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Effect of Dung Beetles on Dung Decomposition and Nutrient Cycling in a Nebraska Rangeland

Kenneth Shay Evans
University of Nebraska-Lincoln

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EFFECT OF DUNG BEETLES ON DUNG DECOMPOSITION AND NUTRIENT CYCLING IN A NEBRASKA RANGELAND

By

Kenneth Shay Evans

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EFFECT OF DUNG BEETLES ON DUNG DECOMPOSITION AND NUTRIENT CYCLING IN A NEBRASKA RANGELAND

Kenneth Shay Evans, M.S.

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Management practice can have impacts on the abundance and frequency of dung beetle populations and nutrient cycling in grazing systems. Also, agriculture and livestock production land use is a considerable source of anthropogenic greenhouse gas (GHG) emissions, which are known to be one of the causes of global climate change. In this study, we evaluated the effect of dung beetle presence on the fluxes of greenhouse gasses (GHG’s) from dung pats in the semi-arid Sandhills region of Nebraska, by using closed chambers to measure the fluxes of carbon dioxide (CO₂), methane (CH₄) and nitrous oxide (N₂O) from dung pats that were exposed and unexposed to dung beetles. We also quantified the effects of dung beetle activity on the timing and magnitude of decomposition of dung, and subsequent fluxes of dung derived C and N into soil. We measured indicators of dung pat decomposition, dung pat C, N, and P variables, and soil C, N, and P variables below dung pats that were either exposed or unexposed to dung beetles. Higher fluxes of GHG’s from dung pats were observed. However, while higher fluxes of CO₂ and N₂O, and lower fluxes of CH₄ due to dung pat exposure to dung beetles were observed, these effects were only significant in one experiment out of the four seasonal experiments performed. We also found that dung pat exposure to dung beetles can increase rates of mass loss in field moist dung pats, as well as rates of
moisture loss. While higher concentrations of nutrients from dung pats in soil were observed, dung beetles had a minimal impact on the soil nutrient concentrations below decomposing dung pats. Environmental factors overall were much more impactful, and dung and soil nutrients, as well as GHG emissions, responded in accordance with temporal fluctuations in the environmental variables that were measured. Our study suggests that management considerations in regards to GHG emissions and nutrient cycling within subirrigated meadows of the Sandhills, might not need to offer as much concern to the effects of dung beetles as perhaps previously believed.
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Table of Contents

Acknowledgements ....................................................................................................................... iv
Table of Contents .......................................................................................................................... vi
List of Tables ................................................................................................................................... ix
List of Figures ............................................................................................................................... xiv
Chapter 1: A Review of Current Literature ............................................................................... 1
  Introduction ........................................................................................................................................ 1
  The Nebraska Sandhills .............................................................................................................. 2
  Nutrient Cycling ........................................................................................................................... 3
  Influence of Grazing Management Practices on Nutrient Cycling .......................................... 4
  Dung Decomposition .................................................................................................................... 5
  Dung Nutrients ............................................................................................................................. 6
  Dung Beetle Effects on Decomposition ....................................................................................... 8
  GHG Production .......................................................................................................................... 10
  Conclusion ...................................................................................................................................... 11
  References ....................................................................................................................................... 13
Chapter 2: Effect of dung beetle colonization on greenhouse gas emissions from cow dung pats in meadows of the Nebraska Sandhills ............................................................ 22
  Abstract ........................................................................................................................................... 22
  Introduction ...................................................................................................................................... 23
  Materials and Methods ............................................................................................................... 29
    Site Description ............................................................................................................................ 29
    Dung Origin .................................................................................................................................. 30
    Dung Pat Placement and Treatments .......................................................................................... 31
    Sample Collection ...................................................................................................................... 34
    Environmental Data .................................................................................................................... 39
    Statistical Design and Analysis .................................................................................................. 40
  Results ............................................................................................................................................ 41
Weather and Soil Conditions .............................................................. 41
Dung Beetle Abundance and Diversity .............................................. 45
GHG Flux .............................................................................................. 48
Experiment Treatment Comparisons ................................................. 69
CO₂ Equivalence of GHG Flux ............................................................ 70
Cumulative Integration of Flux ......................................................... 75
Discussion ............................................................................................ 83
GHG Flux .............................................................................................. 83
Temporal Effects of Dung Beetles ......................................................... 84
Dung Beetle Effect on GHG Flux Density ............................................ 85
Effect of Climatic and Physical Variables on GHG Flux ................. 87
Implications .......................................................................................... 88
References ............................................................................................ 90

Chapter 3: Dung Beetle Effects on Dung Pat Decomposition and Nutrient Translocation in Soil in meadows of the Nebraska Sandhills ........................................................................... 99

Abstract ............................................................................................. 99
Introduction .......................................................................................... 100
Materials and Methods ........................................................................ 107
  Site Description .................................................................................. 107
  Dung Origin ....................................................................................... 108
  Dung Pat Placement and Treatments .................................................. 109
  Dung Pat and Soil Sampling ............................................................... 111
  Environmental Data .......................................................................... 113
  Statistical Design and Analysis .......................................................... 114
Results .................................................................................................. 115
  Weather and Soil Conditions .............................................................. 115
  Dung Beetle Abundance and Diversity .............................................. 119
  Dung Decomposition ........................................................................ 122
  Dung Pat Nutrient Content .................................................................. 141
Experiment Treatment Comparisons ................................................. 152
Soil Nutrients ................................................................................ 152
Experiment Treatment Comparisons ............................................. 184
Discussion ..................................................................................... 185
Dung Pat Characteristics ................................................................. 185
Dung and Soil Nutrients ................................................................. 187
Temporal Effects of Dung Beetles ..................................................... 189
Beetle Effects on Dung Characteristics ........................................... 192
Beetle Effects on Dung and Soil Nutrients ....................................... 193
Effects of Climatic and Physical Variables ..................................... 195
Implications .................................................................................. 197
References ................................................................................... 199
Appendix A ................................................................................. 207
Appendix B .................................................................................. 219
Appendix C .................................................................................. 221
List of Tables

Table 2.1 Monthly cumulative precipitation and mean air temperature May to September 2014 and 2015 and long–term average 1980-2010 values at Barta Brothers Ranch, Eastern Sandhills, NE. ................................................................. 41

Table 2.2 Analysis of Variance for daily CO₂, N₂O, and CH₄ fluxes from 2014 early season experiment. aDays 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ........................................................................................................ 48

Table 2.3 Estimates of average flux (g m⁻² d⁻¹) of CH₄ by treatment and day, with comparisons of exposed with unexposed and no dung treatments. .................. 49

Table 2.3 Analysis of Variance for daily CO₂, N₂O, and CH₄ fluxes from 2014 late season experiment. aDays 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ........................................................................................................ 52

Table 2.4 Environmental covariate significance on 2014 early and late CO₂, N₂O, and CH₄ fluxes, and significance of potential treatment*covariate interaction. aVolumetric water content. ................................................................. 53

Table 2.5 Analysis of Variance for daily CO₂, N₂O, and CH₄ fluxes from 2015 early season experiment. aDays 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ........................................................................................................ 57

Table 2.6 Estimates of average flux (g m⁻² d⁻¹) of CO₂ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments. .......... 58

Table 2.6 Estimates of average flux (g m⁻² d⁻¹) of CO₂ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments. .......... 58

Table 2.6 Analysis of Variance for daily CO₂, N₂O, and CH₄ fluxes from 2015 late season experiment. aDays 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ........................................................................................................ 59

Table 2.7 Estimates of average flux (mg m⁻² d⁻¹) of CH₄ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments. .......... 60
Table 2.9 Estimates of average flux (mg m$^{-2}$ d$^{-1}$) of CO$_2$ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments. .......... 63

Table 2.10 Estimates of average flux (mg m$^{-2}$ d$^{-1}$) of CH$_4$ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments. .......... 64

Table 2.11 Environmental covariate significance on 2014 early and late CO$_2$, N$_2$O, and CH$_4$ fluxes, and significance of potential treatment*covariate interaction. aVolumetric water content. ......................................................... 68

Table 2.12 Analysis of Variance for total experimental CO$_2$, N$_2$O, and CH$_4$ fluxes, across years and seasons. aType 3 F-tests of fixed effects are given. bTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. cDifferences of treatment by least square means. ......................... 68

Table 2.13 Analysis of Variance for sums of CO$_2$-Eq of all GHG fluxes by experiment. aDays 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. .............................................. 78

Table 2.14 Estimates of average cumulative flux (g m$^{-2}$) by treatment and season. P-values of treatment effects, comparisons of exposed against unexposed, and comparisons of dung against no dung treatments are also given. ............................................ 74

Table 2.15 Estimates of average cumulative flux (g m$^{-2}$) across all experiments, by treatment. P-values of treatment effects, comparisons of exposed against unexposed, and comparisons of dung against no dung treatments are also given. ......................... 78

Table 3.1 Monthly cumulative precipitation and mean air temperature May to September 2014 and 2015 and long–term average 1980-2010 values at Barta Brothers Ranch, Eastern Sandhills, NE. ................................................................. 115

Table 3.2 Analysis of Variance for daily dung pat decomposition from 2014 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). cTreatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages. bType 3 F-tests of fixed effects are given. .............................................. 121

Table 3.3 Analysis of Variance for daily dung pat decomposition from 2014 late season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages. ................................................................. 125

Table 3.4 Environmental covariate significance on 2014 early and late dung pat decomposition, and estimation of potential treatment*covariate interaction. aVolumetric water content. bSignificance at p<0.05. ................................................................. 129
Table 3.5 Analysis of Variance for daily dung pat decomposition from 2015 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages. ........................................................................................................................................ 130

Table 3.6. Analysis of Variance for daily dung pat decomposition from 2015 late season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages. ........................................................................................................................................ 134

Table 3.7 Environmental covariate significance on 2015 early and late dung pat decomposition, and estimation of potential treatment*covariate interaction. aVolumetric water content. bSignificance at p<0.05. ........................................................................................................................................ 139

Table 3.8 Analysis of Variance for daily dung pat nutrients from 2014 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages. ........................................................................................................................................ 140

Table 3.9 Analysis of Variance for daily dung pat nutrients from 2014 late season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages. ........................................................................................................................................ 145

Table 3.10 Environmental covariate significance on 2014 early and late dung pat nutrients, and estimation of potential treatment*covariate interaction. aVolumetric water content. bSignificance at p<0.05. ........................................................................................................................................ 150

Table 3.11 Analysis of Variance for experiment-wide dung pat nutrients. aType 3 F-tests of fixed effects are given. bTreatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages. ........................................................................................................................................ 151

Table 3.12 Analysis of Variance for daily soil nutrients from 2014 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. dLocations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away. eDepth in the soil profile; 0-100 and 100-200 mm. ........................................................................................................................................ 153

Table 3.13 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2014 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ........................................................................................................................................ 154
Table 3.14 Analysis of Variance for daily soil nutrients from 2014 late season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. dLocations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away. eDepth in the soil profile; 0- 100 and 100-200 mm. .......................................................... 163

Table 3.15 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2014 late season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ............................................ 164

Table 3.16 Environmental covariate significance on 2014 early and late soil nutrients, and estimation of potential treatment*covariate interaction. aVolumetric water content. bSignificance at p<0.05. ............................................................................. 172

Table 3.17 Analysis of Variance for daily soil nutrients from 2015 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. dLocations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away. eDepth in the soil profile; 0- 100 and 100-200 mm. .......................................................... 173

Table 3.18 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2015 early season experiment. aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP). bType 3 F-tests of fixed effects are given. cTreatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. ............................................ 174

Table 3.19 Environmental covariate significance on 2015 early and late soil nutrients, and estimation of potential treatment*covariate interaction. aVolumetric water content. bSignificance at p<0.05. ............................................................................. 182

Table 3.20 Analysis of Variance for experiment-wide soil nutrients directly below dung pats and within 100 mm of soil depth. a Type 3 F-tests of fixed effects are given. bTreatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages, 3) no dung pat. Significant treatment differences determined by least square means. ............................................................................. 183

Table B.1 Estimates of total average cumulative CO$_2$ flux by treatment. Significance of exposed and unexposed treatment difference. .................................................. 217

Table B.2 Estimates of total average cumulative CO$_2$ flux by treatment. Significance of exposed and unexposed treatment difference. .................................................. 217
Table B.3 Estimates of average flux (g m$^{-2}$ d$^{-1}$) of CO$_2$ in Early Season 2014 by treatment and day. ................................................................. 218

Table B.4 Estimates of average flux (g m$^{-2}$ d$^{-1}$) of CO$_2$ in Late Season 2014 by treatment and day. ................................................................. 218
List of Figures

Figure 2.1 Average normal monthly precipitation and temperatures in Ainsworth, NE . 30

Figure 2.2a Diagram of an experiment layout, with : soil sensors placed at 10, 20, and 60 cm of depth, : soil and O2 sensors placed at 10, 20, and 60 cm of depth and : automated experimental weather station (AEWS) locations indicated. Three distances from AEWS to sensor locations were used, due to cable lengths : 10.7 m, : 7.6 m, and : 3.0 m. Each experiment consisted of 8 replicated blocks. ............................. 32

Figure 2.2b Diagram of treatment and subplot layouts within main plots. HT 1 – 6 subplots were designated randomly within blocks. One GHG subplot at HT 6 in each block contained three permanent chamber anchors, from which GHG samples were repeatedly collected. : Exposed, : Unexposed, and : No Dung treatments were arranged randomly within subplots. : Indicates chamber anchors around dung pats in HT 6. .................................................................................................................. 32

Figure 2.2c Diagram of a subplot with treatments arranged randomly within. ............. 32

Figure 2.2c Picture of subplot with treatments placed within gas chamber anchor rings. .................................................................................................................. 33

Figure 2.2d Picture of subplot with deployed gas chamber lids fitted onto gas chamber. .................................................................................................................. 33

Figure 2.3a Average hourly temperature recorded June to Oct 2014 obtained from automated experimental weather station in the Nebraska Sandhills (42° 13’ 28.40” N, 99° 38’ 19.36” W). ...................................................................................................... 33

Figure 2.3b Average hourly temperature recorded June to Oct 2015 obtained from automated experimental weather station in the Nebraska Sandhills (42° 13’ 36.50” N, 99° 38’ 19.42” W). .................................................................................................................. 36

Figure 2.3c Comparisons of mean air temperature reported by High Plains Regional Climate Center, Barta Station, on the days of sampling in 2014, with observations collected by automated experimental weather station at the time and location of collection. (R^2=0.90). .................................................................................................................. 37

Figure 2.3d Comparisons of mean air temperature reported by High Plains Regional Climate Center, Barta Station, on the days of sampling in 2015, with observations collected by automated experimental weather station at the time and location of collection. (R^2=0.70). .................................................................................................................. 37
Figure 2.4a Average soil temperature over the growing season for 2014, at soil depths 10, 20 and 60 cm. ............................................................. 42

Figure 2.4b Average soil temperature over the growing season for 2015, at soil depths 10, 20 and 60 cm. ............................................................. 42

Figure 2.5a Soil moisture over the 2014 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain. .......................... 43

Figure 2.5b Soil moisture over the 2015 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain. .......................... 43

Figure 2.6a 2014 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. $R^2=0.78$ when averages of $[O_2]$ and WFPS across all soil depths are compared. ...................................................... 44

Figure 2.6b 2015 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. $R^2=0.72$ when averages of $[O_2]$ and WFPS across all soil depths are compared. ...................................................... 44

Figure 2.7a 2014 early season dung beetle counts, by HT. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. ................................................. 45

Figure 2.7b 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure. ................................................................. 46

Figure 2.7c 2014 late season dung beetle counts, by HT. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. ................................................. 46

Figure 2.7d 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure. ................................................................. 47

Figure 2.7a Average CO$_2$ fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ...................................................... 50
Figure 2.7b Average N\textsubscript{2}O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 50

Figure 2.7c Average CH\textsubscript{4} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 51

Figure 2.8a Average CO\textsubscript{2} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 54

Figure 2.8b Average N\textsubscript{2}O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 54

Figure 2.8c Average CH\textsubscript{4} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 55

Figure 2.9a Average CO\textsubscript{2} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 60

Figure 2.9b Average N\textsubscript{2}O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 60

Figure 2.9c Average CH\textsubscript{4} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 61

Figure 2.10a Average CO\textsubscript{2} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 65

Figure 2.10b Average N\textsubscript{2}O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 65

Figure 2.10c Average CH\textsubscript{4} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. ................................................................. 66
Figure 2.11a Sum of all GHG fluxes as CO₂-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. .......... 70

Figure 2.11b Sum of all GHG fluxes as CO₂-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. .......... 70

Figure 2.11c Sum of all GHG fluxes as CO₂-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. .......... 71

Figure 2.11d Sum of all GHG fluxes as CO₂-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP. .......... 71

Figure 2.12a Average cumulative CO₂ fluxes (means and standard errors) by treatment, across years and seasonal experiments. ................................................................. 79

Figure 2.12b Average cumulative N₂O fluxes (means and standard errors) by treatment, across years and seasonal experiments. ................................................................. 79

Figure 2.12c Average cumulative CH₄ fluxes (means and standard errors) by treatment, across years and seasonal experiments. ................................................................. 80

Figure 2.12d Average cumulative sums of CO₂-Eq of all GHG fluxes (means and standard errors) by treatment, across years and seasonal experiments. ....................... 80

Figure 3.1 Average historical monthly precipitation and temperatures in Ainsworth, NE. .................................................................................................................. 107

Figure 3.2a Diagram of an experiment layout, with : soil sensors placed at 10, 20, and 60 cm of depth, : soil and O₂ sensors placed at 10, 20, and 60 cm of depth and : automated experimental weather station (AEWS) locations indicated. Three distances from AEWS to sensor locations were used, due to cable lengths : 10.7 m, : 7.6 m, and : 3.0 m. Each experiment consisted of 8 replicated blocks. .................... 109

Figure 3.2b Diagram of treatment and subplot layouts within main plots. HT 1 – 6 subplots were designated randomly within blocks. One GHG subplot at HT 6 in each block contained three permanent chamber anchors, from which GHG samples were repeatedly collected. : Exposed, : Unexposed, and : No Dung treatments were arranged randomly within subplots. : Indicates chamber anchors around dung pats in HT 6. ................................................................. 109

Figure 3.2c Diagram of a subplot with treatments arranged randomly within. .......... 109
Figure 3.2d Picture of Harvest Time subplot with treatments arranged within. ……… 110

Figure 3.2a Picture of soil probe during sample collection. ……………………….. 111

Figure 3.3b Diagram of points of soil collection with respect to dung pat. Four subsamples are taken directly beneath dung pats after they are removed, and four subsamples taken 300 mm away from dung pats. ……………………………………….. 111

Figure 3.4a Average soil temperature over the growing season for 2014, at soil depths 10, 20 and 60 cm. …………………………………………………………………………………………………………………………… 115

Figure 3.4b Average soil temperature over the growing season for 2015, at soil depths 10, 20 and 60 cm. …………………………………………………………………………………………………………………………… 116

Figure 3.5a Soil moisture over the 2014 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain. …………………. 116

Figure 3.5b Soil moisture over the 2015 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain. …………………. 117

Figure 3.6a 2014 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. R²=0.78 when averages of [O₂] and WFPS across all soil depths are compared. …………………………………………………………………………………………………………………………… 117

Figure 3.6b 2015 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. R²=0.72 when averages of [O₂] and WFPS across all soil depths are compared. …………………………………………………………………………………………………………………………… 118

Figure 3.7a 2014 early season dung beetle counts, by HT. Float method surveys were conducted on 25 % volume of collected dung pats. Dung beetles were counted and species was determined. …………………………………………………………………………………………………………………………… 119

Figure 3.7b 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25 % volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure. …………………………………………………………………………………………………………………………… 119

Figure 3.7c 2014 late season dung beetle counts, by HT. Float method surveys were conducted on 25 % volume of collected dung pats. Dung beetles were counted and species was determined. …………………………………………………………………………………………………………………………… 120
Figure 3.7d 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure.

Figure 3.8a Daily dung pat mass (means and standard errors) from 2014 early season experiment.

Figure 3.8b Daily dung pat moisture content (means and standard errors) from 2014 early season experiment.

Figure 3.8c Daily dung pat dry matter content (means and standard errors) from 2014 early season experiment.

Figure 3.8d Daily change in dung pat dry matter (means and standard errors) from 2014 early season experiment.

Figure 3.9a Daily dung pat mass (means and standard errors) from 2014 late season experiment.

Figure 3.9b Daily dung pat moisture content (means and standard errors) from 2014 late season experiment.

Figure 3.9c Daily dung pat dry matter content (means and standard errors) from 2014 late season experiment.

Figure 3.9d Daily change in dung pat dry matter (means and standard errors) from 2014 late season experiment.

Figure 3.10a Daily dung pat mass (means and standard errors) from 2015 early season experiment.

Figure 3.10b Daily dung pat moisture content (means and standard errors) from 2015 early season experiment.

Figure 3.10c Daily dung pat dry matter content (means and standard errors) from 2015 early season experiment.

Figure 3.10d Daily change in dung pat dry matter (means and standard errors) from 2015 early season experiment.

Figure 3.11a Daily dung pat mass (means and standard errors) from 2015 late season experiment.
Figure 3.11b Daily dung pat moisture content (means and standard errors) from 2015 late season experiment. 

Figure 3.11c Daily dung pat dry matter content (means and standard errors) from 2015 late season experiment. 

Figure 3.11d Daily change in dung pat dry matter (means and standard errors) from 2015 late season experiment. 

Figure 3.12a Daily dung pat WSC concentrations (means and standard errors) from 2014 early season experiment. 

Figure 3.12b Daily dung pat WEN concentrations (means and standard errors) from 2014 early season experiment. 

Figure 3.12c Daily dung pat NO₃⁻ concentrations (means and standard errors) from 2014 early season experiment. 

Figure 3.12d Daily dung pat NH₄⁺ concentrations (means and standard errors) from 2014 early season experiment. 

Figure 3.12e Daily dung pat WEP concentrations (means and standard errors) from 2014 early season experiment. 

Figure 3.13a Daily dung pat WSC concentrations (means and standard errors) from 2014 late season experiment. 

Figure 3.13b Daily dung pat WEN concentrations (means and standard errors) from 2014 late season experiment. 

Figure 3.13c Daily dung pat NO₃⁻ concentrations (means and standard errors) from 2014 late season experiment. 

Figure 3.13d Daily dung pat NH₄⁺ concentrations (means and standard errors) from 2014 late season experiment. 

Figure 3.13e Daily dung pat WEP concentrations (means and standard errors) from 2014 late season experiment. 

Figure 3.14a Daily WSC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2014 early season experiment. 

Figure 3.14b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment.
Figure 3.14c Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment. ............... 156

Figure 3.14d Daily NH$_4^+$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment. ............... 156

Figure 3.14e Daily DMPR soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment. ....... 157

Figure 3.15a Daily NPOC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2014 late season experiment. ............... 164

Figure 3.15b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment. ............... 165

Figure 3.15c Daily NO$_3^-$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment. ............... 165

Figure 3.15d Daily NH$_4^+$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment. ............... 166

Figure 3.15e Daily DMPR soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment. .......... 166

Figure 3.16a Daily WSC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2015 early season experiment. ............... 175

Figure 3.16b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment. ............... 175

Figure 3.16c Daily NO$_3^-$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment. ............... 175

Figure 3.16d Daily NH$_4^+$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment. ............... 176

Figure 3.16e Daily WEP soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment. ............... 177

Figure A.1 Diagram of Sensors Buried at Depth. ......................................................... 206

Figure A.2 Cumulative CO$_2$ fluxes (means and standard errors) integrated over 2014 early season experiment. ................................................................. 206

Figure A.3 Cumulative CO$_2$ fluxes (means and standard errors) integrated over 2014 late season experiment. ................................................................. 207
Figure A.4 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2014 early season experiment. ........................................................................................................ 207

Figure A.5 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2014 late season experiment. ........................................................................................................ 208

Figure A.6 Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2014 early season experiment. ........................................................................................................ 208

Figure A.7 Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2014 late season experiment. ........................................................................................................ 209

Figure A.8 Cumulative CO$_2$ fluxes (means and standard errors) integrated over 2015 early season experiment. ........................................................................................................ 209

Figure A.9 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2015 early season experiment. ........................................................................................................ 210

Figure A.10 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2015 late season experiment. ........................................................................................................ 210

Figure A.11 Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2015 early season experiment. ........................................................................................................ 211

Figure A.12 Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2015 late season experiment. ........................................................................................................ 211

Figure A.13 Cumulative CO$_2$-Eq fluxes (means and standard errors) integrated over 2014 early season experiment. ........................................................................................................ 212

Figure A.14 Cumulative CO$_2$-Eq of GHG fluxes (means and standard errors) integrated over 2014 late season experiment. ........................................................................................................ 212

Figure A.15 Cumulative CO$_2$-Eq of sums of GHG fluxes (means and standard errors) integrated over 2015 early season experiment. ........................................................................................................ 213

Figure A.16 Cumulative integration of sums of CO$_2$-Eq of all GHG fluxes from 2015 late season experiment. ........................................................................................................ 213

Figure A.17 Comparison of [O$_2$] and CO$_2$ flux over 2014 experimental year. .......... 214

Figure A.18 Comparison of [O$_2$] and CO$_2$ flux over 2015 experimental year. .......... 214

Figure A.19 Comparison of [O$_2$] and N$_2$O flux over 2014 experimental year. .......... 215

Figure A.20 Comparison of [O$_2$] and N$_2$O flux over 2015 experimental year. .......... 215
Figure A.21 Comparison of $[O_2]$ and $CH_4$ flux over 2014 experimental year. ............ 216

Figure A.22 Comparison of $[O_2]$ and $CH_4$ flux over 2015 experimental year. ............ 216
CHAPTER 1

LITERATURE REVIEW

Introduction

The impacts of livestock production are substantial, and the intensity and extent of its practice will continue to be equally as significant. It is estimated that livestock production accounts for 30% of the earth’s entire land surface, provides livelihoods for 1.3 billion people, and accounts for 40% of the global agricultural economic output (FOA, 2006b). While livestock production does possess considerable impact in terms of global economic output and extent of land resources invested, its impact is only expected to increase as meat and dairy production is predicted to double by the year 2050 (FOA, 2006b). Across the state of Nebraska, total land area designated for livestock production is estimated to be 23 million acres, almost all of which is used for beef and dairy production in particular (USDA, 2009a). Rangelands are the primary resource used for beef and dairy production across the world, and account for approximately 70% of the necessary forage used for beef and dairy production globally (Lund, 2007). Accordingly, land characterized as rangeland accounts for approximately 23 million acres of the total area of the state of Nebraska (Wilhelmi and Wilhite, 2002). Considering that Nebraska spans 49.5 million acres, land allocated to beef and dairy production accounts for approximately 47% of the total land surface of the state. The economic impact of beef and dairy production within Nebraska is also quite considerable, accounting for approximately 8% of the gross state product according to a report released by the Department of Agricultural Economics at the University of Nebraska-Lincoln (Thompson
et al., 2012). The Sandhills region of Nebraska in particular contains almost half of all rangeland in the state, or approximately 12.5 million acres (Powell et al., 1982). Due to the sizable and rapidly increasing economic and environmental footprints of livestock production in Nebraska and across the world, development of sustainable production practices that allow consistent, or even increasing yield over the long-term future is crucial.

**The Nebraska Sandhills**

The Sandhills region is one of the largest stabilized eolian sand formations in the world, with recent activity being dated approximately between 3,500 to 1,500 YBP (Whitcomb, 1989). Vegetation structure across the Sandhills region is generally variable due to topography and aspect (Barnes et al., 1984; Barnes, 1986; Schacht et al., 2000). Soil moisture content, organic matter, and fine size fraction typically decrease with increasing topographic position, from low to high elevation across perpendicular sand dune profiles (Barnes et al., 1984). This yields a positively correlated gradient of increasing dominance of more drought tolerant species with increasing topographic position (Barnes et al., 1984; Schacht et al., 2000).

Water tables in the wide valleys between dunes can remain within 0.61 – 1.22 m of the soil surface throughout the growing season, and are referred to as subirrigated meadows (Moore and Rhoades, 1966). This high water table provides more consistent available water to plants, and thus greater overall productivity, and higher soil organic matter content compared to areas of higher topographic position (Reece et al., 1994; Barnes, 1986; Nichols et al., 1990). Subirrigated meadows are reliable land of hay production for winter feed, and are also typically grazed for a period of time between
May and June before haying (Adams et al., 1994; Clark et al., 1991; Volesky et al. 2004). However, soil organic carbon (1.0 – 1.1 kg · m$^{-2}$) and soil total nitrogen content (0.731 kg · m$^{-2}$) across the Sandhills region are still generally lower compared to other grassland soils across the central United States (Franzmeier et al., 1985; Leuking and Schepers, 1985).

**Nutrient cycling**

Agro-ecosystems, such as grazed rangelands, are characterized by a diverse array of functional processes and controlling mechanisms which to this point prove difficult to understand, given the complex nature of these systems. The interaction of soil, plants, and animals, along with management strategy, mediates physical and biological processes that exert control on rangeland characteristics such as nutrient availability, diversity and abundance of species, forage quality, primary production, carbon sequestration, and the release of greenhouse gasses (GHGs) (Bryant and Snow, 2008). One essential process that defines the quality and functionality of all ecosystems is that of nutrient cycling (Whisenant, 1999).

Nutrient availability constitutes a dominant control mechanism over primary production and thus the number of grazing animals that can be sustained (Haynes and Williams, 1993). Subsequently, grazing animals exhibit a controlling effect on the fate and movement of nutrients within grazing systems (Haynes and Williams, 1993). Since grazing livestock utilize only a portion of the nutrient value of the biomass they consume, the rest is deposited across the grazing-landscape in the form of urine and dung (Haynes and Williams, 1993). Therefore, decomposition of urine and dung patches represent discrete points of nutrient loss through gaseous emissions or leaching, and nutrient return
to the soil. If the distribution of these discrete points of nutrient loss and return can be affected by management practices, giving substantial and knowledgeable consideration of this nutrient cycling process in grazed rangelands when making management decisions would be conducive to realizing sustainable production.

**Influence of Grazing Management Practices on Nutrient Cycling**

Rangeland cattle production is dependent upon the management of grazing duration and intensity to sustain necessary rangeland characteristics such as plant diversity, productivity, and nutrient content of forage, so that desirable production targets such as animal weight-gain and collective weight-gain per land area over the long-term future can be maintained (Pavlů et al., 2006). Continuous grazing is primarily employed on extensive areas of rangeland, and this type of grazing management system is usually successful when stocking rates are kept at sustainable levels. Rotational grazing involves cycling livestock through smaller pastures, and generally gives greater managerial control over timing and duration of grazing. Mob grazing is a type of rotational grazing management characterized by ultra-high stocking densities in small paddocks over short periods of time, and often requires moving cattle multiple times in one day. Mob grazing reduces the opportunity for selective grazing, as well as decreasing disparities in the spatial distribution of dung accumulation.

The use of rotational grazing has continued to be implemented to more effectively manage biomass utilization, plant diversity, and increase overall animal productivity, in contrast to continuous grazing management (Briske et al., 2008). However, knowledge of the effects of different grazing management strategies on nutrient cycling and other ecosystem functions and services within rangelands is still lacking (Briske et al., 2011).
For instance, livestock attractants such as feed and water troughs increase dung accumulation rates in the vicinity of their placement, with topography and shade also affecting spatial differences in fecal loads (Tate et al., 2003; Augustine et al., 2013). Since livestock ingest nutrients from grazing areas and deposit them non-randomly in the form of dung and urine, nutrient return is often spatially uncoupled from areas of nutrient intake (Augustine et al., 2013).

The cycling of nutrients in grazing systems is largely dependent upon the nutrient intake of cattle, the characteristics of the decomposition process, and the distribution of dung pats that are subsequently deposited within the pasture (Aarons et al., 2004, Augustine et al., 2013, Dickinson et al. 1981, Eghball et al. 2002, Van Vliet et al. 2007), due to the fact that the majority of a cow’s nutritional intake, upwards of 60-90%, is returned to grazing systems in the form of excreta (Haynes and Williams, 1993). Any nutrients contained within the dung material are returned to or lost from the grazing system after the dung is acted upon by a highly variable and extensive set of physical and biological factors that uniquely characterize the decomposition process.

**Dung Decomposition**

Decomposition of dung material and mineralization of dung nutrients is dictated by microbial activity, so therefore the physical conditions under which these microbial communities must live out their life histories serves as a dominant mitigating factor over the intensity of microbial activity, decomposition, and mineralization (Eghball et al., 2002). These physical constraints include the chemical composition of dung, weather, and soil variables (Eghball et al., 2002). The extent of N mineralization and availability of N for microbes and plants from dung is largely dependent on the composition of the C
and N compounds in the dung itself, and not so much the general C:N ratio (Eghball et al., 2002). Dung materials with higher initial concentrations of labile N, as well as other forms of mobile and easily convertible N compounds, exhibit greater total N availabilities over the course of decomposition, regardless of the corresponding C:N ratios (Eghball et al., 2002).

Decomposition of dung pats is assessed by weight loss. In a survey of fresh dung pats in smooth brome pastures in North Dakota, Lysyk et al. (1985) found moisture contents between 400 and 435 %. After deposition, moisture contents typically decrease precipitously over the first 30 DAP, dropping to between 10 to 20 % by the end of that time period (Stevenson & Dindal, 1987). Average pat mass also drops rapidly over the first 28 DAP, in conjunction with rapid losses of moisture after deposition (Aarons et al., 2004; Hirata et al., 2009). Pat masses at deposition can range between 1,200 and 1,600 kg, with mass losses exceeding 50 % over the first 3 to 5 DAP and as high as 90 % by 40 DAP (Aarons et al, 2004; Hirata et al., 2009). Changes in dry matter content are considered to be a more accurate metric of dung decomposition and are much less responsive over early stages of decomposition, in contrast to moisture content and pat mass losses (Dickinson et al., 1981; Hirata et al., 2009). However, dry matter losses can be highly variable and extremely dependent upon environmental conditions, ranging anywhere from 17 to 50 % over the first 50 DAP and weekly changes in dry mass ranging between + 5.1 to -60.7 g (Dickinson & Craig, 1990; Hirata et al., 2009).

**Dung Nutrients**

The greatest fluxes of dung nutrients into soil occur within the first 5 to 10 days after placement, when dung pats are still moist and have not crusted, with subsequent
additional fluxes resulting after precipitation events (Bol et al., 2004; Dickinson et al., 1981; Aarons et al., 2004). Increases in dung pat dry weight accompanying higher dung derived nutrient fluxes within the first 5 days after placement have been observed, and mostly attributed to the incorporation of soil into the dung pats from the activities of dung-feeding invertebrates (Dickinson & Craig, 1990; Aarons et al., 2004).

Dung pats are in essence a heterogeneous mixture of forage materials that exhibit a wide range of mineralization kinetics (Van Kessel et al., 2000). While some inorganic nitrogen can be found in dung pats, primarily in the form of ammonium, the majority of nitrogen found in dung is in organic forms and must be mineralized before it can be assimilated by plants or soil microbes (Calderon et al., 2004; Van Kessel et al., 2000). However, once dung derived N is mineralized, any subsequently available NH$_4^+$ is readily immobilized by microbes, with nitrifiers being responsible for the majority of NH$_4^+$ assimilation and the resulting approximate 7 day lag in measurable increases in NO$_3^-$ concentration (Calderon et al., 2004). Net mineralization of dung-N is reported to be somewhat dependent upon carbon to nitrogen ratios of dung material, however the fraction and form of dung C and N compounds, and their associated mineralization kinetics, have been shown to be much more relevant in regards to dung-N mineralization (Calderon et al., 2004; Eghball et al., 2002; Van Kessel et al., 2000).

Fluxes of dung derived dissolved organic carbon (DOC) in soil generally peak between 7 to 20 days after placement and are attributed to leaching and translocation of soluble organic compounds, and not largely the result of microbial decomposition (Bol et al., 2000; Dickinson et al., 1981; Holter & Hendrickson, 1988). Subsequent peaks in dung derived DOC that begin 20 days after placement are shown to persist, or even
increase, until complete dung pat disappearance, and are largely attributed to microbial decomposition of the more insoluble carbon compounds (Bol et al., 2000; Holter & Hendrickson, 1988).

**Dung Beetle Effects on Decomposition**

Dung pat decomposition can be mediated by a variety of invertebrate organisms, including earthworms, flies, termites, ants, and dung beetles (Denholm-Young, 1978; Freyman et al., 2008; Holter, 1979; Lee and Wall, 2006; O’hea et al., 2010). Dung beetles, in particular, are among the most significant invertebrate contributors to dung decomposition in north temperate rangelands (Lee and Wall, 2006). It has also been shown that dung beetle abundance and diversity can be directly affected by factors associated with land use and management practices such as habitat change, livestock insecticides, and intensity of livestock production (Dadour et al., 1999; Floate, 1998; Hutton and Giller, 2003; Roslin and Koivunen, 2001; Vessby, 2001). To date, there have been 256 different species of dung beetles observed within Nebraska, and it is estimated that 11 to 15 of these can be found within the Sandhills region (Jameson, 1989; Ratcliffe and Paulsen, 2008; Whipple, 2011).

Dung beetles can effectively direct the cycling of dung nutrients into the soil, due to the dung burying activities related to their life histories (Bang et al., 2005; Bertone, 2004; Gillard, 1967; Mittal, 1993). The effect dung beetles on dung nutrients has been documented to include increased yields of forage and crops (Bang et al., 2005; Bornemissza and Williams, 1970; Kabir et al., 1985) and increases in soil nitrogen and other nutrients (Bang et al. 2005; Bertone, 2004; Mittal, 1993; Yamada et al., 2007). Dung pats are also known as a source of GHG’s and other trace gases, which represent
losses of nutrients to the atmosphere (Bellarby et al., 2013; Peterson et al., 1998; Saggar et al., 2004; Van Groenigen et al., 2005). It has been shown that the effect of dung beetle activity can effectively reduce some forms of GHG and trace gas emissions from dung pats, such as NH\textsubscript{3} volatilization and CH\textsubscript{4} emissions (Gillard, 1967; Iwasa et al., 2015; Pentilla et al., 2013; Yokoyama et al., 1991). The net balance effect of dung beetle activity on the loss of nutrients in the form of emission of GHGs is complex, however, there is also evidence that suggests dung beetle activity increasing emissions of N\textsubscript{2}O and CO\textsubscript{2} from dung pats (Iwasa et al., 2015; Penttila et al., 2013; Yokoyama et al., 1991a).

Dung beetle effects on GHG emissions are presumed to be caused by increased aeration of dung material from tunnels that dung beetles create, in contrast to other nutrient cycling responses that are in large part due to the burying of dung material within the soil (Stevenson and Dindal, 1987). However, dung beetle diversity can vary seasonally, and therefore their activity and associated effects on dung decomposition might be expected to vary by the species that are present at different points in time throughout the growing season (Doube, 1991; Holter, 1982; Whipple, 2011).

Further complicating quantification of nutrient cycling is the variability in the decomposition of dung and cycling of dung nutrients due in part to abiotic environmental conditions that are the result of variations in soil, dung characteristics and weather (Bol et al., 2004; Lin et al., 2009; Maljanen et al., 2007; Saggar et al., 2004). However, measurements taken from grasslands within the central U.S. indicate positive ambient fluxes of CO\textsubscript{2} and N\textsubscript{2}O and negative fluxes of CH\textsubscript{4} are typical (Dijkstra et al., 2011; Ingram et al., 2015; Iqbal et al., 2014; Jackson et al., 2015; Liebig et al., 2013). Microbial activity necessary for methanogenesis is particularly sensitive to micro-scale
environmental conditions, such as optimal temperatures, reliable sources of complex carbon compounds, and an anaerobic environment (Chadwick et al., 2000; Jones et al., 2005; Schnell and King 1996).

**GHG Production**

Conditions necessary for peak N$_2$O production are much more wide-ranging and less understood, due largely to the diversity of denitrifying microbes and wide environmental conditions necessary for their activities (Pihlatie et al., 2004, Saggar et al., 2004). Increases in N$_2$O flux after dung soil placements or applications have been observed (Flessa et al., 1996; Lessa et al., 2014; Lin et al., 2009; Yamulki et al., 1998), and were positively correlated to percent water filled pore space (WFPS), temperature, and mineral soil N levels (Dobbie & Smith, 2001; Linn & Duran, 1984; Smith et al., 2003; Lessa et al., 2014). However, other research have shown that N$_2$O fluxes are not well correlated with physical soil variables or mineral soil-N levels (Allen et al., 1996; Velthof et al., 1996; Yamulki et al., 1998). Although, N$_2$O emissions from additions of dung are soil mediated process and dependent on interacting factors including soil texture, soil moisture, aggregate size fraction, pore size distribution, organic carbon, availability N, and temperature (Pihlatie et al., 2004; Saggar et al., 2004; Torbert & Wood, 1992; Uchida et al., 2008; Uchida et al., 2011).

Nitrous oxide emissions from dung applications generally exhibit fluxes larger than those of soil within the first 20 – 30 days after placement (Flessa et al., 1996; Lessa et al., 2014). Peak fluxes have also been documented to be well correlated with high soil moisture content and labile N availability (Smith et al., 2003). Nitrogen losses from dung nitrous oxide emissions has been reported to be on the order of 0.1 – 0.2% (Sordi et al.,
2013; Uchida et al., 2011; Lessa et al., 2014). Such low fluxes of nitrous oxide can be expected considering the low concentrations of labile N found in dung produced by livestock grazed on forage having high C:N ratios, as is usually the case in low-input rangelands (Van Vliet et al., 2007).

Conclusion

The characterization of the cycling of nutrients due to livestock excreta deposition can vary according to the nutrient content of the dung, the rate of decomposition, soil characteristics, the spatial distribution of excreta deposits, abundance and diversity of microbes and invertebrates, and climatic factors such as temperature and precipitation (Aarons et al., 2004; Dennis et al., 2013; Dickinson et al., 1981). Because of the feedback relationship between the nutrient availability control of productivity and fitness of domestic grazing animals, and the control that grazing animals possess over the nutrient cycle, greater understanding of this process is essential to the productivity and sustainability of grazing systems. Nonetheless, given the large number of components of agro-ecosystem functional processes and their complex nature, formulating studies that successfully incorporate all of them proves to be quite challenging.

While grazing management may be a factor affecting nutrient cycling in rangelands, it is not the only one. Dung decomposition and soil nutrient return is a complex process, dependent upon an array of factors including livestock diet, climate, season, soil characteristics, and invertebrate and microbial activity (Dickinson et al., 1981; Eghball et al., 2002; Lee and Wall, 2006; Van Vliet et al., 2007). These physical and biological factors directly mitigate the decomposition and transformation of nutrients from cattle dung within the context of management strategy and depositional distribution.
It would therefore be prudent to seek a better understanding of these processes, biological and physical factors, and their associated effects on dung decomposition, so that more knowledgeable management decisions can be made in regards to nutrient cycling and sustainable production.
References


Bol, R., Petersen, S. O., Christofides, C., Dittert, K., & Hansen, M. N. (2004). Short-term N₂O, CO₂, NH₃ fluxes, and N/C transfers in a Danish grass-clover pasture after


Chapter 2

Effect of dung beetle colonization on greenhouse gas emissions from cow dung pats in meadows of the Nebraska Sandhills

Abstract

Management practice can have impacts on the abundance and frequency of dung beetle populations and nutrient cycling in grazing systems. Also, agriculture and livestock production land use is a considerable source of anthropogenic greenhouse gas (GHG) emissions, which are known to be one of the causes of global climate change. In this study, we evaluated the effect of dung beetle activity on the fluxes of greenhouse gasses (GHG’s) from dung pats in the semi-arid Sandhills region of Nebraska, by using closed chambers to measure the fluxes of carbon dioxide (CO$_2$), methane (CH$_4$) and nitrous oxide (N$_2$O) from dung pats that were exposed and unexposed to dung beetles. While higher fluxes of GHG’s from dung pats were observed, dung beetles had a minimal impact on the loss of nutrients as GHG fluxes from decomposing dung pats. While higher fluxes of CO$_2$ and N$_2$O, and lower fluxes of CH$_4$ due to dung pat exposure to dung beetles were observed, these effects were each only significant in one experiment out of the four seasonal experiments performed. Environmental factors were much more significant, and flux response varied daily, seasonally, and yearly in accordance with temporal fluctuations in the environmental variables that were measured. Our study suggests that management considerations in regards to GHG emissions and nutrient
cycling within subirrigated meadows of the Sandhills, might not need to offer as much concern to the effects of dung beetles as perhaps previously believed.

**KEY WORDS:** Dung Beetles, Greenhouse Gas Flux, Nutrient Cycling, Rangelands, Dung Decomposition

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**Introduction**

The current global demand for livestock production is substantial, and the intensity and extent of its practice will continue to be equally significant in the future, or even more so. It is estimated that livestock production accounts for 30% of the earth’s entire land surface, provides livelihoods for 1.3 billion people, and accounts for 40% of the global agricultural economic output (FOA, 2006b). Land characterized as rangeland continue to be the primary resource for beef and dairy production across the world, and account for approximately 70% of the necessary forage used for beef and dairy production globally (Lund, 2007). Coupled with these large investments of resources and economic dependency on livestock production, is the growing awareness of the effects of global climate change (IPCC, 2014; IPCC, 2007). It is well documented that agriculture and livestock production land use is a considerable source of anthropogenic greenhouse gas (GHG) emissions, while rising atmospheric GHG concentrations are considered to be one of the major causes of global climate change (Garnett, 2009; Gerber et al., 2013; Searchinger et al., 2008). However, while livestock production does currently possess a considerable footprint in terms of global economic output, environmental quality, and
land use, its impact is expected to grow as meat and dairy demands are predicted to double by the year 2050 (FOA, 2006b).

In Nebraska, beef production is the most economically productive agricultural industry, generating $5.4 billion in revenue in 2010 and accounting for approximately 8% of the gross state product (Thompson et al., 2012; Veneman et al. 2004). Across Nebraska, land area designated for livestock production is estimated to be 9.3 million ha, almost all of which is used solely for beef and dairy production (USDA, 2009a). Land characterized as rangeland in Nebraska also accounts for approximately 9.3 million ha, which emphasizes the aforementioned reliance of livestock production on rangelands for forage (Wilhelmi and Wilhite, 2002). The Sandhills region of Nebraska in particular contains almost half of all rangeland in the state, or approximately 5.1 million ha (Powell et al., 1982). The predominant land use within the Nebraska Sandhills is rangeland for beef cattle production, but there is an appreciable amount of corn, soybean, small grains, and potato production (CALMIT, 2005).

The Sand Hills region is one of the largest stabilized eolian sand formations in the world, with recent activity being dated approximately between 3,500 to 1,500 YBP (Whitcomb, 1989). Vegetation structure across the Sand Hills region is generally variable due to topography and aspect (Barnes et al., 1984; Barnes, 1986; Schacht et al., 2000). Soil moisture content, organic matter, and fine size fraction typically decrease with increasing topographic position, from low to high elevation across perpendicular sand dune profiles (Barnes et al., 1984). This yields a positively correlated gradient of increasing dominance of more drought tolerant species with increasing topographic position (Barnes et al., 1984; Schacht et al., 2000). Water tables in the wide valleys
between dunes can remain within 0.61 – 1.22 m of the soil surface throughout the growing season, and are referred to as subirrigated meadows (Moore and Rhoades, 1966). This high water table provides more consistent available water to plants, and thus greater overall productivity, and higher soil organic matter content compared to areas of higher topographic position (Reece et al., 1994; Barnes, 1986; Nichols et al., 1990).

Subirrigated meadows are reliable land of hay production for winter feed, and are also typically grazed for a period of time between May and June before haying (Adams et al., 1994; Clark et al., 1991; Volesky et al. 2004). However, soil organic carbon (1.0 – 1.1 kg \( \cdot \) m\(^{-2} \)) and soil total nitrogen content (0.731 kg \( \cdot \) m\(^{-2} \)) across the Sandhills region are still generally lower compared to other grassland soils across the central United States (Franzmeier et al., 1985; Leuking and Schepers, 1985).

Ecosystems referred to as rangelands can be characterized by a diverse array of functional processes and controlling mechanisms. One essential process that defines the quality and functionality of all ecosystems is that of nutrient cycling (Whisenant, 1999). The interaction of soil, plants, animals, and the management strategy employed thus mediates the cycling of nutrients within rangelands, which in turn can effect diversity and abundance of species, forage quality, primary production, carbon sequestration, and the release of trace gases (Bryant and Snow, 2008). Since grazing livestock utilize only a portion of the nutrient value of the biomass they consume, the rest is deposited across the grazing-landscape in the form of urine and dung (Haynes and Williams, 1993). Once deposited, small patches of livestock excreta become discrete points of nutrient loss or return over the duration of their subsequent decomposition (Jarvis, 2000; Nichols et al., 2008). Dung decomposition and soil nutrient return are complex processes, dependent on
many factors including livestock diet, climate, weather, time of season, soil characteristics, and invertebrate and microbial activity (Dickinson et al., 1981; Eghball et al., 2002; Lee and Wall, 2006; Van Vliet et al., 2007).

Dung pat decomposition can be mediated by a variety of invertebrate organisms, including earthworms, flies, termites, ants, and dung beetles (Denholm-Young, 1978; Freyman et al., 2008; Holter, 1979; Lee and Wall, 2006; O’hea et al., 2010). Dung beetles, in particular, are among the most significant invertebrate contributors to dung decomposition in north temperate rangelands (Lee and Wall, 2006). It has also been shown that dung beetle abundance and diversity can be directly affected by factors associated with land use and management practices such as habitat change, livestock insecticides, and intensity of livestock production (Dadour et al., 1999; Floate, 1998; Vessby 2001; Roslin and Koivunen, 2001; Hutton and Giller, 2003). To date, there have been 256 different species of dung beetles observed within Nebraska, and it is estimated that 11 to 15 of these can be found within the Sandhills region (Ratcliffe and Paulsen, 2008; Jameson, 1998; Whipple, 2011).

Dung beetles can effectively direct the cycling of dung nutrients into the soil, due to the dung burying activities related to their life histories (Bang et al., 2005; Bertone, 2004; Gillard, 1967; Mittal, 1993). The effect dung beetles on dung nutrients has been documented to include increased yields of forage and crops (Bang et al., 2005; Bornemissza and Williams, 1970; Kabir et al., 1985) and increases in soil nitrogen and other nutrients (Bang et al. 2005; Bertone, 2004; Mittal, 1993; Yamada et al., 2007). Dung pats are also known as a source of GHG’s and other trace gases, which represent losses of nutrients to the atmosphere (Bellarby et al., 2013; Peterson et al., 1998; Saggar
et al., 2004; Van Groenigen et al., 2005). It has been shown that the effect of dung beetle activity can effectively reduce some forms of GHG and trace gas emissions from dung pats, such as NH$_3$ volatilization and CH$_4$ emissions (Gillard, 1967; Iwasa et al., 2015; Pentilla et al., 2013; Yokoyama et al., 1991). The net balance effect of dung beetle activity on the loss of nutrients in the form of emission of GHGs is complex, however, there is also evidence that suggests dung beetle activity increasing emissions of N$_2$O and CO$_2$ from dung pats (Iwasa et al., 2015; Penttila et al., 2013; Yokoyama et al., 1991a). Dung beetle effects on GHG emissions are presumed to be caused by increased aeration of dung material from tunnels that dung beetles create, in contrast to other nutrient cycling responses that are in large part due to the burying of dung material within the soil (Stevenson and Dindal, 1987). However, dung beetle diversity can vary seasonally, and therefore their activity and associated effects on dung decomposition might be expected to vary by the species that are present at different points in time throughout the growing season (Doube, 1991; Holter, 1982; Whipple, 2011).

Further complicating quantification is the variability in the decomposition of dung and cycling of dung nutrients due in part to abiotic environmental conditions that are the result of variations in soil, dung characteristics and weather (Bol et al., 2004; Lin et al., 2009; Maljanen et al., 2007; Saggar et al., 2004). However, measurements taken from grasslands within the central U.S. indicate positive ambient fluxes of CO$_2$ and N$_2$O and negative fluxes of CH$_4$ are typical (Dijkstra et al., 2011; Ingram et al., 2015; Iqbal et al., 2014; Jackson et al., 2015; Liebig et al., 2013).

Microbial activity necessary for methanogenesis is particularly sensitive to micro-scale environmental conditions, such as optimal temperatures, reliable sources of
complex carbon compounds, and an anaerobic environment (Chadwick et al., 2000; Jones et al., 2005; Schnell and King 1996).

Conditions necessary for peak N$_2$O production are much more wide-ranging and less understood, due largely to the diversity of denitrifying microbes and wide environmental conditions necessary for their activities (Pihlatie et al., 2004, Saggar et al., 2004). Increases in N$_2$O flux after dung soil placements or applications have been observed (Flessa et al., 1996; Lessa et al., 2014; Lin et al., 2009; Yamulki et al., 1998), and were positively correlated to percent water filled pore space (WFPS), temperature, and mineral soil N levels (Dobbie & Smith, 2001; Linn & Duran, 1984; Smith et al., 2003; Lessa et al., 2014). However, other research have shown that N$_2$O fluxes are not well correlated with physical soil variables or mineral soil-N levels (Allen et al., 1996; Velthof et al., 1996; Yamulki et al., 1998). Although, N$_2$O emissions from additions of dung are soil mediated process and dependent on interacting factors including soil texture, soil moisture, aggregate size fraction, pore size distribution, organic carbon, availability N, and temperature (Pihlatie et al., 2004; Saggar et al., 2004; Torbert & Wood, 1992; Uchida et al., 2008; Uchida et al., 2011).

In this study, we evaluated the effect of dung beetle activity on the fluxes of GHGs (CH$_4$, N$_2$O, and CO$_2$) from dung pats in the semi-arid Sandhills region of Nebraska. Insight into the impact of dung beetles on the cycling of nutrients and GHG fluxes from livestock production could be helpful in soil nutrient conservation practices that can sustain forage quality and productivity of rangelands and reduce GHG emissions. We hypothesized that the effect of dung pat exposure to dung beetles would increase fluxes of CO$_2$ and N$_2$O, and decrease fluxes of CH$_4$, and the intensity of GHG fluxes
would changes across the grazing season with changes in dung beetle species, temperature, and precipitation.

**Materials and Methods**

**Site Description**

Research was conducted at the Barta Brothers Ranch (42°13'28.65"N, 99°38'19.17"W, 773 m.a.s.l), which is a 2,350 ha grazing research site operated by the University of Nebraska-Lincoln. The site is located in the Eastern Nebraska Sandhills, approximately 40 km Southeast of Ainsworth, Nebraska. Experimental plots were placed on a sub-irrigated meadow. Vegetation consists of predominantly mixed cool season (*Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey, *Poa pratensis* L., *Bromus inermis* Leyss., *Agrostis gigantea* Roth, *Elymus repens* (L.) Gould, *Phleum pratense* L.), less abundant warm season grasses (*Andropogon gerardii* Vitman, *Sorghastrum nutans* (L.) Nash, *Panicum virgatum* L., *Spartina pectinata* Bosc ex Link), mixed forbs (*Achillea millefolium* L., *Medicago sativa* L., *Potentilla recta* L., *Rudbeckia hirta* L., *Trifolium pretense* L., *Trifolium repens* L.), and an array of rushes (*Juncus* L. spp.) and sedges (*Carex* L. spp.). Land use in the Eastern Sandhills is predominantly rangeland, mainly used for beef cattle production, but land is also used for growing corn, soybeans, small grains, and potatoes as well (CALMITE, 2005). Soils are of the Els series, classified as a mixed, mesic Aquic Ustipsamments with sandy to fine sandy loam texture (NRCS, 2009). From soil samples taken before each of our experiments, we found average bulk density to 20 cm depth to be 1.44 Mg·m⁻³. The climate is semiarid with long-term average (1981-2010) annual precipitation of 584 mm y⁻¹ (NOAA, 2013), and a mean
annual air temperature of 9.6 °C. Eighty percent of the precipitation falls between April and September with May and June typically being the wettest months. We conducted four seasonal experiments that were performed June 10th to August 5th of 2014, July 15th to September 12th of 2014, June 8th to August 3rd of 2015, and July 14th to September 12th of 2015.

![Figure 2.3 Average normal monthly precipitation and temperatures in Ainsworth, NE.](image)

**Dung Collection**

Dung was collected from grain and pasture-fed yearling steers that did not receive insecticidal treatment. Diet on dry matter (DM) basis consisted of 70.5% Brome Grass, 23.3% dry distillers grains plus solubles, 5.8% dry rolled corn, 0.28% salt, 0.05% beef trace mineral, and 0.03% vitamins A D E. The steers were fed 6.9 kg DM d⁻¹ while held off of pasture for observation. Dung was stored in 19 L plastic buckets at approximately
-20°C until use. Before field experiment layout, dung was thawed, homogenized and reconstituted by adding approximately 4 L of tap water to each bucket. It was assumed that reconstitution had no effect on the nutrient or physical composition of dung, although the effect of freezing and reconstitution was not tested. Dung was frequently mixed inside the bucket during the application of treatments to ensure consistency across dung pats.

**Dung Pat Placement and Treatments**

Dung pats were made by adding 1.5 L of the reconstituted dung into a 20 cm diameter plastic ring. Dung pat diameter and volume was selected following the experiments of Finn and Giller (2000), Hutton and Giller (2004), and Pentillä et al. (2013). Treatments were designated as: Exposed, which consisted of a dung pat placed directly on the soil; Unexposed, which consisted of a dung pat placed into a wire mesh cage with 1 mm² holes and placed on the soil; No Dung, with no dung pat placed on soil. Mesh cage dimensions were approximately 38.1 cm x 38.1 cm x 17.8 cm, and covered the top, bottom, and sides of dung pats to prevent dung beetle colonization. (Figure 2.2). HT subplots represent six different times at which dung and soil samples were collected for nutrient analyses, discussed in Ch. 3.
Figure 2.2a Diagram of an experiment layout, with ⊙: soil sensors placed at 10, 20, and 60 cm of depth, ●: soil and O₂ sensors placed at 10, 20, and 60 cm of depth and □: automated experimental weather station (AEWS) locations indicated. Three distances from AEWS to sensor locations were used, due to cable lengths ——: 10.7 m, ——: 7.6 m, and ——: 3.0 m. Each experiment consisted of 8 replicated blocks.

Figure 2.2b Diagram of treatment and subplot layouts within main plots. HT 1 – 6 subplots were designated randomly within blocks. One GHG subplot at HT 6 in each block contained three permanent chamber anchors, from which GHG samples were repeatedly collected, ●: Exposed, ○: Unexposed, and ◎: No Dung treatments were arranged randomly within subplots. ◎: Indicates chamber anchors around dung pats in HT 6.

Figure 2.2c Diagram of a subplot with treatments arranged randomly within.
Figure 2.2c Picture of subplot with treatments placed within gas chamber anchor rings

Figure 2.2d Picture of subplot with deployed gas chamber lids fitted onto gas chamber
Sample Collection

Greenhouse gas (GHG) samples were taken in accordance with GraceNet Chamber method protocols (Parkin and Venterea, 2010). Chamber-base rings were made of aluminum, with dimensions averaging 0.65 m in diameter, and 0.25 m in height. The base rings were inserted by pushing ring to an average of 0.16 m depth. Chamber lids were made of stainless steel, had an average diameter of 0.66 m, an average height of 0.15 m, and a 1.3 cm thick layer foam board insulation covered with aluminum foil. Gaskets made of rubber bicycle inner tubes were installed on the outside of the lids, attached by metal screws. Circulation fans were attached to the inside of the lids with wire, and were powered by 9V batteries. Septa (pierceable butyl rubber, Labco Limited, High Wycombe, Buckinghamshire, England) was installed on the top of the chamber lids, through which gas samples were collected using a 30 mL syringe (Henke Sass Wolf™, Soft-Ject Luer Lock). Gas chamber-base rings were installed approximately 36 h before initial, baseline gas sampling. Baseline sampling of GHG was done before dung pat placement and at days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after dung pat placement. GHG samples were repeatedly collected from the same dung pats in subplot HT 6. Beetle presence or absence was also determined by both floating and sieving survey methods. The floatation dung beetle survey method is performed by placing approximately 100 g of dung material into 1000 mL of water, stirring until dung is completely broken up, waiting approximately 5 to 45 minutes for dung material to become saturated with water, stirring once more to free beetles from dung material, and then collecting beetles that float to the surface of the water (Whipple, 2011). Beetles were then counted and summed by HT, dung treatment, and season. The effect of treatment on dung pats physical
characteristics was tested by a separate study, and the results suggested that there was no significant effect of mesh exclosures on dung pat moisture or temperature compared to unexposed dung pats.

Gas samples were collected at approximately 9 AM, corresponding with mean diurnal temperature (Figure 2.3). GRACEnet protocols recommends sampling at approximately mid-morning or mid-evening, to account for variations in GHG flux due to diurnal temperature changes (Parkin and Venterea, 2010). Four gas samples were collected in ten minute increments, with the last sample collected at 30 min after chamber lid placement. Chamber temperature was recorded at the end of the 30 minute collection time from a thermometer placed into the chamber. In addition, air samples were taken at the experiment site at each sampling time for reference. Collected sample volumes were 25 mL, and were transferred from the collection syringe into pre-evacuated Labco™ Exetainer 12 mL soda glass vials (Labco Limited, High Wycombe, Buckinghamshire, England). Vials were evacuated less than 24 h before sampling to approximately 400 Pa. Gas samples were then stored cold in insulated Styrofoam container, and transported the same day for analysis. Concentrations of CO₂, CH₄, and N₂O in each sample were determined by gas chromatography (GC) on an automated Varian 450 GC (Agilent Technologies, Inc., Santa Clara, CA) equipped with an electron capture detector to quantify N₂O (Bruker Daltonics, Fremont, CA, United States). The GC was calibrated each sampling time using an external calibration method of comparisons of known samples and ambient air.
Figure 2.3a Average hourly temperature recorded June to Oct 2014 obtained from automated experimental weather station in the Nebraska Sandhills (42° 13’ 28.40” N, 99° 38’ 19.36” W).

Figure 2.3b Average hourly temperature recorded June to Oct 2015 obtained from automated experimental weather station in the Nebraska Sandhills (42° 13’ 36.50” N, 99° 38’ 19.42” W).
Figure 2.3c Comparisons of mean air temperature reported by High Plains Regional Climate Center, Barta Station, on the days of sampling in 2014, with observations collected by automated experimental weather station at the time and location of collection. ($R^2=0.90$)

Figure 2.3d Comparisons of mean air temperature reported by High Plains Regional Climate Center, Barta Station, on the days of sampling in 2015, with observations collected by automated experimental weather station at the time and location of collection. ($R^2=0.70$)
After determination of sample gas concentrations, changes in gas concentrations over
time were used to compute flux following GraceNet procedures (Parkin & Venterea,
2010) as follows:

\[ J = \frac{dc}{dt} \cdot \frac{M}{V^\circ} \cdot \frac{T}{T^\circ} \cdot H \cdot 10^{-6} \quad \text{(Pumpanen et al., 2004)} \]

Eq. 1

Where \( J \) = flux (g·m\(^{-2}\)·d\(^{-1}\)),
\( \frac{dc}{dt} \) = slope of analyte gas to air concentration (\( \mu \text{mol}·\text{mol}^{-1}·\text{d}^{-1} \)),
\( M \) = analyte gas molar mass (g·mol\(^{-1}\)),
\( V^\circ \) = Volume at Standard Condition (0.0224 m\(^3\)·mol\(^{-1}\)),
\( T^\circ \) = Temperature at Standard Condition (273.15 K),
\( T \) = Chamber Temperature (K), and
\( H \) = Chamber Height (m).

*Factor of \( 10^{-6} \) mol·\( \mu \text{mol}^{-1} \) must be applied since concentration slope is originally given
as \( \mu \text{mol}·\text{mol}^{-1}·\text{d}^{-1} \).

Cumulative gas emission was calculated by using numerical integration by
trapezoidal method over a non-uniform grid (reference? Hildebrand, 1974). However,
this method assumes a linear interpolation between data points, and inaccuracies in the
form of underestimations generally become more prominent when time between
sampling increases (Smith and Dobbie, 2001; Parkin, 2008). The equation for this
method is as follows:
\[
\int_{a}^{b} f(x) \, dx \approx \frac{1}{2} \sum_{k=1}^{N} (x_{k+1} - x_{k}) \left( f(x_{k+1}) + f(x_{k}) \right) \quad \text{(Hildebrand, 1974)}
\]

Eq. 2

Equivalent CO\textsubscript{2} values were calculated based upon comparisons of estimates of compound-specific 100-year atmospheric warming potentials to the warming potential of CO\textsubscript{2} (IPCC, 2007). Multipliers of 25 for CH\textsubscript{4} and 298 for N\textsubscript{2}O are suggested by The Intergovernmental Panel on Climate Change (IPCC, 2007).

**Environmental Data**

Soil and air weather station was placed at the experimental site. A programmable data logger was utilized to sequentially record hourly soil and weather information over the month-long period of the experimental trial (Campbell Scientific CR1000, Logan, UT). Soil temperature, volumetric water content, and electrical conductivity, were measured at eighteen different locations and/or depth across the experimental plots (Figure 2a). Absolute oxygen concentration was measured at nine locations and/or depth using Apogee Instruments SO110 sensors (Apogee Instruments Inc., Logan, UT). Air temperature, relative humidity, and vapor pressure were measured with a Campbell Scientific WXT520 weather sensor and precipitation was measured with a tipping bucket pluviometer by Campbell Scientific (Campbell Scientific Inc., Logan, UT). Weather sensors were located on the data logger support tube installed in the center of the experiment site (Figure 2.2a). Soil sensors were buried evenly at six different locations across the experiment site, and placed at 50, 20, and 10 cm depths (Figure 2.2a). Nine oxygen sensors were placed at 50, 20, and 10cm depths, and were buried evenly with soil sensors at three of the 6 different locations across the experiment site.
**Statistical Design and Analysis**

The field experiment consisted of eight replications, or repeated blocks, in which the three treatments were randomly assigned within each block (Figure 2.2). The experiment was conducted twice within the growing season, in June and again in July of both 2014 and 2015, to account for variability in temperature, moisture, and dung beetle populations over the growing season and among years. Data were analyzed for normality and homogeneity of variance. For statistical comparisons of GHG flux measurements, we conducted a multivariate analysis of variance (α=0.05) in a 3 x 9 repeated measures design. The covariance matrix was selected using best fit of infinite population corrected. A generalized linear mixed-effects model was used with a first-order Ante-dependence covariate structure, chosen by considerations of model simplicity and best-fit determined by infinite population corrected Akaike information criterion (SAS 2015, SAS Institute, Cary, NC). Treatment and DAP were considered fixed effects and block was considered a random effect. A least significant difference of means (LSD), or contrast test was used to separate treatment and DAP means. Significance of environmental covariate effect on GHG flux, as well as significance of interaction with treatments, were evaluated using a type I test of fixed effects within a generalized linear mixed-effects model. The general effect of covariates are then estimated by generating regression slope and intercept solutions using SAS. Significance was declared at $p \leq 0.05$. 
Results

Weather and soil conditions

Except for the month of September in 2014 and 2015, which were lower than average, and June in 2014, which was extremely higher than average, precipitation was similar or slightly below long-term average (Table 2.1). Across the two years, soil temperature ranged between 9.6 and 38.6°C for all depths (Figure 2.4). Across all depths, soil temperature increased with increasing air temperatures until approximately the mid-July, and then decreased over the second half of the grazing season. Soil temperature at 10 and 20 cm of depths exhibited greater variability across the season. Soil moisture at 10 cm depth declined over the growing season and fell below 20 % WFPS, except after rainfall events (Figure 2.5). Absolute soil oxygen concentration over the growing season ranged between 8.0 and 17.7 kPa (Figure 2.6a), and was relatively stable across the season. Although, lower soil oxygen concentration were measured at the beginning and end of the growing season, which seems to correlated well with average soil temperatures (Figure 2.6b).

<table>
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<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
<th>Sum</th>
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<td>66.3</td>
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<th>Average</th>
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<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
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<td>22.8</td>
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</table>

Table 2.1 Monthly cumulative precipitation and mean air temperature May to September 2014 and 2015 and long–term average 1980-2010 values at Barta Brothers Ranch, Eastern Sandhills, NE.
Figure 2.4a Average soil temperature over the growing season for 2014, at soil depths 10, 20 and 60 cm.

Figure 2.4b Average soil temperature over the growing season for 2015, at soil depths 10, 20 and 60 cm.
Figure 2.5a Soil moisture over the 2014 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain.

Figure 2.5b Soil moisture over the 2015 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain.
Figure 2.6a 2014 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. $R^2=0.78$ when averages of $[O_2]$ and WFPS across all soil depths are compared.

Figure 2.6b 2015 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. $R^2=0.72$ when averages of $[O_2]$ and WFPS across all soil depths are compared.
**Dung Beetle Abundance and Diversity**

Dung beetle surveys resulted in dung beetle counts ranging from 0 to 12 dung beetles per 25 % volume of collected dung pats. Across seasons, dung beetle abundance was consistently greater in dung pats collected within 3 DAP (Figures 2.7a and 2.7c). By season, 100 % more dung beetles were found in dung pats collected in the early season, when compared to those collected in the late season (Figures 2.7a and 2.7c). Only four beetles were found in unexposed samples, and all of those were found in the same dung pat sample (Figures 2.7b and 2.7d). Surveys of dung pats resulted in the identification of four primary species, *Schaeridium scarabaeoides*, *Aphodius fimetarius*, Histeridae (genus and species unknown), and several other unidentifiable *Aphodius spp.*

*Figure 2.7a* 2014 early season dung beetle counts, by HT. Float method surveys were conducted on 25 % volume of collected dung pats. Dung beetles were counted and species was determined.
Figure 2.7b 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure.

Figure 2.7c 2014 late season dung beetle counts, by HT. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined.
Figure 2.7d 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure.
GHG Flux

Early Season Experiment of 2014

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<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>10.49</td>
<td>8</td>
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<td>DAP x Treatment</td>
<td>0.72</td>
<td>16</td>
<td>0.7666</td>
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<tr>
<td><strong>Daily CH₄ Fluxes</strong></td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>3.60</td>
<td>2</td>
<td>0.0402</td>
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<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>19.55</td>
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<td>DAP x Treatment</td>
<td>1.84</td>
<td>16</td>
<td>0.0480</td>
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</tbody>
</table>

<sup>a</sup>Days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP)

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat.

Table 2.2 Analysis of Variance for daily CO₂, N₂O, and CH₄ fluxes from 2014 early season experiment.
Table 2.3 Estimates of average flux (g m⁻² d⁻¹) of CH₄ by treatment and day, with comparisons of exposed with unexposed and no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>0.5544</td>
<td>1.0365</td>
<td>-1.2919</td>
<td>± 0.7945</td>
<td>F₂₀.₅₃ = 0.18, P = 0.6721</td>
<td>F₂₀.₅₃ = 4.61, P = 0.0439</td>
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<tr>
<td>2</td>
<td>-0.2431</td>
<td>-0.4429</td>
<td>-0.2851</td>
<td>± 0.2261</td>
<td>F₂₀.₈ = 0.40, P = 0.5349</td>
<td>F₂₀.₈ = 0.04, P = 0.8348</td>
</tr>
<tr>
<td>3</td>
<td>0.6143</td>
<td>0.6750</td>
<td>-0.1146</td>
<td>± 0.1273</td>
<td>F₂₀.₃₆ = 0.12, P = 0.7312</td>
<td>F₂₀.₃₆ = 25.28, P = &lt;.0001</td>
</tr>
<tr>
<td>7</td>
<td>-0.1134</td>
<td>0.1253</td>
<td>-0.09913</td>
<td>± 0.06014</td>
<td>F₁₇.₂₉ = 10.85, P = 0.0042</td>
<td>F₁₇.₂₉ = 2.80, P = 0.1121</td>
</tr>
<tr>
<td>10</td>
<td>-0.0820</td>
<td>0.0010</td>
<td>-0.06937</td>
<td>± 0.06684</td>
<td>F₁₇.₉ = 0.99, P = 0.3328</td>
<td>F₁₇.₉ = 0.16, P = 0.6939</td>
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<tr>
<td>14</td>
<td>0.03188</td>
<td>-0.00762</td>
<td>-0.1585</td>
<td>± 0.1599</td>
<td>F₂₀.₅₆ = 0.03, P = 0.8603</td>
<td>F₂₀.₅₆ = 0.79, P = 0.3842</td>
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<tr>
<td>21</td>
<td>-0.2739</td>
<td>-0.1515</td>
<td>-0.2229</td>
<td>± 0.07377</td>
<td>F₁₆.₈ = 1.68, P = 0.2121</td>
<td>F₁₆.₈ = 0.02, P = 0.9023</td>
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<tr>
<td>28</td>
<td>-1.1552</td>
<td>-1.0340</td>
<td>-1.0682</td>
<td>± 0.2404</td>
<td>F₂₀.₅₈ = 0.13, P = 0.7227</td>
<td>F₂₀.₅₈ = 0.01, P = 0.9289</td>
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<tr>
<td>56</td>
<td>-0.7420</td>
<td>-0.6785</td>
<td>-0.5975</td>
<td>± 0.1032</td>
<td>F₁₉.₃₃ = 0.21, P = 0.6528</td>
<td>F₁₉.₃₃ = 0.88, P = 0.3603</td>
</tr>
<tr>
<td>TOTAL</td>
<td>-0.1566</td>
<td>-0.05297</td>
<td>-0.4341</td>
<td>± 0.1093</td>
<td>F₂₈.₉ = 0.49, P = 0.4897</td>
<td>F₂₈.₉ = 6.67, P = 0.0151</td>
</tr>
</tbody>
</table>
Figure 2.7a Average CO$_2$ fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.7b Average N$_2$O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
Across treatments and DAP, daily CO\textsubscript{2}, N\textsubscript{2}O, and CH\textsubscript{4} fluxes ranged from 12 to 56 g m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.7a), -0.04 to 0.96 mg m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.7b), and -1.29 to 1.04 mg m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.7c), respectively. Daily fluxes of CO\textsubscript{2} and N\textsubscript{2}O from the early season experiment exhibited no significant effect of treatment or treatment-DAP interaction (Table 2.2). Daily fluxes of CH\textsubscript{4} in the early season exhibited significant effects of treatment and an interaction of treatment by DAP (Table 2.2). Unexposed treatments exhibited significantly greater flux than the exposed treatments at 7 DAP, and both dung treatments exhibited significantly higher fluxes than the control treatment at 1 and 3 DAP (Table 7c). DAP did exhibit a significant effect on all GHG fluxes. CO\textsubscript{2} fluxes across all treatments exhibited three distinct peaks at 1, 10, and 28 DAP (Table 2.2, Figure 2.7a). These peaks averaged 21, 29, and 57 g CO\textsubscript{2} m\textsuperscript{-2} d\textsuperscript{-1}, respectively (Figure 2.7a). Peak fluxes of N\textsubscript{2}O occurred at 7 and 28 DAP (Figure 2.7b). These peaks averaged 0.52 and

Figure 2.7c Average CH\textsubscript{4} fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
0.73 mg N\textsubscript{2}O m\textsuperscript{2} d\textsuperscript{-1}, respectively (Figure 2.7b). Peak fluxes in CH\textsubscript{4} occurred at 1 and 3 DAP, and these peaks averaged 0.10 and 0.39 mg CH\textsubscript{4} m\textsuperscript{-2} d\textsuperscript{-1}, respectively (Figure 2.7c).

<table>
<thead>
<tr>
<th></th>
<th>Source</th>
<th>F Value\textsuperscript{b}</th>
<th>Num Df</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Daily CO\textsubscript{2} Fluxes</strong></td>
<td>Treatment\textsuperscript{c}</td>
<td>12.84</td>
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<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP\textsuperscript{a}</td>
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<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
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<td>16</td>
<td>0.2994</td>
</tr>
<tr>
<td><strong>Daily N\textsubscript{2}O Fluxes</strong></td>
<td>Treatment\textsuperscript{c}</td>
<td>0.56</td>
<td>2</td>
<td>0.5757</td>
</tr>
<tr>
<td></td>
<td>DAP\textsuperscript{a}</td>
<td>5.19</td>
<td>8</td>
<td>0.0002</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>0.66</td>
<td>16</td>
<td>0.8159</td>
</tr>
<tr>
<td><strong>Daily CH\textsubscript{4} Fluxes</strong></td>
<td>Treatment\textsuperscript{c}</td>
<td>1.53</td>
<td>2</td>
<td>0.2338</td>
</tr>
<tr>
<td></td>
<td>DAP\textsuperscript{a}</td>
<td>16.75</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.37</td>
<td>16</td>
<td>0.1922</td>
</tr>
</tbody>
</table>

Table 2.3 Analysis of Variance for daily CO\textsubscript{2}, N\textsubscript{2}O, and CH\textsubscript{4} fluxes from 2014 late season experiment.

\textsuperscript{a}Days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP)

\textsuperscript{b}Type 3 F-tests of fixed effects are given.

\textsuperscript{c}Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
Table 2.6 Estimates of average flux (g m⁻² d⁻¹) of CO₂ by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>32.9972</td>
<td>27.4822</td>
<td>26.3195</td>
<td>± 1.6886</td>
<td>F&lt;sub&gt;21.85&lt;/sub&gt; = 5.33, P = 0.0308</td>
<td>F&lt;sub&gt;21.85&lt;/sub&gt; = 3.59, P = 0.0713</td>
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<tr>
<td>2</td>
<td>33.9166</td>
<td>32.0253</td>
<td>27.5583</td>
<td>± 1.9079</td>
<td>F&lt;sub&gt;20.01&lt;/sub&gt; = 0.49, P = 0.4914</td>
<td>F&lt;sub&gt;20.01&lt;/sub&gt; = 5.37, P = 0.0313</td>
</tr>
<tr>
<td>3</td>
<td>18.3232</td>
<td>16.4187</td>
<td>10.8941</td>
<td>± 1.3536</td>
<td>F&lt;sub&gt;23.26&lt;/sub&gt; = 0.99, P = 0.3300</td>
<td>F&lt;sub&gt;23.26&lt;/sub&gt; = 15.26, P = 0.0007</td>
</tr>
<tr>
<td>7</td>
<td>27.2261</td>
<td>25.4108</td>
<td>20.2959</td>
<td>± 2.0428</td>
<td>F&lt;sub&gt;21.82&lt;/sub&gt; = 0.39, P = 0.5363</td>
<td>F&lt;sub&gt;21.82&lt;/sub&gt; = 5.79, 0.0250</td>
</tr>
<tr>
<td>10</td>
<td>33.4385</td>
<td>33.0785</td>
<td>29.4351</td>
<td>± 1.8532</td>
<td>F&lt;sub&gt;21.06&lt;/sub&gt; = 0.02, P = 0.8920</td>
<td>F&lt;sub&gt;21.06&lt;/sub&gt; = 2.84, P = 0.1068</td>
</tr>
<tr>
<td>14</td>
<td>18.8957</td>
<td>19.6730</td>
<td>17.3001</td>
<td>± 1.1093</td>
<td>F&lt;sub&gt;13.61&lt;/sub&gt; = 0.25, P = 0.6282</td>
<td>F&lt;sub&gt;13.61&lt;/sub&gt; = 2.13, P = 0.1669</td>
</tr>
<tr>
<td>21</td>
<td>18.9264</td>
<td>18.7968</td>
<td>16.1331</td>
<td>± 1.1051</td>
<td>F&lt;sub&gt;19.66&lt;/sub&gt; = 0.01, P = 0.9347</td>
<td>F&lt;sub&gt;19.66&lt;/sub&gt; = 4.06, P = 0.0577</td>
</tr>
<tr>
<td>28</td>
<td>24.4155</td>
<td>22.9925</td>
<td>22.3190</td>
<td>± 1.1556</td>
<td>F&lt;sub&gt;16.94&lt;/sub&gt; = 0.76, P = 0.3961</td>
<td>F&lt;sub&gt;16.94&lt;/sub&gt; = 0.96, P = 0.3416</td>
</tr>
<tr>
<td>56</td>
<td>10.9633</td>
<td>9.3652</td>
<td>10.0367</td>
<td>± 0.6709</td>
<td>F&lt;sub&gt;15.01&lt;/sub&gt; = 2.84, P = 0.1128</td>
<td>F&lt;sub&gt;15.01&lt;/sub&gt; = 0.02, P = 0.8787</td>
</tr>
<tr>
<td>TOTAL</td>
<td>24.3447</td>
<td>22.8048</td>
<td>20.0324</td>
<td>± 0.6628</td>
<td>F&lt;sub&gt;21.72&lt;/sub&gt; = 2.70, P = 0.1148</td>
<td>F&lt;sub&gt;21.72&lt;/sub&gt; = 19.04, P = 0.0003</td>
</tr>
</tbody>
</table>
Figure 2.8a Average CO$_2$ fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.8b Average N$_2$O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
Across treatments and DAP, daily CO$_2$, N$_2$O, and CH$_4$ fluxes ranged from 9 to 34 g m$^{-2}$ d$^{-1}$ (Figure 2.8a), 0.07 to 0.58 mg m$^{-2}$ d$^{-1}$ (Figure 2.8b), and -1.42 to 0.81 mg m$^{-2}$ d$^{-1}$ (Figure 2.8c), respectively. Daily fluxes of CO$_2$ in the late season exhibited significant differences among treatments (Table 2.3, Figure 2.8a), while N$_2$O and CH$_4$ exhibited none. However, treatment effect on CO$_2$ was due to differences between dung treatments compared to no dung, and there was no significant difference between exposed and unexposed treatments. There was a significant effect of DAP on all GHG fluxes. Peak fluxes of CO$_2$ occurred at 2, 14, and 28 DAP (Figure 2.8a). These peaks exhibited average fluxes of 31, 32, and 23 g m$^{-2}$ d$^{-1}$, respectively (Figure 2.8a). Peak fluxes of N$_2$O were observed at 10 and 56 DAP across all treatments (Figure 2.8b). These peaks exhibited average fluxes of 0.49 and 0.38 mg m$^{-2}$ d$^{-1}$, respectively (Figure 2.8b). Peak fluxes of CH$_4$ occurred at 1 DAP (Figure 2.8c). This peak exhibited an average flux of
0.10 mg CH$_4$ m$^{-2}$ d$^{-1}$ (Figure 2.8c). There was no significant interaction between treatment and DAP observed among any GHG’s.

**Environmental effects**

For both experiments, volumetric water content (WVC), soil O$_2$ concentration, soil temperature, and air temperature all exhibited a significant effect on CO$_2$ flux estimates (Table 2.4). Both, soil O$_2$ concentration and soil VWC exhibited the most significant influence on CO$_2$ flux in 2014.

For both experiments, soil temperature exhibited a significant effect on N$_2$O flux estimates (Table 2.4). In addition, VWC (p=0.0031) and O$_2$ concentration (p<.0001) also exhibited a significant effect on flux estimates in the early season experiment. There were no significant interactions of environmental variables with treatment.

For both experiments, VWC was the only significant covariate on CH$_4$ flux estimates (Table 2.4). In addition, VWC exhibited a significant interaction with treatment in the early season experiment (p=0.0288). This would indicate that there is variability in the effects of soil moisture changes on fluxes of CH$_4$, according to the treatment applied.
<table>
<thead>
<tr>
<th></th>
<th>VWC&lt;sup&gt;a&lt;/sup&gt;</th>
<th>[O&lt;sub&gt;2&lt;/sub&gt;]</th>
<th>Soil Temp</th>
<th>Air Temp</th>
<th>VWC x Trt</th>
<th>O&lt;sub&gt;2&lt;/sub&gt; x Trt</th>
<th>Soil Temp x Trt</th>
<th>Air Temp x Trt</th>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Early</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.5796</td>
<td>0.3037</td>
<td>0.4183</td>
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<tr>
<td>Late</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
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<td><strong>N&lt;sub&gt;2&lt;/sub&gt;O</strong></td>
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<td>Early</td>
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<td>0.1317</td>
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<td><strong>CH&lt;sub&gt;4&lt;/sub&gt;</strong></td>
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<td>Late</td>
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<td>0.2466</td>
<td>0.5237</td>
<td>0.0981</td>
<td>0.1892</td>
<td>0.1355</td>
<td>0.1373</td>
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</table>

Table 2.4 Environmental covariate significance on 2014 early and late CO<sub>2</sub>, N<sub>2</sub>O, and CH<sub>4</sub> fluxes, and significance of potential treatment*covariate interaction.

<sup>a</sup>Volumetric water content.

<table>
<thead>
<tr>
<th>Source</th>
<th>F Value&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Num Df</th>
<th>P Value</th>
</tr>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
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<tr>
<td><strong>DAILY N&lt;sub&gt;2&lt;/sub&gt;O FLUXES</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
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</tr>
<tr>
<td>DAP x Treatment</td>
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<td>16</td>
<td>0.0161</td>
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</tbody>
</table>

Table 2.5 Analysis of Variance for daily CO<sub>2</sub>, N<sub>2</sub>O, and CH<sub>4</sub> fluxes from 2015 early season experiment.

<sup>a</sup>Days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP)

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
Table 2.6 Estimates of average flux (g m\(^{-2}\) d\(^{-1}\)) of CO\(_2\) by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>38.6693</td>
<td>36.0111</td>
<td>31.2895</td>
<td>± 2.2221</td>
<td>(F)(_{16.93} = 1.16, P = 0.2962)</td>
<td>(F)(_{16.93} = 8.03, P = 0.0115)</td>
</tr>
<tr>
<td>2</td>
<td>41.4151</td>
<td>36.8539</td>
<td>31.4529</td>
<td>± 2.1132</td>
<td>(F)(_{13.96} = 4.05, P = 0.0639)</td>
<td>(F)(_{13.96} = 15.31, P = 0.0016)</td>
</tr>
<tr>
<td>3</td>
<td>38.9697</td>
<td>36.4235</td>
<td>36.3446</td>
<td>± 2.3435</td>
<td>(F)(_{15.31} = 0.90, P = 0.3571)</td>
<td>(F)(_{15.31} = 0.34, P = 0.5689)</td>
</tr>
<tr>
<td>7</td>
<td>44.0783</td>
<td>42.8263</td>
<td>34.1381</td>
<td>± 2.1005</td>
<td>(F)(_{14.46} = 0.31, P = 0.5853)</td>
<td>(F)(_{14.46} = 22.99, P = 0.0003)</td>
</tr>
<tr>
<td>10</td>
<td>45.5814</td>
<td>39.2317</td>
<td>34.9661</td>
<td>± 2.7247</td>
<td>(F)(_{15.69} = 3.65, P = 0.0746)</td>
<td>(F)(_{15.69} = 6.68, P = 0.0202)</td>
</tr>
<tr>
<td>14</td>
<td>47.7894</td>
<td>43.7600</td>
<td>40.0898</td>
<td>± 2.1231</td>
<td>(F)(_{16.99} = 3.11, P = 0.0958)</td>
<td>(F)(_{16.99} = 8.25, P = 0.0106)</td>
</tr>
<tr>
<td>21</td>
<td>42.9157</td>
<td>39.6817</td>
<td>32.1751</td>
<td>± 2.1423</td>
<td>(F)(_{15.28} = 1.94, P = 0.1834)</td>
<td>(F)(_{15.28} = 20.60, P = 0.0004)</td>
</tr>
<tr>
<td>28</td>
<td>44.9834</td>
<td>39.2667</td>
<td>36.1093</td>
<td>± 2.2885</td>
<td>(F)(_{19.56} = 4.89, P = 0.0391)</td>
<td>(F)(_{19.56} = 7.22, P = 0.0143)</td>
</tr>
<tr>
<td>56</td>
<td>35.1292</td>
<td>34.7617</td>
<td>31.3008</td>
<td>± 3.1434</td>
<td>(F)(_{16.85} = 0.01, P = 0.9278)</td>
<td>(F)(_{16.85} = 1.11, P = 0.3071)</td>
</tr>
<tr>
<td>TOTAL</td>
<td>42.1702</td>
<td>38.7574</td>
<td>34.2073</td>
<td>± 1.6353</td>
<td>(F)(_{32.3} = 7.49, P = 0.0100)</td>
<td>(F)(_{32.3} = 33.56, P = &lt;.0001)</td>
</tr>
</tbody>
</table>
Table 2.7 Estimates of average flux (mg m\(^{-2}\) d\(^{-1}\)) of CH\(_4\) by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.6507</td>
<td>0.5744</td>
<td>0.2274</td>
<td>± 0.3479</td>
<td>F(_{2,1.3}) = 0.02, P = 0.8773</td>
<td>F(_{2,1.3}) = 0.83, P = 0.3731</td>
</tr>
<tr>
<td>2</td>
<td>-0.7954</td>
<td>-0.5405</td>
<td>-0.2290</td>
<td>± 0.4008</td>
<td>F(_{2,1.44}) = 0.20, P = 0.6558</td>
<td>F(_{2,1.44}) = 0.81, P = 0.3788</td>
</tr>
<tr>
<td>3</td>
<td>0.3807</td>
<td>0.8682</td>
<td>0.4478</td>
<td>± 0.4378</td>
<td>F(_{18.87}) = 0.09, P = 0.4378</td>
<td>F(_{18.87}) = 0.11, P = 0.7438</td>
</tr>
<tr>
<td>7</td>
<td>0.2372</td>
<td>0.3170</td>
<td>0.7946</td>
<td>± 0.5327</td>
<td>F(_{21.17}) = 0.01, P = 0.9165</td>
<td>F(_{21.17}) = 0.63, P = 0.4352</td>
</tr>
<tr>
<td>10</td>
<td>-0.3376</td>
<td>-0.04538</td>
<td>0.3376</td>
<td>± 0.4085</td>
<td>F(_{21.04}) = 0.26, P = 0.6165</td>
<td>F(_{21.04}) = 1.13, P = 0.2999</td>
</tr>
<tr>
<td>14</td>
<td>-0.3651</td>
<td>-0.1121</td>
<td>2.6050</td>
<td>± 1.0236</td>
<td>F(_{21.8}) = 0.03, P = 0.8628</td>
<td>F(_{21.8}) = 5.15, P = 0.0335</td>
</tr>
<tr>
<td>21</td>
<td>-0.7971</td>
<td>-0.3880</td>
<td>0.1972</td>
<td>± 0.4737</td>
<td>F(_{20.89}) = 0.38, P = 0.5466</td>
<td>F(_{20.89}) = 1.87, P = 0.1864</td>
</tr>
<tr>
<td>28</td>
<td>-0.6495</td>
<td>-0.3881</td>
<td>0.1777</td>
<td>± 0.4302</td>
<td>F(_{20.84}) = 0.19, P = 0.6706</td>
<td>F(_{20.84}) = 1.76, P = 0.1986</td>
</tr>
<tr>
<td>56</td>
<td>-0.6429</td>
<td>-1.0023</td>
<td>-1.6544</td>
<td>± 0.3442</td>
<td>F(_{20.8}) = 0.55, P = 0.4657</td>
<td>F(_{20.8}) = 3.95, P = 0.0603</td>
</tr>
<tr>
<td>TOTAL</td>
<td>-0.2577</td>
<td>-0.07964</td>
<td>0.3227</td>
<td>± 0.2763</td>
<td>F(_{23.16}) = 0.21, P = 0.6495</td>
<td>F(_{23.16}) = 2.15, P = 0.1560</td>
</tr>
</tbody>
</table>
Figure 2.9a Average CO₂ fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.9b Average N₂O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
Across treatments and DAP, daily CO\textsubscript{2}, N\textsubscript{2}O, and CH\textsubscript{4} fluxes ranged from 31 to 48 g m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.9a), 0.17 to 1.78 mg m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.9b), and -1.65 to 2.61 mg m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.9c), respectively. Daily fluxes of CO\textsubscript{2} exhibited a significant effect of treatment in the early season experiment of 2015, while N\textsubscript{2}O and CH\textsubscript{4} did not. Averaged across DAP, exposed treatments emitted 9 % greater daily CO\textsubscript{2} flux than unexposed treatments (Table 2.6, Figure 2.9a). The dung treatments on average exhibited flux values that were 18% higher compared to the no dung treatment (Table 2.6, Figure 2.9a). DAP exhibited a significant effect on all GHG fluxes. There were two distinct peaks in fluxes of CO\textsubscript{2} at 7, 21, and 28 DAP (Figure 2.9a). These peaks exhibited average flux values of 40, 44, and 40 g CO\textsubscript{2} m\textsuperscript{-2} d\textsuperscript{-1}, respectively (Table 2.6, Figure 2.9a). Peaks of N\textsubscript{2}O occurred at 14 DAP (Figure 2.9b). Average flux from this peak was approximately 1.18 mg N\textsubscript{2}O m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.9b). Peaks in CH\textsubscript{4} flux were observed at 1, 3, and 14 DAP.
These peaks exhibited average flux values of approximately 0.48, 0.57, and 0.71 mg CH$_4$ m$^{-2}$ d$^{-1}$, respectively (Table 2.7, Figure 2.9c). There was no significant interaction between treatment and DAP factors observed from CO$_2$ and N$_2$O, but a significant interaction was observed from CH$_4$. This DAP-treatment interaction can only be accounted for by the difference between dung and no dung treatments that were observed only at 14 DAP (Table 2.7, Figure 2.9c).

<table>
<thead>
<tr>
<th>Source</th>
<th>Source</th>
<th>F Value</th>
<th>Num Df</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>DAILY CO$_2$ FLUXES</strong></td>
<td>Treatment$^c$</td>
<td>14.29</td>
<td>2</td>
<td>0.0001</td>
</tr>
<tr>
<td></td>
<td>DAP$^a$</td>
<td>60.31</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.58</td>
<td>16</td>
<td>0.1059</td>
</tr>
<tr>
<td><strong>DAILY N$_2$O FLUXES</strong></td>
<td>Treatment$^c$</td>
<td>1.97</td>
<td>2</td>
<td>0.1640</td>
</tr>
<tr>
<td></td>
<td>DAP$^a$</td>
<td>2.48</td>
<td>8</td>
<td>0.0279</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.01</td>
<td>16</td>
<td>0.4586</td>
</tr>
<tr>
<td><strong>DAILY CH$_4$ FLUXES</strong></td>
<td>Treatment$^c$</td>
<td>1.77</td>
<td>2</td>
<td>0.1884</td>
</tr>
<tr>
<td></td>
<td>DAP$^a$</td>
<td>18.31</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.90</td>
<td>16</td>
<td>0.0413</td>
</tr>
</tbody>
</table>

Table 2.8 Analysis of Variance for daily CO$_2$, N$_2$O, and CH$_4$ fluxes from 2015 late season experiment.

$^a$Days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP)

$^b$Type 3 F-tests of fixed effects are given.

$^c$Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
Table 2.9 Estimates of average flux (mg m\(^{-2}\) d\(^{-1}\)) of CO\(_2\) by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>CO(_2) Flux – Late Season 2015</th>
<th>No Dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>46.9956</td>
<td>38.4768</td>
<td>± 2.0443</td>
<td>(F_{22.95} = 6.49, P = 0.0180)</td>
<td>(F_{22.95} = 3.73, P = 0.0658)</td>
</tr>
<tr>
<td>2</td>
<td>36.2735</td>
<td>22.3227</td>
<td>± 2.4592</td>
<td>(F_{22.91} = 1.06, P = 0.3143)</td>
<td>(F_{22.91} = 16.30, P = 0.0005)</td>
</tr>
<tr>
<td>3</td>
<td>33.9573</td>
<td>30.7107</td>
<td>± 2.7075</td>
<td>(F_{23.2} = 0.37, P = 0.5513)</td>
<td>(F_{23.2} = 1.76, P = 0.1971)</td>
</tr>
<tr>
<td>7</td>
<td>30.6787</td>
<td>25.2138</td>
<td>± 2.3075</td>
<td>(F_{22.25} = 0.24, P = 0.6322)</td>
<td>(F_{22.25} = 2.73, P = 0.1123)</td>
</tr>
<tr>
<td>10</td>
<td>30.5740</td>
<td>24.7066</td>
<td>± 3.0677</td>
<td>(F_{23.49} = 0.00, P = 0.9567)</td>
<td>(F_{23.49} = 2.54, P = 0.1244)</td>
</tr>
<tr>
<td>14</td>
<td>31.5018</td>
<td>28.4830</td>
<td>± 1.5573</td>
<td>(F_{16.42} = 0.32, P = 0.5777)</td>
<td>(F_{16.42} = 3.65, P = 0.0737)</td>
</tr>
<tr>
<td>21</td>
<td>51.0462</td>
<td>44.1129</td>
<td>± 2.5877</td>
<td>(F_{25.73} = 2.64, P = 0.1166)</td>
<td>(F_{25.73} = 1.56, P = 0.2225)</td>
</tr>
<tr>
<td>28</td>
<td>32.9910</td>
<td>27.3482</td>
<td>± 1.8402</td>
<td>(F_{28.44} = 1.56, P = 0.2218)</td>
<td>(F_{28.44} = 3.18, P = 0.0854)</td>
</tr>
<tr>
<td>56</td>
<td>16.9889</td>
<td>16.0132</td>
<td>± 2.1184</td>
<td>(F_{20.98} = 0.05, P = 0.8278)</td>
<td>(F_{20.98} = 0.06, P = 0.8059)</td>
</tr>
<tr>
<td>TOTAL</td>
<td>34.5563</td>
<td>28.5987</td>
<td>± 2.0052</td>
<td>(F_{14.74} = 1.06, P = 0.3199)</td>
<td>(F_{14.74} = 8.05, P = 0.0127)</td>
</tr>
</tbody>
</table>
Table 2.10 Estimates of average flux (mg m\(^{-2}\) d\(^{-1}\)) of CH\(_4\) by treatment and day, with comparisons of exposed with unexposed and dung with no dung treatments.

<table>
<thead>
<tr>
<th>DAP</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung</th>
<th>SE</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.7416</td>
<td>0.5891</td>
<td>-0.8356</td>
<td>± 0.4533</td>
<td>(F_{20.81} = 3.23, P = 0.0866)</td>
<td>(F_{20.81} = 13.00, P = 0.0017)</td>
</tr>
<tr>
<td>2</td>
<td>-1.4774</td>
<td>0.1265</td>
<td>-1.7420</td>
<td>± 0.6745</td>
<td>(F_{20.93} = 2.83, P = 0.1075)</td>
<td>(F_{20.93} = 1.67, P = 0.2107)</td>
</tr>
<tr>
<td>3</td>
<td>0.3009</td>
<td>-0.2585</td>
<td>-0.4225</td>
<td>± 0.5124</td>
<td>(F_{20.95} = 0.60, P = 0.4486)</td>
<td>(F_{20.95} = 0.50, P = 0.4872)</td>
</tr>
<tr>
<td>7</td>
<td>-1.3325</td>
<td>-1.1918</td>
<td>-0.8920</td>
<td>± 0.6190</td>
<td>(F_{20.89} = 0.03, P = 0.8738)</td>
<td>(F_{20.89} = 0.24, P = 0.6304)</td>
</tr>
<tr>
<td>10</td>
<td>-2.6296</td>
<td>-2.0180</td>
<td>-3.1310</td>
<td>± 0.7046</td>
<td>(F_{21.06} = 0.38, P = 0.5459)</td>
<td>(F_{21.06} = 0.88, P = 0.3601)</td>
</tr>
<tr>
<td>14</td>
<td>-0.1273</td>
<td>-0.09475</td>
<td>-0.4285</td>
<td>± 0.2363</td>
<td>(F_{20.93} = 0.01, P = 0.9233)</td>
<td>(F_{20.93} = 1.21, P = 0.2844)</td>
</tr>
<tr>
<td>21</td>
<td>0.3044</td>
<td>0.1351</td>
<td>0.3616</td>
<td>± 0.1435</td>
<td>(F_{20.45} = 0.70, P = 0.4120)</td>
<td>(F_{20.45} = 0.66, P = 0.4269)</td>
</tr>
<tr>
<td>28</td>
<td>-0.5280</td>
<td>-1.0699</td>
<td>-1.2057</td>
<td>± 0.3397</td>
<td>(F_{20.84} = 1.27, P = 0.2719)</td>
<td>(F_{20.84} = 0.96, P = 0.3391)</td>
</tr>
<tr>
<td>56</td>
<td>-1.2492</td>
<td>-1.7770</td>
<td>-1.2246</td>
<td>± 0.3900</td>
<td>(F_{20.99} = 0.92, P = 0.3493)</td>
<td>(F_{20.99} = 0.37, P = 0.5521)</td>
</tr>
<tr>
<td>TOTAL</td>
<td>-0.5552</td>
<td>-0.6177</td>
<td>-1.0578</td>
<td>± 0.2102</td>
<td>(F_{30.77} = 0.04, P = 0.8347)</td>
<td>(F_{30.77} = 3.36, P = 0.0763)</td>
</tr>
</tbody>
</table>
Figure 2.10a Average CO₂ fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.10b Average N₂O fluxes (means and standard errors) of exposed, unexposed, and no dung treatments from 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
Across treatments and DAP, daily CO\textsubscript{2}, N\textsubscript{2}O, and CH\textsubscript{4} fluxes ranged from 16 to 51 g m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.10a), -0.71 to 2.79 mg N\textsubscript{2}O m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.10b), and -3.13 to 1.74 mg CH\textsubscript{4} m\textsuperscript{-2} d\textsuperscript{-1} (Figure 2.10c), respectively. Daily fluxes of CO\textsubscript{2} in late season experiment of 2015 exhibited a significant effect of treatment, while N\textsubscript{2}O and CH\textsubscript{4} did not (Table 2.8). Dung treatments exhibited average CO\textsubscript{2} flux values that were approximately 17% higher than no dung, but there was no significant difference between exposed and unexposed treatments (Table 2.9, Figure 2.10a). DAP did exhibit a significant effect on all GHG fluxes. Peak flux of CO\textsubscript{2} was observed at 1 and 21 DAP (Table 2.9, Figure 2.10a). These peaks exhibited average flux values of 42 and 47 g m\textsuperscript{-2} d\textsuperscript{-1}, respectively. Peak flux of N\textsubscript{2}O was observed at 2 DAP (Figure 2.10b). This peak had an average flux of 1.32 mg m\textsuperscript{-2} d\textsuperscript{-1}. Peak fluxes of CH\textsubscript{4} occurred at 1 and 21 DAP (Figure 2.10a). Average flux values for these peaks were approximately 0.50 and 0.27.
mg m$^2$ d$^{-1}$, respectively (Table 2.10, Figure 2.10c). There was no significant interaction between treatment and DAP factors on CO$_2$ or N$_2$O fluxes, while there was a significant treatment-DAP interaction observed from CH$_4$. Differences in average CH$_4$ fluxes between dung and no dung treatments were significant at 1 DAP, and were responsible for the DAP-treatment interaction (Table 2.10).

**Environmental effects**

For both experiments, VWC, O$_2$ concentration, and air temperature exhibited a significant effect on CO$_2$ flux estimates (Table 2.11). In the late season experiment, soil temperature concentration also exhibited a significant effect on CO$_2$ fluxes. Soil temperature exhibited a significant interaction with treatment across both experiments, while air temperature exhibited a significant interaction in the late season experiment only (Table 2.11). This would indicate variability in the effect of soil temperature and air temperature changes on fluxes of CO$_2$, according to the treatment applied.

Soil moisture and soil temperature were the only environmental variables that exhibited a significant effect on N$_2$O fluxes, but they were only significant over the course of the early season experiment (Table 2.11). There were no significant interactions of the effects of environmental variables with treatment.

Soil moisture and soil temperature were the only environmental variables that exhibited a significant effect on CH$_4$ fluxes across both experiments (Table 2.11). Soil O$_2$ concentration also exhibited a significant effect on CH$_4$ fluxes across the early season experiment. Across both experiments, there was a significant interaction of O$_2$ concentration and treatment. This would indicate variability in the effect of O$_2$ concentration changes on fluxes of CH$_4$, according to the treatment applied.
Table 2.11 Environmental covariate significance on 2014 early and late CO$_2$, N$_2$O, and CH$_4$ fluxes, and significance of potential treatment*covariate interaction.

<table>
<thead>
<tr>
<th></th>
<th>Source</th>
<th>F Value$^a$</th>
<th>Num Df</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>CO$_2$ FLUX</td>
<td>Treatment$^b$</td>
<td>17.26</td>
<td>2</td>
<td>0.0001</td>
</tr>
<tr>
<td>Treatment Diff$^c$</td>
<td>UNE - E</td>
<td>-</td>
<td>107.4</td>
<td>0.0840</td>
</tr>
<tr>
<td></td>
<td>E - ND</td>
<td>-</td>
<td>107.4</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>UNE - ND</td>
<td>-</td>
<td>107.4</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>N$_2$O FLUX</td>
<td>Treatment</td>
<td>1.97</td>
<td>2</td>
<td>0.4840</td>
</tr>
<tr>
<td>CH$_4$ FLUX</td>
<td>Treatment</td>
<td>1.77</td>
<td>2</td>
<td>0.4815</td>
</tr>
</tbody>
</table>

Table 2.12 Analysis of Variance for total experimental CO$_2$, N$_2$O, and CH$_4$ fluxes, across years and seasons.

$^a$ Type 3 F-tests of fixed effects are given.

$^b$ Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat

$^c$ Differences of treatment by least square means

Unexposed, exposed, and no dung treatment averages across the entire experiment yielded values of 30.2133, 31.7524, and 26.6949 g CO$_2$ m$^{-2}$ d$^{-1}$, 0.4199, 0.5945, 0.4474 mg N$_2$O m$^{-2}$ d$^{-1}$, and -0.3176, -0.3523, -0.4677 mg CH$_4$ m$^{-2}$ d$^{-1}$, respectively. Significant differences among treatments were observed in fluxes of CO$_2$, but not in fluxes of N$_2$O or CH$_4$ (Table 2.12). However, differences in flux values of CO$_2$ by treatment were due to
differences between dung and no dung treatments, and not due to differences between
exposed and unexposed treatments (Table 2.12).

**CO₂ Equivalence of GHG Flux**

<table>
<thead>
<tr>
<th>Daily CO₂-Eq GHG Flux</th>
<th>Source</th>
<th>F Value&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Num Df</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>2014 Early Season</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2.28</td>
<td>2</td>
<td>0.1200</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>95.95</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.08</td>
<td>16</td>
<td>0.3945</td>
</tr>
<tr>
<td>2014 Late Season</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>12.79</td>
<td>2</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>75.55</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.18</td>
<td>16</td>
<td>0.3146</td>
</tr>
<tr>
<td>2015 Early Season</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>15.12</td>
<td>2</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>8.16</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.40</td>
<td>16</td>
<td>0.1739</td>
</tr>
<tr>
<td>2015 Late Season</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>13.71</td>
<td>2</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>58.51</td>
<td>8</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.49</td>
<td>16</td>
<td>0.1391</td>
</tr>
</tbody>
</table>

*Table 2.13 Analysis of Variance for sums of CO₂-Eq of all GHG fluxes by experiment.*

<sup>a</sup>Days 1, 2, 3, 7, 10, 14, 21, 28, and 56 after placement of dung (DAP)

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat.
Figure 2.11a Sum of all GHG fluxes as CO$_2$-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2014 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.11b Sum of all GHG fluxes as CO$_2$-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2014 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
Figure 11c. Sum of all GHG fluxes as CO$_2$-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2015 early season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.

Figure 2.11d Sum of all GHG fluxes as CO$_2$-Eq (means and standard errors), by day of sampling, from exposed, unexposed, and no dung treatments over 2015 late season experiment. Samples were collected at 1, 2, 3, 7, 10, 14, 21, 28, and 56 DAP.
The CO₂ equivalent fluxes account for all GHG emissions expressed in units of CO₂, with conversion based on metrics of respective GHG potential for atmospheric warming provided by IPCC (2007). Across treatments and DAP, daily CO₂-Eq values ranged from 12 to 57 g CO₂ m⁻² d⁻¹ (Figure 2.11a) over the early season experiment. Daily CO₂-Eq values across the early season experiment of 2014 exhibited no significant effects of treatment (Table 2.13). DAP did exhibit a significant effect on CO₂-Eq values, and there were three distinct peaks, which occurred at 1, 10, and 28 DAP (Figure 2.13a). These peaks exhibited CO₂-Eq values of 21, 29, and 57 g CO₂ m⁻² d⁻¹, respectively. There was no significant interaction between treatment and DAP factors.

Across treatments and DAP, daily CO₂-Eq values ranged from 9 to 34 g CO₂ m⁻² d⁻¹ (Figure 2.11b) over the late season experiment of 2014. Daily CO₂-Eq values over the late season experiment for 2014 exhibited significant effects of treatment (Table 2.13). This effect was due to significant differences between the dung and no dung treatments, with the dung treatments exhibiting average CO₂-Eq values that were 18 % greater than no dung (Figure 2.11b). There was no significant difference found between exposed and unexposed treatments. DAP did exhibit a significant effect on CO₂ equivalent fluxes, and three peaks were observed at 2, 10, and 28 DAP. These peaks had average CO₂-Eq values of 31, 32, and 23 g CO₂ m⁻² d⁻¹, respectively. There was no significant interaction between treatment and DAP factors.

Across treatments and DAP, daily CO₂-Eq values ranged from 31 to 48 g CO₂ m⁻² d⁻¹ (Figure 2.11c) over the early season of 2015. Daily CO₂-Eq values over the early season experiment of 2015 exhibited significant effects of treatment (Table 2.13). This effect was due to significant differences found between dung and no dung treatments,
while there was no difference between exposed and unexposed treatments. Dung treatments exhibited average CO$_2$-Eq values that were 18% greater than no dung (Figure 2.11c). DAP did have a significant effect on daily CO$_2$-Eq values, with peaks observed at 14 and 28 DAP (Figure 2.11c). These peaks had average CO$_2$-Eq values of 44 and 40 g CO$_2$ m$^{-2}$ d$^{-1}$, respectively. There was no significant interaction between treatment and DAP factors.

Across treatments and DAP, daily CO$_2$-Eq values ranged from 16 to 51 g CO$_2$ m$^{-2}$ d$^{-1}$ (Figure 2.11d) over the late season of 2015. Daily CO$_2$ equivalent fluxes over the late season experiment of 2015 exhibited significant effects of treatment (Table 2.13). This effect was due to significant differences found between dung and no dung treatments, while there was no significant difference found between exposed and unexposed treatments (Figure 2.11d). On average dung treatments exhibited CO$_2$-Eq values that were 17% higher than no dung (Figure 2.11d). DAP did have a significant effect on CO$_2$-Eq values, and peaks were observed at 1, 3, and 21 DAP (Figure 2.11d). These peaks had average CO$_2$-Eq values of 42, 34, and 47 g CO$_2$ m$^{-2}$ d$^{-1}$, respectively (Figure 2.11d). There was no significant interaction between treatment and DAP factors (Table 2.13).
Cumulative Integration of Flux

Table 2.14 Estimates of average cumulative flux (g m⁻²) by treatment and season. P-values of treatment effects, comparisons of exposed against unexposed, and comparisons of dung against no dung treatments are also given.

### Cumulative GHG Flux

<table>
<thead>
<tr>
<th></th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung (ND)</th>
<th>SE</th>
<th>Treatment Effect</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>2014 Early Season</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CO₂</td>
<td>1818.65</td>
<td>1851.71</td>
<td>1764.31</td>
<td>± 98.8495</td>
<td>F₁₄ = 0.58, P = 0.5745</td>
<td>F₁₄ = 0.16, P = 0.6935</td>
<td>F₁₄ = 0.99, P = 0.3362</td>
</tr>
<tr>
<td>N₂O</td>
<td>0.02927</td>
<td>0.02475</td>
<td>0.01389</td>
<td>± 0.006885</td>
<td>F₁₄ = 1.35, P = 0.2913</td>
<td>F₁₄ = 0.22, P = 0.6460</td>
<td>F₁₄ = 2.48, P = 0.1378</td>
</tr>
<tr>
<td>CH₄</td>
<td>-0.03118</td>
<td>-0.02598</td>
<td>-0.03194</td>
<td>± 0.005562</td>
<td>F₁₄ = 0.67, P = 0.5282</td>
<td>F₁₄ = 0.86, P = 0.3698</td>
<td>F₁₄ = 0.48, P = 0.5007</td>
</tr>
<tr>
<td>CO₂-Eq</td>
<td>1826.59</td>
<td>1858.43</td>
<td>1767.65</td>
<td>± 98.8417</td>
<td>F₁₄ = 0.61, P = 0.5582</td>
<td>F₁₄ = 0.15, P = 0.7088</td>
<td>F₁₄ = 1.07, P = 0.3183</td>
</tr>
<tr>
<td><strong>2014 Late Season</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CO₂</td>
<td>1142.22</td>
<td>1078.53</td>
<td>994.35</td>
<td>± 44.5187</td>
<td>F₁₄ = 5.97, P = 0.0133</td>
<td>F₁₄ = 2.20, P = 0.1600</td>
<td>F₁₄ = 9.74, P = 0.0075</td>
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<tr>
<td>N₂O</td>
<td>0.01339</td>
<td>0.01604</td>
<td>0.01236</td>
<td>± 0.001495</td>
<td>F₁₄ = 1.81, P = 0.2004</td>
<td>F₁₄ = 1.76, P = 0.2060</td>
<td>F₁₄ = 1.85, P = 0.1947</td>
</tr>
<tr>
<td>CH₄</td>
<td>-0.03732</td>
<td>-0.03741</td>
<td>-0.03528</td>
<td>± 0.004720</td>
<td>F₁₄ = 0.10, P = 0.9032</td>
<td>F₁₄ = 0.00, P = 0.9874</td>
<td>F₁₄ = 0.20, P = 0.6578</td>
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<tr>
<td>CO₂-Eq</td>
<td>1145.28</td>
<td>1082.37</td>
<td>997.15</td>
<td>± 44.4498</td>
<td>F₁₄ = 5.97, P = 0.0134</td>
<td>F₁₄ = 2.14, P = 0.1660</td>
<td>F₁₄ = 9.80, P = 0.0074</td>
</tr>
<tr>
<td><strong>2015 Early Season</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CO₂</td>
<td>2333.59</td>
<td>2143.41</td>
<td>1911.31</td>
<td>± 100.52</td>
<td>F₁₄ = 8.14, P = 0.0045</td>
<td>F₁₄ = 3.29, P = 0.0912</td>
<td>F₁₄ = 12.99, P = 0.0029</td>
</tr>
<tr>
<td>N₂O</td>
<td>0.02586</td>
<td>0.02809</td>
<td>0.03491</td>
<td>± 0.01068</td>
<td>F₁₄ = 0.21, P = 0.8116</td>
<td>F₁₄ = 0.02, P = 0.8799</td>
<td>F₁₄ = 0.40, P = 0.5372</td>
</tr>
<tr>
<td>CH₄</td>
<td>-0.02750</td>
<td>-0.02101</td>
<td>0.000737</td>
<td>± 0.02079</td>
<td>F₁₄ = 0.62, P = 0.5504</td>
<td>F₁₄ = 0.06, P = 0.8099</td>
<td>F₁₄ = 1.19, P = 0.2944</td>
</tr>
<tr>
<td>CO₂-Eq</td>
<td>2340.61</td>
<td>2151.25</td>
<td>1921.73</td>
<td>± 75.3035</td>
<td>F₁₄ = 7.76, P = 0.0054</td>
<td>F₁₄ = 3.16, P = 0.0971</td>
<td>F₁₄ = 12.36, P = 0.0034</td>
</tr>
<tr>
<td><strong>2015 Late Season</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CO₂</td>
<td>1728.32</td>
<td>1617.60</td>
<td>1480.52</td>
<td>± 136.33</td>
<td>F₁₄ = 2.62, P = 0.1078</td>
<td>F₁₄ = 1.04, P = 0.3245</td>
<td>F₁₄ = 4.20, P = 0.0596</td>
</tr>
<tr>
<td>N₂O</td>
<td>0.03230</td>
<td>0.007091</td>
<td>0.01045</td>
<td>± 0.007428</td>
<td>F₁₄ = 3.93, P = 0.0442</td>
<td>F₁₄ = 6.66, P = 0.0218</td>
<td>F₁₄ = 1.20, P = 0.2926</td>
</tr>
<tr>
<td>CH₄</td>
<td>-0.03815</td>
<td>-0.05434</td>
<td>-0.05579</td>
<td>± 0.008603</td>
<td>F₁₄ = 1.30, P = 0.2949</td>
<td>F₁₄ = 1.77, P = 0.1976</td>
<td>F₁₄ = 0.82, P = 0.3754</td>
</tr>
<tr>
<td>CO₂-Eq</td>
<td>1736.99</td>
<td>1618.36</td>
<td>1482.24</td>
<td>± 137.61</td>
<td>F₁₄ = 2.66, P = 0.1049</td>
<td>F₁₄ = 1.15, P = 0.3012</td>
<td>F₁₄ = 4.17, P = 0.0605</td>
</tr>
</tbody>
</table>
Average cumulative fluxes of CO₂ over the early season experiment of 2014 were 1818, 1851, and 1764 g CO₂ m⁻² for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of CO₂ exhibited no significant effects of treatment (Table 2.14).

Over the late season experiment of 2014 average cumulative CO₂ fluxes were 1142, 1078, and 994 g CO₂ m⁻² for exposed, unexposed, and no dung pat treatments, respectively (Table 2.14). Cumulative fluxes of CO₂ exhibited significant effects of treatment (Table 2.14). However, there was no a significant difference found between exposed and unexposed treatments, while a significant difference was found between dung and no dung (Table 2.14). Cumulative fluxes of CO₂ were approximately 12% greater from dung treatments compared to no dung (Table 2.14).

Average cumulative fluxes for the early season 2015 experiment were 2334, 2143, and 1911 g CO₂ m⁻² for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of CO₂ did exhibit a significant effect of treatment (Table 2.14). However, there was no significant difference found between exposed and unexposed treatments, while a significant difference was found between dung and no dung treatments (Table 2.14). Cumulative fluxes of CO₂ were approximately 17% greater from dung treatments compared to no dung (Table 2.14).

Average cumulative fluxes over the late season experiment of 2015 were 1728, 1618, and 1481 g CO₂ m⁻² for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CO₂ fluxes did exhibit a significant effect of treatment (Table 2.14). While there was no significant difference found in cumulative fluxes between
exposed and unexposed treatments, while the dung treatments exhibited average cumulative fluxes that were 13% higher than the no dung treatment (Table 2.14).

Average cumulative fluxes of N\textsubscript{2}O over the early season experiment of 2014 were 29, 25, and 14 mg N\textsubscript{2}O m\textsuperscript{-2} for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of N\textsubscript{2}O exhibited no significant effects of treatment (Table 2.14).

Average cumulative fluxes over the late season experiment of 2014 were 13, 16, and 12 mg N\textsubscript{2}O m\textsuperscript{-2} for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of N\textsubscript{2}O exhibited no significant effect of treatment (Table 2.14).

Average cumulative fluxes over the early season experiment of 2015 were 26, 28, and 35 mg N\textsubscript{2}O m\textsuperscript{-2} for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of N\textsubscript{2}O exhibited no significant effects of treatment (Table 2.14).

Average cumulative fluxes over the late season experiment of 2015 were 32, 7, and 10 mg N\textsubscript{2}O m\textsuperscript{-2} for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative fluxes of N\textsubscript{2}O exhibited a significant effect of treatment (P = 0.0442), suggesting treatment differences that become significant when considering N\textsubscript{2}O flux over longer time scales. There was a significant difference in cumulative flux between exposed and unexposed treatments, and exposed treatments exhibited average cumulative flux that was 355% greater than the unexposed treatment (Table 2.14).

Average cumulative fluxes of CH\textsubscript{4} over the early season experiment of 2014 were -31, -26, and -32 mg CH\textsubscript{4} m\textsuperscript{-2} for exposed, unexposed, and no dung treatments,
respectively (Table 2.14). Cumulative fluxes of CH$_4$ exhibited no significant effects of treatments (Table 2.14).

Average cumulative fluxes over the late season experiment of 2014 were -37, -37, and -35 mg CH$_4$ m$^{-2}$ for exposed, unexposed, and no dung, respectively (Table 2.14). Cumulative fluxes of CH$_4$ exhibited no significant effect of treatment (Table 2.14).

Average cumulative fluxes over the early season experiment of 2015 were approximately -28, -21, and 0.7 mg CH$_4$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CH$_4$ fluxes exhibited no significant effects of treatment (Table 2.14).

Average cumulative fluxes over the late season experiment of 2015 were -38, -54, and -56 mg CH$_4$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CH$_4$ fluxes exhibited no significant effects of treatment (Table 2.14).

Over the early season experiment of 2014 CO$_2$-Eq averages were 1827, 1858, and 1768 g CO$_2$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CO$_2$-Eq values exhibited no significant effects of treatment (Table 2.14).

Over the late season experiment of 2014 average CO$_2$-Eq values were 1145, 1082, 997 g CO$_2$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CO$_2$-Eq values exhibited significant effects of treatment (Table 2.14). There was no significant difference found between exposed and unexposed treatments, but a significant difference was observed between dung and no dung. Dung treatments exhibited average CO$_2$-Eq values that were 4 % greater than no dung (Table 2.14).
Average cumulative fluxes over the early season experiment of 2015 were 2341, 2151, and 1922 g CO$_2$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CO$_2$-Eq values exhibited significant effects of treatment (Table 2.14). While there was no significant difference found between exposed and unexposed treatments, dung treatments exhibited average CO$_2$-Eq values that were 17% greater than no dung (Table 2.14).

Average cumulative values over the late season experiment of 2015 were 1737, 1618, 1482 g CO$_2$-Eq m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Table 2.14). Cumulative CO$_2$-Eq values exhibited no significant effect of treatment (Table 2.14).

Table 2.15 Estimates of average cumulative flux (g m$^{-2}$) across all experiments, by treatment. P-values of treatment effects, comparisons of exposed against unexposed, and comparisons of dung against no dung treatments are also given.

<table>
<thead>
<tr>
<th>Total Average Cumulative GHG Flux</th>
<th>Exposed (E)</th>
<th>Unexposed (UNE)</th>
<th>No Dung (ND)</th>
<th>SE</th>
<th>Treatment Effect</th>
<th>E - UNE</th>
<th>D - ND</th>
</tr>
</thead>
<tbody>
<tr>
<td>CO$_2$</td>
<td>1755.69</td>
<td>1672.81</td>
<td>1537.62</td>
<td>± 84.6156</td>
<td>$F_{62} = 11.67$, $P = &lt;.0001$</td>
<td>$F_{62} = 3.31$, $P = 0.0738$</td>
<td>$F_{62} = 20.02$, $P = &lt;.0001$</td>
</tr>
<tr>
<td>N$_2$O</td>
<td>0.02521</td>
<td>0.01899</td>
<td>0.01790</td>
<td>± 0.003832</td>
<td>$F_{62} = 1.19$, $P = 0.3115$</td>
<td>$F_{62} = 1.48$, $P = 0.2287$</td>
<td>$F_{62} = 0.90$, $P = 0.3467$</td>
</tr>
<tr>
<td>CH$_4$</td>
<td>-0.03354</td>
<td>-0.03468</td>
<td>-0.03057</td>
<td>± 0.006161</td>
<td>$F_{62} = 0.16$, $P = 0.8549$</td>
<td>$F_{62} = 0.02$, $P = 0.8806$</td>
<td>$F_{62} = 0.29$, $P = 0.5911$</td>
</tr>
<tr>
<td>CO$_2$-Eq</td>
<td>1762.37</td>
<td>1677.60</td>
<td>1542.19</td>
<td>± 85.0666</td>
<td>$F_{62} = 11.59$, $P = &lt;.0001$</td>
<td>$F_{62} = 3.38$, $P = 0.0709$</td>
<td>$F_{62} = 19.81$, $P = &lt;.0001$</td>
</tr>
</tbody>
</table>
Figure 2.12a Average cumulative CO$_2$ fluxes (means and standard errors) by treatment, across years and seasonal experiments.

Figure 2.12b Average cumulative N$_2$O fluxes (means and standard errors) by treatment, across years and seasonal experiments.
Figure 2.12c Average cumulative CH₄ fluxes (means and standard errors) by treatment, across years and seasonal experiments.

Figure 2.12d Average cumulative sums of CO₂-Eq of all GHG fluxes (means and standard errors) by treatment, across years and seasonal experiments.
Average cumulative fluxes of CO$_2$ across seasons and years for all 56 day experiments were 1756, 1673, and 11538 g CO$_2$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Figure 2.12a). There were significant differences in both treatment found across all experiments (Table 2.15). However, no significant differences were observed between exposed and unexposed treatments, while dung treatments were significantly greater than the no dung. Averaged together, mean cumulative flux estimates from dung treatments were 11 % larger than the no dung treatments (Table 2.15).

Average cumulative fluxes of N$_2$O across seasons and years for all 56 day experiments were 0.02521, 0.01899, and 0.01790 g N$_2$O m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Figure 2.12b). There were no significant effects of treatment found across all experiments (Table 2.15).

Average cumulative fluxes of CH$_4$ across seasons and years for all 56 day experiments were -0.03354, -0.03468, and -0.03057 g CH$_4$ m$^{-2}$ for exposed, unexposed, and no dung treatments, respectively (Figure 2.12c). There were no significant effects of treatment found across all experiments (Table 2.15).

Average cumulative CO$_2$ equivalents of fluxes across seasons and years for all 56 day experiments were 1762.37, 1677.60, and 1542.19 g CO$_2$-Eq m$^2$ for exposed, unexposed, and no dung treatments, respectively (Figure 2.12d). There was a significant effect of treatment found across all experiments (Table 2.15). However, mean separation indicated no significant difference between exposed and unexposed treatments, while both dung treatments were significantly greater than the no dung. Averaged together,
mean cumulative flux estimates from dung treatments were 12% larger than the no dung treatment (Table 2.15).

**Discussion**

**GHG Flux**

The magnitude and temporal patterns of GHG emissions measured in this study fall within values reported regional GHG measurements in the literature (Dijkstra et al., 2011; Ingram et al., 2015; Iqbal et al., 2014; Jackson et al., 2015; Liebig et al., 2013). The results of CO₂ fluxes were lower than those observed in Pentilla et al. (2013), but were much greater than those observed in Liebig et al. (2013) in North Dakota. Fluxes of N₂O from dung pats were considerably lower than those observed by Pentilla et al. (2013), but were in agreement with ambient fluxes observed by other studies performed across the central US (Ingram et al., 2015; Iqbal et al., 2014; Jackson et al., 2015). While short, positive peaks in CH₄ flux were observed over the first day or two after dung placement, overall CH₄ fluxes from dung pats were generally negative, and served as an overall sink. This negative flux was observed from dung pat treatments as well as the control treatments. This is in contrast to CH₄ fluxes observed by Pentilla et al. (2013), who observed net-positive fluxes of CH₄ from dung pat treatments. The differences in our results compared to those reported by Pentilla et al. (2013) could be due to differences in subarctic and temperate climates, the prevailing soil types that are found in Nebraska and Finland, or differences in experimental treatments. For instance, Pentilla et al. (2013) applied a
predetermined number of dung beetles into enclosures with dung pats, whereas we allowed natural colonization of dung beetles. However, our results were in alignment with observations published by Dijkstra et al. (2011), who also observed overall negative fluxes within short-grass prairie in Wyoming.

**Temporal Effects of Dung Beetles**

The results showed no significant temporal separations of peak pulses due to dung beetle activity. Temporal patterns of CO$_2$ flux were similar with those published by Pentilla et al. (2013), who also observed sharp peaks in flux from dung pats with beetles compared to no beetle and control treatments immediately following dung placement. Early peaks in CO$_2$ were not observed by Iwasa et al. (2015), who observed peaks in CO$_2$ flux from beetle treatments beginning at approximately 4 days. However, secondary peaks in CO$_2$ flux usually occurring at approximately 10 and 21 DAP, like those found in our study, were only observed by Pentilla et al. (2013) from no beetle treatments. However, secondary peaks in CO$_2$ from dung treated with beetles were observed by Iwasa et al. (2015) at 4 and 6 days. Temporal patterns of CO$_2$ equivalent fluxes followed CO$_2$ flux patterns closely.

Temporal patterns of N$_2$O flux in this study were highly variable and peaks were modest in intensity. Late season peak emissions generally occurred within 3 DAP, dissimilar to results found by Pentilla et al. (2013) and Maljanen et al. (2007), but in alignment with those reported by Iwasa et al. (2015). However, early season peak emissions generally occurred at 21 DAP, and in agreement with later peaks found by Pentilla et al. (2013) and Maljanen et al. (2007) who observed peaks in N$_2$O flux from dung at 21 and 28 DAP, respectively. These variations are most likely due to changes in
soil moisture across seasons, as average VWC was approximately twice as high in June compared to July across years.

Temporal patterns of CH4 were consistent across seasons and years. Early positive peaks in CH4 within 3 DAP were observed from dung treatments, and then exhibited negative fluxes 3 DAP. This trend is dissimilar to observations reported by Pentilla et al. (2013) and Iwasa et al. (2015), where they found positive fluxes from all dung treatments across small and large time scales. However, our results are similar to the observation of Maljanen et al. (2012), who found positive CH4 fluxes for only approximately 3 to 4 days after applications of dung in boreal grassland swards. Since CH4 flux was found to be dependent upon soil moisture, it can be assumed that some of these temporal differences in CH4 flux response can likely be attributed to differences in dung moisture evaporation rates and available moisture in dung and soil necessary for methanogenesis.

**Dung Beetle Effect on GHG Flux Density**

Dung pats, whether dung beetles were present or not, were a significant source of GHG emission compared to control treatments with no dung. However, consistent effects of beetle activity on GHG flux were not found. Moreover, the lack of consistent beetle treatment effects, and strong fluctuations in flux by DAP, suggested that physical and climatic factors have a more dominant effect on GHG emission from decomposing dung than the presence or absence of dung beetles in this region and especially since there were no control over the number and type of beetle colonization as was done in Pentilla et al. study (2013).
Dung pats left exposed to colonization by beetles emitted slightly higher CO$_2$ fluxes than the no beetle treatment only in the June 2015 experiment. Thus one out of the four performed experiments is in agreement with the findings of Pentilla et al. (2013). Beetle and no beetle treatments were more consistently not significantly different in fluxes of CO$_2$ that were emitted. However, since the effects of presence or absence of beetles was not consistent among experiments, it cannot be concluded that there is no effect.

Higher peak fluxes of N$_2$O from dung pats left exposed to beetles were observed, but only in the late season experiment of 2015. However, these N$_2$O peak fluxes were lower in intensity and began sooner after dung placement than those reported by Pentilla et al. (2013) and Iwasa et al. (2015). In contrast, June fluxes of N$_2$O were generally greatest from the control treatments, which Pentilla et al. (2013) did not observe. It can be speculated that 2015 late season N$_2$O peaks from beetle treatments could be due to soil moisture and temperature conditions at that point in time. In July 2015 soil volumetric water contents were the lowest and soil temperatures were the highest compared to any other point in time during the study. The general pattern of low N$_2$O fluxes across the entirety of the study can most likely be attributed to the low levels of soil nitrogen found in this region, compared to other grassland soils within the central US.

In accordance to observations made by Pentilla et al. (2013) and Iwasa et al. (2015), higher fluxes of CH$_4$ were observed from dung pats without beetles, but this only occurred during the June 2014 experiment. However, dung pats without beetles still served as an overall sink for CH$_4$ over the course of the 56-day trial, and we observed no cumulative significant differences in CH$_4$ flux from dung treatments. July 2014 CH$_4$
fluxes did not exhibit this pattern, as fluxes were generally lower in intensity, and there were no differences found among dung treatments. This seasonal difference in CH$_4$ flux and beetle effect can likely be attributed to the fact that VWC of soils in July were consistently half of what was observed in June, across years.

**Effect of Climatic and Physical Variables on GHG Flux**

In general, physical variables were found to have a stronger effect on the flux of GHGs from decomposing dung pats, than that of the beetle activity. Soil volumetric water content, soil [O$_2$], and soil temperature were all shown to have a strong effect on the fluxes of CO$_2$, and these relationships have been well documented from many previous studies (Balogh et al., 2011; Lloyd & Taylor, 1994; Smith et al., 2003). CO$_2$ fluxes in 2014 were generally lower than those observed in 2015. This observation could likely be attributed to 2014 average soil temperature being approximately 2° C cooler in June and 1° C cooler in July compared to 2015 values. Precipitation and soil moisture were relatively similar across years. Late season fluxes of CO$_2$ were consistently lower than those observed in the early season, which can most likely be the result of low soil volumetric water content values that were observed in July across both years.

Soil volumetric water content was the only soil variable that was consistently found to have a significant effect on N$_2$O flux. The effect of soil temperature, [O$_2$], and air temperature on N$_2$O flux were each significant in one experiment out of the four performed. It has been shown in previous studies that N$_2$O emission is dependent upon a multiple physical constraints including soil moisture and temperature (Pihlatie et al., 2004; Saggar et al., 2004; Torbert & Wood, 1992; Uchida et al., 2008; Uchida et al., 2011). However, these physical variables responsible for N$_2$O production are very wide
ranging, and strong correlations between a few specific variables and \( \text{N}_2\text{O} \) emission are not clear. The results of our study seem to support that finding. No variations in \( \text{N}_2\text{O} \) flux by season or year were observed.

Soil volumetric water content was found to have a significant effect on \( \text{CH}_4 \) flux, and was the only physical variable that exhibited an effect on \( \text{CH}_4 \) fluxes. The relationship between soil moisture and methanogenesis is also well documented, and the results of our study seem to support those findings (Schnell and King 1996; Chadwick et al., 2000; Jones et al., 2005). \( \text{CH}_4 \) fluxes were the lowest in the late season of 2015, and the lowest monthly averages of soil volumetric water content were correspondingly observed at this time.

**Implications**

In the context of subirrigated meadows within the Sandhills region of Nebraska, our study indicated that dung beetles have a minimal impact on the loss of nutrients as GHG fluxes from decomposing dung pats. While some effects of dung beetle activity were observed, these effects were no consistent across season and years. On the other hand, environmental factors were much more significant, and flux response varied daily, seasonally, and yearly in accordance with temporal fluctuations in physical variables that were measured. This divergence from observations made in recent studies of dung beetle effects on fluxes of GHGs might be due to a number factors. Since the effect of dung beetle activity on dung decomposition can vary by species (Mittal, 1993), it could be plausible that the species of dung beetles found in the Sandhills might exhibit behaviors that are not as effective in modifying dung decomposition in general. It has been postulated that the dung beetle species present throughout much of the U.S. in general,
exhibit activity that is not as effective at removing dung material as the species that are present in other parts of the world (Fincher, 1981). It might also be plausible that dung beetle frequency could vary in accordance with the different soil conditions found at different topographic positions. Perhaps the effect of dung beetles was observed so infrequently due to optimal environmental conditions that existed at the time. Further investigation is needed to adequately resolve questions such as these. However, our study does suggest that management considerations in regards to GHG emissions and nutrient cycling within subirrigated meadows of the Sandhills, might not need to offer as much concern to the effects of dung beetles as perhaps previously thought.
References


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Chapter 3

Dung Beetle Effects on Dung Pat Decomposition and Nutrient Translocation in Soil

Abstract

Livestock production currently yields a considerable footprint in global economic output, environmental quality, and land use, and its impact is only expected to grow over in the future. Management practice can have impacts on the abundance and frequency of dung beetle populations and nutrient cycling in grazing systems. Investigation into the impact of dung beetles on the cycling of nutrients within grazed rangelands could help in formulating management decisions of soil nutrient conservation practices that can sustain forage quality and livestock production. The goal of our study was to quantify the effect of dung beetle presence on the timing and magnitude of decomposition of dung, and subsequent fluxes of dung derived C and N into soil in the semi-arid Sandhills region of Nebraska. We measured indicators of dung pat decomposition, dung pat C, N, and P variables, and soil dung derived C, N, and P variables from dung pats that were either exposed or unexposed to dung beetles. We found that dung beetle presence can increase rates of mass loss in field moist dung pats, as well as rates of moisture loss. The presence of dung beetles had no observable impact on dung pat nutrients. While higher concentrations of nutrients from dung pats in soil were observed, dung beetles had a minimal impact on the nutrient concentrations from decomposing dung pats. Environmental factors were much more impactful, and dung and soil nutrients responded in accordance with temporal fluctuations in the environmental variables that were measured. Our study suggests that management considerations in regards to nutrient
cycling and livestock production within subirrigated meadows of the Sandhills, might not need to offer as much concern to the effects of dung beetles as perhaps previously believed.

**KEY WORDS:** Dung Beetles, Nutrient Cycling, Rangelands, Dung Decomposition, Dung Derived Nutrients

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**Introduction**

The current global demand for livestock production is substantial, and the intensity and extent of its practice will continue to be equally significant in the future. Livestock production accounts for an estimated 30% of the earth’s land use, provides livelihoods for 1.3 billion people, and contributes to 40% of the global agricultural economic output (FOA, 2006b). Land characterized as rangeland continues to be the primary resource for beef and dairy production across the world, and account for approximately 70% of the necessary forage used for beef and dairy production globally (Lund, 2007). Coupled with these large investments of resources and economic dependency on livestock production, is the growing awareness of the effects of global climate change (IPCC, 2014; IPCC, 2007). It is well documented that agriculture and livestock production land use is a considerable source of anthropogenic GHG emissions, while rising atmospheric greenhouse gas (GHG) concentrations are considered to be one of the major indicators of global climate change (Garnett, 2009; Gerber et al., 2013; Searchinger et al., 2008). However, livestock production currently has a considerable
footprint in global economic output, environmental quality, and land use, its impact is only expected to grow as meat and dairy demand is predicted to double by the year 2050 (FOA, 2006b).

In Nebraska, beef production is one of the most economically productive agricultural industry, generating $5.4 billion in revenue in 2010 and accounting for approximately 8% of the gross state product (Thompson et al., 2012; Veneman et al. 2004). Across Nebraska, land area designated for livestock production is estimated to be 9.3 million ha, almost all of which is used solely for beef and dairy production (USDA, 2009a). Land characterized as rangeland also accounts for approximately 9.3 million ha in Nebraska (Wilhelmi and Wilhite, 2002). The Sand Hills region alone contains almost half of all rangeland in the state, at approximately 5.1 million ha (Powell et al., 1982), with the predominant land use being beef cattle production (CALMIT, 2005).

The Sand Hills region of Nebraska is one of the largest stabilized eolian sand formations in the world, with recent activity being dated between 3,500 to 1,500 YBP (Whitcomb, 1989). Vegetation structure across the Sand Hills region is generally variable depending on topography and aspect (Barnes et al., 1984; Barnes, 1986; Schacht et al., 2000). Soil moisture content, organic matter, and fine size fraction typically decrease with increasing topographic position, from low to high elevation across perpendicular sand dune profiles (Barnes et al., 1984), and as such there is dominance of drought tolerant species with higher topographic position (Barnes et al., 1984; Schacht et al., 2000). Water tables in the valleys between dunes can remain at 0.61 to – 1.22 m of the soil surface throughout the growing season, and are referred to as subirrigated meadows (Moore and Rhoades, 1966). This high water table provides more consistent
availability of water to plants, and greater overall productivity compared to areas of higher topographic position (Reece et al., 1994; Barnes, 1986; Nichols et al., 1990). These subirrigated meadows are important hay production areas for winter feed, and are typically grazed between May and June before haying (Adams et al., 1994; Clark et al., 1991; 1994; Volesky et al. 2004). Across 0 to 75 mm of soil depth, organic carbon (1.0 – 1.1 kg · m$^{-2}$) and total nitrogen content (0.731 kg · m$^{-2}$) of soils across the Sandhills region are still generally lower compared to other grassland soils across the central United States (Franzmeier et al., 1985; Leuking and Schepers, 1985).

One essential process that defines the quality and functionality of rangeland ecosystems is nutrient availability and cycling (Whisenant, 1999). The interactions of soil, plants, animals, and management strategy mediate the cycling of nutrients, which in turn can effect diversity and abundance of species, forage quality, primary production, carbon sequestration, and the release of GHGs (Bryant and Snow, 2008). Since grazing livestock utilizes only a portion of the nutrient value of the biomass they consume, the rest is deposited across the grazing-landscape in the form of urine and dung (Haynes and Williams, 1993). Once deposited, small patches of livestock excreta become discrete points of nutrient loss or return during decomposition (Jarvis, 2000; Nichols et al., 2008). Dung decomposition and soil nutrient return are complex processes dependent on factors such livestock diet, climate, time of season, soil characteristics, and invertebrate and microbial activity (Dickinson et al., 1981; Eghball et al., 2002; Lee and Wall, 2006; Van Vliet et al., 2007).

Dung pat decomposition can be mediated by a variety of invertebrate organisms, including earthworms, flies, termites, ants, and dung beetles (Denholm-Young, 1978;
Freyman et al., 2008; Holter, 1979; Lee and Wall, 2006; O’hea et al., 2010). It has been shown that dung beetles are among the most significant invertebrate contributors to dung decomposition in north temperate rangelands (Lee and Wall, 2006). Dung beetle abundance and diversity can be directly affected by land use and management practices such as habitat change, insecticides, and production intensity (Dadour et al., 1999; Floate, 1998; Vessby 2001; Roslin and Koivunen, 2001; Hutton and Giller, 2003). To date, there have been 256 different species of dung beetles observed in Nebraska, and of those species it is estimated that 11 to 15 of those can be found within the Sandhills region (Ratcliffe and Paulsen, 2008; Jameson, 1998; Whipple, 2011).

Dung beetles can influence the cycling of dung nutrients into the soil (Bang et al., 2005; Bertone, 2004; Gillard, 1967; Mittal, 1993) as well as increase forage and grain yields (Bang et al., 2005; Bornemissza and Williams, 1970; Kabir et al., 1985) through more rapid increases in soil available nitrogen and other nutrients (Bang et al. 2005; Bertone, 2004; Gillard, 1967; Miranda et al., 2000; Mittal, 1993; Yamada et al., 2007). The effects of dung beetle activities have also been shown to affect physical soil properties, such as friability, aeration, and water-holding capacity (Bornemissza and Williams 1970; Gillard, 1967; Mittal, 1993). Dung beetles significantly affect the microbial diversity and environmental conditions within the dung pats, which can result in increased mineralization of dung nutrients (Breymeyer et al., 1975; Stephenson & Dindal, 1987; Yokoyama et al., 1991a). However, Dung beetle diversity can vary seasonally, and therefore their activity and associated effects on dung decomposition may vary by the species that are present throughout the growing season (Doube, 1991; Holter, 1982; Whipple, 2011). In the Nebraska Sandhills, 11 to 15 species of dung beetles have
been found, however, their abundance and frequency can vary over the course of the growing season. Different species of dung beetles have been shown to have differing effect on the dung pat with the effect being proportional to species body size (Mittal, 1993). As such, the effect of dung beetle activity on nutrient cycling and GHG emissions would likely be inconsistent depending on species that are present.

In addition to dung beetle influence, decomposition and nutrient cycling may vary due to abiotic and environmental conditions (Bol et al., 2004; Saggar et al., 2004; Maljanen et al., 2007; Lin et al., 2009). The translocation of dung nutrients into the soil is largely related to decomposition rates and the incorporation of dung material into the soil, and complete decomposition can take anywhere from 30 to 1,000 days or more, depending upon environmental conditions (Aarons et al., 2004; Anderson et al., 1984; Dickinson et al., 1981; MacDiarmid & Watkins, 1972; Underhay & Dickinson, 1978). Dung moisture, temperature, and nutrient composition are important variables controlling the processes of dung decomposition (Holter, 1979; Dickinson et al., 1981; Underhay & Dickinson, 1978).

In a survey of fresh dung pats in smooth brome pastures in North Dakota, Lysyk et al. (1985) found moisture contents between 400 and 435 %. After deposition, moisture contents typically decrease precipitously over the first 30 DAP, dropping to between 10 to 20 % by the end of that time period (Stevenson & Dindal, 1987). Average pat mass also drops rapidly over the first 28 DAP, in conjunction with rapid losses of moisture after deposition (Aarons et al., 2004; Hirata et al., 2009). Pat masses at deposition can range between 1,200 and 1,600 kg, with mass losses exceeding 50 % over the first 3 to 5 DAP and as high as 90 % by 40 DAP (Aarons et al, 2004; Hirata et al., 2009). Changes
in dry matter content are considered to be a more accurate metric of dung decomposition and are much less responsive over early stages of decomposition, in contrast to moisture content and pat mass losses (Dickinson et al., 1981; Holter & Hendrickson, 1988; Hirata et al., 2009). However, dry matter losses can be highly variable and extremely dependent upon environmental conditions, ranging anywhere from 17 to 50 % over the first 50 DAP and weekly changes in dry mass ranging between + 5.1 to -60.7 g (Dickinson & Craig, 1990; Hirata et al., 2009).

The greatest fluxes of dung nutrients into soil occur within the first 5 to 10 days after placement, when dung pats are still moist and have not crusted, with subsequent additional fluxes resulting after precipitation events (Bol et al., 2004; Dickinson et al., 1981; Aarons et al., 2004). Increases in dung pat dry weight accompanying higher dung derived nutrient fluxes within the first 5 days after placement have been observed, and mostly attributed to the incorporation of soil into the dung pats from the activities of dung-feeding invertebrates (Dickinson & Craig, 1990; Aarons et al., 2004).

Dung pats are in essence a heterogeneous mixture of forage materials that exhibit a wide range of mineralization kinetics (Van Kessel et al., 2000). While some inorganic nitrogen can be found in dung pats, primarily in the form of ammonium, the majority of nitrogen found in dung is in organic forms and must be mineralized before it can be assimilated by plants or soil microbes (Calderon et al., 2004; Van Kessel et al., 2000). However, once dung derived N is mineralized, any subsequently available NH$_4^+$ is readily immobilized by microbes, with nitrifiers being responsible for the majority of NH$_4^+$ assimilation and the resulting approximate 7 day lag in measurable increases in NO$_3^-$ concentration (Calderon et al., 2004). While net mineralization of dung-N is
reported to be dependent upon carbon to nitrogen ratios of dung material, the fraction and type of dung C and N, and their associated mineralization kinetics, have been shown to be much more relevant in this regard (Calderon et al., 2004; Eghball et al., 2002; Van Kessel et al., 2000).

Fluxes of dung derived dissolved organic carbon (DOC) in soil generally peak between 7 to 20 days after placement and are attributed to leaching and translocation of soluble organic compounds, and not largely the result of microbial decomposition (Bol et al., 2000; Dickinson et al., 1981; Holter & Hendrickson, 1988). Subsequent peaks in dung derived DOC that begin 20 days after placement are shown to persist, or even increase, until complete dung pat disappearance, and are largely attributed to microbial decomposition of the more insoluble carbon compounds (Bol et al., 2000; Holter & Hendrickson, 1988).

The Sandhills are an important beef cattle producing region of the central U.S. Investigation into the impact of dung beetles on the cycling of nutrients within grazed rangelands could help in formulating management decisions of soil nutrient conservation practices that can sustain forage quality and livestock production. As such, this study’s aim was to quantify the effect of dung beetle activity on the timing and magnitude of decomposition of dung, and subsequent fluxes of dung derived C and N into soil in the semi-arid Sandhills region of Nebraska. We hypothesized that the effect of dung beetle activity would: increase rates of dung pat decomposition, indicated by increased rates of pat mass loss, moisture content loss, and dry matter loss; increase the concentrations of peak C and N nutrients and decrease the time at which dung derived nutrient pulses are observed in the soil; and that soil C and N concentrations would be subject to changes
across temporal scales according to seasonal diversity of dung beetle species, and abiotic factors.

Materials and Methods

Site Description

Research was conducted at the Barta Brothers Ranch (42°13’28.65”N, 99°38’19.17”W, 773 m.a.s.l), which is a 2,350 ha grazing research site operated by the University of Nebraska-Lincoln. The site is located in the Eastern Nebraska Sandhills, approximately 40 km Southeast of Ainsworth, Nebraska. Experimental plots were placed on a sub-irrigated meadow. Vegetation consists of predominantly mixed cool season (Thinopyrum intermedium (Host) Barkworth & D.R. Dewey, Poa pratensis L., Bromus inermis Leyss., Agrostis gigantea Roth, Elymus repens (L.) Gould, Phleum pratense L.), less abundant warm season grasses (Andropogon gerardii Vitman, Sorghastrum nutans (L.) Nash, Panicum virgatum L., Spartina pectinata Bosc ex Link), mixed forbs (Achillea millefolium L., Medicago sativa L., Potentilla recta L., Rudbeckia hirta L., Trifolium pretense L., Trifolium repens L.), and an array of rushes (Juncus L. spp.) and sedges (Carex L. spp.). Land use in the Eastern Sandhills is predominantly rangeland, mainly used for beef cattle production, but land is also used for growing corn, soybeans, small grains, and potatoes as well (CALMIT, 2005). Soils are of the Els series, classified as a mixed, mesic Aquic Ustipsamments with sandy to fine sandy loam texture (NRCS, 2009). From soil samples taken before each of our experiments, we found average bulk density to 20 cm depth to be 1.44 Mg·m\(^{-3}\). The climate is semiarid with long-term average (1981-2010) annual precipitation of 584 mm y\(^{-1}\) (NOAA, 2013), and a mean
annual air temperature of 9.6 °C. Eighty percent of the precipitation falls between April and September with May and June typically being the wettest months. We conducted four seasonal experiments that were performed June 10th to August 5th of 2014, July 15th to September 12th of 2014, June 8th to August 3rd of 2015, and July 14th to September 12th of 2015.

![Ainsworth Climate](image)

*Figure 3.1 Average historical monthly precipitation and temperatures in Ainsworth, NE*

**Dung Origin**

Dung was collected from grain and pasture-fed yearling steers that did not receive insecticidal treatment. Diet consisted of 70.51% Brome Grass, 23.33% Dry distillers grains plus solubles, 5.81% Dry Rolled Corn, 0.280% Salt, 0.047% Beef Trace Mineral, and 0.029% Vitamin ADE. These numbers reflect % of the diet inclusion, on a dry matter basis. These steers were also fed 15.2 pounds per day on a dry matter basis while
held off of pasture for observation. Dung was stored in 19 L plastic buckets at approximately -20\(^0\) C until use. Before field experiment layout, dung was thawed, homogenized and reconstituted by adding approximately 4L of tap water to each bucket. Dung was frequently mixed inside the bucket during the application of treatments to ensure consistency across dung pats. It was assumed that freezing and reconstitution had no effect on dung nutrient or physical composition. On analysis of collected dung, we found organic N per dry dung mass concentrations of 20.7 g kg\(^{-1}\), 0.12 g kg\(^{-1}\) NH\(_4\), 20.8 g kg\(^{-1}\) total N, 19.5 g kg\(^{-1}\) P\(_2\)O\(_5\), 4.76 g kg\(^{-1}\) K\(_2\)O, 3.06 g kg\(^{-1}\) S, and 20.8 g kg\(^{-1}\) Ca, and dung C:N ratio was approximately 19.3:1.

**Dung Pat Placement and Treatments**

Dung pats were made by adding 1.5L of the reconstituted dung into a 20 cm diameter plastic ring. Dung pat diameter and volume was chosen by the protocol of previous experiments involving the placement of standardized dung pats and the observation of dung beetle effects or behavior (Finn and Giller 2000; Hutton and Giller 2004; Pentillä et al. 2013). Treatments consisted of dung pat placed directly on the soil; dung placed into a 1 mm wire mesh cage and placed on the soil; and control with no dung pat placement. Mesh cage dimensions were approximately 38.1Lx38.1Wx17.78H cm, and covered the top, bottom, and sides of dung pats to prevent dung beetle colonization. (Figure 3.2). Treatment applications were tested for their effect on dung physical conditions in a separate experiment. It was found that mesh cages had no effect on dung pat moisture or temperature. It was then assumed that mesh exclosures exhibited no significant effect on the physical conditions of dung pats. Each seasonal experimental trial consisted of eight main plots, within each of which there was applied six different
harvest time subplots containing each of the three treatments. The six harvest time subplots were placed randomly within each block, and the three different treatments were also applied randomly within each harvest time (Figure 3.2). Harvest time subplots represented discrete points in time, by which dung and soil samples were collected from each treatment on 1, 3, 7, 14, 28, and 56 days after dung placement (DAP). Thus, each 56-day experimental main plot contained 96 dung treatments, 48 of which were no beetle and 48 beetle, and 48 control units where no dung was placed.

Figure 3.2a Diagram of an experiment layout, with ○: soil sensors placed at 10, 20, and 60 cm of depth, ●: soil and O₂ sensors placed at 10, 20, and 60 cm of depth and ✦: automated experimental weather station (AEWS) locations indicated. Three distances from AEWS to sensor locations were used, due to cable lengths — — : 10.7 m, — — : 7.6 m, and — — : 3.0 m. Each experiment consisted of 8 replicated blocks.

Figure 3.2b Diagram of treatment and subplot layouts within main plots. HT 1 – 6 subplots were designated randomly within blocks. One GHG subplot at HT 6 in each block contained three permanent chamber anchors, from which GHG samples were repeatedly collected. ●: Exposed, ○: Unexposed, and ●: No Dung treatments were arranged randomly within subplots. ○: Indicates chamber anchors around dung pats in HT 6.

Figure 3.2c Diagram of a subplot with treatments arranged randomly within.
Dung Pat and Soil Sampling

At each sampling date, dung pats from each treatment were collected from subplot within each of the eight block. A total of sixteen dung pats were sampled at each sampling date. After dung pat sampling, four soil cores were immediately collected below each dung pat, as well as from the control with no dung pat. Soil cores were also collected from four orthogonal points located 30 cm away from the edge of the dung pat (Figure 3.3). Soil cores were divided by depth, 0 – 10 cm and 10 – 20 cm, and then combined by main plot, depth, distance from pat, and treatment. One sample or harvest time therefore consisted of eighty samples, four each for the mesh and no-mesh
treatments, two from the control treatment, and these collected from eight replicated blocks.

Dung and soil samples were placed into Ziploc freezer bags and stored at approximately -20° C until analyses. Prior to analysis, dung samples were thawed, weighed, and homogenized. Approximately 25 % of the dung sample was used for beetle survey, another 25 % was used for moisture determination, and the rest was used for chemical analyses. Moisture content was determined after dung pat oven-drying at 60° C for 72 hours. Beetle presence or absence was determined by both floating and sieving survey methods. The floatation dung beetle survey method is performed by placing...
approximately 100 g of dung material into 1000 mL of water, stirring until dung is completely broken up, waiting approximately 5 to 45 minutes for dung material to become saturated with water, stirring once more to free beetles from dung material, and then collecting beetles that float to the surface of the water (Whipple, 2011). Beetles were then counted and summed by HT, dung treatment, and season.

Field moist dung and soil sample analyses included ammonium and nitrate, water soluble organic carbon, and water soluble total nitrogen, and molybdate reactive phosphorus. Dung and soil ammonium and nitrate were extracted in 2 M KCL, and determined by flow injection method (Ružicka & Hansen, 1988) using a Lachat Quikchem 8000 (Lachat Instruments, Inc., Loveland, CO). Water soluble organic carbon, nitrogen, and phosphorus were obtained after 1-hr extraction of field moist dung or soil in deionized water at a ratio (m/V) of 5:1 for soil and 200:1 for dung. Extracts were analyzed for soluble organic carbon and nitrogen on Shimadzu 5200 Liquid analyzer (Shimadzu corp., Kyoto, Japan). Phosphorus was determined colorimetrically by the molybdate method (Murphy & Riley, 1962) at 880 nm using a Thermo Scientific Genesys 10S VIS Spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA). Total carbon and nitrogen by mass were determined by combustion using LECO TruMac C/N/S analyzer (LECO corp., Saint Joseph, MI).

**Environmental Data**

A soil and air weather station was placed at the experimental site. A Campbell Scientific brand CR1000 programmable data logger was utilized to sequentially record hourly soil and weather information over the month-long period of the experimental trial. Soil temperature, volumetric water content, and electrical conductivity, were measured
with eighteen Campbell Scientific CR655 soil water content reflectometer sensors. Absolute oxygen concentration was measured with 9 different Apogee Instruments SO110 sensors. Air temperature, relative humidity, and vapor pressure were measured with a Campbell Scientific WXT520 weather sensor and precipitation was measured with a tipping bucket pluviometer by Campbell Scientific. Weather sensors were located on the data logger support tube installed in the center of the experiment site. Soil sensors were buried evenly at six different locations across the experiment site, and placed at 50, 20, and 10 cm depths. Oxygen sensors were placed at 50, 20, and 10 cm depths at three different locations across the experiment site.

**Statistical Design and Analysis**

The field experiment was a split-plot design with eight blocks, in each of which the six subplots were randomly assigned. The experiment was conducted twice within the grazing season in consecutive years, in June and again in July of 2014 and 2015, to account for variability in temperature, moisture, and dung beetle population. Data were analyzed for normality and homogeneity of variance. For statistical comparisons of soil nutrients, a multivariate analysis of variance (α=0.05) in a 3 x 2 repeated measures design. Distance from pat and depth in soil were considered to be repeated measurements across space, within a fixed time of collection. A generalized linear mixed-effects model was used for soil data analyses with a first-order auto-regressive covariate structure, chosen by considerations of model simplicity and best-fit determined by infinite population corrected Akaike information criterion (SAS 2015, SAS Institute, Cary, NC).
Treatment, days after pat placement (pat age), location, and Depth were considered fixed effects, while block and block-treatment interactions were considered random effects. For statistical comparisons of dung nutrient and physical quality measurements, a multivariate analysis of variance (α=0.05), with no repeated measure was done. A least significant Difference of means (LSD), or contrast test was used to separate means. Significance of environmental covariate effects on measured soil chemical variables, as well as significance of interactions with treatments, were evaluated using a type I test of fixed effects within a generalized linear mixed-effects model.

**Results**

**Weather and Soil Conditions**

Except for the month of September, in 2014 and 2015, precipitation was similar or slightly below long-term average (Table 3.1). Across the two years, soil temperature ranged between 9.6 and 38.6°C for all depths (Figure 3.4). Across all depths, soil temperature increased with increasing air temperatures until approximately the mid-July, and then decreased over the second half of the grazing season. Soil temperature at 10 and 20 cm of depths exhibited greater variability across the season. Soil moisture at 10 cm depth declined over the growing season and fell below 20 % WFPS, except after rainfall events (Figure 3.5). Absolute soil oxygen concentration over the growing season ranged between 8.0 and 17.7 kPa (Figure 3.6a), and was relatively stable across the season. Although, lower soil oxygen concentration were measured at the beginning and end of the growing season, which seems to correlated well with average soil temperatures (Figure 3.6b).
<table>
<thead>
<tr>
<th>Precipitation (mm)</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>2014</td>
<td>19.6</td>
<td>195.8</td>
<td>55.9</td>
<td>72.1</td>
<td>50.3</td>
<td>393.7</td>
</tr>
<tr>
<td>2015</td>
<td>71.9</td>
<td>92.7</td>
<td>49.8</td>
<td>52.6</td>
<td>78.7</td>
<td>345.7</td>
</tr>
<tr>
<td>1980-2010</td>
<td>86.1</td>
<td>83.6</td>
<td>90.7</td>
<td>66.3</td>
<td>63.5</td>
<td>390.2</td>
</tr>
<tr>
<td>Temperature (°C)</td>
<td>14.1</td>
<td>20.5</td>
<td>20.7</td>
<td>21.5</td>
<td>16.1</td>
<td>18.6</td>
</tr>
<tr>
<td>2015</td>
<td>13.0</td>
<td>20.3</td>
<td>22.2</td>
<td>20.7</td>
<td>19.5</td>
<td>19.1</td>
</tr>
<tr>
<td>1980-2010</td>
<td>15.2</td>
<td>20.6</td>
<td>23.7</td>
<td>22.8</td>
<td>17.7</td>
<td>20.0</td>
</tr>
</tbody>
</table>

Table 3.1 Monthly cumulative precipitation and mean air temperature May to September 2014 and 2015 and long-term average 1980-2010 values at Barta Brothers Ranch, Eastern Sandhills, NE.

Figure 3.4a Average soil temperature over the growing season for 2014, at soil depths 10, 20 and 60 cm.
Figure 3.4b Average soil temperature over the growing season for 2015, at soil depths 10, 20 and 60 cm.

Figure 3.5a Soil moisture over the 2014 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain.
Figure 3.5b Soil moisture over the 2015 growing season at soil depths 10, 20 and 50 cm. Arrows indicate rainfall events and numbers indicate mm of rain.

Figure 3.6a 2014 regression between WFPS and oxygen concentration at 10, 20, and 60 cm of soil depth. $R^2=0.78$ when averages of $[O_2]$ and WFPS across all soil depths are compared.
Dung Beetle Abundance and Diversity

Dung beetle surveys resulted in dung beetle counts ranging from 0 to 12 dung beetles per 25% volume of collected dung pats. Across seasons, dung beetle abundance was consistently greater in dung pats collected within 3 DAP (Figures 3.7a and 3.7c). By season, 100% more dung beetles were found in dung pats collected in the early season, when compared to those collected in the late season (Figures 7a and 7c). Only four beetles were found in unexposed samples, and all of those were found in the same dung pat sample (Figures 3.7b and 3.7d). Surveys of dung pats resulted in the identification of four primary species, *Schaeridium scarabaeoides*, *Aphodius fimetarius*, Histeridae (genus and species unknown), and several other unidentifiable *Aphodius spp.*
Figure 3.7a 2014 early season dung beetle counts, by HT. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined.

Figure 3.7b 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure.
Figure 3.7c 2014 late season dung beetle counts, by HT. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined.

Figure 3.7d 2014 early season total dung beetle counts by treatment. Float method surveys were conducted on 25% volume of collected dung pats. Dung beetles were counted and species was determined. Unexposed treatment indicates dung pats that were placed in 1 mm wire mesh exclosure, while exposed treatment indicates dung pats with no exclosure.
## Dung Decomposition

<table>
<thead>
<tr>
<th>2014 EARLY SEASON</th>
<th>SOURCE</th>
<th>F VALUE&lt;sup&gt;b&lt;/sup&gt;</th>
<th>NUM DF</th>
<th>P VALUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAT MASS</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2.00</td>
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<td>0.1617</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>486.19</td>
<td>5</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>1.40</td>
<td>5</td>
<td>0.2354</td>
</tr>
<tr>
<td>MOISTURE CONTENT</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>0.12</td>
<td>1</td>
<td>0.7252</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>283.96</td>
<td>5</td>
<td>&lt;.0001</td>
</tr>
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<td></td>
<td>DAP x Treatment</td>
<td>0.62</td>
<td>5</td>
<td>0.6823</td>
</tr>
<tr>
<td>DRY MATTER CONTENT</td>
<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
<td>0.03</td>
<td>1</td>
<td>0.8544</td>
</tr>
<tr>
<td></td>
<td>DAP&lt;sup&gt;a&lt;/sup&gt;</td>
<td>11.32</td>
<td>5</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>DAP x Treatment</td>
<td>0.79</td>
<td>5</td>
<td>0.5581</td>
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</tbody>
</table>

*Table 3.2 Analysis of Variance for daily dung pat decomposition from 2014 early season experiment.*

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)

<sup>c</sup>Treatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages.

<sup>b</sup>Type 3 F-tests of fixed effects are given.
Figure 3.8a Daily dung pat mass (means and standard errors) from 2014 early season experiment.

Figure 3.8b Daily dung pat moisture content (means and standard errors) from 2014 early season experiment.
Figure 3.8c Daily dung pat dry matter content (means and standard errors) from 2014 early season experiment.

Figure 3.8d Daily change in dung pat dry matter (means and standard errors) from 2014 early season experiment.
Across treatments and time, daily dung pat mass ranged from 289 to 1556 g (Figure 3.8a). Daily dung pat mass exhibited no significant differences between exposed and unexposed treatments (Table 3.2, Figure 3.8a). DAP did exhibit a significant effect on dung pat mass, and over the course of the early season experiment of 2014 dung pat mass loss exhibited a negative exponential decay. There was no significant interaction between treatment and DAP factors.

Across treatments and DAP, daily dung pat moisture content ranged from 17 to 421 % (Figure 3.8b). Daily dung pat moisture content exhibited no significant differences between exposed and unexposed treatments (Table 3.2, Figure 3.8b). DAP did exhibit a significant effect on dung pat moisture content, and over the course of the early season experiment of 2014 dung pat moisture content exhibited a pattern of negative exponential decay. There was no significant interaction between treatment and DAP factors.

Across treatments and DAP, daily dung pat dry matter ranged from 246 to 308 g (Figure 3.8c). Daily dung pat dry matter exhibited no significant differences between exposed and unexposed treatments (Table 3.2, Figure 3.8c). DAP did exhibit a significant effect on dung pat dry matter, and over the course of the early season experiment of 2014 dung pat dry matter exhibited a pattern of negative exponential decay, approaching a lower bound of 250 g. There was no significant interaction between the treatment and DAP factors. Across treatments and DAP, daily dung pat change in dry matter ranged from -26 to 8 g (Figure 3.8d). Dung pat dry matter change exhibited a damped oscillatory pattern, resolving to a steady state dry matter change of -9 g in the latter stages of the experiment.
Table 3.3 Analysis of Variance for daily dung pat decomposition from 2014 late season experiment.

<table>
<thead>
<tr>
<th>Source</th>
<th>F VALUE ^B</th>
<th>NUM DF</th>
<th>P VALUE</th>
</tr>
</thead>
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<td><strong>MASS</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treatment c</td>
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<tr>
<td>DAP a</td>
<td>486.07</td>
<td>5</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>DAP x Treatment</td>
<td>2.09</td>
<td>5</td>
<td>0.0767</td>
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<tr>
<td><strong>MOISTURE CONTENT</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treatment c</td>
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<td>1</td>
<td>0.0429</td>
</tr>
<tr>
<td>DAP a</td>
<td>478.90</td>
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<td>&lt;.0001</td>
</tr>
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<td>DAP x Treatment</td>
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<td>5</td>
<td>0.2151</td>
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<td><strong>DRY MATTER CONTENT</strong></td>
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<td></td>
<td></td>
</tr>
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<td>Treatment c</td>
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<td>DAP a</td>
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</tr>
<tr>
<td>DAP x Treatment</td>
<td>1.41</td>
<td>5</td>
<td>0.2329</td>
</tr>
</tbody>
</table>

^a Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)
^b Type 3 F-tests of fixed effects are given.
^c Treatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages.

Figure 3.9a Daily dung pat mass (means and standard errors) from 2014 late season experiment.
Figure 3.9b Daily dung pat moisture content (means and standard errors) from 2014 late season experiment.

Figure 3.9c Daily dung pat dry matter content (means and standard errors) from 2014 late season experiment.
Across treatments and DAP, daily dung pat mass ranged from 463 to 1535 g (Figure 3.9a). Daily dung pat mass exhibited significant differences between exposed and unexposed treatments (Table 3.3, Figure 3.9a). Dung pats from unexposed treatment averaged 802 g, while dung pats from exposed treatments averaged 702 g. DAP did exhibit a significant effect on dung pat mass, and over the course of the late season experiment of 2014 dung pat mass exhibited a pattern of negative exponential decay. There was no significant interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat moisture content ranged from 107 to 437 % (Figure 3.9b). Daily dung pat moisture content exhibited a significant between exposed and unexposed treatments (Table 3.3, Figure 3.9b). Dung pats from unexposed treatments averaged 246 % MC, while dung pats from exposed treatments averaged 216 % MC. DAP did exhibit a significant effect on dung pat moisture content, and over the course of the late season experiment of 2014 dung pat moisture content exhibited a
pattern of negative exponential decay. There was no significant interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat dry matter ranged from 202 to 288 g (Figure 3.9c). Daily dung pat dry matter exhibited no significant differences between exposed and unexposed treatments (Table 3.3, Figure 3.9c). DAP did exhibit a significant effect on dung pat dry matter, and over the course of the late season experiment of 2014 dung pat dry matter exhibited a pattern of negative exponential decay, approaching a lower bound of 210 g. There was no significant interaction between the treatment and DAP factors. Across treatments and DAP, daily dung pat change in dry matter ranged from -41 to 14 g (Figure 3.9d). Dung pat dry matter change exhibited a damped oscillatory pattern, resolving to a steady state dry matter change of -10 g in the latter stages of the experiment. Dry matter loss was significantly greater within exposed treatments on 1 and 7 DAP, and dry matter loss was significantly greater within unexposed treatments on 3 and 14 DAP (Figure 3.9c).

**Environmental effects**

For both experiments, volumetric water content, soil O$_2$ concentration, and soil temperature had significant effects on dung pat mass (Table 3.4). Air temperature was significant on dung pat mass in the late season experiment only. For both experiments, volumetric water content had a significant effect on dung pat moisture content (Table 3.4). Additionally, soil O$_2$ concentration, soil temperature, and air temperature were significant on dung pat moisture in the late season experiment. There was significant interaction of treatment with soil O$_2$ concentration and soil moisture in the late season. For both experiments, volumetric water content exhibited a significant effect on dung pat
dry matter (Table 3.4). Also, soil moisture exhibited a significant interaction with treatment in the late season.

<table>
<thead>
<tr>
<th>2014</th>
<th>VWC\textsuperscript{a}</th>
<th>[O\textsubscript{2}]</th>
<th>Soil Temp</th>
<th>Air Temp</th>
<th>VWC x Trt</th>
<th>O\textsubscript{2} x Trt</th>
<th>Soil Temp x Trt</th>
<th>Air Temp x Trt</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pat Mass</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Early</td>
<td>&lt;.0001</td>
<td>0.0058</td>
<td>0.0015</td>
<td>0.1687</td>
<td>0.5922</td>
<td>0.3916</td>
<td>0.6386</td>
<td>0.9550</td>
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<tr>
<td>Late</td>
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<td>&lt;.0001</td>
<td>0.0058</td>
<td>0.0178</td>
<td>0.0039</td>
<td>0.0286</td>
<td>0.9274</td>
<td>0.9915</td>
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<td>Water Content</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Early</td>
<td>0.0125</td>
<td>0.1899</td>
<td>0.6781</td>
<td>0.6671</td>
<td>0.9246</td>
<td>0.9206</td>
<td>0.7970</td>
<td>0.4367</td>
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<tr>
<td>Late</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.0004</td>
<td>0.0091</td>
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<td>0.9659</td>
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<td>Dry Matter</td>
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<tr>
<td>Early</td>
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<td>0.7067</td>
<td>0.0825</td>
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<tr>
<td>Late</td>
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<td>0.8957</td>
<td>0.0121</td>
<td>0.5913</td>
<td>0.0615</td>
<td>0.1474</td>
</tr>
</tbody>
</table>

Table 3.4 Environmental covariate significance on 2014 early and late dung pat decomposition, and estimation of potential treatment*covariate interaction.
\textsuperscript{a}Volumetric water content.
\textsuperscript{b}Significance at p<0.05.
### Table 3.5 Analysis of Variance for daily dung pat decomposition from 2015 early season experiment.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Source</th>
<th>F VALUE</th>
<th>NUM DF</th>
<th>P VALUE</th>
</tr>
</thead>
<tbody>
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<td>DAILY PAT MASS</td>
<td>Treatment</td>
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<td>DAP</td>
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<td>&lt;.0001</td>
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<td></td>
<td>DAP x Treatment</td>
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<tr>
<td>DAILY PAT MOISTURE CONTENT</td>
<td>Treatment</td>
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</tr>
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<td>DAP</td>
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<td>DAP x Treatment</td>
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<td>Treatment</td>
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<td>DAP</td>
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<tr>
<td></td>
<td>DAP x Treatment</td>
<td>0.39</td>
<td>5</td>
<td>0.8525</td>
</tr>
</tbody>
</table>

aDays 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)
bType 3 F-tests of fixed effects are given.
cTreatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages.
Figure 3.10a Daily dung pat mass (means and standard errors) from 2015 early season experiment.

Figure 3.10b Daily dung pat moisture content (means and standard errors) from 2015 early season experiment.
Across treatments and DAP, daily dung pat mass ranged from 309 to 1498 g (Figure 3.10a). Daily dung pat mass exhibited a significant difference between exposed and unexposed treatments (Table 3.5, Figure 3.10a). DAP did exhibit a significant effect.
on dung pat mass, as well as a significant DAP-treatment interaction. Across all DAP, dung pats under exposed and unexposed treatments averaged 859 and 960 g respectively. Across treatments, dung pat mass exhibited a pattern of negative exponential decay, approaching a lower bound of approximately 300 g. DAP-treatment interaction is due to average pat mass from exposed treatments being less than unexposed treatments on 1, 7, 14, and 28 DAP, but being not significantly different from each other on 0, 3, and 56 DAP.

Across treatments and DAP, daily dung pat moisture content ranged from 46 to 449 % (Figure 3.10b). Daily dung pat moisture content exhibited a significant difference between exposed and unexposed treatments (Table 3.5, Figure 3.10b). DAP did exhibit a significant effect on dung pat moisture content, as well as DAP-treatment interaction. Across all DAP, dung pats under exposed and unexposed treatments averaged 151 and 175 % respectively. Across treatments, dung pat moisture content exhibited a pattern of negative exponential decay, approaching a lower bound of approximately 45 %. DAP-treatment interaction is due to average pat moisture content from exposed treatments being less than unexposed treatments on 1, 7, 14, and 28 DAP, and pat moisture content exhibiting no significant differences by treatment on 0, 3, and 56 DAP.

Across treatments and DAP, daily dung pat dry matter ranged from 209 to 283 g (Figure 3.10c). Daily dung pat dry matter exhibited no significant differences between exposed and unexposed treatments (Table 3.5, Figure 3.10c). DAP did exhibit a significant effect on dung pat dry matter. Over the course of the early season experiment of 2015 experiment dung pat dry matter exhibited a pattern of negative exponential decay, approaching a lower bound of 210 g. There was no significant interaction between
the treatment and DAP factors. Across treatments and DAP, daily dung pat change in dry matter ranged from -45 to 8 g (Figure 3.10d). Dung pat dry matter change exhibited a driven oscillatory pattern across DAP, possibly indicating an increasing input of energy over time. Oscillations were seemingly out of phase by treatment, resulting in changes in differences among treatments at almost every different sampling time.

<table>
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<th>2015 LATE SEASON</th>
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<th>P VALUE</th>
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<td>&lt;.0001</td>
</tr>
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<td></td>
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<td>5</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>DAILY PAT MOISTURE CONTENT</td>
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<td>&lt;.0001</td>
</tr>
<tr>
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<td>1181.52</td>
<td>5</td>
<td>&lt;.0001</td>
</tr>
<tr>
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<td>DAP x Treatment</td>
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</table>

Table 3.6. Analysis of Variance for daily dung pat decomposition from 2015 late season experiment.

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)
<sup>b</sup>Type 3 F-tests of fixed effects are given.
<sup>c</sup>Treatments: 1) exposed dung pats and 2) unexposed dung pats inside wire mesh cages.
Figure 3.11a Daily dung pat mass (means and standard errors) from 2015 late season experiment.

Figure 3.11b Daily dung pat moisture content (means and standard errors) from 2015 late season experiment.
**Figure 3.11c** Daily dung pat dry matter content (means and standard errors) from 2015 late season experiment.

**Figure 3.11d** Daily change in dung pat dry matter (means and standard errors) from 2015 late season experiment.
Across treatments and DAP, daily dung pat mass ranged from 268 to 1468 g (Figure 3.11a). Daily dung pat mass exhibited a significant difference between exposed and unexposed treatments (Table 3.6, Figure 3.11a). DAP did exhibit a significant effect on dung pat mass, as well as a significant DAP-treatment interaction. Across all DAP, dung pats under exposed and unexposed treatments averaged 695 and 785 g respectively. Across treatments, dung pat mass exhibited a pattern of negative exponential decay, approaching a lower bound of approximately 250 g. DAP-treatment interaction is due to average pat mass from exposed treatments being less than unexposed treatments on all DAP except 0 and 56 DAP, when pat mass by treatment were not significantly different from each other.

Across treatments and DAP, daily dung pat moisture content ranged from 41 to 526 % (Figure 3.11b). Daily dung pat moisture content exhibited a significant difference between exposed and unexposed treatments (Table 3.6, Figure 3.11b). DAP did exhibit a significant effect on dung pat moisture content, as well as DAP-treatment interaction. Across all DAP, dung pats under exposed and unexposed treatments averaged 118 and 137 % respectively. Across treatments, dung pat moisture content exhibited a pattern of negative exponential decay, approaching a lower bound of approximately 40 %. DAP-treatment interaction is due to average pat mass from exposed treatments being less than unexposed treatments on all DAP except 0 and 56 DAP, when pat mass by treatment were not significantly different from each other.

Across treatments and DAP, daily dung pat dry matter ranged from 193 to 236 g (Figure 3.11c). Daily dung pat dry matter exhibited no significant differences between exposed and unexposed treatments (Table 3.6, Figure 3.11c). DAP did exhibit a
significant effect on dung pat dry matter. Over the course of the late season experiment of 2015 dung pat dry matter exhibited a pattern of negative exponential decay, approaching a lower bound of 195 g. There was no significant interaction between the treatment and DAP factors. Across treatments and DAP, daily dung pat change in dry matter ranged from -16 to 19 g (Figure 3.11d). Dung pat dry matter change exhibited a harmonic oscillatory pattern, with a mitigated amplitude. Oscillations in dry matter change were out of phase by treatment, with changes in treatments differences occurring at almost every DAP.

**Environmental effects**

For both experiments, soil moisture, O<sub>2</sub> concentration, soil temperature, and air temperature all exhibited a significant effect on dung pat mass (Table 3.7). Air temperature only exhibited a significant effect on pat mass in the late season experiment. Both, soil moisture and air temperature exhibited the most significance of the environmental variables that were monitored. There were no significant interactions among environmental variables and treatment effects. For both experiments, volumetric water content exhibited a significant effect on dung pat moisture content (Table 3.7). Additionally, soil O<sub>2</sub> concentration, soil temperature, and air temperature were all significant in the late season experiment. Both, soil O<sub>2</sub> concentration and soil moisture exhibited the most significance of the environmental variables that were monitored, and also exhibited a significant interaction with treatment in the late season. For both experiments, volumetric water content exhibited a significant effect on dung pat dry matter (Table 3.7). Also, soil moisture exhibited a significant interaction with treatment in the late season.
<table>
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<th>Air Temp</th>
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<th>O$_2$ x Trt</th>
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Table 3.7 Environmental covariate significance on 2015 early and late dung pat decomposition, and estimation of potential treatment*covariate interaction.
$^a$Volumetric water content.
$^b$Significance at p<0.05.
### Dung Pat Nutrient Content

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<th>P VALUE</th>
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<tr>
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<td>DAP(^a)</td>
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<td>DAP(^a)</td>
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*Table 3.8 Analysis of Variance for daily dung pat nutrients from 2014 early season experiment.*

\(^a\)Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)

\(^b\)Type 3 F-tests of fixed effects are given.

\(^c\)Treatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages
Figure 3.12a Daily dung pat WSC concentrations (means and standard errors) from 2014 early season experiment.

Figure 3.12b Daily dung pat WEN concentrations (means and standard errors) from 2014 early season experiment.
**Figure 3.12c** Daily dung pat NO$_3^-$ concentrations (means and standard errors) from 2014 early season experiment.

**Figure 3.12d** Daily dung pat NH$_4^+$ concentrations (means and standard errors) from 2014 early season experiment.
Across treatments and DAP, daily dung pat WSC ranged from 6908 to 11875 mg kg\(^{-1}\) (Figure 3.12a). There was no treatment effect in daily dung pat WSC (Table 8, Figure 12a). DAP did exhibit a significant effect on WSC. Over the course of the early season experiment of 2014 dung pat WSC concentrations generally exhibited decreases over the first 14 DAP, after which WSC concentrations began to increase (Figure 3.12a). There was no significant interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat change in dry matter ranged from 1158 to 2165 mg kg\(^{-1}\) (Figure 3.12b). Daily dung pat WEN exhibited no significant differences between beetle and no beetle treatments (Table 3.8, Figure 3.12b). DAP did exhibit a significant effect on WEN. Over the course of the early season experiment of 2014 dung pat WEN concentrations generally exhibited decreases over the first 14 DAP, after which WEN concentrations began to increase (Figure 3.12b). There was no interaction between the treatment and DAP factors.

Figure 3.12e Daily dung pat WEP concentrations (means and standard errors) from 2014 early season experiment.
Across treatments and DAP, daily dung pat NO$_3^-$ concentrations ranged from 0 to 29 mg kg$^{-1}$ (Figure 3.12c). Both treatment and DAP exhibited no effect on dung pat NO$_3^-$ concentrations in the early season experiment of 2014 (Table 3.8, Figure 3.12c).

Across treatments and DAP, daily dung pat NH$_4^+$ concentrations ranged from 132 to 930 mg kg$^{-1}$ (Figure 3.12d). Daily dung pat NH$_4^+$ exhibited no significant differences between exposed and unexposed treatments (Table 3.8, Figure 3.12d). DAP did exhibit a significant effect on NH$_4^+$. Over the course of the early season experiment of 2014 dung pat NH$_4^+$ concentrations generally exhibited increases over the first 3 DAP, after which NH$_4^+$ concentrations decreased (Figure 3.12d). There was no interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat WEP concentrations ranged from 1109 to 3499 mg kg$^{-1}$ (Figure 3.12e). Daily dung pat DMPR exhibited no significant differences between beetle and no beetle treatments (Table 3.8, Figure 3.12e). DAP did was not a significant effect on DMPR. There was no interaction between the treatment and DAP factors.
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Table 3.9 Analysis of Variance for daily dung pat nutrients from 2014 late season experiment.

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages
Figure 3.13a Daily dung pat WSC concentrations (means and standard errors) from 2014 late season experiment.

Figure 3.13b Daily dung pat WEN concentrations (means and standard errors) from 2014 late season experiment.
Figure 3.13c Daily dung pat NO$_3^-$ concentrations (means and standard errors) from 2014 late season experiment.

Figure 3.13d Daily dung pat NH$_4^+$ concentrations (means and standard errors) from 2014 late season experiment.
Across treatments and DAP, daily dung pat WSC concentrations ranged from 3581 to 10539 mg kg\(^{-1}\) (Figure 3.13a). Daily dung pat WSC exhibited no significant differences between exposed and unexposed treatments (Table 3.9, Figure 3.13a). DAP did exhibit a significant effect on WSC. Over the course of the late season experiment of 2014 dung pat WSC concentrations generally exhibited decreases only after the first 14 DAP (Figure 3.12a). There was no interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat WEN concentrations ranged from 474 to 1,566 mg kg\(^{-1}\) (Figure 3.13b). Daily dung pat WEN exhibited no significant differences between exposed and unexposed treatments (Table 3.9, Figure 3.13b). DAP did exhibit a significant effect on WEN. Over the course of the late season experiment 2014 dung pat WEN concentrations generally exhibited decreases only after the first 14 DAP (Figure 3.13b). There was no interaction between the treatment and DAP factors.
Across treatments and DAP, daily dung pat NO$_3^-$ concentrations ranged from 0 to 9 mg kg$^{-1}$ (Figure 3.13c). Both treatment and DAP exhibited no effect on dung pat NO$_3^-$ concentrations in the late season experiment of 2014 (Table 3.9, Figure 3.13c).

Across treatments and DAP, daily dung pat NH$_4^+$ concentrations ranged from 36 to 460 mg kg$^{-1}$ (Figure 3.13d). Daily dung pat NH$_4^+$ exhibited no significant differences between exposed and unexposed treatments (Table 3.9, Figure 3.13d). DAP did exhibit a significant effect on NH$_4^+$. Over the course of the late season experiment of 2014 dung pat NH$_4^+$ concentrations generally exhibited increases over the first 7 DAP, after which NH$_4^+$ concentrations decreased (Figure 3.13d). There was no interaction between the treatment and DAP factors.

Across treatments and DAP, daily dung pat WEP concentrations ranged from 819 to 1882 mg kg$^{-1}$ (Figure 3.13e). Daily dung pat WEP exhibited no significant differences between exposed and unexposed treatments (Table 3.9, Figure 3.13e). DAP did not exhibit a significant effect on WEP. There was no interaction between the treatment and DAP factors.

**Environmental effects**

There were no significant effects of any measured environmental variable on dung pat WSC concentrations observed in 2014 (Table 3.10). Over both early and late season experiments, soil moisture, O$_2$ concentration, and air temperature all exhibited a significant effect on dung pat WEN concentrations (Table 3.10). There was no interaction between environmental and treatment effects. There were no significant effects of any measured environmental variable on dung pat NO$_3^-$ concentrations observed in 2014 (Table 3.10). Over both early and late season experiments O$_2$ concentration exhibited a
significant effect on dung pat NH$_4^+$ concentrations (Table 3.10). Soil temperature exhibited a significant effect on NH$_4^+$ over the early season experiment, and soil moisture and air temperature exhibited significant effects on NH$_4^+$ over the late season experiment. There was no interaction between environmental and treatment effects. The only environmental variable that exhibited an effect on dung pat WEP concentrations was air temperature, and that effect was observed only during the early season experiment (Table 3.10). There were no other effects of environmental variables on dung pat WEP (Table 3.10).

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Table 3.10 Environmental covariate significance on 2014 early and late dung pat nutrients, and estimation of potential treatment*covariate interaction.
$^a$Volumetric water content.
$^b$Significance at $p<0.05$. 
Experiment Treatment Comparisons

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<th>P VALUE</th>
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Table 3.11 Analysis of Variance for experiment-wide dung pat nutrients.

a Type 3 F-tests of fixed effects are given.
b Treatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages

Across seasons and years, experiment-wide estimates of exposed and unexposed treatment averages of dung nutrients were 8801.69 and 8767.40 mg kg⁻¹ WSC, 1421.77 and 1418.99 mg kg⁻¹ WEN, 3.0236 and 1.6628 mg kg⁻¹ NO₃⁻, 273.24 and 312.40 mg kg⁻¹ NH₄⁺, and 1344.63 and 1575.28 mg kg⁻¹ WEP. There were no significant treatment differences observed when considering values measured across the entire experiment.
Soil Nutrients
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Table 3.12 Analysis of Variance for daily soil nutrients from 2014 early season experiment.
<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP).
<sup>b</sup>Type 3 F-tests of fixed effects are given.
<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat.
<sup>d</sup>Locations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away.
<sup>e</sup>Depth in the soil profile; 0-100 and 100-200 mm.
### Table 3.13 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2014 early season experiment.

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<th>P VALUE</th>
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</table>

\(^a\)Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)

\(^b\)Type 3 F-tests of fixed effects are given.

\(^c\)Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
Figure 3.14a Daily WSC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2014 early season experiment.

Figure 3.14b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment.
Figure 3.14c Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment.

Figure 3.14d Daily NH$_4^+$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 early season experiment.
Across treatments, DAP, depth, and location, daily soil WSC concentrations ranged from 77 to 399 mg kg\(^{-1}\) (Figure 3.14a). Daily soil WSC exhibited no significant differences among treatments under a repeated measure analysis (Table 3.12, Figure 3.14a). DAP, location, and depth factors did exhibit a significant effect on WSC concentrations. There was a significant interaction between treatment and DAP, but only within the first 100 mm of soil depth and directly under dung pats. Mean separation indicated that across treatments soil WSC concentration was greatest on 56 DAP, and there was no other significant difference among DAP. WSC concentration by depth averaged approximately 116 mg kg\(^{-1}\) from 200 to 100 mm, and 169 mg kg\(^{-1}\) from 0 to 100 mm of soil depth. By location, WSC ranged from 136 mg kg\(^{-1}\) 300 mm away from dung pats, to 148 mg kg\(^{-1}\) directly under dung pats. Over the course of the early season experiment of 2014 soil directly under dung pat treatments and within 0 to 100 mm of soil depth did exhibit a significant effect of treatment, DAP, and DAP-treatment.
interaction (Table 3.13). Within this same spatial context, mean separation indicated that there was no significant difference in WSC concentrations among dung treatments, however exposed treatment was greater than no dung, while the unexposed treatment was not (Table 3.13). WSC concentrations in soil under dung pats increased to over 300 mg kg\(^{-1}\) beginning after 14 DAP, while control treatments only ranged between 89 and 212 mg kg\(^{-1}\) (Figure 3.14a). The DAP-treatment interaction is a result of no difference in treatments by DAP until 28 DAP, at which time WSC concentrations under dung treatments exhibited significantly greater concentrations than no dung treatments.

Across treatments, DAP, depth, and location, daily soil WEN concentrations ranged from 28 to 102 mg kg\(^{-1}\) (Figure 3.14b). Daily soil WEN exhibited no significant difference among treatments under a repeated measure analysis (Table 3.12, Figure 3.14b). DAP, location, and depth factors did exhibit a significant effect on WEN concentrations, as well as a significant location-depth interaction. WEN concentrations by location ranged from 30 mg kg\(^{-1}\) at 300 mm of distance to 37 mg kg\(^{-1}\) directly below dung pats. By depth, WEN ranged from 21 mg kg\(^{-1}\) within 100 to 200 mm to 46 mg kg\(^{-1}\) within 0 to 100 mm of soil depth. The location-treatment interaction was due to changes in average WEN concentration differences between exposed and unexposed treatments by location. Mean separation indicated that exposed treatments were estimated to be approximately 3.8 mg kg\(^{-1}\) greater than unexposed treatments directly below dung pats, and approximately -1.9 mg kg\(^{-1}\) less than unexposed treatments 300 mm away from dung pats. Over the course of the early season experiment of 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant effect of treatment (Table 3.13). Within this same spatial context, mean separation indicated greater
concentrations of WEN in soil below dung treatments compared to no dung treatments beginning at 7 DAP, and lasting for the duration of the experiment (Figure 3.14b). Soil WEN concentrations increased to over 40 mg kg\(^{-1}\) at 7 DAP, and increased to a peak high of approximately 95 mg kg\(^{-1}\) at 14 DAP below the dung treatments. Conversely, no dung treatments only ranged between 28 and 55 mg kg\(^{-1}\) over the same time period. Across all DAP, there was no significant difference in soil WEN concentration between dung treatments directly under dung pats and within 100 mm of soil depth, however dung treatments were both significantly greater than no dung. Exposed and unexposed averaged 58 and 56 mg kg\(^{-1}\) in WEN concentration respectively, while control treatments averaged to 40 mg kg\(^{-1}\) (Figure 3.14b).

Across treatments, DAP, depth, and location, daily soil NO\(_3^-\) concentrations ranged from 3 to 43 mg kg\(^{-1}\) (Figure 3.14c). Daily soil NO\(_3^-\) exhibited no significant differences among treatments under a repeated measure analysis (Table 3.12, Figure 3.14c). However, DAP, location, and depth factors did exhibit a significant effect on NO\(_3^-\) concentrations, as well as location-treatment interaction (Table 3.12). By location, NO\(_3^-\) concentrations ranged from 9 mg kg\(^{-1}\) at 300 mm of distance to 13 mg kg\(^{-1}\) directly below dung pats. By depth, NO\(_3^-\) ranged from 5 mg kg\(^{-1}\) within 100 to 200 mm to 17 mg kg\(^{-1}\) within 0 to 100 mm of soil depth. The location-treatment interaction was due to changes in average NO\(_3^-\) concentration differences between exposed and unexposed treatments by location. Mean separation indicated that exposed treatments were estimated to be approximately 2.6 mg kg\(^{-1}\) greater than unexposed treatments 300 mm away from dung pats, and approximately 0.5 mg kg\(^{-1}\) greater than unexposed treatments directly below dung pats. Over the course of the early season experiment of 2014
experiment soil directly under dung pats and within 0 to 100 mm of soil depth did exhibit a significant effect of treatment (Table 3.13). Within this same spatial context, mean separation indicated that across all DAP, average concentrations of NO$_3^-$ in soil below dung treatments were greater than no dung treatments, but exposed and unexposed treatments were not significantly different from each other. Average soil NO$_3^-$ concentrations for exposed, unexposed, and no dung treatments were 23, 24, and 15 mg kg$^{-1}$ respectively. Beginning at 7 DAP, greater soil NO$_3^-$ concentrations below dung treatments compared to no dung were first observed and persisted through 28 DAP, when no differences among treatments were again observed (Figure 3.14c). By DAP, peak NO$_3^-$ concentrations were observed at 14 DAP and reached 42 and 36 mg kg$^{-1}$ for exposed and unexposed treatments, compared to only 15 mg kg$^{-1}$ in soil beneath no dung treatments.

Across treatments, DAP, depth, and location, daily soil NH$_4^+$ concentrations ranged from 0 to 154 mg kg$^{-1}$ (Figure 3.14d). Daily soil NH$_4^+$ exhibited no significant differences among treatments under a repeated measure analysis (Table 3.12, Figure 3.14d). However, DAP, location, and depth factors did exhibit a significant effect on NH$_4^+$ concentrations, as well as DAP-treatment interaction (Table 3.12). By location, NH$_4^+$ concentrations ranged from 9 mg kg$^{-1}$ at 300 mm of distance to 15 mg kg$^{-1}$ directly below dung pats. By depth, NH$_4^+$ ranged from 5 mg kg$^{-1}$ within 100 to 200 mm to 20 mg kg$^{-1}$ within 0 to 100 mm of soil depth. The DAP-treatment interaction was due to changes in average NH$_4^+$ concentration differences between exposed and unexposed treatments at 7 DAP. At 7 DAP, mean separation showed that exposed treatments were estimated to be approximately 9.4 mg kg$^{-1}$ greater than unexposed treatments, and were
not significantly different at any other point in time (Figure 3.14d). Over the course of the early season experiment of 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did not exhibit a significant effect of treatment (Table 3.13). By DAP, peak $\text{NH}_4^+$ concentrations were observed at 7 DAP and reached 122 mg kg$^{-1}$ averaged across all treatments, and there were no differences among all other DAP.

Across treatments, DAP, depth, and location, daily soil WEP concentrations ranged from 1 to 12 mg kg$^{-1}$ (Figure 3.14e). Daily soil WEP exhibited no significant differences among treatments under a repeated measure analysis (Table 3.12, Figure 3.14e). However, DAP, location, and depth factors did exhibit a significant effect on WEP concentrations (Table 3.12). By location, WEP concentrations ranged from 3.8 mg kg$^{-1}$ at 300 mm of distance to 4.4 mg kg$^{-1}$ directly below dung pats. By depth, WEP ranged from 2.3 mg kg$^{-1}$ within 100 to 200 mm to 5.8 mg kg$^{-1}$ within 0 to 100 mm of soil depth. Over the course of the early season experiment 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant effect of treatment, and a significant DAP-treatment interaction (Table 3.13). Mean separation indicated that the DAP-treatment interaction was due to changes in treatments differences in WEP concentration at 28 DAP. Soil below exposed treatments exhibited WEP concentrations that were significantly greater than unexposed and no dung treatments, while unexposed treatments were significantly greater than no dung at this time. There were no significant difference among treatments by DAP at any other point of the experiment. Across all DAP, exposed treatments were significantly greater than both unexposed and no dung treatments, with exposed, unexposed, and no dung averaging to approximately 7.4, 5.9,
and 6.0 mg kg\(^{-1}\) respectively. Peak soil WEP concentrations of 11 mg kg\(^{-1}\) were observed at 3 DAP, with a smaller peak of 8.3 mg kg\(^{-1}\) observed at 28 DAP.
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Table 3.14 Analysis of Variance for daily soil nutrients from 2014 late season experiment.

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP).
<sup>b</sup>Type 3 F-tests of fixed effects are given.
<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat.
<sup>d</sup>Locations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away.
<sup>e</sup>Depth in the soil profile; 0- 100 and 100-200 mm.
Table 3.15 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2014 late season experiment.

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\textsuperscript{a}Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)  
\textsuperscript{b}Type 3 F-tests of fixed effects are given.  
\textsuperscript{c}Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat

Figure 3.15a Daily NPOC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2014 late season experiment.
Figure 3.15b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment.

Figure 3.15c Daily NO₃⁻ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment.
Figure 3.15d Daily NH$_4^+$ soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment.

Figure 3.15e Daily DMPR soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2014 late season experiment.
Across treatments, DAP, depth, and location, daily soil WSC concentrations ranged from 74 to 215 mg kg\(^{-1}\) (Figure 3.15a). Daily soil WSC exhibited no significant differences among treatments under a repeated measure analysis (Table 3.14, Figure 3.15a). DAP and depth factors did exhibit a significant effect on WSC concentrations. Mean separation indicated that across treatments soil WSC concentrations were greatest on 3 and 14 DAP, averaging 152 and 179 mg kg\(^{-1}\) respectively. By depth, WSC concentrations ranged from 100 mg kg\(^{-1}\) within 200 to 100 mm, and 135 mg kg\(^{-1}\) within 0 to 100 mm of soil depth. Over the course of the late season experiment of 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant effect of treatment (Table 3.15). Within this same spatial context, mean separation indicated greater concentrations of WSC from dung treatments observed on 3 and 56 DAP, compared to no dung treatments (Figure 3.15a). At these points in time soil WSC concentrations increased to over 160 mg kg\(^{-1}\) at 3 DAP and 134 mg kg\(^{-1}\) at 56 DAP below the dung treatments, while no dung treatments were approximately 124 and 153 mg kg\(^{-1}\) at these times. Compared to unexposed and no dung, soil WSC concentrations were significantly greater below exposed treatments at 14 DAP, and reached 215 mg kg\(^{-1}\) (Figure 3.15a). Across all DAP, there was no significant difference in soil WSC concentration between dung treatments directly under dung pats and within 100 mm of soil depth, however dung treatments were both significantly greater than no dung. Exposed and unexposed averaged 153 and 138 mg kg\(^{-1}\) in WSC concentration respectively, while no dung treatments averaged to 120 mg kg\(^{-1}\) (Figure 3.15a).

Across treatments, DAP, depth, and location, daily soil WEN concentrations ranged from 17 to 83 mg kg\(^{-1}\) (Figure 3.15b). Daily soil WEN exhibited no significant
differences among treatments under a repeated measure analysis (Table 3.14, Figure 3.15b). However, DAP, location, and depth factors did exhibit a significant effect on WEN concentrations (Table 3.14). By location, WEN concentrations ranged from 34 mg kg\(^{-1}\) at 300 mm of distance to 40 mg kg\(^{-1}\) directly below dung pats. By depth, WEN concentrations ranged from 26 mg kg\(^{-1}\) within 100 to 200 mm to 50 mg kg\(^{-1}\) within 0 to 100 mm of soil depth. Over the course of the late season experiment of 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant effect of treatment and DAP-treatment interaction (Table 3.15). Within this same spatial context, mean separation indicated that across all DAP average concentrations of WEN in soil below exposed treatments were greater than unexposed and no dung treatments, and across all DAP, average WEN concentrations of exposed, unexposed, and no dung treatments were 62, 51, and 48 mg kg\(^{-1}\) respectively. Beginning at 7 DAP, greater soil WEN concentrations below exposed treatments compared to unexposed and no dung were first observed and persisted until 56 DAP, when no differences among treatments were again observed (Figure 3.15b). Soil WEN concentrations below unexposed treatments were only found to be greater than no dung treatments at 14 DAP (Figure 3.15b). These observed changes in differences among treatments by DAP are responsible for the DAP-treatment interaction (Table 3.15). Soil WEN concentrations below exposed treatments peaked at 83 mg kg\(^{-1}\) at 28 DAP, in comparison to unexposed and no dung treatments which only peaked at 63 and 67 mg kg\(^{-1}\) respectively.

Across treatments, DAP, depth, and location, daily soil NO\(_3^-\) concentrations ranged from 2 to 22 mg kg\(^{-1}\) (Figure 3.15c). Daily soil NO\(_3^-\) exhibited no significant differences among treatments under a repeated measure analysis (Table 3.14, Figure
However, DAP, location, and depth factors did exhibit a significant effect on NO\textsubscript{3}\textsuperscript{−} concentrations (Table 3.14). By location, NO\textsubscript{3}\textsuperscript{−} concentrations ranged from 7 mg kg\textsuperscript{−1} at 300 mm of distance to 9 mg kg\textsuperscript{−1} directly below dung pats by location. By depth, NO\textsubscript{3}\textsuperscript{−} ranged from 4 mg kg\textsuperscript{−1} within 100 to 200 mm to 13 mg kg\textsuperscript{−1} within 0 to 100 mm of soil depth. Over the course of the late season experiment of 2014 soil directly under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant effect of treatment (Table 3.15). Within this same spatial context, mean separation indicated that across all DAP average concentrations of NO\textsubscript{3}\textsuperscript{−} in soil below exposed treatments were greater than no dung treatments, but exposed and unexposed treatments were not significantly different from each other. Average soil NO\textsubscript{3}\textsuperscript{−} concentrations for exposed, unexposed, and no dung treatments were 16, 14, and 12 mg kg\textsuperscript{−1} respectively. At 14 DAP, average soil NO\textsubscript{3}\textsuperscript{−} concentrations below dung treatments were greater than those under no dung, but unexposed treatments were no longer significantly greater than no dung at 28 DAP and exposed treatments were no longer significantly greater than no dung at 56 DAP (Figure 3.15c). By DAP, peak NO\textsubscript{3}\textsuperscript{−} concentrations were observed at 28 DAP and reached an average of 18 mg kg\textsuperscript{−1}, with exposed, unexposed, and no dung treatments respectively averaging 22, 16, and 16 mg kg\textsuperscript{−1}.

Across treatments, DAP, depth, and location, daily soil NH\textsubscript{4}\textsuperscript{+} concentrations ranged from 0 to 16 mg kg\textsuperscript{−1} (Figure 3.15d). Daily soil NH\textsubscript{4}\textsuperscript{+} exhibited no significant differences among treatments under a repeated measure analysis (Table 3.14, Figure 3.15d). By depth, NH\textsubscript{4}\textsuperscript{+} concentrations ranged from 1 mg kg\textsuperscript{−1} within 100 to 200 mm to 5 mg kg\textsuperscript{−1} within 0 to 100 mm of soil depth. Over the course of the late season experiment of 2014 experiment soil directly under dung pat treatments within 0 to 100 mm of soil
depth did exhibit a significant effect of treatment (Table 3.15). Both exposed and unexposed treatments exhibited soil NH$_4^+$ concentrations that were significantly greater than that found below no dung treatments, but no significant differences were found in soil below the two dung treatments. Average soil NH$_4^+$ concentrations by treatment were approximately 7.1, 6.5, and 3.8 mg kg$^{-1}$ from exposed, unexposed, and no dung respectively. By DAP, peak NH$_4^+$ concentrations were observed at 7 DAP and reached 12 mg kg$^{-1}$ averaged across all treatments.

Across treatments, DAP, depth, and location, daily soil DMPR concentrations ranged from 0.1 to 3.6 mg kg$^{-1}$ (Figure 3.15e). Daily soil WEP exhibited no significant differences among treatments under a repeated measure analysis (Table 3.14, Figure 3.15e). However, DAP, location, and depth factors did exhibit a significant effect on WEP concentrations (Table 3.14). Average WEP concentrations by location ranged from 1.1 mg kg$^{-1}$ at 300 mm of distance to 1.4 mg kg$^{-1}$ directly below dung pats, and from 0.5 mg kg$^{-1}$ within 100 to 200 mm to 1.9 mg kg$^{-1}$ within 0 to 100 mm by soil depth. Over the course of the late season experiment of 2014 experiment soil directly under dung pat treatments within 0 to 100 mm of soil depth did not exhibit a significant effect of treatment (Table 3.15). Mean separation indicated that across treatments, peak WEP concentrations were observed at 1 DAP, averaging to approximately 3.3 mg kg$^{-1}$ (Figure 3.15e). There were no other significant differences in WEP concentrations among any other DAP.

**Environmental effects**

Soil moisture, O$_2$ concentration, and air temperature all exhibited a significant effect on soil WSC concentrations across both early and late seasonal experiments (Table 16). Soil O$_2$ concentration and air temperature exhibited a potential interaction with
treatment. Soil O₂ concentration was the only environmental variable that exhibited a significant effect on soil WEN concentrations across both experiments (Table 16). However, soil moisture and air temperature were significant over the early season experiment, and soil temperature was significant over the late season experiment. Soil O₂ concentration and air temperature exhibited a significant interaction with treatment, but only over the course of the late season experiment. Soil moisture was the only environmental variable that exhibited a significant effect on soil NO₃⁻ concentrations over the early season experiment (Table 16). Soil O₂ concentration and soil temperature exhibited a significant effect on NO₃⁻ concentration over the late season experiment. There was no interaction of environmental variables with treatment observed in either the early or late season experiments. Soil moisture and soil temperature both exhibited a significant effect on soil NH₄⁺ concentrations over both the early and late season experiments (Table 16). Soil O₂ concentration was significant over the early season experiment, and air temperature exhibited a significant effect over the late season experiment. There was no interaction of environmental variables with treatment observed in either early or late season experiments. O₂ concentration and soil temperature both exhibited a significant effect on soil WEP concentrations over both the early and late season experiments (Table 16). While soil moisture and air temperature exhibited significant effects on soil WEP over the late season experiment only. There was also a significant O₂ concentration-treatment interaction over the early season experiment, and soil temperature-treatment interaction over the late season experiment.
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*Table 3.16 Environmental covariate significance on 2014 early and late soil nutrients, and estimation of potential treatment\(^a\)covariate interaction.

\(^a\)Volumetric water content.

\(^b\)Significance at \(p<0.05\).*
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<td>Location x Trt</td>
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<td>Depth x Trt</td>
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Table 3.17 Analysis of Variance for daily soil nutrients from 2015 early season experiment.

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP).

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat.

<sup>d</sup>Locations where soil cores were taken in respect to dung pat; directly beneath and 300 mm away.

<sup>e</sup>Depth in the soil profile; 0-100 and 100-200 mm.
<table>
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<th>NUM DF</th>
<th>P VALUE</th>
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<td>DAP x Treatment</td>
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<tr>
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<td>Treatment&lt;sup&gt;c&lt;/sup&gt;</td>
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<td>DAP x Treatment</td>
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*Table 3.17 Analysis of Variance for daily soil nutrients directly below dung pats and within 100 mm of soil depth from 2015 early season experiment.*

<sup>a</sup>Days 1, 3, 7, 14, 28, and 56 after placement of dung (DAP)

<sup>b</sup>Type 3 F-tests of fixed effects are given.

<sup>c</sup>Treatments: 1) exposed dung pats to dung beetle colonization, 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
Figure 3.16a Daily WSC soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats 2015 early season experiment.

Figure 3.16b Daily WEN soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment.
Figure 3.16c Daily \( \text{NO}_3^- \) soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment.

Figure 3.16d Daily \( \text{NH}_4^+ \) soil concentrations (means and standard errors) from 0-100 mm of soil depth and directly below dung pats in 2015 early season experiment.
Across treatments, DAP, depth, and location, daily soil WSC concentrations ranged from 44 to 356 mg kg$^{-1}$ (Figure 3.16a). Daily soil WSC exhibited no significant differences among treatments under a repeated measure analysis (Table 3.17, Figure 3.16a). DAP, location, and depth factors did exhibit a significant effect on WSC concentrations. WSC concentrations by depth averaged approximately 167 mg kg$^{-1}$ from 200 to 100 mm, and 219 mg kg$^{-1}$ from 0 to 100 mm of soil depth. By location, WSC concentrations ranged from 181 mg kg$^{-1}$ 300 mm away from dung pats, to 208 mg kg$^{-1}$ directly under dung pats. There was a significant effect of treatment on WSC concentrations directly under dung pats and within 100 mm of soil depth (Table 3.18). Mean separation indicated that although not significantly different from each other, soil WSC concentrations under dung treatments were greater than soil under no dung treatments. Soil WSC concentrations under exposed, unexposed, and no dung treatments
averaged approximately 252, 248, and 203 mg kg\textsuperscript{-1} respectively. Across treatments soil WSC concentrations were greatest on 7 DAP, and averaged approximately 343 mg kg\textsuperscript{-1} at that time.

Across treatments, DAP, depth, and location, daily soil WEN concentrations ranged from 6 to 86 mg kg\textsuperscript{-1} (Figure 3.16b). Daily soil WEN exhibited a significant difference among treatments under a repeated measure analysis (Table 3.17, Figure 3.16b). DAP, location, and depth factors did exhibit a significant effect on WEN concentrations as well. Across location, depth, and DAP, exposed, unexposed, and no dung treatments averaged 29, 29, and 27 mg kg\textsuperscript{-1} respectively. Mean separation indicated that there was no significant difference between dung treatments, but average WEN concentrations under dung treatments were significantly greater than no dung treatments. By location, WEN concentrations ranged from 25 mg kg\textsuperscript{-1} at 300 mm of distance to 34 mg kg\textsuperscript{-1} directly below dung pats by location. By depth, WEN ranged from 19 mg kg\textsuperscript{-1} within 100 to 200 mm to 39 mg kg\textsuperscript{-1} within 0 to 100 mm of soil depth. Directly under dung pats and within 0 to 100 mm of soil depth, treatment was again found to have a significant effect on soil WEN (Table 3.18). Mean separation indicated that WEN concentrations in soil under dung treatments were not significantly different from each other, but were both greater than no dung treatments. Peak WEN across treatments occurred at 14 DAP, averaging approximately 71 mg kg\textsuperscript{-1} at that time.

Across treatment, DAP, depth, and location, daily soil NO\textsubscript{3}\textsuperscript{-} concentrations ranged from 3 to 43 mg kg\textsuperscript{-1} (Figure 3.16c). Daily soil NO\textsubscript{3}\textsuperscript{-} exhibited a significant difference among treatments under a repeated measure analysis (Table 3.17, Figure 3.16c). DAP, location, and depth factors also exhibited a significant effect on NO\textsubscript{3}\textsuperscript{-} concentrations, as
well as location-treatment interaction (Table 3.17). Soil NO$_3^-$ concentrations under exposed treatments were significantly greater than both unexposed and no dung treatments. Across all DAP, soil below exposed, unexposed, and no dung treatments exhibited average NO$_3^-$ concentrations of 11, 8, and 9 mg kg$^{-1}$, respectively. By location, NO$_3^-$ concentrations ranged from 7 mg kg$^{-1}$ at 300 mm of distance to 12 mg kg$^{-1}$ directly below dung pats. By depth, NO$_3^-$ ranged from 4 mg kg$^{-1}$ within 100 to 200 mm to 15 mg kg$^{-1}$ within 0 to 100 mm of soil depth. The location-treatment interaction was due to changes in average NO$_3^-$ concentration differences between exposed and unexposed treatments by location. Across depth and DAP, mean separation indicated that exposed treatments were estimated to be approximately 0.8 mg kg$^{-1}$ less than unexposed treatments 300 mm away from dung pats, and approximately 6 mg kg$^{-1}$ greater than unexposed treatments directly below dung pats. Over the course of the early season experiment of 2015 soil directly under dung pat treatments within 0 to 100 mm of soil depth did not exhibit a significant effect of treatment (Table 3.18). Average soil NO$_3^-$ concentrations for exposed, unexposed, and no dung treatments were 24, 14, and 14 mg kg$^{-1}$, respectively. By DAP, peak NO$_3^-$ concentrations were observed at 3 and 14 DAP, and reached 24 and 23 mg kg$^{-1}$, respectively.

Across treatments, DAP, depth, and location, daily soil NH$_4^+$ concentrations ranged from 7 to 54 mg kg$^{-1}$ (Figure 3.16d). Daily soil NH$_4^+$ exhibited no significant differences among treatments or DAP under a repeated measure analysis (Table 3.17, Figure 3.16d). However, location and depth factors did exhibit a significant effect on NH$_4^+$ concentrations (Table 3.17). By location, NH$_4^+$ concentrations ranged from 6 mg kg$^{-1}$ at 300 mm of distance to 15 mg kg$^{-1}$ directly below dung pats. By depth, NH$_4^+$
ranged from 3 mg kg$^{-1}$ within 100 to 200 mm to 17 mg kg$^{-1}$ within 0 to 100 mm of soil depth. Soil NH$_4^+$ concentrations directly under dung pat treatments within 0 to 100 mm of soil depth did not exhibit a significant effect of treatment, DAP, or DAP-treatment interaction (Table 3.18).

Across treatments, DAP, depth, and location, daily soil WEP concentrations ranged from 0.2 to 22 mg kg$^{-1}$ (Figure 3.16e). Daily soil WEP exhibited significant differences among treatments under a repeated measure analysis (Table 3.17, Figure 3.16e). Significant effects of DAP, location, and depth all exhibited a significant effect on WEP concentrations, as well as depth-treatment interaction (Table 3.17). Across DAP, depth, and location WEP concentrations in soil below dung treatments were significantly greater than in soil below no dung treatments, but no difference was found between exposed and unexposed treatments. Average WEP concentrations below dung treatments were approximately 4.1 mg kg$^{-1}$, compared to 2.1 mg kg$^{-1}$ below no dung treatments. By location, WEP concentrations ranged from 1.9 mg kg$^{-1}$ at 300 mm of distance to 6.4 mg kg$^{-1}$ directly below dung pats. By depth, WEP ranged from 1.3 mg kg$^{-1}$ within 100 to 200 mm to 6.2 mg kg$^{-1}$ within 0 to 100 mm of soil depth. Mean separation indicated that the depth-treatment interaction is due to significant differences found in WEP concentrations in soil below dung treatments and no dung treatment within 0 to 100 mm of soil depth, but no difference was found among treatments within 100 to 200 mm of soil depth. Average soil WEP concentrations below exposed, unexposed, and no dung treatments within 0-100 mm of soil depth were 7.4, 6.6, and 3.0 mg kg$^{-1}$, respectively, while treatment averages within 100 to 200 mm of soil depth were 1.4, 1.3, and 1.3 mg kg$^{-1}$, respectively. Over the course of the early season experiment of 2015 soil directly
under dung pat treatments within 0 to 100 mm of soil depth did exhibit a significant
effect of treatment, as well as a significant DAP-treatment interaction (Table 3.18). Soil
directly under dung pats and within 0 to 100 mm of soil depth exhibited similar
differences among treatments compared with the repeated measures analysis, except
concentration averages were 11.9, 10.5, and 3.0 mg kg\(^{-1}\) beneath exposed, unexposed,
and no dung treatments, respectively. Peak soil WEP concentrations of 12 mg kg\(^{-1}\) were
observed at both 3 and 14 DAP. DAP-treatments interaction was due to changes in
differences among treatments by DAP. At 3 DAP, soil WEP below dung treatments was
significantly greater than in soil below no dung treatments, but not significantly different
from each other. By 14 DAP, soil WEP below exposed treatments was significantly
greater than both unexposed and no dung treatments, while unexposed was significantly
greater than no dung at this same point in time. At 56 DAP, soil WEP below exposed
treatments was significantly greater than no dung treatments, while there was no
significant difference between unexposed and exposed, or unexposed and no dung
treatments.

**Environmental effects**

Over the early experiment, soil moisture, \(O_2\) concentration, soil temperature, and
air temperature all exhibited a significant effect on soil WSC concentrations (Table 19).
Air temperature exhibited a significant interaction with treatment. Soil moisture, soil
temperature, and air temperature all exhibited a significant effect on soil WEN
concentrations over the early season experiment (Table 19). There was no significant
interaction of any environmental variable with treatment. Soil moisture, \(O_2\) concentration,
and soil temperature all exhibited a significant effect on soil NO\(_3^-\) concentrations over the
early season experiment (Table 19). There was no interaction of any environmental variable with treatment over the early season experiment. Soil moisture, soil temperature, and air temperature all exhibited a significant effect on soil NH$_4^+$ over the 2015 early season experiment (Table 19). Soil moisture and air temperature both exhibited a significant effect on soil WEP concentrations over the early season experiment (Table 19). There was no significant interaction of any environmental variable with treatment over the early season experiment of 2015.

<table>
<thead>
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<th>Air Temp</th>
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<th>O$_2$ x Trt</th>
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Table 3.19 Environmental covariate significance on 2015 early and late soil nutrients, and estimation of potential treatment*covariate interaction.
$^a$Volumetric water content.
$^b$Significance at p<0.05.
Experiment Treatment Comparisons

<table>
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<tr>
<th>EXPERIMENTAL COMPARISONS</th>
<th>SOURCE</th>
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<td>E - ND</td>
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<td>E - ND</td>
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Table 3.20 Analysis of Variance for experiment-wide soil nutrients directly below dung pats and within 100 mm of soil depth.

a Type 3 F-tests of fixed effects are given.
b Treatments: 1) exposed dung pats to dung beetle colonization and 2) unexposed dung pats inside wire mesh cages, 3) no dung pat
c Significant treatment differences determined by least square means

Treatment means for experiment-wide observations of soil nutrient concentrations were 210.43, 221.25, and 174.68 mg kg⁻¹ WSC, 49.8761, 55.2581, and 40.2290 mg kg⁻¹ WEN, 18.2555, 20.9684, and 14.4970 mg kg⁻¹ NO₃⁻, 19.1895, 19.3242, and 11.2418 mg kg⁻¹ NH₄⁺, and 6.6481, 7.7478, and 4.5616 mg kg⁻¹ WEP. Significant treatment differences were observed for WSC, WEN, and WEP in soil directly under dung pats and within 100 mm of soil depth (Table 3.20). However, for all of these soil nutrient variables treatment differences were due to significant differences between dung and no dung treatments, and not due to differences between exposed and unexposed treatments.
Discussion

This study sought to quantify the effect of dung beetle activity on the flux of dung derived nutrients into soil, within the context of the environmental constraints of the semi-arid Sandhills region of Nebraska. The Sandhills are an important beef cattle producing region of the central U.S., and its value as a resource for beef production will only continue to increase with the large increases in demand for beef that are projected over the next fifty years. The livestock production potential of any rangeland is largely tied to forage productivity, and as such managing the availability of soil nutrients that are necessary to sustain forage productivity is of great importance. The results of our research thus provide additional knowledge that could prove useful in making management decisions that are in alignment with the goals of conserving soil nutrients and the sustainability of forage quality and productivity within livestock producing regions like the Nebraska Sandhills. We hypothesized that dung beetle activity would have an effect on observed changes in the physical characteristics of dung pats, that the effect of dung beetle activity would increase the concentrations of measured nutrients within dung pats and in the soil, environmental variables, particularly soil volumetric water content and air temperature, would have a significant effect on changes in the concentrations of nutrients within dung pats and the soil, and soil nutrient concentrations would be subject to changes across both day and season time scales in accordance with general dung beetle species, climate, and weather variations.

Dung Pat Characteristics

While published observations of dung pat physical attributes, and their corresponding changes in value over time, are not generously reported, the physical
characteristics of dung pats observed in this study were largely consistent with observations published from other research. While initial dung pat masses observed in our study were slightly larger than those of Aarons et al. (2004), initial pat masses were well correlated with those reported by Hirata et al. (2009). Discrepancies between our study and the one performed by Aarons et al. (2004) are mitigated by similar observations of pat mass over later collection times, and pat mass differences at initial placement can be attributed to the difference in dung volume used to create pats in respective studies. Aarons et al. (2004) used 1 L of dung per pat while our study used 1.5 L per pat.

In the study performed by Lysyk et al. (1985), the authors observed moisture contents ranging from 400 to 435 % among fresh, field-collected dung pats found in smooth brome pastures in South Dakota. These values are in agreement with initial moisture contents observed in our study. Stevenson & Dindal (1987) found moisture contents ranging from 5 to 700 %, which were similar to the values measured across our experiments. However, moisture contents observed in samples taken at the late stages of both late season experiments did not approach such low values, likely due to decreasing temperatures and increasing precipitation.

Pat dry matter ranged from 193 to 308 g across all harvest times, seasons, and experiments, and these are similar to the values reported by Hirata et al. (2009) in their study. Change in dung pat dry matter between consecutive sampling times ranged from +19 to -45 g across experiments and years, which is a reasonable observation considering the reported range of +5.1 to -60.7 g by Dickinson & Craig (1990). While pat mass increases were moderately greater across our study, it is not inconceivable to
attribute these increases to differences in the abundance of coprophagous fauna or weather at the time of the experiment, when considering differences between Nebraska and the United Kingdom.

**Dung and Soil Nutrients**

Dung nutrient concentrations measured in this study were also consistent with those reported in other published results. Dung pat percentage carbon by mass for 2014 was also well within the range of values reported by Lovell & Jarvis (1996) and Bol et al. (2000), and our observations of dung pat C:N ratios, which ranged from 14 to 20 across 2014, were similar to results published by Lovell & Jarvis (1996), Dickenson et al. (1981), and Chatigny et al. (2002) in their respective studies. Comparisons of dung pat NPOC and WEN to other studies are difficult since most analyses are performed in terms of % C or % N by mass, or concentration determinations by sample combustion using CHN analyzers. However, it is noteworthy that in analyses performed by Bol et al. (1999), dung C concentrations were reported to be between 350,100 to 383,300 ppm by CHN analysis. As would be expected, due to the method the authors employed, these values are considerably greater than our observations of concentrations of dissolved organic carbon from extractions of the sampled dung material used in our study.

The range of percent nitrogen by mass from 2014 was well within the range of total nitrogen from dung pats from smooth brome pastures observed by Lysyk et al. (1985), Lovell & Jarvis (1996), and Karn & Hoffman (1990). Average dung pat NH$_4^+$ concentrations were moderately higher than values reported by Saarijärvi & Virkajärvi (2009), but these differences are not unreasonable considering the differences in
vegetation and climate that exist between temperate and subarctic pasture. NO$_3^-$ concentrations in dung pats was largely negligible, and this was to be expected.

Observed dung pat DMPR concentrations from our study were well within the range of 2237 ppm observed in cattle dung that was measured by McDowell & Stewart (2005), and was moderately lower than the 4,940 to 7,620 ppm range reported by Dickinson et al. (1981).

Soil NPOC concentrations ranged from 28 to 356 ppm across all experiments. These values are in alignment with those observed by Chatigny et al. (2002) by K$_2$SO$_4$ extraction, and initial soil values were similar to soil concentrations reported by Bol et al. (1999) before dung had been applied.

Soil WEN concentrations ranged from 6 to 102 ppm, NO$_3^-$ ranged from 2 to 43 ppm, and NH$_4^+$ ranged from 0 to 154 ppm across all experiments. Soil NO$_3^-$ concentrations were similar to those observed by Hatch et al. (2000) and Lovell & Jarvis (1996), but were much larger than those reported by Chatigny et al. (2002). Soil NH$_4^+$ concentrations observed across our study were much more wide ranging, but this variability was in large part due to a few extremely large measurements that were found only at 7 DAP in the early season experiment. Soil NH$_4^+$ concentrations never exceeded 29 ppm at any other time across all experiments. Taking this into consideration, soil NH$_4^+$ concentrations were largely in agreement with those observed by Chatigny et al. (2002) and Hatch et al. (2000) in their respective studies. Soil DMPR concentrations were moderately lower compared to results published by Aarons et al. (2004).
Temporal Effects of Dung Beetles

Regarding temporal patterns of measured variables, pat mass, pat moisture content, pat dry matter change, soil WEN, and soil DMPR were found to exhibit significant temporal separations of peak pulses due to the effects of dung beetle activity. Significant temporal effects of exposure to dung beetles on dung pat mass were only found across both early and late experiments in 2015, and this was the case with significant beetle effects on dung pat moisture content as well. Significant temporal effects of exposure to dung beetles on change in dry matter were observed across the late season experiment in 2014, as well as both experiments in 2015.

Across experiments in 2015, pat mass exhibited treatment differences between exposed and unexposed that were observed early on at 1 DAP, but these differences were mitigated by 56 DAP in both experiments. Between these sampling times, the exposed treatments consistently exhibited pat masses that were less than unexposed pats. These results closely resemble the results of pat mass by dry weight reported by Yamada et al. (2007), when no beetle and 120 beetle treatment differences were significant and then mitigated over this same period of time.

Moisture content in exposed treatments became significantly lower than unexposed by 3 DAP, and these conditions persisted through 28 DAP. However, these effects were diminished by the last sampling at 56 DAP, after unexposed pats with lower rates of moisture loss had effectively desiccated. These results are consistent with those found by Stevenson & Dindal (1987), who found that dung pats exposed to dung beetles exhibited increased rates of moisture loss and lower moisture contents through approximately 35 days after exposure.
While treatment had no effect on dry matter mass, as observed by Yamada et al. (2007), changes in dry matter between sampling times exhibited significant effects of DAP by treatment, across 2015 and late 2014. Exposed treatments exhibited significantly greater losses of dry matter at 3 and 1 DAP in early 2015 and both late seasons respectively, significantly greater losses at 28 DAP in the early season 2015, and significantly lower losses at 56 DAP in both 2015 experiments. In the late season of 2014, dry matter increases in exposed treatments were observed at 3 and 14 DAP, and significantly greater losses in dry matter compared to unexposed treatments at 7 DAP. It might be plausible that these changing rates of dry matter loss in exposed treatments are associated with changes in dung beetle activities and behavior as they progress through different stages of their respective life histories.

While soil NPOC concentrations did exhibit a significant effect of interaction between DAP and treatment, there was no separation of temporal peaks due to exposure to dung beetles compared to dung pats that were unexposed. Direct comparisons of the effect of dung beetle activity on soil NPOC concentrations cannot be made, but Yokoyama et al. (1991a) did find significant increases in % C by mass in soil below dung pats exposed to beetles as early as 7 days after exposure. These kinds of early peaks were not observed in soil treated with exposed or unexposed dung, and NPOC concentrations generally peaked at the end of experiments, on 56 DAP.

Exposed treatments exhibited soil exhibited significantly greater WEN concentrations, compared to unexposed or no dung, by 7 DAP in the late season experiment of 2014, and again at 28 DAP when WEN concentrations under exposed treatments exhibited peak concentrations. Published results of effect of beetles on soil
nitrogen typically focus on measurements of mineral concentrations or % N, so direct comparisons cannot be made to published results. However, Yokoyama et al. (1991a) observed increases in % N and NH$_4^+$ concentrations in soil due to dung beetle effects at 5 and 30 days after exposure, and Yamada et al. (2007) found greater concentrations of inorganic N in soil below beetle treatments by 7 days but not at 28 days after exposure. Early increases in soil N has been attributed to the movement of dung material into the upper portions of the soil profile by dung beetles (Yokoyama et al., 1991a). While later increases are speculated to be due secondary effects of differences in microbial decomposition of dung that occur in response to physical effects on dung pats by dung beetles, and not a primary effect of the dung beetles themselves (Yokoyama et al., 1991a).

Exposed treatments exhibited significant peaks in DMPR concentrations in comparison to unexposed and no dung treatments at 28 DAP during the early seasons of both years. In comparison, Yamada et al. (2007) found singular peaks in soil P$_2$O$_5$ concentrations below beetle treatments at 14 and 56 days after exposure, and a significant peak in no beetle treatments at 28 days after exposure when comparing treatments by day. The exact mechanism responsible for this movement of P due to beetle activity at 28 DAP is not clear. The forms of P present in dung material generally exhibit low water solubility, so perhaps this delayed peak is due to the low water solubility of P forms within dung pats in conjunction with the early movement of dung by dung beetles into the soil (Hakamata et al., 1971).
Beetle Effects on Dung Characteristics

Dung pats, whether they were exposed or not, exhibited significant changes in physical characteristics over time. However, consistent effects of exposure to beetle activity on these physical characteristics were not found across all experiments. While the effects of dung beetles on the physical character of decomposing dung pats were apparent across experiments in 2015, these same effects were not observed across 2014. Moreover, the lack of consistent exposed treatment effects, and strong significance by DAP, suggest that physical environmental factors have a more dominant effect on dung pat decomposition than exposure to or exclusion of dung beetles in this region. Perhaps the effect of exposure to dung beetles is significant only under the constraints of optimal environmental conditions and necessary dung beetle abundance to produce such effects.

Pat mass by treatment showed significant effects of exposed dung pats in the form of greater decreases in mass over 7 to 14 DAP, followed by decelerated mass loss over the final 14 DAP compared to unexposed across both 2015 experiments and the late season experiment of 2014. Across all DAP, average pat mass in exposed treatments were significantly lower than those left unexposed to dung beetles. These results are comparable to those reported by Yamada et al. (2007), who found higher dry weights of dung pats left unexposed to dung beetles in their 56 day study in 2000. This effect is likely attributable to dung beetles moving dung material into the soil early after dung placement.

Moisture content by treatment showed significant effects of exposed dung pats in the form of higher rates of dung pat moisture loss, and lower average moisture contents in exposed dung pats compared to unexposed across all DAP in both 2015 experiments and
the late season experiment of 2014. These results are consistent with those reported by Stevenson & Dindal et al. (1987), who found similar effects of dung beetles on moisture content. It has been postulated that higher moisture losses in dung pats exposed to dung beetles is due to increased surface area and aeration created by the dung tunneling activities of dung beetles.

Surprisingly, dry matter mass showed no significant effect of exposure to dung beetles. However, change in dry matter mass between sampling dates did show significant effects, but only across the early experiment of 2015. Across all DAP, exposed treatments exhibited average changes in dry matter mass that were significantly more negative than unexposed treatments. These effects of beetles on the change in dry matter are consistent with those reported by Yamada et al. (2007), who found larger decreases in dry matter weights in dung pats exposed to dung beetles. However, unlike Yamada et al. (2007), we found no significant differences among treatments in average dry matter mass even across the duration of the early 2015 experiment when change in dry matter mass was significant by treatment.

**Beetle Effects on Dung and Soil Nutrients**

Dung pats, whether dung beetles were present or not, were a significant source of C, N, and P compared to control treatments with no dung. However, consistent effects of beetle activity on soil nutrients were not found. Moreover, the lack of consistent beetle treatment effects, and strong fluctuations in flux by DAP, suggest that physical and climatic factors have a more dominant effect on the movement of nutrients from dung to soil than the presence or absence of dung beetles in this region.
There was no effect of exposure to beetles found across any dung nutrients measured over the course of our study. These results are not consistent with those reported by Stevenson & Dindal (1987), Yokoyama et al. (1991a), and Yamada et al. (2007) who observed lower total carbon content, lower total nitrogen content, and higher concentrations of NH$_4^+$ in dung pats exposed to beetles. These differences in results may be attributed to differences in any number of constraints that exist between the locations in which the studies were performed. Any or all of the different factors such as climate, soil type, weather, and the specific activity of the dung beetle species present could have been responsible for the contrasts between their results and ours.

While soil NPOC concentrations below dung treatments did exhibit significantly greater values than soil below treatments with no dung across all experiments, there was no significant difference found between exposed and unexposed treatments in any of our four experiments. Therefore, we found no evidence that exposure of dung to dung beetles has any effect on the movement of water soluble, labile, organic C into the soil from dung pats. However, NPOC concentrations seemed to continue to increase across our 56 day experiments, and effects of beetle activity on soil NPOC concentrations may very well be observed after this point of dung pat decomposition. These results were unexpected considering the observations of Yokoyama et al. (1991a), who reported significantly higher soil total C by % mass under dung exposed to dung beetles than either dung left unexposed to beetles or soil with no dung.

Significant effects of exposure to dung beetles was found in soil WEN and NO$_3^-$ across the late season of 2014, and the early season of 2015 respectively. No significant effects of exposure to dung beetles on soil N variables were found at any other time in
our study. In the study performed by Yamada et al. (2007), the authors found concentrations of inorganic N reaching approximately 20 ppm below dung pats exposed to beetles, compared to 3 to 7 ppm found in soil above which no dung was applied. These results are comparable to those observed in our study across late season experiments, but early season concentrations of inorganic N were approximately double these values across years. The reason for some of these inconsistencies across years could be due to lower soil moisture and slightly warmer soil temperatures in the early season of 2015, as the experimental site was subject to unusually large precipitation totals in June of 2014.

Soil DMPR concentrations did exhibit a significant effect of exposure to dung beetles, but this only occurred over the course of the early season experiment of 2014. The results of early season 2014 are consistent with those found by Yamada et al. (2007), although DMPR concentrations were considerably lower than the P$_2$O$_5$ concentrations reported in their study. This result might again be due to the considerably large precipitation totals experienced in the region in June of 2014, as dung P forms exhibit low water solubility in general (Hakamata et al., 1971).

Effects of Climatic and Physical Variables

In general, physical variables were found to have a stronger effect on the dung and soil variables measured over the course of this study, than that of the beetle activity. Soil moisture and soil temperature were found to exhibit consistent and strong effects on changes in all dung physical variables, which is in alignment with published reports of environmental effects on the decomposition of dung pats (Holter, 1979; Dickinson et al., 1981; Underhay & Dickinson, 1978).
Soil moisture, $O_2$ concentration, and air temperature were shown to have significant effects on NPOC concentrations in soil. This relationship is consistent with published observations of dung decomposition in regards to $CO_2$ fluxes from dung pats, which is a significant metric of the decomposition of C compounds in dung pats (Balogh et al., 2011; Lloyd & Taylor, 1994; Smith et al., 2003). However, higher concentrations of soil NPOC were consistently observed in the early season experiments, and could be an indication of incomplete decomposition or lower rates of C uptake by microbes and vegetation as growing season productivity is expected to reach maximum rates at this point in time.

Soil moisture, $O_2$ concentration, soil temperature, and air temperature all exhibited a significant effect on soil WEN, $NO_3^-$, and $NH_4^+$ concentrations in one or more of our four experiments, but not consistently across all experiments. However, the dynamics and pathways of dung N nutrients are as wide ranging as the microbes responsible for their uptake and conversion, so this result is to be expected (Pihlatie et al., 2004, Saggar et al., 2004). Ultimately, these processes are acknowledged to be a soil mediated process, and are dependent upon an interaction of physical soil variables that include soil moisture, soil texture, aggregate size fraction, pore size distribution, availability of organic carbon, availability of nitrogen, and temperature (Pihlatie et al., 2004, Saggar et al., 2004). Therefore, it can be expected that the significance of environmental effects would vary according to the conditions of the experiment, and the limiting factors at the time of observation.

All measured environmental variables exhibited a significant effect on soil DMPR concentrations across both 2014 experiments, but only soil moisture and air temperature
were significant in the early season experiment of 2015. Since P forms in dung exhibit low water solubility in general, it would be reasonable to expect soil DMPR concentrations to be reliant upon those same variables exhibiting significant effects on dung pat physical characteristics and higher measurements of soil moisture accompanying precipitation events (Hakamata et al., 1971). Thus, the results of 2015 would be more in alignment with these expectations. However, since available P in dung can be occluded within more recalcitrant complex C compounds, its release might also be closely tied to the optimal environmental conditions necessary for the decomposition of these C compounds. So perhaps it is not unreasonable to see such relationships between soil DMPR, O\textsubscript{2} concentration, and air temperature, in addition to those environmental variables that exhibit effects on the physical characteristics of dung pats.

**Implications**

In the context of subirrigated meadows within the Sandhills region of Nebraska, our study indicates that while dung beetles have a significant impact on the physical changes in dung pats over time, their impact is minimal in regards to nutrient dynamics in dung and soil. While some effects of dung beetle activity were observed, these effects were not consistent across season and years. On the other hand, environmental factors were much more significant, and the variables measured in our study varied daily, seasonally, and yearly in accordance with temporal fluctuations in environmental variables that were measured. The divergence observed between the results of our study and those found in other recent studies of dung beetle effects on dung and soil nutrients might be due to a number factors. Since the effect of dung beetle activity on dung decomposition can vary by species (Mittal, 1993), it could be plausible that the species of
dung beetles found in the Sandhills might exhibit behaviors that are not as effective in mitigating dung decomposition. It has been postulated that the dung beetle species present throughout much of the U.S. in general, exhibit activity that is not as effective at removing dung material as the species that are present in other parts of the world (Fincher, 1981). It might also be plausible that dung beetle frequency could vary in accordance with the different soil conditions found at different topographic positions, and so there effect may be more significant in upland areas compared to the meadows. Perhaps the effect of dung beetles was observed so infrequently due to the specific environmental conditions that existed at the time. Further investigation is needed to adequately resolve questions such as these. However, our study does suggest that management considerations in regards to nutrient cycling within subirrigated meadows of the Sandhills, might not need to offer as much concern to the effects of dung beetles as perhaps previously believed.
References


Appendix A

Figure A.1 Diagram of Sensors Buried at Depth

Figure A.2 Cumulative CO₂ fluxes (means and standard errors) integrated over 2014 early season experiment.
Figure A.3 Cumulative CO₂ fluxes (means and standard errors) integrated over 2014 late season experiment.

Figure A.4 Cumulative N₂O fluxes (means and standard errors) integrated over 2014 early season experiment.
Figure A.5 Cumulative N\textsubscript{2}O fluxes (means and standard errors) integrated over 2014 late season experiment.

Figure A.6 Cumulative CH\textsubscript{4} fluxes (means and standard errors) integrated over 2014 early season experiment.
**Figure A.7** Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2014 late season experiment.

**Figure A.8** Cumulative CO$_2$ fluxes (means and standard errors) integrated over 2015 early season experiment.
Figure A.9 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2015 early season experiment.

Figure A.10 Cumulative N$_2$O fluxes (means and standard errors) integrated over 2015 late season experiment.
Figure A.11 Cumulative CH$_4$ fluxes (means and standard errors) integrated over 2015 early season experiment.

Figure A.12 Cumulative CH$_4$ fluxes (means and standard errors integrated over 2015 late season experiment.)
Figure A.13 Cumulative CO₂-Eq fluxes (means and standard errors) integrated over 2014 early season experiment.

Figure A.14 Cumulative CO₂-Eq of GHG fluxes (means and standard errors) integrated over 2014 late season experiment.
Figure A.15 Cumulative CO$_2$-Eq of sums of GHG fluxes (means and standard errors) integrated over 2015 early season experiment.

Figure A.16 Cumulative integration of sums of CO$_2$-Eq of all GHG fluxes from 2015 late season experiment.
Figure A.17 Comparison of $[O_2]$ and CO$_2$ flux over 2014 experimental year.

Figure A.18 Comparison of $[O_2]$ and CO$_2$ flux over 2015 experimental year.
**2014 $[O_2]$ vs. Avg. N$_2$O Flux**

*Figure A.19 Comparison of $[O_2]$ and N$_2$O flux over 2014 experimental year.*

**2015 $[O_2]$ vs. Avg. N$_2$O Flux**

*Figure A.20 Comparison of $[O_2]$ and N$_2$O flux over 2015 experimental year.*
Figure A.21 Comparison of \( \text{[O}_2\text{]} \) and \( \text{CH}_4 \) flux over 2014 experimental year.

Figure A.22 Comparison of \( \text{[O}_2\text{]} \) and \( \text{CH}_4 \) flux over 2015 experimental year.
# Appendix B

## Table B.1

Estimates of total average cumulative CO\(_2\) flux by treatment. Significance of exposed and unexposed treatment difference.

**Cumulative CO\(_2\) Flux – Early Season 2014**

<table>
<thead>
<tr>
<th>Treatment</th>
<th>CO(_2) Flux</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beetle (B)</td>
<td>1818.65</td>
</tr>
<tr>
<td>No Beetle (NB)</td>
<td>1851.71</td>
</tr>
<tr>
<td>Control</td>
<td>1764.31</td>
</tr>
<tr>
<td>SE</td>
<td>± 98.8495</td>
</tr>
<tr>
<td>E - UNE</td>
<td>(F_{14} = 0.16, P = 0.6935)</td>
</tr>
</tbody>
</table>

## Table B.2

Estimates of total average cumulative CO\(_2\) flux by treatment. Significance of exposed and unexposed treatment difference.

**Cumulative CO\(_2\) Flux – Late Season 2014**

<table>
<thead>
<tr>
<th>Treatment</th>
<th>CO(_2) Flux</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beetle (B)</td>
<td>1142.22</td>
</tr>
<tr>
<td>No Beetle (NB)</td>
<td>1078.53</td>
</tr>
<tr>
<td>Control</td>
<td>994.35</td>
</tr>
<tr>
<td>SE</td>
<td>± 44.5187</td>
</tr>
<tr>
<td>B - NB</td>
<td>(F_{14} = 2.20, P = 0.1600)</td>
</tr>
</tbody>
</table>
### Table B.3 Estimates of average flux (g m\(^{-2}\) d\(^{-1}\)) of CO\(_2\) in Early Season 2014 by treatment and day.

<table>
<thead>
<tr>
<th>CO(_2) Flux – Early Season 2014</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>DAP</td>
<td>Beetle (B)</td>
<td>No Beetle (NB)</td>
<td>Control</td>
<td>SE</td>
<td>B - NB</td>
</tr>
<tr>
<td>1</td>
<td>21.3690</td>
<td>23.2462</td>
<td>17.9470</td>
<td>± 1.3184</td>
<td>F(_{18,48} = 1.06,) P = 0.3159</td>
</tr>
<tr>
<td>2</td>
<td>16.7793</td>
<td>17.6715</td>
<td>17.8506</td>
<td>± 1.4799</td>
<td>F(_{20,29} = 0.19,) P = 0.6686</td>
</tr>
<tr>
<td>3</td>
<td>16.3914</td>
<td>15.7157</td>
<td>12.0620</td>
<td>± 0.8304</td>
<td>F(_{14,4} = 0.37,) P = 0.5501</td>
</tr>
<tr>
<td>7</td>
<td>23.3991</td>
<td>26.9759</td>
<td>20.3080</td>
<td>± 1.7351</td>
<td>F(_{15,43} = 2.18,) P = 0.1597</td>
</tr>
<tr>
<td>10</td>
<td>29.1111</td>
<td>30.5014</td>
<td>26.2077</td>
<td>± 1.4070</td>
<td>F(_{17,76} = 0.51,) P = 0.4849</td>
</tr>
<tr>
<td>14</td>
<td>27.2077</td>
<td>29.8364</td>
<td>24.7547</td>
<td>± 1.3734</td>
<td>F(_{15,43} = 1.91,) P = 0.1863</td>
</tr>
<tr>
<td>21</td>
<td>25.7216</td>
<td>21.8462</td>
<td>21.2593</td>
<td>± 1.9234</td>
<td>F(_{20,72} = 2.07,) P = 0.1647</td>
</tr>
<tr>
<td>28</td>
<td>56.4337</td>
<td>56.5144</td>
<td>56.9658</td>
<td>± 3.9693</td>
<td>F(_{22,32} = 0.00,) P = 0.9886</td>
</tr>
<tr>
<td>56</td>
<td>17.0325</td>
<td>18.8789</td>
<td>18.1239</td>
<td>± 1.9067</td>
<td>F(_{17,95} = 0.69,) P = 0.4975</td>
</tr>
<tr>
<td>Total</td>
<td>25.9384</td>
<td>26.7985</td>
<td>23.9411</td>
<td>± 0.9605</td>
<td>F(_{29,62} = 0.44,) P = 0.5127</td>
</tr>
</tbody>
</table>

### Table B.4 Estimates of average flux (g m\(^{-2}\) d\(^{-1}\)) of CO\(_2\) in Late Season 2014 by treatment and day.

<table>
<thead>
<tr>
<th>CO(_2) Flux – July 2014</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>DAP</td>
<td>Beetle (B)</td>
<td>No Beetle (NB)</td>
<td>Control</td>
<td>SE</td>
<td>B - NB</td>
</tr>
<tr>
<td>1</td>
<td>32.9972</td>
<td>27.4822</td>
<td>26.3195</td>
<td>± 1.7732</td>
<td>F(_{20,72} = 5.58,) P = 0.0283</td>
</tr>
<tr>
<td>2</td>
<td>33.9166</td>
<td>32.0253</td>
<td>27.5583</td>
<td>± 1.9938</td>
<td>F(_{19,95} = 0.50,) P = 0.4865</td>
</tr>
<tr>
<td>3</td>
<td>18.3232</td>
<td>16.4187</td>
<td>10.8941</td>
<td>± 1.4886</td>
<td>F(_{19,61} = 1.01,) P = 0.3275</td>
</tr>
<tr>
<td>7</td>
<td>27.2261</td>
<td>25.4108</td>
<td>20.2959</td>
<td>± 2.1651</td>
<td>F(_{19,84} = 0.39,) P = 0.5415</td>
</tr>
<tr>
<td>10</td>
<td>33.4385</td>
<td>33.0785</td>
<td>29.4351</td>
<td>± 2.1545</td>
<td>F(_{19,61} = 0.02,) P = 0.9027</td>
</tr>
<tr>
<td>14</td>
<td>18.8957</td>
<td>19.6730</td>
<td>17.3001</td>
<td>± 1.1642</td>
<td>F(_{19,4} = 0.32,) P = 0.5768</td>
</tr>
<tr>
<td>21</td>
<td>18.9264</td>
<td>18.7968</td>
<td>16.1331</td>
<td>± 1.2081</td>
<td>F(_{18,43} = 0.01,) P = 0.9294</td>
</tr>
<tr>
<td>28</td>
<td>24.4155</td>
<td>22.9925</td>
<td>22.3190</td>
<td>± 1.2186</td>
<td>F(_{16,82} = 0.95,) P = 0.3438</td>
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<tr>
<td>56</td>
<td>10.9633</td>
<td>9.3652</td>
<td>10.0367</td>
<td>± 1.0026</td>
<td>F(_{14,65} = 2.17,) P = 0.1624</td>
</tr>
<tr>
<td>Total</td>
<td>24.3447</td>
<td>22.8048</td>
<td>20.0324</td>
<td>± 0.8676</td>
<td>F(_{35,26} = 1.88,) P = 0.0682</td>
</tr>
</tbody>
</table>
Appendix C

```sas
proc import
datafile="C:\Users\Green Thumb\Documents\AFRI Data\GasFluxData.csv"
dbms=csv
out=Sasdata.Gasdata
replace;
proc print;
run;
proc contents data=Sasdata.Gasdata;
proc freq data=Sasdata.Gasdata;
run;
data Sasdata.Co2(keep=Year DAA Ring Block Treatment Experiment CO2 BaseCO2 VWC O2 SoilTemp AirTemp) Sasdata.Co2equiv(keep=Year DAA Ring Block Treatment Experiment CO2equiv BaseCo2E VWC O2 SoilTemp AirTemp) Sasdata.N2o(keep=Year DAA Ring Block Treatment Experiment N2O BaseN2O VWC O2 SoilTemp AirTemp) Sasdata.Ch4(keep=Year DAA Ring Block Treatment Experiment CH4 BaseCH4 VWC O2 SoilTemp AirTemp);
set Sasdata.Gasdata;
*if DAA=0 then delete;
*if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
*where Experiment=2;
proc print;
run;
data Sasdata.Co2y1exp2(keep=DAA Ring Block Treatment Experiment CO2 BaseCO2 VWC O2 SoilTemp AirTemp) Sasdata.Co2equivy1exp2(keep=DAA Ring Block Treatment Experiment CO2equiv BaseCo2E VWC O2 SoilTemp AirTemp) Sasdata.N2oy1exp2(keep=DAA Ring Block Treatment Experiment N2O BaseN2O VWC O2 SoilTemp AirTemp) Sasdata.Ch4y1exp2(keep=DAA Ring Block Treatment Experiment CH4 BaseCH4 VWC O2 SoilTemp AirTemp);
set Sasdata.Gasdata;
*if DAA=0 then delete;
if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=2;
proc print;
run;
data Sasdata.Co2y1exp1(keep=DAA Ring Block Treatment Experiment CO2 BaseCO2 VWC O2 SoilTemp AirTemp) Sasdata.Co2equivy1exp1(keep=DAA Ring Block Treatment Experiment CO2equiv BaseCo2E VWC O2 SoilTemp AirTemp) Sasdata.N2oy1exp1(keep=DAA Ring Block Treatment Experiment N2O BaseN2O VWC O2 SoilTemp AirTemp) Sasdata.Ch4y1exp1(keep=DAA Ring Block Treatment Experiment CH4 BaseCH4 VWC O2 SoilTemp AirTemp);
set Sasdata.Gasdata;
*if DAA=0 then delete;
if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=2;
proc print;
run;
```

where Experiment=1;
proc print;
run;

data Sasdata.C02y1exp1(keep=DAA Ring Block Treatment Experiment CO2 BaseCO2 VWC O2 SoilTemp AirTemp) Sasdata.C02equivy1exp1(keep=DAA Ring Block Treatment Experiment CO2equiv BaseCo2E VWC O2 SoilTemp AirTemp) Sasdata.N2oy1exp1(keep=DAA Ring Block Treatment Experiment N2O BaseN2O VWC O2 SoilTemp AirTemp) Sasdata.Ch4y1exp1(keep=DAA Ring Block Treatment Experiment CH4 BaseCH4 VWC O2 SoilTemp AirTemp);
set Sasdata.Gasdata;
*if DAA=0 then delete;
if year=1 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=1;
proc print;
run;

data Sasdata.C02y2exp1(keep=DAA Ring Block Treatment Experiment CO2 BaseCO2 VWC O2 SoilTemp AirTemp) Sasdata.C02equivy2exp1(keep=DAA Ring Block Treatment Experiment CO2equiv BaseCo2E VWC O2 SoilTemp AirTemp) Sasdata.N2oy2exp1(keep=DAA Ring Block Treatment Experiment N2O BaseN2O VWC O2 SoilTemp AirTemp) Sasdata.Ch4y2exp1(keep=DAA Ring Block Treatment Experiment CH4 BaseCH4 VWC O2 SoilTemp AirTemp);
set Sasdata.Gasdata;
*if DAA=0 then delete;
if year=1 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=2;
proc print;
run;
proc import datafile="C:\Users\Green Thumb\Documents\AFRI Data\Integrated Flux.csv"
dbms=csv
out=Sasdata.IntegratedGas replace;
proc print;
run;
proc contents data=Sasdata.IntegratedGas;
proc freq data=Sasdata.IntegratedGas;
run;
data Sasdata.C02intyle1e2(keep=Ring Block Treatment CO2_Integration VWC O2 Soil_TEMP Air_Temp) Sasdata.C02eqintyle1e2(keep=Ring Block Treatment CO2_Equiv_Integration VWC O2 Soil_TEMP Air_Temp) Sasdata.N2ointyle1e2(keep=Ring Block Treatment N2O_Integration VWC O2 Soil_TEMP Air_Temp) Sasdata.Ch4intyle1e2(keep=Ring Block Treatment CH4_Integration VWC O2 Soil_TEMP Air_Temp);
set Sasdata.IntegratedGas;
*if DAA=0 then delete;
if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=2;

proc print;
run;
data Sasdata.Co2intyle1(keep=Ring Block Treatment CO2_Integration VWC O2 Soil Temp Air Temp) Sasdata.Co2eqintyle1(keep=Ring Block Treatment CO2_Equiv Integration VWC O2 Soil Temp Air Temp) Sasdata.N2ointyle1(keep=Ring Block Treatment N2O_Integration VWC O2 Soil Temp Air Temp) Sasdata.Ch4intyle1(keep=Ring Block Treatment CH4_Integration VWC O2 Soil Temp Air Temp);
set Sasdata.IntegratedGas;
*if DAA=0 then delete;
if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=1;
proc print;
run;
data Sasdata.Co2inty2e1(keep=Ring Block Treatment CO2_Integration VWC O2 Soil Temp Air Temp) Sasdata.Co2eqinty2e1(keep=Ring Block Treatment CO2_Equiv Integration VWC O2 Soil Temp Air Temp) Sasdata.N2ointy2e1(keep=Ring Block Treatment N2O_Integration VWC O2 Soil Temp Air Temp) Sasdata.Ch4inty2e1(keep=Ring Block Treatment CH4_Integration VWC O2 Soil Temp Air Temp);
set Sasdata.IntegratedGas;
*if DAA=0 then delete;
if year=1 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=3;
proc print;
run;
data Sasdata.Co2inty2e2(keep=Ring Block Treatment CO2_Integration VWC O2 Soil Temp Air Temp) Sasdata.Co2eqinty2e2(keep=Ring Block Treatment CO2_Equiv Integration VWC O2 Soil Temp Air Temp) Sasdata.N2ointy2e2(keep=Ring Block Treatment N2O_Integration VWC O2 Soil Temp Air Temp) Sasdata.Ch4inty2e2(keep=Ring Block Treatment CH4_Integration VWC O2 Soil Temp Air Temp);
set Sasdata.IntegratedGas;
*if DAA=0 then delete;
if year=1 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=4;
proc print;
run;
proc import
   datafile="C:\Users\Green Thumb\Documents\AFRI Data\Dungdata.csv"
   dbms=csv
data Sasdata.Dungdata;
out=Sasdata.Dungdata;
replace;
proc print;
run;
data Sasdata.Pmylexp1(keep=DAA Block Treatment PM VWC O2 SoilTemp
AirTemp) Sasdata.Wcylexp1(keep=DAA Block Treatment WC VWC O2 SoilTemp
AirTemp) Sasdata.Wxmyexp1(keep=DAA Block Treatment Waterbymass VWC
O2 SoilTemp AirTemp) Sasdata.Dmyexp1(keep=DAA Block Treatment
Drymatter VWC O2 SoilTemp AirTemp) Sasdata.Chdmyexp1(keep=DAA Block
Treatment ChDMat VWC O2 SoilTemp AirTemp) Sasdata.Npocdy1exp1(keep=DAA
Block Treatment NPOC VWC O2 SoilTemp AirTemp)
Sasdata.Tndy1exp1(keep=DAA Block Treatment TN VWC O2 SoilTemp AirTemp)
Sasdata.Dmprdy1exp1(keep=DAA Block Treatment DMPR VWC O2 SoilTemp
AirTemp) Sasdata.No3dy1exp1(keep=DAA Block Treatment NO3 VWC O2
SoilTemp AirTemp) Sasdata.Nh4dy1exp1(keep=DAA Block Treatment NH4 VWC
O2 SoilTemp AirTemp);
set Sasdata.Dungdata;
if DAA=0 then delete;
where Experiment=1;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*where Experiment=1;
proc print;
run;
data Sasdata.Npocd(keep=DAA Year Block Treatment NPOC VWC O2 SoilTemp
AirTemp) Sasdata.Tnd(keep=DAA Year Block Treatment TN VWC O2 SoilTemp
AirTemp) Sasdata.Dmprd(keep=DAA Year Block Treatment DMPR VWC O2
SoilTemp AirTemp) Sasdata.No3d(keep=DAA Year Block Treatment NO3 VWC O2
SoilTemp AirTemp) Sasdata.Nh4d(keep=DAA Year Block Treatment NH4 VWC O2
SoilTemp AirTemp);
set Sasdata.Dungdata;
if DAA=0 then delete;
proc print;
run;
data Sasdata.Pmylexp2(keep=DAA Block Treatment PM VWC O2 SoilTemp
AirTemp) Sasdata.Wcylexp2(keep=DAA Block Treatment WC VWC O2 SoilTemp
AirTemp) Sasdata.Wxmyexp2(keep=DAA Block Treatment Waterbymass VWC
O2 SoilTemp AirTemp) Sasdata.Dmyexp2(keep=DAA Block Treatment
Drymatter VWC O2 SoilTemp AirTemp) Sasdata.Chdmyexp2(keep=DAA Block
Treatment ChDMat VWC O2 SoilTemp AirTemp) Sasdata.Npocdy1exp2(keep=DAA
Block Treatment NPOC VWC O2 SoilTemp AirTemp)
Sasdata.Tndy1exp2(keep=DAA Block Treatment TN VWC O2 SoilTemp AirTemp)
Sasdata.Dmprdy1exp2(keep=DAA Block Treatment DMPR VWC O2 SoilTemp
AirTemp) Sasdata.No3dy1exp2(keep=DAA Block Treatment NO3 VWC O2
SoilTemp AirTemp) Sasdata.Nh4dy1exp2(keep=DAA Block Treatment NH4 VWC
O2 SoilTemp AirTemp);
set Sasdata.Dungdata;
if DAA=0 then delete;
where Experiment=2;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*where Experiment=1;
proc print;
run;
set Sasdata.Dungdata;
if DAA=0 then delete;
if year=1 then delete;
where Experiment=3;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*where Experiment=1;
proc print;
run;
set Sasdata.Dungdata;
if DAA=0 then delete;
if year=1 then delete;
where Experiment=4;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*where Experiment=1;
proc print;
run;
proc import
datafile="C:\Users\Green Thumb\Documents\AFRI Data\Soil Data.csv"
dbms=csv
out=Sasdata.Soildata
replace;
proc print;
run;
proc contents data=Sasdata.Soildata;
proc freq data=Sasdata.Soildata;
run;
data Sasdata.N03yexp110cm(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 SoilTemp AirTemp) Sasdata.Nh4yexp110cm(keep=HT Sample Location VWC O2 SoilTemp AirTemp) Sasdata
Block Treatment NH4 Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Dmpry1exp110cm(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Tn1exp10cm(keep=HT Sample Block Treatment TN Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Npoc10cm(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 Soil Temp Air Temp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=2 then delete;
where Experiment=1;
if location=2 then delete;
*where Experiment=1;
if depth=2 then delete;
*where Experiment=1;
proc print;
run;

data Sasdata.No310cm(keep=HT Year Sample Block Treatment NO3 Depth Location VWC O2 Soil Temp Air Temp) Sasdata.Nh410cm(keep=HT Year Sample Block Treatment NH4 Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Dmpr10cm(keep=HT Year Sample Block Treatment DMPR Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Tn10cm(keep=HT Year Sample Block Treatment TN Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Npoc10cm(keep=HT Year Sample Block Treatment NPOC Depth Location VWC O2 Soil Temp Air Temp);
set Sasdata.Soildata;
*if DAA=0 then delete;
*if year=2 then delete;
*where Experiment=1;
if location=2 then delete;
*where Experiment=1;
if depth=2 then delete;
*where Experiment=1;
proc print;
run;

data Sasdata.No3y1exp1(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 Soil Temp Air Temp) Sasdata.Nh4y1exp1(keep=HT Sample Block Treatment NH4 Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Dmpry1exp1(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Tn1exp1(keep=HT Sample Block Treatment TN Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Npoc1exp1(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 Soil Temp Air Temp);
set Sasdata.Soildata;
*if DAA=0 then delete;
*if year=2 then delete;
*where Experiment=1;
if location=2 then delete;
*where Experiment=1;
if depth=2 then delete;
*where Experiment=1;
proc print;
run;

data Sasdata.No3y1exp2(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 Soil Temp Air Temp) Sasdata.Nh4y1exp2(keep=HT Sample Block Treatment NH4 Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Dmpry1exp2(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Tn1exp2(keep=HT Sample Block Treatment TN Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Npoc1exp2(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 Soil Temp Air Temp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=2 then delete;
where Experiment=1;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
*where Experiment=1;
proc print;
run;

data Sasdata.No3y1exp3(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 Soil Temp Air Temp) Sasdata.Nh4y1exp3(keep=HT Sample Block Treatment NH4 Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Dmpry1exp3(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Tn1exp3(keep=HT Sample Block Treatment TN Depth Location VWC O2 Soil Temp Air Temp)
Sasdata.Npoc1exp3(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 Soil Temp Air Temp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=2 then delete;
where Experiment=1;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
*where Experiment=1;
proc print;
run;
VWC O2 SoilTemp AirTemp) Sasdata.Tnylexp2(keep=HT Sample Block Treatment TN Depth Location VWC O2 SoilTemp AirTemp)
Sasdata.Npocy1exp2(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 SoilTemp AirTemp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=2 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=2;
proc print;
run;
data Sasdata.No3y1exp210cm(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 SoilTemp AirTemp) Sasdata.Nh4y1exp210cm(keep=HT Sample Block Treatment NH4 Depth Location VWC O2 SoilTemp AirTemp)
Sasdata.Dmpry1exp210cm(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 SoilTemp AirTemp) Sasdata.Tnylexp210cm(keep=HT Sample Block Treatment TN Depth Location VWC O2 SoilTemp AirTemp)
Sasdata.Npocy1exp210cm(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 SoilTemp AirTemp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=2 then delete;
where Experiment=2;
if location=2 then delete;
*where Experiment=1;
if depth=2 then delete;
*where Experiment=1;
proc print;
run;
data Sasdata.No3y2exp210cm(keep=HT Sample Block Treatment NO3 Depth Location VWC O2 SoilTemp AirTemp) Sasdata.Nh4y2exp210cm(keep=HT Sample Block Treatment NH4 Depth Location VWC O2 SoilTemp AirTemp)
Sasdata.Dmpry2exp210cm(keep=HT Sample Block Treatment DMPR Depth Location VWC O2 SoilTemp AirTemp) Sasdata.Tnylexp210cm(keep=HT Sample Block Treatment TN Depth Location VWC O2 SoilTemp AirTemp)
Sasdata.Npocy2exp210cm(keep=HT Sample Block Treatment NPOC Depth Location VWC O2 SoilTemp AirTemp);
set Sasdata.Soildata;
*if DAA=0 then delete;
if year=1 then delete;
*if location=2 then delete;
*where Experiment=1;
*if depth=2 then delete;
*if location=2 then delete;
where Experiment=3;
proc print;
run;
data Sasdata.No3y2exp310cm(keep=HT Sample Block Treatment NO3 VWC O2 SoilTemp AirTemp) Sasdata.Nh4y2exp310cm(keep=HT Sample Block Treatment NH4 VWC O2 SoilTemp AirTemp) Sasdata.Dmpry2exp310cm(keep=HT Sample Block Treatment DMPR VWC O2 SoilTemp AirTemp)
Sasdata.Tnylexp310cm(keep=HT Sample Block Treatment TN VWC O2 SoilTemp AirTemp) Sasdata.Npocy2exp310cm(keep=HT Sample Block Treatment NPOC VWC O2 SoilTemp AirTemp);
set Sasdata.Soildata;
*if DAA=0 then delete;
where Experiment=3;
if year=1 then delete;
if location=2 then delete;
if depth=2 then delete;
*where Experiment=1;
proc print;
run;

proc glimmix data=Sasdata.Ch4y1exp1 plot=residualpanel;
class Block Treatment Ring DAA;
model CH4=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Ch4y1exp1;
class Block Treatment Ring DAA;
model CH4= Block Treatment|DAA /ddfm=kr;
random Block Ring(Treatment);
random _residual_ / type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA / diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*contrast 'D - ND' treatment 1 1 -2;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y1exp1;
class Block Treatment Ring;
model CH4= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCH4 / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y1exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model CH4=Treatment|DAA / ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Ch4y1exp2;
class Block Treatment Ring DAA;
model CH4= Block Treatment|DAA / ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*lsmeans Treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Ch4y1exp2;
class Block Treatment Ring;
model CH4=Block Treatment VWC Treatment*VWC 02 Treatment*02 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCH4 / solution htype=1
ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y2exp1 plot=residualpanel;
class Block Treatment Ring DAA;
model CH4=Treatment|DAA /ddfm=kr;
random Block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Ch4y2exp1;
class Block Treatment Ring DAA;
model CH4=Block Treatment|DAA /ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ar(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*estimate 'D vs ND' treatment 1 1 -2/ divisor=2;
*contrast 'D - ND' treatment 1 1 -2;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2, 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2, 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2, 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2, 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2, 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2, 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2, 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2, 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2, 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y2exp1;
class Block Treatment Ring;
model CH4=Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCH4 / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y2exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model CH4=Treatment|DAA / ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Ch4y2exp2;
class Block Treatment Ring DAA;
model CH4= Block Treatment|DAA / ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4y2exp2;
class Block Treatment Ring;
model CH4= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCH4 / solution htype=1
ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Ch4 plot=residualpanel;
class Block Treatment Ring DAA;
model CH4=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Ch4;
class Block Year Treatment Ring DAA;
model CH4= Block Year Treatment|DAA /ddfm=kr;
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA / diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*contrast 'D - ND' treatment 1 1 -2;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y1exp1 plot=residualpanel;
  class Block Treatment DAA;
  model CO2=Treatment|DAA / ddfm=kr;
  random Block;
  random _residual_ / group=treatment;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2y1exp1;
  class Block Treatment Ring DAA;
  model CO2= Block Treatment|DAA / ddfm=kr;
  *random Treatment(DAA);
  random Block Ring(Treatment);
  random _residual_ / type=ante(1) subject=ring(Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl plot=diff;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
  *contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
  *contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
  *contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
  *contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
  *contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
  *contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
  *contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
  *contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
  *contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
  *contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
  *contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
  *contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
  *contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
  *contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
  *contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
  *contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
  *contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
  *contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y1exp1;
  class Block Treatment Ring;
  model CO2= Block Treatment VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2 / solution htype=1 ddfm=kr;
  *random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Co2ylexp2 plot=residualpanel;
class Block Treatment Ring DAA;
model CO2=Treatment|DAA /ddfm=kr;
random Block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2ylexp2;
class Block Treatment Ring DAA;
model CO2= Block Treatment|DAA /ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*lsmeans treatment/ diff plot=diff;
*lsmeans treatment DAA treatment*DAA/ cl;
*lsmeans Treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D - ND' treatment 1 1 -2;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y1exp2;
  class Block Treatment Ring;
  model CO2= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2 / solution htype=1 ddfm=kr;
  *random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y2exp1 plot=residualpanel;
  class Block Treatment Ring DAA;
  model CO2=Treatment|DAA / ddfm=kr;
  random Block; random _residual_ /group=treatment; covtest homogeneity; output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2y2exp1;
  class Block Treatment Ring DAA;
  model CO2= Block Treatment|DAA / ddfm=kr;
  *random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*lsmeans Treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D - ND' treatment 1 1 -2;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DA 0 0 0 -1 1 0 0 0 0 0;
*contrast '21DAP - 14DAP' DA 0 0 0 0 -1 1 0 0 0 0;
*contrast '28DAP - 21DAP' DA 0 0 0 0 0 -1 1 0 0 0;
*contrast '56DAP - 28DAP' DA 0 0 0 0 0 0 -1 1 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y2exp1;
 class Block Treatment Ring;
model CO2= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2 / solution htype=1 ddfm=kr;
 *random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2y2exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model CO2= Treatment|DAA /ddfm=kr;
random Block;
random residual /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Co2y2exp2;
class Block Treatment Ring DAA;
model CO2= Block Treatment|DAA /ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random residual /type=ante(1) subject=ring(Treatment);
lsmeans treatment/ diff plot=diff;
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D - ND' treatment 1 1 -2;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc glimmix data=Sasdata.Co2y2exp2;
class Block Treatment Ring;
model CO2= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2 / solution htype=1
ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc glimmix data=Sasdata.Co2 plot=residualpanel;
class Block Treatment Ring DAA;
model CO2=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Co2;
class Block Treatment Ring DAA;
model CO2= Block Year Treatment|DAA /ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl plot=diff;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.N2oy1exp1 plot=residualpanel;
class Block Treatment Ring DAA;
model N2O=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.N2oy1exp1;
class Block treatment ring DAA;
model N2O= Block treatment|DAA /ddfm=kr;
random Block Ring(Treatment);
random _residual_ /type=ar(1) subject=ring(treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
proc glimmix data=Sasdata.N2oy1exp1;
class Block treatment ring;
model N2O= Block treatment|DAA /ddfm=kr;
random Block Ring(Treatment);
random _residual_ /type=ar(1) subject=ring(treatment);
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.N2oy1exp1;
class Block DAA Treatment Ring;
model N2O= Treatment VWC Treatment*VWC O2 Treatment*O2 / solution htype=1 ddfm=kr;
*model N2O= Block Treatment SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block ring(Treatment);
random residual /type=ante(1) subject=ring(Treatment);
nloptimizations maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.N2oy1exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model N2O=Treatment|DAA / ddfm=kr;
random Block;
random residual /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.N2oy1exp2;
class Block Treatment Ring DAA;
model N2O= Block Treatment|DAA / ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random residual /type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA/ diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.N2oy1exp2;
   class Block Treatment Ring;
   model N2O= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseN2O / solution htype=1 ddfm=kr;
   *random Treatment(DAA);
   random Block Ring(Treatment);
   random _residual_ /type=ante(1) subject=ring(Treatment);
   *ods output covparms=Sasdata.covco2y1exp1;
   *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.N2oy2exp1 plot=residualpanel;
   class Block Treatment Ring DAA;
   model N2O=Treatment|DAA / ddfm=kr;
   random Block;
   random _residual_ /group=treatment;
   covtest homogeneity;
   output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.N2oy2exp1;
   class Block Treatment Ring DAA;
   model N2O= Block Treatment|DAA / ddfm=kr;
   *random Treatment(DAA);
   random Block Ring(Treatment);
   random _residual_ /type=ar(1) subject=ring(Treatment);
   *lsmeans treatment DAA treatment*DAA/ diff cl;
   *lsmeans Treatment/ diff=control('3') plot=diff;
   lsmeans DAA/ diff plot=diff;
   *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrcor2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.N2oy2exp1;
class Block Treatment Ring;
model N2O= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseN2O / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ar(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrcor2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.N2oy2exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model N2O=Treatment|DAA / ddfm=kr;
random Block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.N2oy2exp2;
class Block Treatment Ring DAA;
model N2O= Block Treatment|DAA / ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0; 
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0; 
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0; 
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0; 
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0; 
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0; 
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0; 
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1; 
*contrast 'beetle - no beetle' treatment -1 1 0; 
*ods output covparms=Sasdata.covco2y1exp1; 
*ods output rcorr=Sasdata.corrco2y1exp1; 
run;

proc print;
proc glimmix data=Sasdata.N2o plot=residualpanel;
class Block Treatment Ring DAA;
model N2O=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment; 
covtest homogeneity;* 
output out=outd pred=pred residual=resid; 
run;
proc glimmix data=Sasdata.N2o;
class Block Year treatment ring DAA;
model N2O= Block Year treatment|DAA /ddfm=kr;
random Block Ring(Treatment);
random _residual_ /type=ar(1) subject=ring(treatment); 
*lsmeans treatment DAA treatment*DAA/ diff cl; 
*lsmeans Treatment/ diff=control('3') plot=diff; 
lsmeans treatment/ diff=plot=diff;*
lsmeans DAA/ diff=plot=diff; 
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff; 
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1]; 
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2]; 
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3]; 
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4]; 
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5]; 
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2equivy1exp1;
class Block Treatment Ring;
model CO2Equiv= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2E /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2equivy1exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model TotalCO2Equiv=Treatment|DAA /ddfm=kr;
random Block;
random _residual_ /group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2equivy1exp2;
class Block Treatment Ring DAA;
model TotalCO2Equiv= Block Treatment|DAA /ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ /type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*contrast 'dung - no dung' treatment -1 -1 2;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2equivy1exp2;
  class Block Treatment Ring;
  model CO2Equiv= BlockTreatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2E /
    solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block(Ring(Treatment));
  random _residual_/type=ante(1) subject=ring(Treatment);
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2equivy2exp1 plot=residualpanel;
  class Block Treatment Ring DAA;
  model CO2Equiv=Treatment|DAA /ddfm=kr;
  random Block;
  random _residual_/group=treatment;
  covtest homogeneity;
  output out=oud pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2equivy2exp1;
  class Block Treatment Ring DAA;
  model TotalCO2Equiv= BlockTreatment|DAA /ddfm=kr;
  *random Treatment(DAA);
  random Block(Ring(Treatment));
  random _residual_/type=ante(1) subject=ring(Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans Treatment/ diff plot=diff;
  lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D - ND' treatment 1 1 -2;
*contrast 'B1DAP - NB1DAP' treatment -1 1 0 treatment*DAA [1, 2 1] [-1, 1 1];
*contrast 'B2DAP - NB2DAP' treatment -1 1 0 treatment*DAA [1, 2 2] [-1, 1 2];
*contrast 'B3DAP - NB3DAP' treatment -1 1 0 treatment*DAA [1, 2 3] [-1, 1 3];
*contrast 'B7DAP - NB7DAP' treatment -1 1 0 treatment*DAA [1, 2 4] [-1, 1 4];
*contrast 'B10DAP - NB10DAP' treatment -1 1 0 treatment*DAA [1, 2 5] [-1, 1 5];
*contrast 'B14DAP - NB14DAP' treatment -1 1 0 treatment*DAA [1, 2 6] [-1, 1 6];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0; 
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0; 
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0; 
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0; 
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0; 
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0; 
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0; 
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1; 
*contrast 'beetle - no beetle' treatment -1 1 0; 
*contrast 'dung - no dung' treatment -1 -1 2; 
*ods output covparms=Sasdata.covco2y1exp1; 
*ods output rcorr=Sasdata.corrco2y1exp1; 
run; 
proc print; 
proc glimmix data=Sasdata.Co2equivy2exp1; 
class Block Treatment Ring; 
model CO2Equi= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2E / solution htype=1 ddfm=kr; 
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ / type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Co2equivy2exp2 plot=residualpanel;
class Block Treatment Ring DAA;
model CO2Equiv=Treatment|DAA / ddfm=kr;
random Block;
random _residual_ / group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2equivy2exp2;
class Block Treatment Ring DAA;
model TotalCO2Equiv= Block Treatment|DAA / ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_ / type=ante(1) subject=ring(Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment/ diff plot=diff;
lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D4DAP - C4DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D5DAP - C5DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D6DAP - C6DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D8DAP - C8DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D9DAP - C9DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 10] [1, 1 10] [-2, 3 10];
*contrast 'D11DAP - C11DAP' treatment 1 1 -2 treatment*DAA [1, 2 11] [1, 1 11] [-2, 3 11];
*contrast 'D12DAP - C12DAP' treatment 1 1 -2 treatment*DAA [1, 2 12] [1, 1 12] [-2, 3 12];
*contrast 'D13DAP - C13DAP' treatment 1 1 -2 treatment*DAA [1, 2 13] [1, 1 13] [-2, 3 13];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 14] [1, 1 14] [-2, 3 14];
*contrast 'D15DAP - C15DAP' treatment 1 1 -2 treatment*DAA [1, 2 15] [1, 1 15] [-2, 3 15];
*contrast 'D16DAP - C16DAP' treatment 1 1 -2 treatment*DAA [1, 2 16] [1, 1 16] [-2, 3 16];
*contrast 'D17DAP - C17DAP' treatment 1 1 -2 treatment*DAA [1, 2 17] [1, 1 17] [-2, 3 17];
*contrast 'D18DAP - C18DAP' treatment 1 1 -2 treatment*DAA [1, 2 18] [1, 1 18] [-2, 3 18];
*contrast 'D19DAP - C19DAP' treatment 1 1 -2 treatment*DAA [1, 2 19] [1, 1 19] [-2, 3 19];
*contrast 'D20DAP - C20DAP' treatment 1 1 -2 treatment*DAA [1, 2 20] [1, 1 20] [-2, 3 20];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 21] [1, 1 21] [-2, 3 21];
*contrast 'D22DAP - C22DAP' treatment 1 1 -2 treatment*DAA [1, 2 22] [1, 1 22] [-2, 3 22];
*contrast 'D23DAP - C23DAP' treatment 1 1 -2 treatment*DAA [1, 2 23] [1, 1 23] [-2, 3 23];
*contrast 'D24DAP - C24DAP' treatment 1 1 -2 treatment*DAA [1, 2 24] [1, 1 24] [-2, 3 24];
*contrast 'B21DAP - NB21DAP' treatment -1 1 0 treatment*DAA [1, 2 7] [-1, 1, 1 7];
*contrast 'B28DAP - NB28DAP' treatment -1 1 0 treatment*DAA [1, 2 8] [-1, 1, 1 8];
*contrast 'B56DAP - NB56DAP' treatment -1 1 0 treatment*DAA [1, 2 9] [-1, 1, 1 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Co2equivy2exp2;
class Block Treatment Ring;
model CO2Equiv= Block Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp BaseCO2E /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Ring(Treatment);
random _residual_/type=ante(1) subject=ring(Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc glimmix data=Sasdata.Co2inty1e1 plot=residualpanel;
class Block Treatment;
model CO2_Integration=Treatment /ddfm=satterth;
random Block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Co2inty1e2;
class block treatment;
model CO2Int= treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.Co2inty2e1;

```plaintext
class block treatment;
model CO2Int= treatment / ddfm=satterth;
random block block*treatment;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.Co2inty2e2;
class block treatment;
model CO2Int= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.N2ointyle1;
class block treatment;
model N2OInt= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.N2ointyle2;
class block treatment;
model N2OInt= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.N2ointy2e1;
class block treatment;
model N2OInt= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.N2ointy2e2;
class block treatment;
model N2OInt= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.CH4intyle1;
class block treatment;
model CH4Int= treatment / ddfm=satterth;
random block;
lsmeans treatment / cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;

proc glimmix data=Sasdata.CH4intyle2;
class block treatment;
```
model CH4Int= treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CH4inty2e1;
class block treatment;
model CH4Int= treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CH4inty2e2;
class block treatment;
model CH4Int= treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CO2eqinty1e1;
class block treatment;
model CO2EqInt= block treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CO2eqinty1e2;
class block treatment;
model CO2EqInt= block treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CO2eqinty2e1;
class block treatment;
model CO2EqInt= block treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.CO2eqinty2e2;
class block treatment;
model CO2EqInt= block treatment /ddfm=satterth;
random block;
lsmeans treatment/ cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class block treatment experiment;
```plaintext
model CO2_Int= treatment experiment treatment*experiment;
random block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment;
model CO2Int= treatment/ddfm=satterth;
random block;
lsmeans treatment/ plot=diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc anova data=Sasdata.IntegratedGas;
class block treatment;
model CO2Int= treatment;
means treatment;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class block treatment;
model CH4Int= treatment;
random block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment;
model CH4Int= treatment/ddfm=satterth;
random block;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
lsmeans treatment/ plot=diff cl;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class block treatment;
model N2OInt= treatment;
random block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment experiment;
model N2OInt= treatment/ddfm=satterth;
random block;
lsmeans treatment/ plot=diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class Block treatment;
model CO2EqInt= treatment;
random block;
random _residual_/group=treatment;
covtest homogeneity;
```

output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment;
model CO2EqInt= treatment /ddfm=satterth;
random block;
lsmeans treatment/ plot=diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
contrast 'D - ND' treatment 1 1 -2;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class treatment experiment Block;
model CH4_CO2_Equiv_Int= treatment experiment treatment*experiment;
random block;
random _residual_/group=treatment;
contrast 'beetle - no beetle' treatment -1 1 0;
lsmeans treatment experiment treatment*experiment/ cl;
lsmeans treatment experiment treatment*experiment/diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
lsmeans treatment experiment treatment*experiment/diff lines cl
plot=diffplot adjust=sidak;
lsmeans t*water/diff plot=diffplot adjust=sidak;
lsmeans treatment experiment treatment*experiment/cl adjust=sidak;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class treatment experiment Block;
model N2O_CO2_Equiv_Int= treatment experiment treatment*experiment;
random block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment experiment;
model N2O_CO2_Equiv_Int= treatment experiment treatment*experiment /
ddfm=satterth;
random block block*treatment;
*lsmeans treatment experiment treatment*experiment/ cl;
*lsmeans treatment experiment treatment*experiment/diff cl;
lsmeans treatment/diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
*lsmeans treatment experiment treatment*experiment/diff lines cl
plot=diffplot adjust=sidak;
*lsmeans t*water/diff plot=diffplot adjust=sidak;
*lsmeans treatment experiment treatment*experiment/cl adjust=sidak;
run;
proc glimmix data=Sasdata.IntegratedGas plot=residualpanel;
class treatment experiment Block;
model N2O_CH4_CO2_Equiv_Int= treatment experiment treatment*experiment; random block;
random _residual_/group=treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.IntegratedGas;
class block treatment experiment;
model N2O_CH4_CO2_Equiv_Int= treatment experiment treatment*experiment /ddfm=satterth;
random block treatment*block;
*lsmeans treatment experiment treatment*experiment/ cl;
*lsmeans treatment experiment treatment*experiment/diff cl;
lsmeans treatment/diff cl;
contrast 'beetle - no beetle' treatment -1 1 0;
*lsmeans treatment experiment treatment*experiment/diff lines cl plot=diffplot adjust=sidak;
*lsmeans t*water/diff plot=diffplot adjust=sidak;
*lsmeans treatment experiment treatment*experiment/treatment/cl adjust=sidak;
run;

proc glimmix data=Sasdata.Pmy1exp1 plot=residualpanel;
class Block Treatment DAA;
model PM = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Pmy1exp1;
class Block Treatment DAA;
model PM=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/diff cl;
lsmeans DAA/diff plot=diff;
*lsmeans Treatment*DAA/slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Pmy1exp1;
class Block Treatment;
model PM = Block Block*Treatment Treatment VWC Treatment*VWC O2
  Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
  *random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Pmy1exp2 plot=residualpanel;
class Block Treatment DAA;
model PM = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Pmy1exp2;
class Block Treatment DAA;
model PM=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA / diff cl;
  lsmeans treatment/ diff plot=diff;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;  
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Pmy1exp2;
  class Block Treatment;
  model PM = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
    solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_ /type=ar(1) subject=Treatment;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Pmy2exp1 plot=residualpanel;
  class Block Treatment DAA;
  model PM = Block Block*Treatment Treatment|DAA /ddfm=kr;
  random Block Block*Treatment;
  random _residual_ /group=Treatment;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Pmy2exp1;
  class Block Treatment DAA;
  model PM = Block Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA / diff cl;
  *lsmeans Treatment/ diff plot=diff;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Pmy2exp1;
class Block Treatment;
model PM = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Pmy2exp2 plot=residualpanel;
class Block Treatment DAA;
model PM = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Pmy2exp2;
class Block Treatment DAA;
model PM=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*lsmeans _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA / diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Pmy2exp2;
class Block Treatment;
*model PM = Block Block*Treatment Treatment VWC Treatment*VWC /
solution htype=1 ddfm=kr;
model PM = O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp
Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Wcylexp1 plot=residualpanel;
class Block Treatment DAA;
model WC = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Wcylexp1;
class Block Treatment DAA;
model WC=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA / diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;  
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;  
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;  
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;  
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;  
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;  
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;  
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;  
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;  
*ods output rcorr=Sasdata.corrco2y1exp1;  
run;

proc glimmix data=Sasdata.Wcylexp1;
  class Block Treatment;
  model WC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
    solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_ /type=ar(1) subject=Treatment;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc glimmix data=Sasdata.Wcylexp2 plot=residualpanel;
  class Block Treatment DAA;
  model WC = Block Block*Treatment Treatment|DAA /ddfm=kr;
  random Block Block*Treatment;
  random _residual_ /group=Treatment;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Wcylexp2;
  class Block Treatment DAA;
  model WC=Block Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Wcylexp2;
class Block Treatment;
model WC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block*Treatment;
random _residual_ /type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Wcylexp1 plot=residualpanel;
class Block Treatment DAA;
model WC = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Wcylexp1;
class Block Treatment DAA;
model WC=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff = DAA plot = diff;

*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Wcy2exp1;
class Block Treatment;
model WC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Wcy2exp2 plot=residualpanel;
class Block Treatment DAA;
model WC = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Wcy2exp2;
class Block Treatment DAA;
model WC=Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff plot=diff;
*lsmeans Treatment/ diff=control(3') plot=diff;
*lsmeans DAA/ diff plot=diff;
lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Wcy2exp2;
class Block Treatment;
*model WC = Block Block*Treatment Treatment VWC Treatment*VWC /
solution htype=1 ddfm=kr;
model WC = Block Block*Treatment Treatment O2 Treatment*O2 SoilTemp
Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1
ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Dmylexp1 plot=residualpanel;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmylexpl;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA treatment|DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
  *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
  *contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
  *contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
  *contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
  *contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
  *contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
  *contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
  *contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
  *contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
  *contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
  *contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
  *contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
  *contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
  *contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
  *contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Dmylexpl;
class Block Treatment;
model Drymatter = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
  solution htype=1 ddfm=kr;
  *random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Dmylexp2 plot=residualpanel;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random _residual_ / group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmylexp2;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmylexp2;
class Block Treatment;
model Drymatter = Block Block*Treatment Treatment VWC Treatment|VWC O2 Treatment|O2 SoilTemp Treatment|SoilTemp AirTemp Treatment|AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrc2y1expl;
run;
proc print;
proc glimmix data=Sasdata.Dmy2exp1 plot=residualpanel;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmy2exp1;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
ods output covparms=Sasdata.covco2y1expl;
ods output rcorr=Sasdata.corrc2y1expl;
run;
proc print;
proc glimmix data=Sasdata.Dmy2exp1;
class Block Treatment;
model Drymatter = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmy2exp2 plot=residualpanel;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=oud pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmy2exp2;
class Block Treatment DAA;
model Drymatter = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA / diff cl;
*lsmeans Treatment/diff=control('3') plot=diff;
*lsmeans DAA/diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmy2exp2;
class Block Treatment;
model Drymatter = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy1exp1 plot=residualpanel;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Chdmy1exp1;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*1means treatment DAA treatment*DAA/ diff cl;
*1means Treatment/ diff=control('3') plot=diff;
*1means DAA/ diff plot=diff;
*1means Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D1DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Chdmyexp1;
class Block Treatment;
model ChDMat = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random_residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Chdmyexp2 plot=residualpanel;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random_residual_/group=Treatment;
covtest homogeneity;
output out=oudt pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Chdmyexp2;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random_residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans Treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy1exp2;
class Block Treatment;
model ChDMat = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy2exp1 plot=residualpanel;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Chdmy2exp1;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA /ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;  
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;  
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;  
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;  
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy2exp1;
class Block Treatment;
model ChDMat = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy2exp2 plot=residualpanel;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA / ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Chdmy2exp2;
class Block Treatment DAA;
model ChDMat = Block Block*Treatment Treatment|DAA/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Chdmy2exp2;
class Block Treatment;
model ChDMat = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) group=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocdy1exp1 plot=residualpanel;
class Block Treatment DAA;
model NPOC = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Npocdy1exp1;
class Block Treatment DAA;
model NPOC = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/diff cl;
*lsmeans Treatment/diff=control('3') plot=diff;
*lsmeans DAA/diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2AP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3AP - 2DAP' DAA 0 -1 1 0 0 0 0 0;
*contrast 'D7AP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covpar=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocdylexpl;
  class Block Treatment;
  model NPOC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_/type=ar(1) subject=Treatment;
*ods output covpar=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocdylexpl plot=residualpanel;
  class Block Treatment DAA;
  model NPOC = Block Block*Treatment Treatment|DAA /ddfm=kr;
  random Block Block*Treatment;
  random _residual_/group=Treatment;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Npocdylexpl2;
  class Block Treatment DAA;
  model NPOC = Block Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_/type=ante(1) subject=Sample(HT Treatment);
  *lsmeans Treatment*DAA treatment*DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *contrast '1D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast '2D1DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast '3D1DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast '7D1DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
  *contrast '10D1DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
  *contrast '14D1DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocdy1exp2;
class Block Treatment;
model NPOC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocd plot=residualpanel;
class Block Treatment DAA;
model NPOC = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outed pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Npocd;
class Block Year Treatment DAA;
model NPOC = Block Block*Treatment Year Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0 0 0 0 0 0 0 0;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc glimmix data=Sasdata.Tndy1exp1 plot=residualpanel;
class Block Treatment DAA;
model TN = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Tndy1exp1;
class Block Treatment DAA;
model TN = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Tndylexp1;
class Block Treatment;
model TN = Block Block*Treatment Treatment*VWC Treatment*VWC O2
Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block*Treatment;
random _residual_/type=ar(1) subject=Training;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Tndylexp2 plot=residualpanel;
class Block Treatment DAA;
model TN = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block*Treatment;
random _residual_/type=ar(1) subject=Training;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Tndylexp2;
class Block Treatment DAA;
model TN = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Tndy1exp2;
  class Block Treatment;
  model TN = Block Treatment VWC Treatment*VWC / solution htype=1 ddfm=kr;
  *model TN = Block Treatment O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_ /type=ar(1) subject=Sample;  
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Tnd plot=residualpanel;
  class Block Treatment DAA;
  model TN = Block Block*Treatment Treatment|DAA / ddfm=kr;
  random Block Block*Treatment;
  random _residual_ /group=Sample;  
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc glimmix data=Sasdata.Tnd;
  class Block Year Treatment DAA;
  model TN = Block Year Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl;  
  *lsmeans treatment/ diff plot=diff;  
  *lsmeans Treatment/ diff=control('3') plot=diff;  
  *lsmeans DAA/ diff plot=diff;  
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
  *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 0 0 1 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 0 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Dmprdylexpl plot=residualpanel;
class Block Treatment DAA;
model DMPR = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmprdylexpl;
class Block Treatment DAA;
model DMPR = Block Block*Treatment Treatment|DAA /ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*1means treatment DAA treatment*DAA/ diff cl;
*1means Treatment/ diff=control('3') plot=diff;
*1means DAA/ diff plot=diff;
*1means Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmprdylexpl;
class Block Treatment;
model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random_residual_ /type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmprdylexpl2 plot=residualpanel;
class Block Treatment DAA;
model DMPR = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random_residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmprdylexpl2;
class Block Treatment DAA;
model DMPR = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random_residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA /diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmprdy1exp2;
class Block Treatment;
model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
  solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_ /type=ar(1) group=Treatment;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmprd plot=residualpanel;
class Block Treatment DAA;
model DMPR = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
  covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmprd;
class Block Year Treatment DAA;
model DMPR = Block Year Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl;
  lsmeans treatment/ diff plot=diff;
  *lsmeans Treatment/ diff=control(3) plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
  *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment 1 -1 0;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.No3dylexp1 plot=residualpanel;
   class Block Treatment DAA;
   model NO3 = Block Block*Treatment Treatment|DAA /ddfm=kr;
   random Block Block*Treatment;
   random _residual_ /group=Sample(HT Treatment);
   covtest homogeneity;
   output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3dylexp1;
   class Block Treatment DAA;
   model NO3 = Block Block*Treatment Treatment|DAA/ddfm=satterth;
   random Block Block*Treatment;
   *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
   *1means treatment DAA treatment*DAA/ diff cl;
   *1means Treatment/ diff=control('3') plot=diff;
   *1means DAA/ diff plot=diff;
   *1means Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.No3dylexp1;
class Block Treatment;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) subject=Treatment;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.No3dylexp2 plot=residualpanel;
class Block Treatment DAA;
model NO3 = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3dylexp2;
class Block Treatment DAA;
model NO3 = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3dy1exp2;
class Block Treatment;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random_residual_/type=ar(1) subject=Treatment;
*ods output covpars=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3d plot=residualpanel;
class Block Treatment DAA;
model NO3 = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random_residual_/group=Treatment;
covtest homogeneity;
output out=oudt pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3d;
class Block Year Treatment DAA;
model NO3 = Block Year Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random_residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans treatment/ diff plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covpreams=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Nh4dy1exp1 plot=residualpanel;
class Block Treatment DAA;
model NH4 = Block Block*Treatment Treatment|DAA /ddfm=kr;
random Block Block*Treatment;
random _residual_/ group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh4dy1exp1;
class Block Treatment DAA;
model NH4 = Block Block*Treatment Treatment|DAA/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*1means treatment DAA treatment*DAA/ diff cl;
*1means Treatment/ diff=control('3') plot=diff;
*1means DAA/ diff plot=diff;
*1means Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 1;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4dy1exp2;
  class Block Treatment;
  model NH4 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random _residual_ /type=ar(1) subject=Block;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4d plot=residualpanel;
  class Block Treatment DAA;
  model NH4 = Block Block*Treatment Treatment|DAA /ddfm=kr;
  random Block Block*Treatment;
  random _residual_ /group=Treatment;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh4d;
  class Block Year Treatment DAA;
  model NH4 = Block Year Block*Treatment Treatment|DAA/ddfm=satterth;
  random Block Block*Treatment;
  *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans Treatment DAA treatment*DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  lsmeans treatment/ diff plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
  *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;

proc glimmix data=Sasdata.No3y1exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block;
random _residual_/group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3y1exp1;
class Block Treatment Sample HT location depth;
model NO3 = Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block*Treatment Sample(HT Treatment);
random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*location/ slicediff=location plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D1DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0 0;
*contrast 'D2DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0 0 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y1exp110cm;
class Block Treatment Sample HT;
model NO3=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0 0 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc glimmix data=Sasdata.No3y1exp1;
class Block Treatment Sample HT;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y1exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3y1exp2;
class Block Treatment Sample HT location depth;
model NO3=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans location/ diff plot=diff;
*lsmeans depth/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment|HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y1exp210cm;
class Block Treatment Sample HT;
model NO3=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans treatment/diff plot=diff;
*lsmeans Treatment/ diff=control(3') plot=diff;
*lsmeans HT/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y1exp2;
class Block Treatment Sample HT;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 
Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glmmix data=Sasdata.No3y2exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth 
Depth*Treatment/ddfm=kr;
random Block;
random _residual_ /group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glmmix data=Sasdata.No3y2exp1;
class Block Treatment Sample HT location depth;
model NO3=Block Block*Treatment Treatment|HT Location 
Location*Treatment Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*THT/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
lsmeans Treatment*location/ slicediff=location plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DA 1 1 1 
[1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DA 1 1 2 
[1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DA 1 1 3 
[1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DA 1 1 4 
[1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DA 1 1 5 
[1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DA 1 1 6 
[1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DA 1 1 7 
[1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DA 1 1 8 
[1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DA 1 1 9 
[1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc glimmix data=Sasdata.No3y2exp310cm;
class Block Treatment Sample HT;
model NO3=Block Block*Treatment Treatment|HT/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans Treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc glimmix data=Sasdata.No3y2exp1;
class Block Treatment Sample HT;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y2exp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block;
random _residual_ /group=Treatment;
contrast homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No3y2exp2;
class Block Treatment Sample HT location depth;
model NO3=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment|HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans location/ diff plot=diff;
*lsmeans depth/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;  
*contrast 'D3DAP - 2DAP' DAA 0 0 1 1 0 0 0 0 0 0; 
*contrast 'D7DAP - 3DAP' DAA 0 0 0 0 1 1 0 0 0 0; 
*contrast 'D10DAP - 7DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0 0 0 0 0 0 0 0; 
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 0 0 0 0 -1 1 0 0 0; 
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0; 
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0; 
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0; 
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.No3y2exp2410cm;
class Block Treatment Sample HT;
...
proc print;
proc glimmix data=Sasdata.No3y1exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment O2;
random Block Block*Treatment HT Location Location*Treatment Depth*Treatment/ ddfm=kr;
*ncontrasts, 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*ncontrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*ncontrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*ncontrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*ncontrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*ncontrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*ncontrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*ncontrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*ncontrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*ncontrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*ncontrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*ncontrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*ncontrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*ncontrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*ncontrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*ncontrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*ncontrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*ncontrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.No3y2exp2;
class Block Treatment Sample HT;
model NO3 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*VWC Treatment*SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
random _residual_ / group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No310cm plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NO3 = Block Treatment|HT Location Location*Treatment Depth*Treatment|ddfm=kr;
random Block;
random _residual_ / group=Treatment;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.No310cm;
class Block Year Treatment Sample HT;
model NO3=Block Block*Treatment Year Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NH4 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random residual /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh4y1exp1;
class Block Treatment Sample HT Location Depth;
model NH4=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/

ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random residual /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment*location/ slicediff=depth plot=diff;
*lsmeans DAA/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 0 0 0 0 1 1 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 0 0 1 1 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 0 1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp110cm;
class Block Treatment Sample HT;
model NH4=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp1;
class Block Treatment Sample HT;
model NH4 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=l ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_/type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NH4 = Block Block*Treatment HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random _residual_/group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh4y1exp2;
class Block Treatment Sample HT Location Depth;
model NH4=Block Block*Treatment Treatment|HT Location
Location*Treatment Depth*Treatment/ ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_/type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment HT treatment*Treatment/ diff cl;
*lsmeans treatment/ diff=control('3') plot=diff;
*lsmeans treatment/ diff plot=diff;
*lsmeans treatment*Treatment slicediff=HT plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment*Treatment slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 0 0 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 0 0 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 0 0 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 0 0 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 0 0 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 -1 0 0 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 0 0 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 0 0;
*contrast 'beetle - no beetle' treatment -1 0 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp210cm;
class Block Treatment Sample HT;
model NH4=Block Block*Treatment Treatment|HT/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*Treatment/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans treatment*HT slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 -2 treatment*DA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 -2 treatment*DA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 -2 treatment*DA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 -2 treatment*DA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 -2 treatment*DA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 -2 treatment*DA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 -2 treatment*DA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y1exp2;
class Block Treatment Sample HT;
model NH4 = Block Block*Treatment Treatment VWC Treatment*O2
Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random_residual_/type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y2exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NH4 = Block Block*Treatment|HT Location Location*Treatment Depth
  Depth*Treatment /ddfm=kr;
  random Block;
  random residual_/group= Treatment;
  nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh4y2exp1;
class Block Treatment Sample HT Location Depth;
model NH4=Block Block*Treatment|HT Location Location*Treatment Depth
  Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random_residual_/type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans Treatment*location/ slicediff=depth plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;

*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Nh4y2exp310cm;
class Block Treatment Sample HT;
model NH4=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;

*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Nh4y2exp1;
class Block Treatment Sample HT;
model NH4 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random residual /type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Nh4y2exp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NH4 = Block Block*Treatment|HT Location Location*Treatment Depth Depth*Treatment /
ddfm=kr;
random Block;
random residual /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc print;
proc glimmix data=Sasdata.Nh4y2exp2;
class Block Treatment Sample HT Location Depth;
model NH4=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Nh4y2exp410cm;
class Block Treatment Sample HT;
model NH4=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*1means Treatment HT/ diff cl;
*1means Treatment/ diff plot=diff;
*1means HT/ diff plot=diff;
*1means Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '1DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 29DAP' DAA 0 0 0 0 0 0 -1 1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh4y2exp2;
class Block Treatment Sample HT;
model NH4 = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Nh410cm plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NH4 = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random residual /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
*contrast homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Nh410cm;
class Block Year Treatment Sample HT;
model NH4=Block Block*Treatment Year Treatment|HT/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'A4DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Dmpry1exp1 plot=residualpanel;
  class Block Treatment Sample HT Location Depth;
  model DMPR = Block Treatment|HT Location Location*Treatment Depth
               Treatment /ddfm=kr;
  random Block;
  random _residual_ /group= Treatment;
  nloptions maxiter=500 maxfunc=5000;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Dmpry1exp1;
  class Block Treatment Sample HT Location Depth;
  model DMPR = Block Block*Treatment HT Location
               Location*Treatment/ Treatment/ddfm=kr;
  random Block Block*Treatment Sample(HT Treatment);
  random residual /type=ante(1) subject=Sample(HT Treatment);
  nloptions maxiter=1000 maxfunc=10000;
  *lsmeans treatment DAA treatment*DAA / diff cl;
  lsmeans location/ diff plot=diff;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Dmpry1exp110cm;
class Block Treatment Sample HT;
model DMPR=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexpl;
*ods output rcorr=Sasdata.corrco2ylexpl;
run;
proc print;
proc glimmix data=Sasdata.Dmpry1exp1;
  class Block Treatment Sample HT;
  model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
    solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment;
  random residual /type=ar(1) subject=Sample(HT Treatment);
  nloptions maxiter=1000 maxfunc=10000;
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry1exp2 plot=residualpanel;
  class Block Treatment Sample HT Location Depth;
  model DMPR = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /
    ddfm=kr;
  random Block;
  random residual /group= Treatment;
  nloptions maxiter=500 maxfunc=5000;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmpry1exp2;
  class Block Treatment Sample HT Location Depth;
  model DMPR=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/
    ddfm=kr;
  random Block Block*Treatment Sample(HT Treatment);
  random residual /type=ante(1) subject=Sample(HT Treatment);
  nloptions maxiter=1000 maxfunc=10000;
  *lsmeans treatment HT treatment/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans HT/ diff plot=diff;
  *lsmeans Treatment*HT/ slicediff=HT plot=diff;
  *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
  *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
  *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
  *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
  *contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
  *contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
  *contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
  *contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
  *contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
  *contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
  *contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
  *contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
  *contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Dmpry1exp210cm;
class Block Treatment Sample HT;
model DMPR=Block Block*Treatment Treatment|HT/htype=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=dif;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 1] [1, 2 3] [1, 4] [-2, 3 4];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 1] [1, 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Dmpry1exp2;
class Block Treatment Sample HT;
model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry2exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model DMPR = Block Treatment|HT Location Location*Treatment Depth
         Treatment*Depth / dfm=kr;
random _residual_ / group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Dmpry2exp1;
class Block Treatment Sample HT Location Depth;
model DMPR=Block Block*Treatment Treatment|HT Location
         Location*Treatment Depth Depth*Treatment/
         dfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_/ type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans location/ diff plot=diff;
*lsmeans Depth*treatment/ slicediff=depth plot=diff;
lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans DAA/ diff plot=diff;
lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP-C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1]
[-2, 3 1];
*contrast 'D2DAP-C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2]
[-2, 3 2];
*contrast 'D3DAP-C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3]
[-2, 3 3];
*contrast 'D7DAP-C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4]
[-2, 3 4];
*contrast 'D10DAP-C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5]
[-2, 3 5];
*contrast 'D14DAP-C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6]
[-2, 3 6];
*contrast 'D21DAP-C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7]
[-2, 3 7];
*contrast 'D28DAP-C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8]
[-2, 3 8];
*contrast 'D56DAP-C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9]
[-2, 3 9];
*contrast '2DAP-1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP-2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP-3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP-7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP-10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP-14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP-21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP-28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle-no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry2exp310cm;
where Block|Treatment
model DMPR=Block Block*Treatment Treatment|HT
random Block Block*Treatment;
    *lsmeans Treatment HT Treatment*HT/ diff plot=diff;
*lsmeans Treatment/ diff=control(3') plot=diff;
*lsmeans HT/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry2exp1;
where Block|Treatment
model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp
solution htype=1 ddfm=kr;
random Treatment(DAA);
random Block Block*Treatment;
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry2exp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model DMPR = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random residual /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Dmpry2exp2;
class Block Treatment Sample HT Location Depth;
model DMPR=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random residual /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=10000;
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control("3") plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Dmpry2exp410cm;
class Block Treatment Sample HT;
model DMPR=Block Block*Treatment Treatment|HT/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control(’3’) plot=diff;
lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpry2exp2;
class Block Treatment Sample HT;
model DMPR = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment;
random_residual_ /type=ante(1) subject=Sample(HT Treatment);
nloptions maxiter=1000 maxfunc=100000;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Dmpr10cm plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model DMPR = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /
ddfm=kr;
random Block;
random_residual_ /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
& run;
& proc glimmix data=Sasdata.Dmpr10cm;
 class Block Year Treatment Sample HT;
 model DMPR=Block Block*Treatment Year Treatment|HT/ddfm=satterth;
 random Block Block*Treatment;
 *random _residual_ /type=ante(1) subject=Sample(HT Treatment);
 *lsmeans treatment HT treatment*HT/ diff cl;
 lsmmeans treatment/ diff plot=diff;
 *lsmeans Treatment/ diff=control('3') plot=diff;
 *lsmeans HT/ diff plot=diff;
 *lsmeans Treatment*HT/ slicediff=HT plot=diff;
 *contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
 *contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
 *contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
 *contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
 *contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
 *contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
 *contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
 *contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
 *contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
 *contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
 *contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
 *contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
 *contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
 *contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
 *contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
 *contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
 *contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
 *contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
& proc print;
& proc glimmix data=Sasdata.Tny1exp1 plot=residualpanel;
 class Block Treatment Sample HT Location Depth;
 model TN = Block Treatment|HT Location Location*Treatment Depth*Treatment /ddfm=kr;
 random Block Block*Treatment Sample(HT Treatment);
 nloptions maxiter=500 maxfunc=5000;
 covtest homogeneity;
 output out=outd pred=pred residual=resid;
run;
& proc glimmix data=Sasdata.Tny1exp1;
 class Block Treatment Sample HT Location Depth;
 model TN=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
 random Block Block*Treatment Sample(HT Treatment);
random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
lsmeans Treatment*location/ slicediff=location plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tnyexp110cm;
class Block Block*Treatment Treatment HT;
model TN=Block Block*Treatment Treatment*HT/ddfm=satterth;
random Block Block*Treatment;
*lsmeans treatment DAA treatment*DAA/ diff cl;
lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tnylexp1;
class Block Treatment Sample HT;
model TN = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covp parms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tnylexp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model TN = Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment / ddfm=kr;
random Block;
random _residual_ /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Tnylexp2;
class Block Treatment Sample HT Location Depth;
model TN=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff=plot=diff;
*lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tny1exp210cm;
class Block Treatment Sample HT;
model TN=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*lsmeans treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans Treatment/ diff plot=diff;
*lsmeans DAA/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Tny1exp2;
class Block Treatment Sample HT;
model TN = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tny2exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model TN = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment / ddfm=kr;
random Block;
random _residual_ /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Tny2exp1;
class Block Treatment Sample HT Location Depth;
model TN=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
lsmeans treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*lsmeans Treatment*location/ slicediff=location plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tny2exp310cm;
class Block Treatment Sample HT;
model TN=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0 0 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tny2exp1;
  class Block Treatment Sample HT;
  model TN = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
        solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment Sample(HT Treatment);
  random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tny2exp2 plot=residualpanel;
  class Block Treatment Sample HT Location Depth;
  model TN = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /
        ddfm=kr;
  random Block;
  random _residual_ /group= Treatment;
  nloptions maxiter=500 maxfunc=5000;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Tny2exp2;
  class Block Treatment Sample HT Location Depth;
  model TN=Block Block*Treatment Treatment|HT Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
  random Block Block*Treatment Sample(HT Treatment);
  random _residual_ /type=ante(1) subject=Sample(HT Treatment);
  *lsmeans treatment DAA treatment*DAA/ diff cl;
  *lsmeans Treatment/ diff=control('3') plot=diff;
  *lsmeans DAA/ diff plot=diff;
  *lsmeans Treatment*DAA/ slicediff=DAA plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 1 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 1 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 1 3] [1, 1 3] [-2, 3 3];
*contrast 'D4DAP - C4DAP' treatment 1 1 -2 treatment*DAA [1, 1 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 1 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 1 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 1 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 1 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 1 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;  
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;  
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;  
*contrast 'beetle - no beetle' treatment -1 1 0;  
*ods output covparms=Sasdata.covco2y1exp1;  
*ods output rcorr=Sasdata.corrco2y1exp1;  
run;

proc print;  
proc glimmix data=Sasdata.Tny2exp410cm;  
class Block Treatment Sample HT;  
model TN=Block Block*Treatment Treatment|HT/ddfm=satterth;  
random Block Block*Treatment;  
*lsmeans treatment DAA treatment*DAA/ diff cl;  
*lsmeans Treatment/ diff=control('3') plot=diff;  
lsmeans Treatment/ diff plot=diff;  
*lsmeans DAA/ diff plot=diff;  
lsmeans Treatment*HT/ slicediff=HT plot=diff;  
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];  
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];  
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];  
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];  
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];  
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];  
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];  
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];  
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];  
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;  
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;  
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;  
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;  
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;  
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;  
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;  
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;  
*contrast 'beetle - no beetle' treatment -1 1 0;  
*ods output covparms=Sasdata.covco2y1exp1;  
*ods output rcorr=Sasdata.corrco2y1exp1;  
run;

proc print;  
proc glimmix data=Sasdata.Tny2exp2;  
class Block Treatment Sample HT;  
model TN = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp / solution htype=1 ddfm=kr;  
*random Treatment(DAA);  
random Block Block*Treatment Sample(HT Treatment);  
random _residual_/ type=ante(1) subject=Sample(HT Treatment);  
*ods output covparms=Sasdata.covco2y1exp1;
ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Tn10cm plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model TN = Block Treatment|HT Location Location*Treatment Depth
Depth*Treatment /ddfm=kr;
random Block;
random residual /group= Treatment;
 nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Tn10cm;
class Block Year Treatment Sample HT;
model TN=Block Block*Treatment Year Treatment|HT/
 ddfm=satterth;
random Block Block*Treatment;
*lsmeans treatment DAA treatment*DAA/ diff cl;
 lsmeans Treatment/ diff plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy1exp1 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NPOC = Block Treatment|HT Location Location*Treatment Depth
Depth*Treatment /ddfm=kr;
random Block;
random _residual_ /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Npocy1exp1;
class Block Treatment Sample HT location depth;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=kr;
*random Block Block*Treatment;
*model NPOC=Block Block*Treatment Treatment|HT Sample Location Location*Treatment Depth Depth*Treatment/ddfm=satterth;
*random Block Block*Treatment Sample(HT Treatment);
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*Treatment/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans depth/ diff plot=diff;
*lsmeans location/ diff plot=diff;
*lsmeans Treatment*depth/ slicediff=depth plot=diff;
*lsmeans Treatment*location/ slicediff=location plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy1exp110cm;
class Block Treatment Sample HT;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control(’3’) plot=diff;
*lsmeans HT/ diff plot=diff;
lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocylexpl;
class Block Treatment Sample HT;
model NPOC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocylexpl2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NPOC = Block Treatment|HT Location Location*Treatment Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random _residual_ /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Npocy1exp2;
class Block Treatment Sample HT location depth;
*model NPOC=Block Block*Treatment Treatment|HT/ddfm=kr;
*random Block Block*Treatment;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
*lsmeans maxiter=1000 maxfunc=5000;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy210cm;
class Block Treatment Sample HT;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans Treatment/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocy1exp2;
class Block Treatment Sample HT;
model NPOC = Block Block*Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
  solution htype=1 ddfm=kr;
  *random Treatment(DAA);
  random Block Block*Treatment Sample(HT Treatment);
  random _residual_ /type=ar(1) subject=Sample(HT Treatment);
  *ods output covparms=Sasdata.covco2y1exp1;
  *ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy2exp1 plot=residualpanel;
class Block Treatment Sample HT location Depth;
model NPOC = Block Block*Treatment|HT Location Location*Treatment Depth Depth*Treatment /
  ddfm=kr;
  random Block;
  random residual /group= Treatment;
  nloptions maxiter=500 maxfunc=5000;
  covtest homogeneity;
  output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Npocy2exp1;
class Block Treatment Sample HT location depth;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=kr;
  *random Block Block*Treatment;
*model NPOC=Block Block*Treatment Treatment|HT Sample Location
Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_/type=ar(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff plot=diff;
*lsmeans Treatment/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans depth/ diff plot=diff;
*lsmeans location/ diff plot=diff;
*lsmeans Treatment*depth/ slicediff=depth plot=diff;
*lsmeans Treatment*location/ slicediff=location plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covpvars=Sasdata.covco2ylexp1;
*ods output rcorr=Sasdata.corrco2ylexp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy2exp310cm;
class Block Treatment Sample HT;
model NPOC=Block Block*Treatment Treatment|HT/ ddfm=satterth;
random Block Block*Treatment;
*random _residual_/type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff plot=diff;
*lsmeans Treatment/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocy2exp1;
class Block Treatment Sample HT;
model NPOC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random _residual_ /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;

proc print;
proc glimmix data=Sasdata.Npocy2exp2 plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NPOC = Block Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random _residual_ /group= Treatment;
noptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=oudt pred=pred residual=resid;
run;

proc glimmix data=Sasdata.Npocy2exp2;
class Block Treatment Sample HT location depth;
*model NPOC=Block Block*Treatment Treatment|HT/ddfm=kr;
*random Block Block*Treatment;
model NPOC=Block Block*Treatment Treatment|HT Sample Location Location*Treatment Depth Depth*Treatment/ddfm=kr;
random Block Block*Treatment Sample(HT Treatment);
random _residual_ / subject=Sample(HT Treatment);
*nloptions maxiter=1000 maxfunc=5000;
*lsmeans treatment HT treatment*HT/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast 'D2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast 'D3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast 'D7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast 'D10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D14DAP - 10DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast 'D21DAP - 14DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast 'D28DAP - 21DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast 'D56DAP - 28DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy2exp410cm;
class Block Treatment Sample HT;
model NPOC=Block Block*Treatment Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random _residual_ /type=ante(1) subject=Sample(HT Treatment);
*lsmeans Treatment/ diff plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment DAA treatment*DAA/ diff cl;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans DAA/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0;
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0;
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0;
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0;
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0;
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0;
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0;
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1;
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npocy2exp2;
class Block Treatment Sample HT;
model NPOC = Block Block*Treatment Treatment VWC Treatment*VWC O2 Treatment*O2 SoilTemp Treatment*SoilTemp AirTemp Treatment*AirTemp /
solution htype=1 ddfm=kr;
*random Treatment(DAA);
random Block Block*Treatment Sample(HT Treatment);
random residual /type=ar(1) subject=Sample(HT Treatment);
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;
proc glimmix data=Sasdata.Npoc10cm plot=residualpanel;
class Block Treatment Sample HT Location Depth;
model NPOC = Block Block*Treatment|HT Location Location*Treatment Depth Depth*Treatment /ddfm=kr;
random Block;
random residual /group= Treatment;
nloptions maxiter=500 maxfunc=5000;
covtest homogeneity;
output out=outd pred=pred residual=resid;
run;
proc glimmix data=Sasdata.Npoc10cm;
class Block Year Treatment Sample HT;
model NPOC=Block Block*Treatment Year Treatment|HT/ddfm=satterth;
random Block Block*Treatment;
*random residual /type=ante(1) subject=Sample(HT Treatment);
*lsmeans treatment HT treatment*HT/ diff cl;
lsmeans Treatment/ diff plot=diff;
*lsmeans Treatment/ diff=control('3') plot=diff;
*lsmeans HT/ diff plot=diff;
*lsmeans Treatment*HT/ slicediff=HT plot=diff;
*contrast 'D1DAP - C1DAP' treatment 1 1 -2 treatment*DAA [1, 2 1] [1, 1 1] [-2, 3 1];
*contrast 'D2DAP - C2DAP' treatment 1 1 -2 treatment*DAA [1, 2 2] [1, 1 2] [-2, 3 2];
*contrast 'D3DAP - C3DAP' treatment 1 1 -2 treatment*DAA [1, 2 3] [1, 1 3] [-2, 3 3];
*contrast 'D7DAP - C7DAP' treatment 1 1 -2 treatment*DAA [1, 2 4] [1, 1 4] [-2, 3 4];
*contrast 'D10DAP - C10DAP' treatment 1 1 -2 treatment*DAA [1, 2 5] [1, 1 5] [-2, 3 5];
*contrast 'D14DAP - C14DAP' treatment 1 1 -2 treatment*DAA [1, 2 6] [1, 1 6] [-2, 3 6];
*contrast 'D21DAP - C21DAP' treatment 1 1 -2 treatment*DAA [1, 2 7] [1, 1 7] [-2, 3 7];
*contrast 'D28DAP - C28DAP' treatment 1 1 -2 treatment*DAA [1, 2 8] [1, 1 8] [-2, 3 8];
*contrast 'D56DAP - C56DAP' treatment 1 1 -2 treatment*DAA [1, 2 9] [1, 1 9] [-2, 3 9];
*contrast '2DAP - 1DAP' DAA -1 1 0 0 0 0 0 0 0; 
*contrast '3DAP - 2DAP' DAA 0 -1 1 0 0 0 0 0 0; 
*contrast '7DAP - 3DAP' DAA 0 0 -1 1 0 0 0 0 0; 
*contrast '10DAP - 7DAP' DAA 0 0 0 -1 1 0 0 0 0; 
*contrast '14DAP - 10DAP' DAA 0 0 0 0 -1 1 0 0 0; 
*contrast '21DAP - 14DAP' DAA 0 0 0 0 0 -1 1 0 0; 
*contrast '28DAP - 21DAP' DAA 0 0 0 0 0 0 -1 1 0; 
*contrast '56DAP - 28DAP' DAA 0 0 0 0 0 0 0 -1 1; 
*contrast 'beetle - no beetle' treatment -1 1 0;
*ods output covparms=Sasdata.covco2y1exp1;
*ods output rcorr=Sasdata.corrco2y1exp1;
run;
proc print;