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Characterization and Selection of Hop Cultivars Adapted to Nebraska

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Characterization and Selection of Hop Cultivars Adapted to Nebraska

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Characterization and Selection of Hop Cultivars Adapted to Nebraska

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Hop (*Humulus lupulus* L.) is an ingredient in the beer brewing industry that provides beer its flavor and aroma. High demand from the brewing industry has encouraged production outside of the traditional Pacific Northwest, the primary production region. Producers in the Midwest are attempting to grow cultivars adapted to the Pacific Northwest, but environmental differences have caused low yields and changes in secondary metabolite content. To aid producers, a regional breeding program was initiated to develop cultivars adapted to the Midwest. Success of any breeding program relies on the selection of genetically superior parents to generate progeny with the traits of interest and genetically superior progeny for potential release. Therefore, objectives of this study included identifying superior parents, breeding populations, and progeny that could be used as foundational germplasm in a newly created hop breeding project. Traits characterized included performance ratings, flowering time, alpha acid content, and cohumulone content. Performance ratings and flowering time were evaluated annually from 2019 to 2021, and alpha acid content and cohumulone content were evaluated in 2020 and 2021. Data for this study were unbalanced, number of progeny from each parent and breeding population varied. Progeny genotypes changed from year to year, and number of replicates of individual genotypes also varied. Breeding values of both parents and populations varied widely for the traits measured, indicating that parents were diverse and that improved cultivars can be developed from germplasm used in this study. Sixteen

maternal parents, 18 paternal parents, and 23 breeding populations were selected as superior and advanced for use in future progeny development. Genetic values (BLUPs) of the progeny were variable for all traits evaluated. Forty-nine female progeny were selected as superior and will be advanced with potential for release as locally adapted cultivars. Information gained from this study will support future breeding decisions contributing to the development of new Midwest adapted hop cultivars.

DEDICATION

To Luella,

Thank you for your unconditional love, loyalty, and support.

You always believed in me and never left my side throughout this journey.

You are the best dog in the world.

"Dogs are our link to paradise. They don't know evil or jealousy or discontent. To sit with a dog on a hillside on a glorious afternoon is to be back in Eden, where doing nothing was not boring -- it was peace." ~Milan Kundera, The Unbearable Lightness of Being

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LIST OF ABBREVIATIONS

Abbreviation	Meaning
ALP	Alpha acid content
ANOVA	Analysis of variance
BLUEs	Best Linear Unbiased Estimators
BLUPs	Best Linear Unbiased Predictors
BVs	Breeding Values
COH	Cohumulone content
EBVs	Estimated breeding values
EGVs	Estimated genetic values
FT	Flowering time
HSI	Hop storage Index
ICE-4	International calibration extract
LC-MS-MS	Liquid chromatography with tandem mass spectrometry
LMM	Linear mixed model
LSD	Least significant difference
PRs	Performance ratings
USDA	U. S. Department of Agriculture

CHAPTER ONE

Literature Review

Genus: *Humulus* (Hop)

Humulus is a genera in the botanical family Cannabaceae with three recognized species, one species having economic importance in the beer brewing and pharmaceutical industries. The three recognized *Humulus* species are: *H. yunnanesis* Hu., *H. japonicus* Siebold & Zucc., and *H. lupulus* L. Very little information exists on *H. yunnanensis,* and it has only been found in the Yunnan province of China. Small (1978) recognized that *H. yunnanesis* is often mistaken for *H. lupulus* but is more closely related to *H. japonicus*. *H. japonicus* is indigenous to Eastern Asia, and it was introduced to North America in the mid to late 1800s. Although this species is cultivated primarily for ornamental value, it is often considered a weed, and even an invasive species because of its aggressive growth habit. *H. japonicus* is dioecious, and the chromosome number and sex chromosomes for females is 2n=2x=14+XX, and for males is 2n=2x=14+XY1Y2 (Shephard et al., 2000).

H. lupulus is a perennial bine which is native to temperate regions in the northern hemisphere. Because of its use in the beer brewing and pharmaceutical industry, it is currently the only commercially important species. It is predominantly dioecious and usually diploid. Compared to *H. japonicus*, it differs in chromosome number and sex chromosome system, with females having chromosome numbers of 2n=2x=18+XX and males having chromosome numbers of 2n=2x=18+XY (Shephard et al., 2000). Because *H. japonicus* and *H. lupulus* differ in chromosome number and sex chromosome systems, crossing attempts between the two species have never been successful (Winge, 1914). However, *H. lupulus* and *H. japonicus* have the same sex determination system, X

chromosome to autosome set balance system. When the X chromosome to autosome set ratio is 1.0, a female results, and when the sex determination ratio is 0.5 or less, a male results. A ratio between 0.5 and 1.0 results in a monoecious plant (Shephard et al, 2000), which can exhibit different sex phenotypes, and can either be diploid or polyploid (Skof et al., 2012). There are monoecious plants that possess sterile male flowers suggesting the Y chromosomes are unessential in determining the sex phenotype but are essential for pollen development (Shephard et al., 2000).

Humulus lupulus

Humulus lupulus is classified into five botanical varieties based on leaf and stem morphological traits and geographical distribution (Small, 1978). Differentiating between the varieties by morphological traits may be challenging since the variation within each trait is highly variable, even in a single population. (Bassil et al., 2008). Therefore, geographical distribution is typically used to distinguish the varieties. Two of the five varieties of *H. lupulus* are not native to the United States: var. *cordifulus* and var. *lupulus*. *H. lupulus* var. *cordifulus* is found in eastern Asia, primarily Japan, while *H. lupulus* var. *lupulus* is indigenous to Europe but was introduced into Japan and North America (Small, 1978). In North America, it is prominent in the Northeast region, with sporadic populations occurring throughout the United States. Three of the five botanical varieties of *H. lupulus* are native to North America: var. *lupuloides*, var. *neomexicanus*, and var. *pubescence*. *H. lupulus* var. *lupuloides* is prominent in the North Central and Northeast regions of the continent, while *H. lupulus* var. *neomexicanus* is mainly found in the North and Southwest regions of the United States and North Central Canada. The final cultivar,

H. lupulus var. *pubescence*, is most prevalent in the Midwest region of the United States (Tembrock et al., 2016). Differentiating between the North American varieties may be challenging since there are areas of the continent where they occur in the same region (Tembrock et al., 2016). Each variety can coincide with one of the other varieties in areas of the Midwest. In eastern Nebraska, all three coincide. Because they all inhabit this region, there is the possibility for gene flow between them (Reeves & Richards, 2010).

Traditionally, cultivated hops only comprised the European variety, *H. lupulus* var. *lupulus* (Moir, 2000). During the twentieth century, a traditional European variety was crossed with an indigenous North American wild hop (*H. lupulus* var. *lupuloides*) to improve beer brewing qualities and disease resistance (Moir, 2000). This cross produced renowned hop cultivars such as 'Brewers Gold', 'Northern Brewer', and 'Bullion'. Many modern cultivars used in beer production descend from these renowned cultivars; therefore, they have a common ancestry.

Importance of Crop

The hop female inflorescence (cones) are an essential ingredient used by the beer brewing industry. The cones form glandular trichomes (lupulin glands), which produce bitter acid and essential oil compounds that give beer its flavor, bitterness, aroma, and antimicrobial properties. The bitter acids, composed of alpha acids (humulone, cohumulone, and adhumulone) and beta acids (lupulone, colupulone, and adlupulone), provide beer its bitter flavor and antimicrobial properties (Castro et al., 2008). Of the bitter acids, the alpha acids are the main contributor. The essential oils, predominantly composed of caryophyllene, farnesene, humulene, and myrcene, provide beer with unique

flavors and aromas (McAdam et al., 2013). The ratio of the bitter acid and essential oil compounds are cultivar dependent, providing each cultivar a unique flavor and aroma profile.

Hop cultivars are divided into three categories based on their alpha acid and essential oil content, (1) aroma, (2) dual-purpose, and (3) bittering. Aroma hops are typically low in alpha acid content and high in essential oils. Dual-purpose hops are high in both alpha acid and essential oil content. Bittering hops have high alpha acid content and low essential oil content. The type of cultivar selected by brewers varies depending on their recipes.

Commercial Production

The majority of the world's hop production occurs between the 35th and 55th parallels, north, and south of the equator. Areas between these parallels provide the adequate climate and photoperiod hops need to flower. Commercially, hops are grown on a trellis system, typically 6 m tall, to maximize growth and yields (Kneen, n.d., pp. 20-23). The shoots are trained and grow in a clockwise direction around a string, usually coir. Currently, the top producing countries are the United States and Germany. Most hops produced in the U.S. come from the Pacific Northwest region, Washington, Oregon, and Idaho. In 2021, 116.5 million pounds of hops were produced in the United States, with 115.6 million pounds (99.9 %) coming from the Pacific Northwest (Hop Growers of America, 2022). Total U.S. production nearly doubled from 2012 to 2021 (Hop Growers of America, 2022). Hop production has increased worldwide because of the recent and steady increase in the number of craft beer breweries (Brewers Association, 2021). Even

though production has nearly doubled, producers are still not able to fill demand, causing scarce supply and the cost of hops to increase. To help lower costs and fulfill demand, regions outside of the Pacific Northwest have begun producing hops.

Production in the Midwest

In the Midwest, producers are attempting to grow popular commercial cultivars developed for the Pacific Northwest, but because of the different climate and photoperiod, the flavor profiles and yields are inconsistent. The climate in the Midwest is considerably more unpredictable than in the Pacific Northwest. The Midwest is prone to having late spring and early fall frosts; in some years, both can occur. Late spring frosts will kill any initial growth and extend the time until harvest. Early fall frosts can damage the cones, causing poor yields or, if severe enough, can destroy the entire crop. Hail-producing storms that occur in the Midwest, typically during the spring and summer, can damage hop leaves and trained shoots, again, extending the time until harvest. The Midwest is also more susceptible to higher winds throughout the growing season, which cause the plants to dry out. Water stress affects the plants at all developmental growth stages, but mostly during cone development, reducing yields and alpha acid content (Nakawuka et al., 2017).

Cool temperatures and rainy conditions during the spring and fall in the Midwest are ideal for hop diseases to occur. Two of the most devastating diseases that thrive in these conditions are powdery mildew caused by *Podosphaera macularis* and downy mildew caused by *Pseudoperonospora humuli*. Powdery mildew is a fungal disease common in hop yards in the Pacific Northwest. It is an emerging disease in the Midwest

and was recently found in Michigan (Lizotte & Miles, 2021b). The disease is not extensive outside of the Pacific Northwest because hop production is relatively new in these regions (O'Neal et al., 2015). Powdery mildew infects all areas of the bine, including the cones; it disrupts alpha and beta acid production and, if severe enough, will ultimately lead to yield loss (Plant Disease Diagnostic Clinic, 2017). It overwinters on the crown of hop plants and, in the spring, infected shoots emerge. If left untreated, spores will produce and spread by wind, causing further infection. The disease will appear as circular powdery white colonies on all above-ground plant organs, and the cones will also appear malformed (O'Neal et al., 2015). If the cones are infected during later stages of development, they will have a red discoloration.

The prevalent disease found in the Midwest is downy mildew; like powdery mildew, it can infect the whole bine, including the cones, inevitably leading to yield and quality loss (Lizotte & Miles, 2021a). As well as thriving during the spring and fall, downy mildew also favors the humid Midwest summer months when there are high-temperature fluctuations. The fungal-like oomycetes pathogen typically first appears in the spring on emerging shoots from infected crowns. Infected shoots, referred to as basal spikes, have curled leaves, short internodes and, overall, a stunted, chlorotic appearance (Lizotte & Miles, 2021a). Basal spikes cannot be trained to grow up a trellis; only if uninfected shoots emerge can the bine be trained and continue growing throughout the season. If infection occurs after training, the main bine becomes stunted and can cease growth (O'Neal et al., 2015). Lateral shoots also become stunted and potentially unable to produce cones. The upper sides of leaves form brown angular lesions. Sporangia, appearing as black masses, form on the underside of leaves. Infected flowers will

desiccate and fall off the bine. Cones infected during early development will become hard and brown and may stop developing. Infections on mature cones may cause discolored bracts, which can reduce their value or destroy the entire crop. The severity of infection depends on the time of infection and cultivar susceptibility (Infante-Casella & Bamka, 2017).

Photoperiod and temperature impact hop growth and development because their interaction regulates flowering (Thomas & Schwabe, 1969). The increase in photoperiod and temperature during the spring signals the end of dormancy. Vegetative growth is promoted as the photoperiod and temperature continually increase into the summer. Hops are short-day sensitive and transition from vegetative to reproductive growth when the photoperiod begins to decrease (Bauerle, 2019). The daylength required is specific to each genotype; this transition typically takes place around the summer solstice. Cultivars developed for the Pacific Northwest do not flower at the same time in the Midwest. If cultivars flower too early, they may have reduced yields if they switch to reproductive growth before reaching their potential height.

Development of Midwest Cultivars

It is essential to develop locally adapted cultivars to help solve production challenges in the Midwest. The demand for locally adapted cultivars has created a need for regional hop breeding programs. To support this need, the University of Nebraska-Lincoln established a hop breeding program in 2016. The goal of the program is to develop downy mildew-resistant, locally adapted cultivars with unique brewing qualities through conventional plant breeding methods. Developing cultivars resistant to downy

mildew is fundamental because of its prevalence and the negative impacts it has on yield and production. Cultivars adapted to the Midwest should flower between mid-June to mid-August, so they can maximize their growth and yield and avoid damage caused by unfavorable weather in the spring and fall. Because the yield and flavor profiles depend on environmental conditions, having locally adapted cultivars will provide producers with a consistent yield and provide brewers with a consistent flavor profile.

Parental Germplasm Diversity

Development of new cultivars begins with the selection of parental genotypes. Public elite cultivars are generally crossed with wild hops to combine brewing qualities with local adaptation traits. Female parents are typically public elite cultivars popular amongst brewers. However, because many modern cultivars descend from a few common ancestors, locally adapted female wild hops can be included as a source of genetic variation. The wild hops introduce new genetics since they are acclimated to different environments and exposed to distinct pressures and populations of insects and diseases (Livingston-Garcia, 2018). Male parents are usually wild hop varieties found locally or from a clonal germplasm repository that are adapted to or perform well in the region**.**

Conventional Breeding Selection

Conventional breeding is a long and laborious process that can take up to a decade or longer to release a new cultivar. The chances of developing an improved cultivar that possesses all the desired traits from a single cross are relatively low. Breeders must conduct numerous crosses and evaluate an extensive amount of progeny. To reduce the

number of progeny evaluated each year, breeders must select parental genotypes that develop progeny with the desired traits of interest. Typically, breeders select parental genotypes by evaluating their progeny's phenotype and eliminating those that generate inferior progeny. However, phenotypes are influenced by both genetic and environmental factors, and selection decisions need to be based solely on genetics. To make selection decisions based on genetic effects, breeders implement statistical analyses.

Henning & Townsend (2005) conducted a study by crossing five maternal and five paternal genotypes and assessing their progeny for two years. To determine which parents developed the best progeny based on genetic effects, they used an analysis of variance (ANOVA) and Fisher's protected least significant difference (LSD) test. From the results, they were able to identify superior parents and crosses that developed progeny with the traits of interest. In their study, an equal number of progeny represented each parent and cross. The progeny also had the same number of replicates and were grown in one location and evaluated in that location for several years.

Often in a breeding program, parents and crosses will not have an equal number of progeny. Their progeny also will not be evaluated in the same year or possibly the same location. Each season, progeny is developed, the genotypes evaluated with no or an unequal number of replicates, those that perform well are kept for reevaluation, and all others eliminated. The unequal number of progeny and replicates cause unbalanced data. An ANOVA and Fisher’s LSD test are not the best techniques for selection decisions when there is unbalanced data, because they assume data is balanced.

To aid in selection decisions when there is unbalanced data, a linear mixed model analysis (LMM) can be used to obtain the Best Linear Unbiased Predictors (BLUPs) of

random effects (Henderson, 1975). To correct for unequal progeny and replicates, the analysis implements pedigree information. Including the pedigree provides genetic trends for a more precise prediction. The analysis also separates genetic and environmental effects, allowing for a direct comparison of progeny.

BLUPs predict the breeding values of parents and crosses. The predicted breeding values, referred to as estimated breeding values (EBVs), convey the genetic merit of a parent or a cross for a certain trait. These values are expressed as a deviation from the population mean, which is zero. BLUPs feature a shrinkage property, which adjusts above-average and below-average values towards the population mean to provide a more accurate prediction of the breeding value (Piepho et al., 2007). The shrinkage factor is based on the trait heritability and the number of observations for each genotype.

Heritability, defined as the ratio of the phenotypic variation due to genetic variation is measured on a scale from zero (low) to one (high). Traits with high heritability indicate a strong connection between the progeny's phenotype and the parent's genotype, these traits are easier to breed for and improve. Traits with low heritability can indicate the genetic variation is small. However, it can also indicate a strong environmental influence or unreliable phenotype documentation. The higher the heritability, the more observations, the more accurate the breeding values are and less shrinkage towards the mean occurs.

It is not only important to accurately select parents in a breeding program, but progeny for advancement and potential release. The LMM can be used to obtain BLUPs of predicted genetic values to aid in the selection of progeny for a trait of interest. BLUPs

of predicted genetic values, referred to as estimated genetic values (EGVs) describe how the genes of progeny impact their performance.

Early Progeny Evaluations

Early progeny evaluations can be limited because hops are perennials and the yield and flavor profiles take several years to mature (Cerenak et al., 2009). Since the actual yield of progeny can't be assessed until maturation, potential yield can be evaluated by morphological traits such as internode length and lateral branch length. Bines that have short internodes produce more nodes which is where the lateral branches develop. The lateral branches are where the flowers form, and eventually, the cones. Therefore, bines that have shorter internodes and develop more lateral branches will potentially produce more cones, having a higher yield (Skomra et al., 2013). However, this also depends on the length of the lateral branches, as bines with short internodes and short laterals are not likely to have a high yield. Roberts et al. (1980) observed that the length of lateral branches positively correlated with yield. Even though yield increases as the length of lateral branches increase, bines with longer branches need to be spaced further apart in commercial production. Spacing them further apart helps prevent neighboring bines from shading each other and tangling. By spacing them further apart, fewer bines are planted, decreasing the overall yield. So, when evaluating potential yield, it's important to consider both the internode length and lateral branch length, as both traits determine a genotype's potential yield.

Even though the secondary metabolites take several years to mature, they can still be assessed early in a breeding program to determine the variation that exists within the

population. It can also help eliminate progeny with undesirable proportions. Because brewers select for high alpha acid content or high essential oil content, progeny with low levels of both compounds can be eliminated since they will not provide good brewing qualities.

Progeny evaluations typically begin with evaluating for disease resistance because of the negative effects disease can have on growth and development. Because the severity of disease depends on the time of infection and environmental conditions, disease resistance should continue to be evaluated as progeny advance through the program. Selection for traits such as the time of flowering, gender, and vigor are also typically evaluated early in a breeding program. The time of flowering breeders select for depends on the environment where the cultivars will be commercially produced. Usually, breeders select for a range of flowering times, so producers can spread out the time of harvest. While mainly female progeny are selected for advancement, it is also important to select males as they contribute desired traits to progeny and can be used in future breeding efforts. Vigor is a selection criterion in a breeding program because it informs how progeny will perform in a particular environment. Vigor can be determined by the growth rate of the main bine from the time of transplantation or emergence in the spring until the plant transitions from vegetative to reproductive growth.

Summary & Objectives

Even though the selection of traits can be limited during early progeny evaluations, which traits to evaluate and how to evaluate them are important decisions in a breeding program. Ineffective selection of traits and evaluation protocols can lengthen

the time to develop improved cultivars. Not only are the selection of traits important to the success of a breeding program, but the selection of parental genotypes and the appropriate crosses to generate progeny with the traits of interest. Likewise, once progeny are generated, superior genotypes must be selected for advancement and potential release. While the selection of superior parental genotypes, crosses, and progeny genotypes can be accomplished based on phenotypic progeny evaluations, these decisions need to be based on genetic factors. To assist in selection based on genetic factors, a LMM can be used to determine the Best Linear Unbiased Predictors (BLUPs).

Currently, Midwest hop producers rely on cultivars adapted to the Pacific Northwest. The inconsistent yields and brewing qualities of these cultivars caused by the different environmental conditions have created a need for locally adapted cultivars. The University of Nebraska-Lincoln established a regional hop breeding program to develop these cultivars and aid Midwest producers. Success of the program begins with the accurate selection of superior parental genotypes and crosses. For this study, crosses will be referred to as breeding populations. Additionally, the program depends on the selection of superior progeny for advancement. Therefore, the purpose of this study was to utilize the LMM analysis to select superior parental genotypes, breeding populations, and progeny genotypes to support hop breeding in Nebraska. The objectives were to: 1) select superior parental genotypes and breeding populations by estimates of their breeding value (EBVs); 2) select superior progeny genotypes by estimates of their genetic value (EGVs); and 3) determine heritability estimates for the traits evaluated in this study, which were performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH).

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CHAPTER TWO

Introduction

Hop (*Humulus lupulus* L.) is a dioecious perennial bine native to temperate regions in the northern hemisphere. Female inflorescence (cones) of the hop plant produces secondary metabolites used by the beer brewing industry, bitter acid and essential oil compounds. Bitter acids, which consist of alpha acids and beta acids, provide beer with antimicrobial properties and bitter flavor, with alpha acids being the main contributor. Essential oil compounds provide beer with unique flavor and aromas. Each hop cultivar has a unique ratio of bitter acid and essential oils, providing a distinct profile of flavor and aroma.

Cultivars are divided into three categories, (1) aroma, (2) dual-purpose, and (3) bittering. Aroma cultivars are high in essential oils and low in alpha acids; dual-purpose cultivars are high in both essential oils and alpha acids; bittering cultivars are low in essential oils and high in alpha acids. The type of cultivar selected by a brewer depends on the recipe of the beer they are brewing. When selecting cultivars having high alpha acid content, brewers also consider the proportions of the component acids. These three main component acids are humulone, adhumulone, and cohumulone, with brewers preferring low levels of cohumulone because it produces a harsh quality of bitterness.

The United States is the largest hop-producing country, with 116.5 million pounds produced in 2021 (Hop Growers of America, 2022). The majority of hops (99.9 %) produced in the United States come from the Pacific Northwest, with 73 % produced in Washington, 16 % in Idaho, and 11 % in Oregon (Hop Growers of America, 2022). Only 900,000 pounds of hops were grown outside of the Pacific Northwest in 2021 (Hop

Growers of America, 2022). Hop production has nearly doubled in the last decade because of the recent steady increase of the number of craft beer breweries (Brewers Association, 2021). Even though production has increased, producers in the Pacific Northwest are still unable to fill demand, causing a shortage of hops. To help fulfill demand, there is interest in increasing production in regions outside of the Pacific Northwest.

To meet this increase in demand, Midwest producers are attempting to grow cultivars developed for the Pacific Northwest, however environmental conditions in the Midwest are more unpredictable than those in the Pacific Northwest. For example, temperature fluctuations in the Midwest are more extreme than those in the Pacific Northwest, with fluctuations in the Midwest frequently resulting in late spring or early fall frosts. Late spring frosts can damage initial spring growth and extend time to harvest. Cones can be damaged by early fall frosts, lowering yield, and potentially destroying the entire crop. Likewise, there is less precipitation in the Midwest, which can result in water stress. Water stress impacts hop growth and development across all growth stages but is most significant during cone development causing reductions in yield and secondary metabolite content (Nakawuka et al., 2017).

Hop diseases also negatively impact growth, development, and yield. In the Midwest, conditions are conducive to downy mildew, caused by *Psuedoperonospora humuli* throughout the growing season. Downy mildew can thrive during cool and rainy springs and falls but is most severe during the humid summer months when temperature fluctuates. Downy mildew can cause complete yield loss depending on the cultivar's susceptibility and timing of infection (Infante-Casella & Bamka, 2017).

Hops are short day sensitive, and day length required to transition from vegetative growth to flowering is specific to each genotype. Because of the latitudinal differences, there are day-length differences between the Pacific Northwest and the Midwest, and consequently time to flowering of cultivars developed for the Pacific Northwest is altered when the same cultivars are grown in the Midwest, with potential negative consequences. Transition from vegetative to reproductive growth typically occurs close or immediately after the summer solstice when day length begins to decrease. Flowering early tends to shorten the overall height and reduce number of lateral branches. As cones develop on lateral branches, any reduction in number of lateral branches reduces yield. Likewise, cultivars flowering late during the season, are more likely exposed to early fall frosts which can damage the cones.

Because of the production challenges associated with growing Pacific Northwest cultivars in the Midwest there is demand from Midwest producers for the development of locally adapted cultivars. In 2016 the University of Nebraska-Lincoln initiated a regional hop breeding program targeting development of adapted cultivars useful to Midwest producers. Goal of the program is to develop downy mildew-resistant, locally adapted cultivars with unique brewing qualities using conventional breeding methods.

An approach to develop cultivars adapted to the Midwest is to start with breeding crosses made between public elite cultivars and wild hops collected regionally and/or other genotypes retrieved from a clonal germplasm repository, with intent of combining the brewing qualities of Pacific Northwest genotypes with the local adaptation of wild hops collected. Because conventional breeding requires evaluating a large number of progeny at the cost of labor, space, and other resources, selection of parental genotypes

contributing desired traits to progeny is essential. Evaluation of parents and progeny resulting from parental crosses frequently consist of phenotypic evaluations, with selected progeny being retained for further evaluation and characterization.

However, selection based on phenotypic data can be difficult when evaluations are conducted across years and locations, and especially when genotypes are unequally represented across those years and locations. Breeding crosses amongst parents typically result in unequal number of progeny within each population and depending on availability of nursery space and/or available seed, progeny may not be equally replicated. Phenotypic measurements are a function of both genetic and environmental effects, yet cultivars must be selected and advanced based upon genetic effects, not on phenotypic observations.

To assist with making accurate selection decisions based upon genetic effects, linear mixed model analyses (LMM) based upon Henderson's Best Linear Unbiased Predictors (BLUPs; Henderson 1975) can be used. Such analyses are especially useful when data are widely unbalanced. LMM adjusts for unequal number of experimental units and/or of replicates when analyzing phenotypic data. Additionally, the methodology separates genetic effects from environmental effects, so the genetic value of genotypes can be directly compared. The methodology has been a standard in animal breeding (Henderson, 1975) and is widely used in plant breeding programs for crops such as buffalograss (Serba et al., 2012), maize (Oliveira et al., 2016), and peanut (Milla-Lewis & Isleib, 2005).

Best Linear Unbiased Predictors are the predictors of relative breeding values (BVs) of parents and their breeding populations. BVs, also called estimated breeding

values (EBVs), express the genetic value of parents or populations. For progeny genotypes, BLUPs are the predictors of their relative genetic value for the trait of interest. Predicted genetic values, sometimes referred to as estimated genetic values (EGVs), predict the long-term genetic value, i.e., the expected performance of a genotype. BLUPs are expressed as a deviation from the population mean. The population mean of BLUPs, by definition, is zero.

To adjust for unequal replication of genotypes, thereby ensuring accurate selection and reducing the risk of misinterpretation, BLUPs are a function of a shrinkage or regression property. The shrinkage property shifts above-average and below-average values closer towards the population mean (Piepho et al., 2007), with the degree of shrinkage based on number of observations per genotype and the heritability of the trait in question. So, a greater number of observations for a given genotype contributes to more accurate values. Likewise, high heritability results in less shrinkage towards the population mean.

When data are unbalanced, with unequal number of genotypes and replicates, it is difficult to estimate additive and non-additive genetic variances and classify the type of heritability estimated. Therefore, for this study heritability will be defined as the ratio of genetic variance to total variance where total variance equals the sum of genetic variance and all other variances. Therefore, heritability is an expression of the proportion of the phenotypic variation that is attributed to genetic factors and is expressed on a scale from zero to one. Traits with a heritability close to one indicate that phenotypic variation is mainly due to genetic variation, whereas low heritability indicates that genetic variation

is small and/or there is significant error variance, which may be due to environmental factors or inaccurate phenotyping.

Success of a breeding program relies on the accurate selection of genetically superior parents, using those parents to make appropriate breeding crosses, and accurately identifying and selecting genetically superior progeny for advancement and release. Therefore, the purpose of this study was to select superior parents, identify superior breeding populations, and to select superior resulting progeny in development of the foundation of the hop breeding program at the University of Nebraska. Due to the unbalanced nature of the data, analysis and selection was facilitated by using linear mixed model analyses. Specific objectives were to: 1) select superior parental genotypes and breeding populations based upon estimates of their breeding values (EBVs); 2) select superior progeny based upon estimates of their genetic values (EGVs); and 3) estimate heritability for traits deemed important to producers and brewer. Those traits included performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH).

Materials & Methods

Nurseries

Maternal and paternal nurseries were established at the University of Nebraska-Lincoln's East Campus Research Farm in 2016. The nurseries were in two separate areas of the farm to prevent unwanted cross-pollination and to facilitate controlled crosses. The maternal nursery was established on a 6 m tall V trellis system similar to systems used by

commercial producers (Kneen, n.d., pp. 20–23). The nursery consisted of three rows that were 46 m long. Rows were spaced 4 m apart. Genotypes in the maternal nursery were public elite cultivars popular amongst brewers and local wild hops collected from Midwest Hop Producers near Plattsmouth, Nebraska (Table 2.1). The number of genotypes and replicates within each row varied.

The paternal nursery was established using a teepee-style trellis system (Kneen, n.d., pp. 20–23). Three 4 m tall teepee-style trellises were placed 6 m apart. Genotypes in the paternal nursery consisted of accessions retrieved from the U. S. Department of Agriculture (USDA), Agricultural Research Service, National Clonal Germplasm Repository in Corvallis, Oregon, as well as locally found wild hops retrieved from Midwest Hop Producers near Plattsmouth, Nebraska (Table 2.1). Number of unique genotypes as well as the number of replicates at each trellis varied.

In 2019, two progeny nurseries were constructed at the research farm, near the maternal nursery. The two nurseries were parallel to each other and spaced 9 m apart. Genotypes included in the progeny nurseries changed across evaluation seasons (Appendix A), with evaluations being conducted in a given progeny nursery in alternate years, as follows: Progeny were evaluated in one nursery for one season, then selected progeny were propagated by cuttings and overwintered in a greenhouse. Progeny not selected were eradicated from the nursery. The next growing season, selected progeny were transplanted from the greenhouse to the alternate nursery, along with any newly developed progeny. This system of using alternate nurseries prevented the reemergence of eradicated genotypes due to remaining viable rhizomes.

Nurseries used for each annual evaluation were arranged in rows 46 m long, with the number of rows varying from three to six each season, depending on the number of progeny. Progeny were arranged in a completely randomized design, spaced 0.3 m apart, and trained to grow up 2 m bamboo stakes. Biodegradable plastic was placed on the soil surface to prevent growth of weeds, and drip irrigation was installed for efficient watering.

Progeny Development

Progeny were created during the 2018, 2019, and 2020 growing seasons using genotypes from the nurseries located on the East Campus Research Farm. Parental genotypes used to develop progeny differed across seasons. Progeny were first developed in 2018 from crosses made between genotypes established in the maternal and paternal nurseries (Table 2.1). Crosses were not made prior to the 2018 growing season, allowing the parental genotypes time to establish and mature. Crosses were made in the 2019 and 2020 growing seasons again using genotypes from the parental nurseries (Table 2.1). Additional crosses were made in 2019 and 2020 using progeny in the progeny nursery as parents.

Crossing, harvest, and processing was done as described below. Pollen was collected from the desired male plant(s) in 4-1/4 X 4-3/4 X 2-1/2 X 15-1/2 water repellant Canvasback tassel bags manufactured by Seedburo Equipment Company, part No. T415 (Des Plaines, IL). A bag containing pollen from a specific male was then placed over a lateral branch of a receptive female and tied to the bine. Once mature, cones were individually collected by cutting the lateral branch off at the end of the bag.

Cones were then air-dried for three weeks in preparation for seed removal. Seeds were removed by breaking apart the cones and manually removing the seeds. Once removed, seeds were cleaned using a solution of ethanol, bleach, and water in a 2:4:10 ratio, rinsed and placed in Petri dishes. Seeds were then treated with 20ppm Captan fungicide and stratified in a Fisher Scientific Isotemp Refrigerator at 5°C for eight weeks. After stratification, seeds were germinated, and individual resulting plants grown in a greenhouse. Resulting progeny remained in the greenhouse until the following June when they were transplanted to the progeny nurseries in the field.

Progeny Nursery Evaluations

Progeny were evaluated the first growing season after the season in which the seed was produced e.g., progeny resulting from summer 2018 crosses were evaluated in the summer of 2019. Therefore, progeny were evaluated in 2019, 2020, and 2021. There was no replication of genotypes during their first year of evaluation. Genotypes advanced from the non-replicated first year evaluations were evaluated in subsequent years, replicated one to five times each year.

In each season of evaluation, progeny were transplanted into the progeny nurseries during the first two weeks of June. Data collection began two weeks after all progeny were transplanted. In all three years the time of flowering was recorded, and gender was identified (Table 2.2). Time of flowering (FT) was documented as the week the first flowers on the individual plant fully opened. Gender was recorded as either female, male, or monoecious.

Progeny were also given a numeric performance rating based on observed performance in the field (Table 2.2). Performance ratings (PRs) were scored using a scale of one to five, one being the worst score and five being the best score. Rating scores were recorded three times throughout the season, in mid-June, mid-July, and mid-August. Ratings were based on visual observations as a single aggregate score of four traits: downy mildew resistance, vigor, internode length, and lateral branch length. Occurrence of downy mildew was the result of natural inoculation and was characterized by the magnitude of lesions on leaves. Vigor was characterized by comparing length of the main bine to the 2 m bamboo stake. Progeny were classified as 1) highly vigorous if their main bine was over 2 m tall, 2) vigorous was between 1 m and 2 m, and 3) not vigorous if below 1 m. Because hops are perennials and take several years to mature, yield of cones could not be measured in the progeny nurseries. As an alternative measure of yield, length of internodes on the main bine and length of the lateral branches were used as indicators of potential yield. As ratings were assigned as an aggregate assessment of several traits, a given rating does not imply equal value for any of the single traits contributing to the rating in question. For example, a performance rating of five could have been recorded for a given genotype because the genotype showed no signs of downy mildew and appeared to be highly vigorous or because they appeared to be highly vigorous and had the potential to produce a high yield.

In 2020 and 2021, cones were collected from a subset of the genotypes in the progeny nurseries (Table 2.3, Appendix B), and characterized for alpha acids using liquid chromatography with tandem mass spectrometry (LC-MS-MS) analysis, using the international calibration extract hop standard (ICE-4). Ten cones from the subset were

placed in Ziploc quart freezer bags and sent to the Proteomics and Metabolomics Facility at the Center for Biotechnology at the University of Nebraska-Lincoln for analysis. The analysis quantified the total concentration of alpha acid content (ALP) and the total concentration of cohumulone content (COH) in mg/g of fresh hop cones (Table 2.2, Appendix B).

For the PRs and FT traits, data were collected on 589 progeny, consisting of 379 unique progeny genotypes and 210 replicated progeny (Table 2.3, Appendix A), and were analyzed using LMM. Number of replicates for each unique progeny genotype varied from one to eight (Table 2.3, Appendix A). These progeny originated from 74 breeding populations (Table 2.3, Table 2.4) created from crosses between 53 maternal (Table 2.5) and 46 paternal parents (Table 2.6). Number of progeny genotypes within each breeding population varied from 1 to 70 (Table 2.4). The number of progeny originating from each parent ranged from 1 to 130 (Table 2.5, Table 2.6).

The analyses for ALP and COH contained 105 progeny, consisting of 67 unique progeny genotypes and 38 replicated progeny (Table 2.3, Appendix B). Number of replicates for each unique progeny genotype varied from one to eight (Table 2.3, Appendix B). These progeny were derived from 35 breeding populations (Table 2.3, Table 2.4), that originated from crosses between 26 maternal (Table 2.5) and 26 paternal parents (Table 2.6). The number of progeny from each breeding population ranged from 1 to 13 (Table 2.4), and from 1 to 26 for each parent (Table 2.5, Table 2.6).

Mixed Linear Model

Best Linear Unbiased Predictors (BLUPs), estimates of breeding values (EBVs) and genetic values (EGVs), as well as estimates of variance components were calculated using Echidna Mixed Models Software (Gilmour, 2020). Using matrix notation, the linear mixed model equation used for the analysis is expressed as follows:

$$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Zu} + \boldsymbol{e}$$

$\boldsymbol{y}$ = vector of observations,

$\boldsymbol{X}$= design matrix of fixed effects (relates $\boldsymbol{y}$ to $\boldsymbol{b}$),

$\boldsymbol{b}$ = vector of fixed effects,

$\boldsymbol{Z}$= design matrix of random effects (relates $\boldsymbol{y}$ to $\boldsymbol{u}$)

$\boldsymbol{u}$ = vector of random effects, and

$\boldsymbol{e}$ = vector of residual errors

Years were set as fixed effects and expressed as Best Linear Unbiased Estimators, BLUEs. Genotypes were set as random effects and solutions expressed as Best Linear Unbiased Predictors, BLUPs. BLUEs ($\widehat{\boldsymbol{b}}$) and BLUPs ($\widehat{\boldsymbol{u}}$), have solutions:

$$\widehat{\boldsymbol{b}} = (\boldsymbol{X^1 V^{-1} X})^{-1} \ \boldsymbol{X^1 V^{-1} y}$$

$$\widehat{\boldsymbol{u}} = \boldsymbol{G Z^1 V^{-1}} \ (\boldsymbol{y} - \boldsymbol{X}\widehat{\boldsymbol{b}})$$

where:

$\boldsymbol{G}$ = genetic variance-covariance matrix for $\boldsymbol{u}$,

$\boldsymbol{V}$ = variance-covariance matrix for $\boldsymbol{y}$,

The BLUPs are expressed as a deviation from the population mean. As noted above, solutions to these equations were obtained using the algorithms of Echidna Mixed Models Software (Gilmour, 2020).

Heritability

Estimates of heritability (h^2) were calculated as:

$$h^2 = \frac{V_g}{V_g + V_e}$$

h^2 = heritability

V_g = genetic variance

V_e = environmental variance

Results

Estimated Breeding Values (EBVs)

The first objective of this study was to select superior maternal genotypes, paternal genotypes, and breeding populations based upon estimates of their breeding values (EBVs) for the following traits: performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH). EBVs of the traits assessed for the maternal genotypes, paternal genotypes, and breeding populations, are presented in Table 2.7, Table 2.8, and Table 2.9, respectively.

The PRs provided information on relative progeny performance throughout the season in Eastern Nebraska. Parental genotypes and breeding populations with positive EBVs for the June, July, and August PRs were desired. EBVs for June PRs had similar variation for the parental genotypes and breeding populations. July and August PRs for the breeding populations had more variable EBVs than the parental genotypes. The

amount of variation for the breeding populations demonstrates the diversity of progeny generated from the crosses.

Sixteen maternal genotypes (Table 2.7), 18 paternal genotypes (Table 2.8), and 30 breeding populations (Table 2.9) had positive EBVs for the June, July, and August PRs, indicating that progeny adapted to the nurseries located on the East Campus Research Farm can be developed using germplasm currently in the program. Maternal parent 18NEHOPS009 had the highest EBVs for the June, July, and August PRs (Table 2.7) and should be used to generate progeny that perform well in Nebraska in future breeding efforts. Of the paternal genotypes, 18NEHOPS031 had the highest EBV for the June PR, and PI 635403 had the highest EBVs for the July and August PRs. Paternal genotypes with positive EBVs for the monthly PRs included six USDA accessions and two wild hops (Table 2.8), which was expected since they were found locally or adapted to the region. Seventeen of the breeding populations with positive EBVs for the June, July and August PRs were developed from crosses with the USDA accessions as paternal parents (Table 2.9). Twenty-five of the breeding populations were developed from a cross between the 16 maternal and 18 paternal genotypes that had positive EBVs for the monthly PRs (Table 2.9), indicating that crosses between these parental genotypes are the most suitable to develop progeny adapted to Nebraska.

Ideal time for hops to flower in Nebraska is mid-June to mid-August. The goal of the breeding program is to develop cultivars that flower during this time interval. Genotypes that flower during this interval maximize height and avoid unfavorable weather conditions in the spring and fall. Additionally, having cultivars that flower at different times throughout the season will aid producers by spreading out the time of

harvest. The 589 progeny that flowered in this study did so from late June to early September, most from early August to mid-August (Figure 2.1). Parental genotypes and breeding populations with negative EBVs are more likely to develop progeny that flower early during the growing season before August. Those with positive EBVs close to the mean, 0, will likely generate progeny that flower from early August to mid-August and those with positive EBVs that deviate far from the mean are more likely to develop progeny that flower after August. Therefore, parental genotypes and breeding populations were desired with negative EBVs and positive EBVs that did not deviate too far from the mean, such as maternal genotype 19NEHOPS041-39 (Table 2.7).

There was more variation of FT EBVs for the paternal genotypes and breeding populations than the maternal genotypes. The public elite cultivars were selected because they flower within a certain range for production in the Pacific Northwest, which may help explain the lower variation for the maternal genotypes. Because most progeny flowered in August, it will be important to generate progeny that flower before August in future breeding efforts. To generate early flowering progeny, crosses will need to be conducted between parents with negative EBVs. Thirty maternal genotypes (Table 2.7), 24 paternal genotypes (Table 2.8), and 39 breeding populations (Table 2.9) had negative FT EBVs. Maternal genotypes 18NEHOPS009 and 19NEHOPS053-16 had the lowest FT EBVs (Table 2.7) and would be ideal to cross with PI 635403 or PI 635246, which had the lowest FT EBVs of the paternal genotypes (Table 2.8). 18NEHOPS009/PI 635246 and 18NEHOPS009/PI 635403 were assessed in this study. These crosses developed breeding populations with two of the five lowest FT EBVs (Table 2.9). The two populations with the lowest EBVs were ‘Sorachi Ace’/PI 635246 and 19NEHOPS053-

16/19NEHOPS052-11 (Table 2.9). 19NEHOPS053-16 was a progeny of ‘Sorachi Ace’/PI 635246, and 19NEHOPS052-11 was a progeny of ‘Sorachi Ace’/PI 635287 (Table 2.3). ‘Sorachi Ace’, PI 635246, and PI 635287 all typically mature and flower during the month of June on the East Campus Research Farm.

Similar to the FT EBV variation, the ALP EBVs varied more for the paternal genotypes and breeding populations than for the maternal genotypes. However, the maternal genotypes had more variability for COH EBVs but only slightly more than the breeding populations. The alpha acid content of the 105 progeny assayed in this study ranged from 1.278 % to 27.521 %, with a mean of 8.251 % (Appendix B). Therefore, parental genotypes and breeding populations with positive ALP EBVs would be the most suitable to develop bittering hop cultivars, those with high alpha acid content. Bittering hops were the focus of this study because essential oil content was not evaluated but should be in future studies. Cohumulone is the least desired type of alpha acid by brewers because of its harsh bitter flavor. Cohumulone content for the 105 progeny ranged from 0.434 % to 8.579 %, with a mean of 3.140 % (Appendix B). So, parental genotypes and breeding populations with negative EBVs would likely develop progeny with the lowest COH and were desired in this study.

Ten maternal genotypes had a positive ALP EBV, 13 had a negative COH EBV (Table 2.7). ‘Sorachi Ace’ had the highest ALP EBV (Table 2.7), which was expected since it is a bittering hop cultivar. Seven maternal genotypes had a positive ALP EBV and a negative COH EBV (Table 2.7), ideally suited to develop bittering hops with low cohumulone content. Six paternal genotypes and eight breeding populations also had a positive ALP EBV and a negative COH EBV (Table 2.8, Table 2.9). Four of the six

paternal genotypes were USDA accessions (Table 2.8). The other paternal genotypes were 19NEHOPS052-11 and 19NEHOPS056-2, which were progeny of USDA accessions (Table 2.3). Four of the eight populations were crosses between ‘Sorachi Ace’ and a USDA accession (Table 2.9).

Five maternal genotypes, five paternal genotypes, and seven breeding populations had the desired EBVs for all traits of interest, which were positive for the June, July, and August PRs, positive for ALP, and negative for COH. They also had negative FT EBVs and would develop progeny that flowers from mid-June to mid-August. The five maternal genotypes were ‘Sorachi Ace’, 18NEHOPS005, 18NEHOPS009, 19NEHOPS53-16, and 19NEHOPS59-217 (Table 2.7). The paternal genotypes were PI 635242, PI 635246, PI 635287, PI 635403, and 19NEHOPS052-11 (Table 2.8). The breeding populations comprised crosses between the five maternal and five paternal genotypes previously listed (Table 2.9). These parents should be used, and the crosses repeated in future breeding efforts to develop bittering hop cultivars with low cohumulone levels adapted to Nebraska.

Estimated Genetic Values (EGVs)

The second objective was to identify superior progeny genotypes based upon estimates of their genetic values (EGVs) for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH). Variation of EGVs for the PRs, FT, ALP and COH are shown in Figure 2.2, Figure 2.3, and Figure 2.4, respectively. The amount of variation for the trait EGVs indicates there are diverse progeny genotypes in the program.

Progeny were desired that performed well throughout the season in the nurseries, those with positive EGVs for the June, July, and August PRs. Eighty-four of the genotypes had positive EGVs for the monthly PRs, which consisted of 61 females (Table 2.10) and 23 males (Table 2.11). Sixty-four of the 84 progeny were developed from a breeding population that had positive EBVs for the June, July, and August PRs, confirming that these crosses are a source of environmental adaptation to eastern Nebraska.

It is important to advance progeny with a range of flowering times while maintaining diversity, so progeny with positive and negative FT EGVs were selected. Progeny with negative FT EGVs such as 19NEHOPS041-39 and 20NEHOPS077-17 will flower before August (Table 2.10, Appendix A). Progeny with positive EGVs close to the mean, 0, are more likely to flower from early August to mid-August, such as 19NEHOPS59-121 (Table 2.10, Appendix A). Progeny with positive FT EGVs that deviated far from the mean, such as 21NEHOPS117-3 and 21NEHOPS126-3, flower after mid-August (Appendix A). Genotypes that flower after mid-August were not selected for advanced evaluations as a potential cultivar because they are susceptible to early weather-related damage in the fall. Most of the progeny genotypes, 209, had a positive FT EGV (Figure 2.3).

Progeny ALP EGVs, presented in figure 2.4, was similar to the ALP EBV variation for the breeding populations (Table 2.9). However, the COH EGV variation was wider than the COH EBV variation for the paternal genotypes and breeding populations. Progeny were desired with a positive ALP EGV and a negative COH EGV to develop bittering hop cultivars with low cohumulone levels. Of the subset of progeny included in

the analysis, 17 had both a positive ALP EGV and a negative COH EGV (Figure 2.4). Thirteen of the 17 also had positive EGVs for the monthly PRs and flowered from mid-June to mid-August (Table 2.10). These genotypes have the potential to be released as bittering hop cultivars with low cohumulone content adapted to Nebraska. Seven were developed from a cross between ‘Sorachi Ace’ and a USDA accession.

Heritability Estimates

The final objective was to determine heritability estimates for the traits evaluated. Heritability estimates for the parental genotypes, progeny genotypes, and breeding populations were low for all traits, ranging from 0.165 to 0.337 (Table 2.12). The low estimates indicate that selection for these traits based on phenotypic observations is unreliable. Progeny genotypes had the highest heritability estimates for most of the traits evaluated, which included: July PRs, August PRs, FT, and COH. Heritability estimates for ALP were similar for the parents, progeny, and breeding populations. The lowest heritability estimates for parental genotypes were the August PRs, and for progeny genotypes the June PRs. Surprisingly, the lowest estimate for the breeding populations was for COH.

Discussion

Overview of Study

Development of hop cultivars adapted to the Midwest is essential for regional producers to have consistent yields and brewers to have consistent ingredients for their

recipes. Cultivar development in conventional breeding is time-consuming because of the large number of progeny evaluated each season. Selection of superior parents and crosses that generate progeny with the traits of interest can reduce the number of progeny evaluated and therefore reduce the length of time to develop improved cultivars. Typically, selection in conventional hop breeding is achieved by phenotypic observations of their progeny and retaining those that develop progeny with the traits of interest. However, selection based on phenotypic observations can lead to erroneous selection decisions when evaluations are conducted in different years and locations and when parents have different numbers of progeny and progeny replicates evaluated. Moreover, phenotypic observations confound both genetic and environmental effects, and these selection decisions must be based on genetic effects, not phenotypic observations.

To make selection decisions based on genetic effects when data is unbalanced, a linear mixed model analysis (LMM) based on Henderson's Best Linear Unbiased Predictors (BLUPs), Henderson 1975) can be used. Linear mixed model analysis accounts for different numbers of progeny and replicates by using phenotypic data and pedigree information to account for genetic trends. It accounts for progeny evaluated in different years and locations by separating environmental effects from genetic effects for a direct comparison. The analysis is characterized by a shrinkage property, which shifts above and below-average values closer to the population mean and further reduces the risk of erroneous selection decisions (Piepho et al., 2007). The level of shrinkage depends on the trait heritability and the number of observations per genotype.

Heritability, for this study, cannot be categorized into broad or narrow sense due to the unbalanced nature of the data. Heritability was defined as the proportion of

phenotypic variation present due to total genetic variation. Traits with a high heritability indicate phenotypic variation is mainly attributed to genetic variation. These traits are easier to improve and can typically be selected based on phenotypic observations. Traits with a low heritability indicate that selection based on phenotypic data is unreliable and is attributed to environmental influence and/or inaccurate phenotypic data. These traits are more effectively selected by LMM based on BLUPs.

BLUPs are the predictors of parents and crosses breeding values for the trait of interest. The predicted breeding values also called estimated breeding values (EBVs), predict the value of the genes a parent passes to its progeny. The predicted breeding values also called estimated breeding values (EBVs), predict the value of the genes a parent passes to its progeny. Likewise, this LMM can be used to select genetically superior progeny. BLUPs are the predictors of a progeny's genetic values for the trait of interest. The predicted genetic values, commonly referred to as estimated genetic values (EGVs), describe a progeny's performance.

Estimated Breeding Values (EBVs)

Variation of the EBVs for the traits evaluated in this study indicates the potential to develop improved hops for those traits using the parental genotypes currently in the program. Genotypes in the program had desirable EBVs for one or several traits of interest. Desirable EBVs in this study were positive for the June, July, and August performance ratings (PRs), positive for alpha acid content (ALP), and negative for cohumulone content (COH). For flowering time (FT), negative and positive EBVs were desired, except positive EBVs that deviated far from the mean.

The most pivotal trait assessed were the June, July, and August PRs because they provided insight on potential yield, downy mildew resistance, and how progeny performed in eastern Nebraska. For that reason, superior parental genotypes for this study are the 16 maternal and 18 paternal genotypes with positive EBVs for the monthly PRs. These genotypes will be retained in the program for future progeny development regardless of their EBV for FT, ALP, and COH.

The majority of the superior parental genotypes, those with positive EBVs for the monthly PRs, had a FT EBV that was negative or was positive and did not deviate far from the mean. These parents would likely develop progeny that flower from mid-June to mid-August, the ideal time for hops to flower in Eastern Nebraska. Two of the superior parental genotypes, maternal genotype 19NEHOPS059-208 and paternal genotype 19NEHOPS049-12, had a FT EBV that deviated significantly from the mean (Table 2.7, Table 2.8). These genotypes may develop progeny that flower too late in the growing season, after mid-August, increasing the risk of injury due to early frost. Hops that flower between mid-June to mid-August were most likely to maximize their yield while being ready to harvest before the risk of late-season temperature injury. To avoid developing progeny that flowers after mid-August, these genotypes can be crossed to parents with a low FT EBV. For example, maternal genotype 20NEHOPS095-2 had a FT EBV of -0.005 (Table 2.7) and was crossed to paternal genotype 20NEHOPS096-3, which had an EBV of 0.475 (Table 2.8). Their cross developed a breeding population with an EBV of 0.052 (Table 2.9) and their progeny would likely flower from early to mid-August. Conversely, a cross between 20NEHOPS095-17 and 20NEHOPS096-3, both with

positive FT EBVs (Table 2.7, Table 2.8), had progeny with more positive FT EBVs, a less desirable FT phenotype.

Positive ALP EBVs and negative COH EBVs were desired to develop bittering hops with low cohumulone content. Bittering hops were the focus of this study because essential oils were not evaluated but should be in future studies to determine a parent's value for developing aroma or dual-purpose hops. Cohumulone, a type of alpha acid, is least preferred by brewers because it imparts a harsh bitterness to beer. A subset of parental genotypes was included in the analyses for ALP and COH due to associated costs. Of the superior parental genotypes included, five maternal and five paternal parents had a positive ALP EBV and a negative COH EBV (Table 2.7, Table 2.8).

Superior parents not included in the analyses for ALP and COH, should be assessed in future studies. While essential oil content was not evaluated in this study, superior parents that had a negative ALP EBV may still develop aroma cultivars. Parents with a positive COH EBV can be crossed to parents with a negative COH EBV to create a breeding population with low COH. For example, maternal genotype 'Glacier' had a COH EBV of -0.029 (Table 2.7). When crossed to paternal genotype 18NEHOPS026, which had an EBV of 0.002 (Table 2.8), the breeding population resulted in an EBV of -0.004 (Table 2.9).

There were 30 breeding populations that had positive EBVs for the June, July, and August PRs (Table 2.9). Twenty-five of the 30 breeding populations were developed from crosses between the superior parental genotypes, further suggesting these parental genotypes are the most suitable to develop progeny adapted to Eastern Nebraska. The superior parental genotypes selected are the only parents that will be retained in the

breeding program. Therefore, in future breeding efforts, only crosses between the superior parental genotypes will be conducted. Crosses between the superior parental genotypes that developed the 25 breeding populations should be repeated in future evaluations except for those with a negative ALP EBV and a positive COH EBV, such as Arp/18NEHOPS031 and 19NEHOPS052-12/19NEHOPS052-6 (Table 2.9). While crosses with breeding populations that have a negative ALP EBV may develop aroma cultivars, these types of cultivars are typically characterized by low cohumulone levels. Therefore, 23 of the 25 breeding populations with positive EBVs for the monthly PRs were considered superior and will be repeated to generate progeny in future breeding efforts (Table 2.9). Twenty of the 23 populations had a negative FT EBV, and three had a positive FT EBV close to the mean, indicating their progeny should flower within the preferred range (Table 2.9).

Maternal Genotypes

Maternal genotypes had less EBV variation for FT and ALP than the paternal genotypes and breeding populations. Henning & Townsend (2005) conducted a field-based study to determine the genetic variances for several morphological and chemical hop traits for maternal and paternal genotypes. The study was conducted by crossing five maternal and five paternal genotypes and assessing their progeny for two years. They found a lack of variation for several of the chemical traits between the maternal parents, which were public elite cultivars, and determined it was because they had an ancestral relationship; they were all descendants of ‘Brewer's Gold’. Compared to the Henning & Townsend (2005) study that found a lack of variation between maternal genotypes, this

study found less variation compared to the paternal genotypes and breeding populations. In this study, maternal wild hops were used as a source of genetic variation, which contributed to the maternal genotypes having more variation.

The 16 maternal genotypes with positive EBVs for the June, July, and August PRs consisted of three public elite cultivars, one local wild hop, five of unknown origin, and seven developed by the program. The public elite cultivars were ‘Sorachi Ace’, ‘Glacier’, and ‘Galena’. ‘Sorachi Ace’, a bittering hop cultivar, had the maximum ALP EBV (Table 2.7). ‘Glacier’, a dual-purpose cultivar, is characterized by low COH. It was anticipated this genotype would have a negative COH EBV (Table 2.7). Bittering hop cultivar ‘Galena’ was not assessed in the ALP and COH analyses.

Arp, a Nebraska wild hop, had a positive ALP and COH EBV (Table 2.7). It was unexpected for Arp to have a positive ALP EBV because studies, such as Haunold et al. (1993) and Patzak et al. (2010), that have analyzed the chemical characteristics of North American wild hops found they typically have low levels of ALP and high levels of COH. The Haunold et al. (1993) study found a few rare wild genotypes with high levels of ALP and noted that these genotypes would be best for future breeding efforts; this may be the case with ARP because of its positive ALP EBV. Haunold et al. (1993) also found that the genotypes they analyzed from Nebraska matured later in the growing season, from early August to mid-October. In this study, Arp had a FT EBV of -0.0367 (Table 2.7), indicating this genotype is more likely to develop progeny than matures around early August. Flowering time and chemical characteristics of the parental genotypes were not collected for this study. It may be beneficial to collect this data in future studies for progeny comparison.

The unknown genotypes with positive EBVs for the June, July, and August PRs were 18NEHOPS005, 18NEHOPS007, 18NEHOPS008, 18NEHOPS009, and 18NEHOPS014. They were of unknown origin because several of the genotypes established in the maternal nursery when the program began were not spaced appropriately (Table 2.1). Because they were spaced incorrectly, rhizomes from a genotype would integrate with other genotypes in proximity. Therefore, the unknown genotypes were either one of the public elite cultivars or wild hops. 18NEHOPS009 was one of the best maternal parents in this study because it had the highest EBVs for the June, July, and August PRs, second lowest FT EBV, second highest ALP EBV, and the lowest for COH (Table 2.7).

The genotypes developed by the program were 19NEHOPS048-4, 19NEHOPS052-12, 19NEHOPS053-16, 19NEHOPS056-12, 19NEHOPS059-208, 19NEHOPS059-217, and 19NEHOPS059-94. These genotypes were progeny of either ‘Sorachi Ace’, Arp, or 18NEHOPS005 that also had positive EBVs for the monthly PRs (Table 2.7). 19NEHOPS053-16, progeny of ‘Sorachi Ace’, had the lowest FT EBV (Table 2.7) and would develop progeny that flower earlier in the season. 19NEHOPS059-208 and 19NEHOPS056-12, progeny of Arp, were the only two maternal genotypes with positive EBVs for the monthly PRs that had a positive FT EBV (Table 2.7).

Paternal Genotypes

The 18 paternal genotypes with positive EBVs for the June, July, and August PRs consisted of six USDA accessions, two wild hops, and ten genotypes developed by the program. The accessions were PI 635242, PI 635246, PI 635287, PI 635403, PI 635458,

and PI 635472. PI 635403 and PI 635246 had the lowest FT EBVs of all the paternal genotypes (Table 2.8). Four accessions were included in the ALP and COH analyses and had a positive ALP EBV and a negative COH EBV (Table 2.8). PI 635403 and PI 635242 had the lowest COH EBVs (Table 2.8) and could be crossed to a maternal genotype with a positive COH EBV, such as Arp, to produce progeny with desired high ALP and low COH (Table 2.7).

The wild hops, 18NEHOPS026 and 18NEHOPS031, had positive EBVs for the monthly PRs further supporting their regional adaptation. As previously stated, North American wild hops typically have low levels of ALP and high levels of COH, so it was also expected the two wild hops would have a negative ALP EBV and a positive COH EBV (Table 2.8). These genotypes would be best crossed to maternal genotypes with positive ALP EBVs and negative COH EBVs to potentially develop bittering or dual-purpose hop cultivars.

18NEHOPS031 and three genotypes developed by the program, 19NEHOPS049-12, 19NEHOPS056-144, and 20NEHOPS094-2, had a positive FT EBV (Table 2.8). They would be best crossed to maternal genotypes with a negative FT EBV to avoid developing progeny that flowers too late in the growing season. The other genotypes developed by the program with positive EBVs for the June, July, and August PRs were 19NEHOPS048-22, 19NEHOPS052-11, 19NEHOPS052-6, 19NEHOPS054-1, 19NEHOPS059-178, 19NEHOPS059-93, and 20NEHOPS069-2. The genotypes developed by the program were derived from one of the USDA accessions, 18NEHOPS031, 19NEHOPS056-144, or 19NEHOPS054-1, which also had positive EBVs for the monthly PRs (Table 2.8).

Breeding Populations

The analysis of breeding populations revealed that transgressive segregation is possible in some crosses. Typically, EBVs of the breeding populations for the traits assessed in this study were similar to the EBVs of the parental genotypes crossed. For example, maternal genotype ‘Sorachi Ace’ and paternal genotype PI 635242 had positive EBVs for the June, July, and August PRs and a negative FT EBV (Table 2.7, Table 2.8). Their cross resulted in a breeding population with the same EBVs, positive for the monthly PRs and negative for FT (Table 2.9). However, this was not true for all crosses, such as 18NEHOPS009/PI 635246. Both parents had a negative COH EBV (Table 2.7, Table 2.8), but their breeding population had a positive COH EBV (Table 2.9). The varying results show the importance of determining the breeding values of the breeding populations in addition to the individual parents. Traits of the breeding populations will not always reflect those of parents because hops are characterized by quantitative traits and have a non-mendelian inheritance. Many studies have been conducted, such as McAdam et al., 2013, McAdam et al. 2014, and Zhang et al., 2017, to try and better understand the transmission of traits in hops.

As previously mentioned, 23 of the 30 breeding populations with positive EBVs for the June, July, and August PRs are superior and can be repeated for future progeny development. Additionally, maternal and paternal genotypes with positive EBVs for the monthly PRs that were not crossed as part of this study can be hybridized, such as ‘Sorachi Ace’/18NEHOPS026. All parental genotypes were not crossed in this study because hops flower at different times throughout the season, making it challenging to cross some genotypes. Pollen could be collected and preserved to cross parents that

flower at different times. The storage length and requirements to preserve pollen depend on the timing of male flowering in relation to the timing of female flowering. A male flowering before the female would only require short-term pollen storage, whereas the female flowering before the male would require long-term pollen storage. The preservation requirements for short and long-term storage have been researched by Haunold & Stanwood (1985). They identified successful ways to keep pollen viable and develop seeds that germinate after one week of storage and up to several years of pollen storage. While it is feasible to store pollen to conduct crosses between parents that flower at different times, it would also require more time and labor. Pollen would need to be collected, dried, and properly prepared before storage.

Estimated Genetic Values (EGVs)

The progeny genotypes had variable EGVs for the traits evaluated. The amount of variation suggests the progeny were highly diverse, and improved genotypes for the traits can be selected from the genotypes present. The desired EGVs in this study were: positive for the June, July, and August performance ratings (PRs), positive for alpha acid content (ALP), and negative for cohumulone content (COH). Negative and positive FT EGVs were desired, except positive EGVs that deviated significantly from the mean, to avoid late maturing genotypes. For progeny to be considered for advancement and potential release, they must be adapted to Nebraska. Therefore, the most important trait assessed was the monthly PRs, and progeny selected for advanced evaluations must have positive EGVs for the monthly PRs.

Eighty-four progeny genotypes had positive EGVs for the June, July, and August PRs. There were 61 females (Table 2.10) and 23 males (Table 2.11). Because the cones are of agronomic importance, only female progeny can be potentially released. The males can be used in future progeny development and would be good candidates as parents since they thrive in Nebraska and can potentially pass the genes of interest onto their progeny. Seven of the males were evaluated as parents in this study. Two genotypes, 19NEHOPS048-22 and 19NEHOPS052-6 were selected as superior paternal genotypes because they had positive EBVs for the June, July, and August PRs (Table 2.8) and will continue to be used to develop progeny. 20NEHOPS096-3, 19NEHOPS041-23, 19NEHOPS041-34, 19NEHOPS053-8, and 19NEHOPS052-17 did not have positive EBVs for the June, July, and August PRs (Table 2.8) and will be eliminated from the program.

The 61 female progeny genotypes had a variable range of FT EGVs (Table 2.10). All except two flowered within the desired range, mid-June to mid-August. 19NEHOPS059-208 had a FT EGV of 0.728, and 20NEHOPS090-2 had a FT EGV of 0.656 (Table 2.10). These genotypes had several replicates evaluated in this study, and both had one or more replicates that flowered after the desired range (Appendix A).

From the subset of progeny that were evaluated for ALP and COH, 13 had a positive ALP EGV and a negative COH EGV (Table 2.10). Ten were progeny of maternal genotype ‘Sorachi Ace’ or a descendent of ‘Sorachi Ace’, 19NEHOPS053-16. Progeny with a positive ALP EGV and a positive COH EGV can still be advanced, as there are popular public elite cultivars with moderate to high levels of cohumulone, such as ‘Chinook’. Essential oil content was not evaluated in this study, so progeny with a

negative ALP EGV and COH EGV have the potential as aroma cultivars. Progeny with a negative ALP EGV and a positive COH EGV do not have the potential for release because aroma cultivars typically have low COH. Therefore, the ten genotypes with a negative ALP EGV and a positive COH EGV will not be advanced for future evaluations (Table 2.10). Overall, this study found 49 superior female progeny genotypes that will be advanced and potentially released as a cultivar. The 12 that will not be advanced can be evaluated as potential parents, as none were used to develop progeny as part of this study.

Thirty-four of the 49 superior female genotypes originated from the 23 superior breeding populations and therefore developed from a cross between the superior parental genotypes. Because most of the superior progeny were developed from the superior parental genotypes, it further emphasizes the value of these parents for developing superior progeny. The parents not selected as superior that developed the other 15 superior progeny genotypes will not be crossed in future evaluations because they will not be retained in the program. Not crossing these parental genotypes may cause the potential to miss several superior genotypes in future progeny development. However, more superior genotypes would be developed by focusing on the superior parents with the desired EBVs. It would also reduce the amount of inferior progeny evaluated and maintained in the breeding nurseries, saving time, space, and labor, making the program more efficient. Witcombe et al. (2013) compared the number of crosses conducted and the number of improved varieties released in several rice breeding programs. They found that the probability of developing improved varieties increased by strategically targeting specific crosses and making fewer crosses.

In advanced evaluations, the superior female genotypes will be grown in replicates on the V trellis system in the maternal nursery. They will be allowed to establish and mature for evaluation under commercial scale conditions. During advanced evaluations, downy mildew resistance, flowering time, vigor, alpha acid content, and cohumulone content can continue to be assessed. Because downy mildew is prevalent in Nebraska and the Midwest, more emphasis should be placed on assessing the genotypes for resistance. The disease can be rated on a scale, such as the one implemented by Henning et al. (2015), where the percentage of lesions on the leaf was estimated on a scale of 0 (no lesions) to 10 (100 % of leaf area diseased). Progeny should be assessed regularly throughout the season for the disease, especially during periods with high humidity. This scale can also be implemented in early evaluations of the progeny nursery, separating downy mildew resistance from the performance ratings. Vigor for advanced evaluations can be estimated using a scale similar to the one Henning et al. (2010) implemented in their study. They used a scale of 1-10, where one indicated the plant was dead, and ten indicated the plant had several vines reaching the top of the trellis with vigorous side arm development. Typically, vigor is measured as the growth rate from the date of emergence in the spring until the plant transitions from vegetative to reproductive growth, with the height, measured weekly to determine their growth rate. However, using a scale like Henning et al. (2010) would reduce the time and labor of taking weekly measurements, requiring only one scoring of plants at the end of the growing season. Furthermore, when cones reach maturity, they can be harvested, and yield can be measured as the weight of cones per plant, as in the study conducted by Henning & Townsend (2005). Measurements of the actual yield would replace measurements of

traits relating to potential yield. A sample of the cones can be used to assess the secondary metabolite content, which would consist of alpha acid content, cohumulone proportion, and essential oil content.

In commercial production, hops are dried, typically to around 10 % moisture, and pelletized after harvest for preservation and storage. Secondary metabolite content begins to degrade after harvest during processing and storage. Measurements of the degradation of the secondary metabolites, referred to as the hop storage index (HSI), is an important quality factor for producers and brewers. Degradation of the metabolites is caused by different factors such as length of time, temperature, and exposure to oxygen and light, the rate of degradation is cultivar dependent (Mikyska & Krofta, 2012). Because HSI is an important factor, it would be beneficial to dry and store the cones to determine HSI for the advanced genotypes. Because the value of a cultivar is ultimately dependent on its acceptance by beer brewers, brewers should have access to the cones of the advanced genotypes to use in recipes. If brewers find no value in the cones of a genotype, then the genotype can be eliminated from the program.

A concern that should be addressed is authenticity of pedigrees of progeny in this study. The maternal and paternal nurseries were in separate locations, but the progeny nursery neighbored the maternal nursery. Males were included in the progeny nursery because their gender was not identified until they developed flowers. Most of the males had their flowers removed before pollen matured, except males selected for progeny development. Therefore, cross-contamination of the females in the progeny and maternal nursery could have occurred. In future progeny development, female lateral branches will

be bagged before they are receptive to avoid cross-contamination, such as in the study conducted by Henning & Townsend (2005).

Heritability

The low heritability found for all traits evaluated in this study confirms that selection in this program, based on phenotypic observations would be unreliable and use of predicted breeding and genetic values would be a more effective selection method. The low estimates for the PRs were likely because they were based on several traits of interest, downy mildew resistance, vigor, lateral branch length, and internode length. To obtain better heritability estimates for these traits, they should be evaluated separately in future studies.

Heritability estimates for FT and ALP in a study conducted by Roberts. et al. (1975) were relatively higher than the estimates found here. The Roberts. et al. (1975) study determined the heritability estimates based on data collected from 29 mature female hops. The data was collected from the same females, with an equal number of replicates. FT data was collected for two years, and ALP for one year. The difference in estimates between this study and the Roberts. et al. (1975) study shows the main factor for low heritability in this study were likely due to the unbalanced data. Heritability estimates would have been higher if the same progeny were evaluated each season with the same number of replicates.

Conclusion

This study characterized the current germplasm in the University of Nebraska-Lincoln's regional hop breeding program to assist in the development and selection of locally adapted cultivars. Linear mixed model analysis based upon the Best Linear Unbiased Predictors (BLUPs) was used to evaluate the germplasm based upon genetic effects. Best Linear Unbiased Predictors of predicted breeding values identified several parental genotypes and breeding populations that develop progeny with one or several traits of interest. Identification of these parents and populations will reduce the amount of progeny developed each season and reduce the length of time to develop improved cultivars. Multiple progeny genotypes were identified by BLUPs of predicted genetic values that possess one or multiple traits of interest. Data collected in the program was unbalanced, which could cause bias in selection decisions, so the analysis helped overcome this bias to improve and make accurate selections.

The University of Nebraska-Lincoln's regional breeding program is still establishing the best strategies to implement for field evaluations and this research contributes to more efficient use of space in the nurseries by making informed breeding decisions and reducing the numbers of progeny evaluated. As evaluations improve and additional data is collected, the more informative the BLUPs will be to the program. Overall, the information gained from the analysis will help the program's success to develop hop cultivars adapted to Nebraska.

Table 2.1. Hop (*Humulus lupulus* L.) genotypes established in the maternal and paternal nurseries at the University of Nebraska-Lincoln East Campus Research Farm in 2016. Genotypes consisted of public elite cultivars, local wild hops, and USDA accessions.

Genotype	Accession type	Parental type
Arp	Nebraska wild hop	Maternal
Cascade	Public elite cultivar	Maternal
Cashmere	Public elite cultivar	Maternal
Chinook	Public elite cultivar	Maternal
Columbus	Public elite cultivar	Maternal
Crystal	Public elite cultivar	Maternal
Doris Mae	Nebraska wild hop	Maternal
Galena	Public elite cultivar	Maternal
Glacier	Public elite cultivar	Maternal
Joplin 1	Nebraska wild hop	Maternal
Joplin 2	Nebraska wild hop	Maternal
Joplin 3	Nebraska wild hop	Maternal
Magnum	Public elite cultivar	Maternal
Sorachi Ace	Public elite cultivar	Maternal
Triple Pearl	Public elite cultivar	Maternal
18NEHOPS024	Nebraska wild hop	Maternal
18NEHOPS025	Nebraska wild hop	Paternal
18NEHOPS026	Nebraska wild hop	Paternal
18NEHOPS031	Nebraska wild hop	Paternal
PI 635242	USDA accession	Paternal
PI 635246	USDA accession	Paternal
PI 635287	USDA accession	Paternal
PI 635367	USDA accession	Paternal
PI 635403	USDA accession	Paternal
PI 635458	USDA accession	Paternal
PI 635472	USDA accession	Paternal

Table 2.2. Traits evaluated on hop (*Humulus lupulus* L.) progeny genotypes developed at the University of Nebraska-Lincoln.

Trait	Description	Years evaluated
Performance ratings (PRs)[a]	Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. Ratings were given in mid-June, mid-July, and mid-August and were assigned as an aggregate assessment of several traits: downy mildew resistance[b], vigor[c], internode length[d] and lateral branch length[d].	2019-2021
Gender	Documented as female, male, or monoecious.	2019-2021
Flowering time (FT)	Documented as the week the first flowers on an individual plant fully opened.	2019-2021
Alpha acid content (ALP)	Concentration of alpha acid content (mg/g of fresh hops)	2020-2021
Cohumulone content (COH)	Concentration of cohumulone content (mg/g of fresh hops)	2020-2021

[a] Ratings were not assigned equally to progeny for a single trait. For example, a score of five was assigned if the progeny showed no signs of downy mildew and were highly vigorous or showed no signs of downy mildew and had the potential to produce a high yield.
[b] Assessed by the presence of lesions on the leaves.
[c] Assessed by comparing the length of the main bine to the six-foot bamboo stakes progeny were trained on.
[d] Assessed as an indicator of potential yield.

Table 2.3. Hop (*Humulus lupulus* L.) progeny genotypes, their pedigree (breeding population), and the number of replicates assessed for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) in the linear mixed model analysis based upon Henderson's Best Linear Unbiased Predictors (BLUPs).

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS037-1	18NEHOPS014/PI 635242	1	0
19NEHOPS037-5	18NEHOPS014/PI 635242	1	0
19NEHOPS040-3	18NEHOPS009/PI 635246	4	1
19NEHOPS040-5	18NEHOPS009/PI 635246	1	0
19NEHOPS040-6	18NEHOPS009/PI 635246	1	0
19NEHOPS040-8	18NEHOPS009/PI 635246	1	0
19NEHOPS040-9	18NEHOPS009/PI 635246	1	0
19NEHOPS041-1	18NEHOPS009/PI 635403	1	0
19NEHOPS041-13	18NEHOPS009/PI 635403	1	0
19NEHOPS041-23	18NEHOPS009/PI 635403	1	0
19NEHOPS041-25	18NEHOPS009/PI 635403	1	0
19NEHOPS041-27	18NEHOPS009/PI 635403	1	0
19NEHOPS041-29	18NEHOPS009/PI 635403	6	1
19NEHOPS041-3	18NEHOPS009/PI 635403	1	0
19NEHOPS041-34	18NEHOPS009/PI 635403	1	0
19NEHOPS041-35	18NEHOPS009/PI 635403	1	0
19NEHOPS041-39	18NEHOPS009/PI 635403	6	1
19NEHOPS041-40	18NEHOPS009/PI 635403	1	0
19NEHOPS041-43	18NEHOPS009/PI 635403	1	0
19NEHOPS041-47	18NEHOPS009/PI 635403	2	0
19NEHOPS042-1	18NEHOPS008/PI 635472	1	0
19NEHOPS043-1	18NEHOPS007/PI 635242	2	0
19NEHOPS044-1	Glacier/PI 635246	1	0
19NEHOPS045-1	Galena/PI 635287	1	0
19NEHOPS045-2	Galena/PI 635287	1	0
19NEHOPS046-1	Galena/PI 635246	1	0
19NEHOPS047-1	Galena/PI 635242	2	0
19NEHOPS048-11	18NEHOP005/PI 635403	1	0
19NEHOPS048-17	18NEHOP005/PI 635403	1	0
19NEHOPS048-20	18NEHOP005/PI 635403	1	0
19NEHOPS048-22	18NEHOP005/PI 635403	1	0
19NEHOPS048-4	18NEHOP005/PI 635403	1	0
19NEHOPS048-8	18NEHOP005/PI 635403	4	2

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS049-11	18NEHOPS005/PI 635287	5	1
19NEHOPS049-12	18NEHOPS005/PI 635287	1	0
19NEHOPS049-16	18NEHOPS005/PI 635287	1	0
19NEHOPS049-17	18NEHOPS005/PI 635287	1	0
19NEHOPS049-18	18NEHOPS005/PI 635287	1	0
19NEHOPS049-4	18NEHOPS005/PI 635287	1	0
19NEHOPS050-1	18NEHOPS005/PI 635246	1	0
19NEHOPS050-5	18NEHOPS005/PI 635246	1	0
19NEHOPS051-1	Sorachi Ace/PI 635242	5	5
19NEHOPS052-10	Sorachi Ace/PI 635287	1	0
19NEHOPS052-11	Sorachi Ace/PI 635287	1	0
19NEHOPS052-12	Sorachi Ace/PI 635287	5	2
19NEHOPS052-14	Sorachi Ace/PI 635287	1	0
19NEHOPS052-15	Sorachi Ace/PI 635287	4	2
19NEHOPS052-17	Sorachi Ace/PI 635287	1	0
19NEHOPS052-2	Sorachi Ace/PI 635287	1	0
19NEHOPS052-20	Sorachi Ace/PI 635287	1	0
19NEHOPS052-5	Sorachi Ace/PI 635287	1	0
19NEHOPS052-6	Sorachi Ace/PI 635287	2	0
19NEHOPS052-7	Sorachi Ace/PI 635287	1	0
19NEHOPS053-1	Sorachi Ace/PI 635246	1	0
19NEHOPS053-10	Sorachi Ace/PI 635246	1	0
19NEHOPS053-16	Sorachi Ace/PI 635246	1	0
19NEHOPS053-17	Sorachi Ace/PI 635246	4	2
19NEHOPS053-18	Sorachi Ace/PI 635246	7	8
19NEHOPS053-19	Sorachi Ace/PI 635246	1	0
19NEHOPS053-2	Sorachi Ace/PI 635246	1	0
19NEHOPS053-3	Sorachi Ace/PI 635246	1	0
19NEHOPS053-7	Sorachi Ace/PI 635246	6	3
19NEHOPS053-8	Sorachi Ace/PI 635246	1	0
19NEHOPS054-1	Sorachi Ace/PI 635403	1	0
19NEHOPS054-10	Sorachi Ace/PI 635403	1	0
19NEHOPS054-12	Sorachi Ace/PI 635403	1	0
19NEHOPS054-13	Sorachi Ace/PI 635403	1	0
19NEHOPS054-14	Sorachi Ace/PI 635403	1	0
19NEHOPS054-15	Sorachi Ace/PI 635403	1	0

Continued next page.

Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS054-16	Sorachi Ace/PI 635403	1	0
19NEHOPS054-3	Sorachi Ace/PI 635403	1	0
19NEHOPS054-4	Sorachi Ace/PI 635403	1	0
19NEHOPS054-5	Sorachi Ace/PI 635403	5	1
19NEHOPS054-6	Sorachi Ace/PI 635403	1	0
19NEHOPS054-8	Sorachi Ace/PI 635403	1	0
19NEHOPS054-9	Sorachi Ace/PI 635403	5	1
19NEHOPS055-1	Chinook/PI 635246	2	0
19NEHOPS055-2	Chinook/PI 635246	2	0
19NEHOPS056-110	Arp/PI 635246	1	0
19NEHOPS056-12	Arp/PI 635246	5	1
19NEHOPS056-128	Arp/PI 635246	2	2
19NEHOPS056-130	Arp/PI 635246	1	0
19NEHOPS056-133	Arp/PI 635246	1	0
19NEHOPS056-139	Arp/PI 635246	1	0
19NEHOPS056-142	Arp/PI 635246	1	0
19NEHOPS056-144	Arp/PI 635246	1	0
19NEHOPS056-146	Arp/PI 635246	6	3
19NEHOPS056-148	Arp/PI 635246	1	0
19NEHOPS056-151	Arp/PI 635246	1	0
19NEHOPS056-19	Arp/PI 635246	1	0
19NEHOPS056-2	Arp/PI 635246	1	0
19NEHOPS056-20	Arp/PI 635246	1	0
19NEHOPS056-25	Arp/PI 635246	1	0
19NEHOPS056-37	Arp/PI 635246	1	0
19NEHOPS056-38	Arp/PI 635246	1	1
19NEHOPS056-45	Arp/PI 635246	1	0
19NEHOPS056-48	Arp/PI 635246	1	0
19NEHOPS056-50	Arp/PI 635246	1	0
19NEHOPS056-51	Arp/PI 635246	1	0
19NEHOPS056-53	Arp/PI 635246	1	0
19NEHOPS056-56	Arp/PI 635246	1	0
19NEHOPS056-61	Arp/PI 635246	1	0
19NEHOPS056-65	Arp/PI 635246	1	0
19NEHOPS056-71	Arp/PI 635246	1	0
19NEHOPS056-76	Arp/PI 635246	1	0

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS056-79	Arp/PI 635246	1	0
19NEHOPS056-83	Arp/PI 635246	1	0
19NEHOPS056-98	Arp/PI 635246	1	0
19NEHOPS057-1	Arp/PI 635458	1	0
19NEHOPS058-104	Arp/PI 635458	1	0
19NEHOPS058-34	Arp/PI 635458	1	0
19NEHOPS058-43	Arp/PI 635458	1	0
19NEHOPS058-50	Arp/PI 635458	1	0
19NEHOPS058-52	Arp/PI 635458	1	0
19NEHOPS058-75	Arp/PI 635458	1	0
19NEHOPS058-8	Arp/PI 635458	1	0
19NEHOPS058-83	Arp/PI 635458	1	0
19NEHOPS058-96	Arp/PI 635458	1	0
19NEHOPS059-103	Arp/18NEHOPS031	2	0
19NEHOPS059-111	Arp/18NEHOPS031	5	1
19NEHOPS059-118	Arp/18NEHOPS031	1	0
19NEHOPS059-12	Arp/18NEHOPS031	1	0
19NEHOPS059-120	Arp/18NEHOPS031	1	0
19NEHOPS059-121	Arp/18NEHOPS031	8	2
19NEHOPS059-124	Arp/18NEHOPS031	1	0
19NEHOPS059-140	Arp/18NEHOPS031	1	0
19NEHOPS059-160	Arp/18NEHOPS031	1	0
19NEHOPS059-161	Arp/18NEHOPS031	1	0
19NEHOPS059-162	Arp/18NEHOPS031	4	0
19NEHOPS059-165	Arp/18NEHOPS031	1	0
19NEHOPS059-173	Arp/18NEHOPS031	7	2
19NEHOPS059-178	Arp/18NEHOPS031	1	0
19NEHOPS059-182	Arp/18NEHOPS031	1	0
19NEHOPS059-189	Arp/18NEHOPS031	1	0
19NEHOPS059-196	Arp/18NEHOPS031	1	0
19NEHOPS059-204	Arp/18NEHOPS031	5	3
19NEHOPS059-208	Arp/18NEHOPS031	7	0
19NEHOPS059-213	Arp/18NEHOPS031	1	0
19NEHOPS059-217	Arp/18NEHOPS031	1	0
19NEHOPS059-224	Arp/18NEHOPS031	1	0
19NEHOPS059-227	Arp/18NEHOPS031	1	0

Continued next page.

Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS059-44	Arp/18NEHOPS031	1	0
19NEHOPS059-46	Arp/18NEHOPS031	1	0
19NEHOPS059-47	Arp/18NEHOPS031	1	0
19NEHOPS059-61	Arp/18NEHOPS031	1	0
19NEHOPS059-71	Arp/18NEHOPS031	1	0
19NEHOPS059-74	Arp/18NEHOPS031	1	0
19NEHOPS059-8	Arp/18NEHOPS031	1	0
19NEHOPS059-80	Arp/18NEHOPS031	1	0
19NEHOPS059-84	Arp/18NEHOPS031	6	0
19NEHOPS059-92	Arp/18NEHOPS031	1	0
19NEHOPS059-93	Arp/18NEHOPS031	1	0
19NEHOPS059-94	Arp/18NEHOPS031	1	0
19NEHOPS105-1	18NEHOPS014/PI635246	2	0
20NEHOPS061-11	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-15	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-16	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-2	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-4	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-5	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-7	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-8	19NEHOPS105-1/19NEHOPS052-11	1	0
20NEHOPS061-9	19NEHOPS105-1/19NEHOPS052-11	4	1
20NEHOPS064-3	19NEHOPS041-13/19NEHOPS041-34	4	1
20NEHOPS065-1	19NEHOPS041-25/19NEHOPS041-27	1	0
20NEHOPS065-2	19NEHOPS041-25/19NEHOPS041-27	3	1
20NEHOPS065-3	19NEHOPS041-25/19NEHOPS041-27	1	0
20NEHOPS066-2	19NEHOPS041-29/19NEHOPS041-23	1	0
20NEHOPS068-6	19NEHOPS042-1/19NEHOPS052-11	1	0
20NEHOPS068-8	19NEHOPS042-1/19NEHOPS052-11	1	0
20NEHOPS069-1	19NEHOPS043-1/19NEHOPS054-1	1	0
20NEHOPS069-2	19NEHOPS043-1/19NEHOPS054-1	1	0
20NEHOPS069-3	19NEHOPS043-1/19NEHOPS054-1	1	0
20NEHOPS069-4	19NEHOPS043-1/19NEHOPS054-1	1	0
20NEHOPS069-6	19NEHOPS043-1/19NEHOPS054-1	1	0
20NEHOPS069-7	19NEHOPS043-1/19NEHOPS054-1	4	0
20NEHOPS069-8	19NEHOPS043-1/19NEHOPS054-1	1	0

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
20NEHOPS072-11	19NEHOPS045-2/PI 635287	3	0
20NEHOPS072-2	19NEHOPS045-2/PI 635287	1	0
20NEHOPS072-3	19NEHOPS045-2/PI 635287	1	0
20NEHOPS072-5	19NEHOPS045-2/PI 635287	1	0
20NEHOPS072-6	19NEHOPS045-2/PI 635287	1	0
20NEHOPS073-1	19NEHOPS048-4/19NEHOPS048-22	1	1
20NEHOPS073-11	19NEHOPS048-4/19NEHOPS048-22	4	0
20NEHOPS073-13	19NEHOPS048-4/19NEHOPS048-22	4	1
20NEHOPS073-18	19NEHOPS048-4/19NEHOPS048-22	1	1
20NEHOPS073-22	19NEHOPS048-4/19NEHOPS048-22	4	1
20NEHOPS073-23	19NEHOPS048-4/19NEHOPS048-22	1	0
20NEHOPS073-24	19NEHOPS048-4/19NEHOPS048-22	1	0
20NEHOPS073-3	19NEHOPS048-4/19NEHOPS048-22	1	0
20NEHOPS073-4	19NEHOPS048-4/19NEHOPS048-22	1	0
20NEHOPS073-7	19NEHOPS048-4/19NEHOPS048-22	3	2
20NEHOPS074-12	19NEHOPS048-11/19NEHOPS041-34	1	0
20NEHOPS074-5	19NEHOPS048-11/19NEHOPS041-34	1	0
20NEHOPS074-6	19NEHOPS048-11/19NEHOPS041-34	1	0
20NEHOPS074-8	19NEHOPS048-11/19NEHOPS041-34	1	0
20NEHOPS075-11	19NEHOPS050-1/19NEHOPS047-1	1	0
20NEHOPS075-13	19NEHOPS050-1/19NEHOPS047-1	1	0
20NEHOPS075-3	19NEHOPS050-1/19NEHOPS047-1	1	0
20NEHOPS076-2	19NEHOPS052-12/19NEHOPS047-1	1	1
20NEHOPS076-3	19NEHOPS052-12/19NEHOPS047-1	1	0
20NEHOPS076-5	19NEHOPS052-12/19NEHOPS047-1	1	0
20NEHOPS076-6	19NEHOPS052-12/19NEHOPS047-1	1	0
20NEHOPS077-1	19NEHOPS053-16/19NEHOPS052-11	4	2
20NEHOPS077-13	19NEHOPS053-16/19NEHOPS052-11	4	3
20NEHOPS077-15	19NEHOPS053-16/19NEHOPS052-11	1	0
20NEHOPS077-17	19NEHOPS053-16/19NEHOPS052-11	4	2
20NEHOPS077-18	19NEHOPS053-16/19NEHOPS052-11	1	0
20NEHOPS077-19	19NEHOPS053-16/19NEHOPS052-11	4	1
20NEHOPS077-4	19NEHOPS053-16/19NEHOPS052-11	1	0
20NEHOPS078-10	19NEHOPS053-18/19NEHOPS046-1	4	1
20NEHOPS078-16	19NEHOPS053-18/19NEHOPS046-1	1	1
20NEHOPS078-20	19NEHOPS053-18/19NEHOPS046-1	3	2

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
20NEHOPS078-27	19NEHOPS053-18/19NEHOPS046-1	1	0
20NEHOPS078-28	19NEHOPS053-18/19NEHOPS046-1	1	0
20NEHOPS078-30	19NEHOPS053-18/19NEHOPS046-1	4	1
20NEHOPS078-31	19NEHOPS053-18/19NEHOPS046-1	1	0
20NEHOPS078-33	19NEHOPS053-18/19NEHOPS046-1	4	2
20NEHOPS078-5	19NEHOPS053-18/19NEHOPS046-1	1	0
20NEHOPS078-7	19NEHOPS053-18/19NEHOPS046-1	4	1
20NEHOPS078-8	19NEHOPS053-18/19NEHOPS046-1	1	0
20NEHOPS078-9	19NEHOPS053-18/19NEHOPS046-1	4	2
20NEHOPS079-1	19NEHOPS053-18/19NEHOPS053-8	1	0
20NEHOPS080-7	19NEHOPS054-9/19NEHOPS053-3	1	0
20NEHOPS080-9	19NEHOPS054-9/19NEHOPS053-3	1	0
20NEHOPS082-5	19NEHOPS054-6/19NEHOPS054-4	1	0
20NEHOPS082-7	19NEHOPS054-6/19NEHOPS054-4	4	0
20NEHOPS083-2	19NEHOPS054-16/19NEHOPS054-14	1	0
20NEHOPS083-4	19NEHOPS054-16/19NEHOPS054-14	1	0
20NEHOPS084-1	19NEHOPS056-25/19NEHOPS056-2	1	0
20NEHOPS084-2	19NEHOPS056-25/19NEHOPS056-2	4	1
20NEHOPS084-3	19NEHOPS056-25/19NEHOPS056-2	1	0
20NEHOPS085-7	19NEHOPS058-43/19NEHOPS052-14	1	0
20NEHOPS085-8	19NEHOPS058-43/19NEHOPS052-14	4	1
20NEHOPS086-2	19NEHOPS059-61/19NEHOPS059-46	1	0
20NEHOPS086-4	19NEHOPS059-61/19NEHOPS059-46	1	0
20NEHOPS086-6	19NEHOPS059-61/19NEHOPS059-46	3	1
20NEHOPS088-1	19NEHOPS059-217/19NEHOPS059-178	1	0
20NEHOPS088-4	19NEHOPS059-217/19NEHOPS059-178	1	0
20NEHOPS089-5	19NEHOPS059-208/19NEHOPS049-12	1	0
20NEHOPS090-1	19NEHOPS059-224/19NEHOPS049-4	1	0
20NEHOPS090-2	19NEHOPS059-224/19NEHOPS049-4	4	0
20NEHOPS091-2	19NEHOPS059-217/19NEHOPS059-178	4	2
20NEHOPS091-3	19NEHOPS059-217/19NEHOPS059-178	1	0
20NEHOPS092-1	19NEHOPS056-142/19NEHOPS056-110	1	0
20NEHOPS093-1	19NEHOPS056-146/19NEHOPS046-1	1	0
20NEHOPS093-12	19NEHOPS056-146/19NEHOPS046-1	1	0
20NEHOPS093-13	19NEHOPS056-146/19NEHOPS046-1	1	0
20NEHOPS093-14	19NEHOPS056-146/19NEHOPS046-1	1	1

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
20NEHOPS093-17	19NEHOPS056-146/19NEHOPS046-1	4	1
20NEHOPS093-2	19NEHOPS056-146/19NEHOPS046-1	1	1
20NEHOPS093-5	19NEHOPS056-146/19NEHOPS046-1	1	0
20NEHOPS093-6	19NEHOPS056-146/19NEHOPS046-1	1	0
20NEHOPS094-2	Arp/19NEHOPS056-144	1	0
20NEHOPS094-3	Arp/19NEHOPS056-144	4	1
20NEHOPS094-4	Arp/19NEHOPS056-144	4	0
20NEHOPS095-12	Columbus/18NEHOPS026	1	0
20NEHOPS095-15	Columbus/18NEHOPS026	1	0
20NEHOPS095-16	Columbus/18NEHOPS026	1	0
20NEHOPS095-17	Columbus/18NEHOPS026	1	0
20NEHOPS095-18	Columbus/18NEHOPS026	1	0
20NEHOPS095-19	Columbus/18NEHOPS026	1	0
20NEHOPS095-2	Columbus/18NEHOPS026	4	1
20NEHOPS095-4	Columbus/18NEHOPS026	1	0
20NEHOPS095-5	Columbus/18NEHOPS026	1	0
20NEHOPS095-7	Columbus/18NEHOPS026	1	0
20NEHOPS095-8	Columbus/18NEHOPS026	1	0
20NEHOPS096-1	Glacier/18NEHOPS026	1	0
20NEHOPS096-2	Glacier/18NEHOPS026	4	1
20NEHOPS096-3	Glacier/18NEHOPS026	1	0
20NEHOPS096-5	Glacier/18NEHOPS026	4	1
20NEHOPS096-6	Glacier/18NEHOPS026	1	0
20NEHOPS097-1	Sorachi Ace/19NEHOPS052-5	1	0
20NEHOPS097-12	Sorachi Ace/19NEHOPS052-5	1	0
20NEHOPS097-2	Sorachi Ace/19NEHOPS052-5	1	0
20NEHOPS097-6	Sorachi Ace/19NEHOPS052-5	4	2
20NEHOPS097-7	Sorachi Ace/19NEHOPS052-5	1	0
20NEHOPS097-8	Sorachi Ace/19NEHOPS052-5	1	0
20NEHOPS098-10	Sorachi Ace/19NEHOPS052-11	1	0
20NEHOPS098-15	Sorachi Ace/19NEHOPS052-11	1	0
20NEHOPS098-8	Sorachi Ace/19NEHOPS052-11	1	0
20NEHOPS099-12	Sorachi Ace/19NEHOPS053-8	1	0
20NEHOPS099-6	Sorachi Ace/19NEHOPS053-8	1	0
20NEHOPS101-1	19NEHOPS056-19/19NEHOPS056-83	4	2
20NEHOPS101-2	19NEHOPS056-19/19NEHOPS056-83	4	1

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
20NEHOPS102-1	19NEHOPS059-94/19NEHOPS059-93	1	0
20NEHOPS102-2	19NEHOPS059-94/19NEHOPS059-93	4	2
20NEHOPS102-3	19NEHOPS059-94/19NEHOPS059-93	1	0
20NEHOPS104-1	19NEHOPS052-12/19NEHOPS052-6	1	0
20NEHOPS104-2	19NEHOPS052-12/19NEHOPS052-6	4	3
20NEHOPS104-3	19NEHOPS052-12/19NEHOPS052-6	2	1
20NEHOPS104-4	19NEHOPS052-12/19NEHOPS052-6	1	0
21NEHOPS107-1	20NEHOPS078-11/20NEHOPS078-8	1	0
21NEHOPS107-2	20NEHOPS078-11/20NEHOPS078-8	1	0
21NEHOPS108-2	19NEHOPS043-1/20NEHOPS069-4	1	0
21NEHOPS109-1	20NEHOPS095-2/20NEHOPS096-3	1	1
21NEHOPS109-2	20NEHOPS095-2/20NEHOPS096-3	1	1
21NEHOPS109-3	20NEHOPS095-2/20NEHOPS096-3	1	0
21NEHOPS110-1	19NEHOPS056-12/20NEHOPS094-2	1	0
21NEHOPS111-1	20NEHOPS072-2/19NEHOPS045-1	1	0
21NEHOPS112-1	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-11	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-13	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-14	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-15	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-18	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-19	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-20	20NEHOPS104-2/19NEHOPS052-17	1	1
21NEHOPS112-21	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-22	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-23	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-24	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-25	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-3	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-4	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-5	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-7	20NEHOPS104-2/19NEHOPS052-17	1	1
21NEHOPS112-8	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS112-9	20NEHOPS104-2/19NEHOPS052-17	1	0
21NEHOPS113-10	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-11	20NEHOPS093-14/20NEHOPS093-12	1	0

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
21NEHOPS113-12	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-13	20NEHOPS093-14/20NEHOPS093-12	1	1
21NEHOPS113-14	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-15	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-18	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-19	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-20	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-21	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-3	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-4	20NEHOPS093-14/20NEHOPS093-12	1	1
21NEHOPS113-5	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-6	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS113-8	20NEHOPS093-14/20NEHOPS093-12	1	0
21NEHOPS114-2	20NEHOPS093-5/20NEHOPS093-6	1	0
21NEHOPS114-3	20NEHOPS093-5/20NEHOPS093-6	1	0
21NEHOPS114-4	20NEHOPS093-5/20NEHOPS093-6	1	1
21NEHOPS115-1	19NEHOPS052-12/19NEHOPS052-17	1	0
21NEHOPS115-2	19NEHOPS052-12/19NEHOPS052-17	1	0
21NEHOPS115-3	19NEHOPS052-12/19NEHOPS052-17	1	0
21NEHOPS115-4	19NEHOPS052-12/19NEHOPS052-17	1	0
21NEHOPS115-5	19NEHOPS052-12/19NEHOPS052-17	1	0
21NEHOPS116-1	19NEHOPS051-1/PI 635242	1	0
21NEHOPS116-2	19NEHOPS051-1/PI 635242	1	0
21NEHOPS116-3	19NEHOPS051-1/PI 635242	1	0
21NEHOPS116-4	19NEHOPS051-1/PI 635242	1	0
21NEHOPS117-1	20NEHOPS095-17/20NEHOPS096-3	1	0
21NEHOPS117-2	20NEHOPS095-17/20NEHOPS096-3	1	1
21NEHOPS117-3	20NEHOPS095-17/20NEHOPS096-3	1	0
21NEHOPS117-4	20NEHOPS095-17/20NEHOPS096-3	1	0
21NEHOPS118-2	19NEHOPS052-15/19NEHOPS052-17	1	0
21NEHOPS118-3	19NEHOPS052-15/19NEHOPS052-17	1	0
21NEHOPS118-4	19NEHOPS052-15/19NEHOPS052-17	1	0
21NEHOPS118-6	19NEHOPS052-15/19NEHOPS052-17	1	0
21NEHOPS119-10	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-11	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-19	19NEHOPS043-1/20NEHOPS069-8	1	0

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Table 2.3 continued.

Progeny genotype[a]	Breeding population[b]	Number of replicates[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
21NEHOPS119-2	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-3	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-4	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-6	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS119-7	19NEHOPS043-1/20NEHOPS069-8	1	1
21NEHOPS119-8	19NEHOPS043-1/20NEHOPS069-8	1	0
21NEHOPS120-1	19NEHOPS043-1/20NEHOPS069-2	1	0
21NEHOPS122-1	20NEHOPS074-8/20NEHOPS074-5	1	0
21NEHOPS123-1	20NEHOPS061-5/20NEHOPS077-1	1	0
21NEHOPS124-2	20NEHOPS096-1/20NEHOPS095-8	1	0
21NEHOPS124-4	20NEHOPS096-1/20NEHOPS095-8	1	0
21NEHOPS125-1	20NEHOPS077-15/20NEHOPS080-9	1	0
21NEHOPS125-2	20NEHOPS077-15/20NEHOPS080-9	1	0
21NEHOPS126-1	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-10	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-12	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-16	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-17	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-18	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-3	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-5	19NEHOPS041-39/19NEHOPS041-23	1	0
21NEHOPS126-9	19NEHOPS041-39/19NEHOPS041-23	1	0

[a] Progeny genotypes were developed at the University of Nebraska-Lincoln from 2018-2020.
[b] Breeding populations consisted of crosses between public elite cultivars, wild hops, USDA accessions, and the progeny genotypes listed in this table.
[c] Total number of replicates assessed from 2019-2021 for the PRs & FT, and from 2020-2021 for ALP & COH.
[d] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.
[e] Documented as the week the first flowers on an individual plant fully opened.
[f] Concentration of alpha acid content (mg/g of fresh hops).
[g] Concentration of cohumulone content (mg/g of fresh hops).

Table 2.4. The number of hop (*Humulus lupulus* L.) progeny observations assessed for 74 breeding populations for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) in the linear mixed model analysis based upon Henderson's Best Linear Unbiased Predictors (BLUPs).

Breeding population[a]	**Number of progeny observations[b]**	
	PRs[c] & FT[d]	**ALP[e] & COH[f]**
18NEHOP005/PI 635403	9	2
18NEHOPS005/PI 635246	2	0
18NEHOPS005/PI 635287	10	1
18NEHOPS007/PI 635242	2	0
18NEHOPS008/PI 635472	1	0
18NEHOPS009/PI 635246	8	1
18NEHOPS009/PI 635403	24	2
18NEHOPS014/PI 635242	2	0
18NEHOPS014/PI 635246	2	0
19NEHOPS041-13/19NEHOPS041-34	4	1
19NEHOPS041-25/19NEHOPS041-27	5	1
19NEHOPS041-29/19NEHOPS041-23	1	0
19NEHOPS041-39/19NEHOPS041-23	9	0
19NEHOPS042-1/19NEHOPS052-11	2	0
19NEHOPS043-1/19NEHOPS054-1	10	0
19NEHOPS043-1/20NEHOPS069-2	1	0
19NEHOPS043-1/20NEHOPS069-4	1	0
19NEHOPS043-1/20NEHOPS069-8	9	1
19NEHOPS045-2/PI 635287	7	0
19NEHOPS048-11/19NEHOPS041-34	4	0
19NEHOPS048-4/19NEHOPS048-22	21	6
19NEHOPS050-1/19NEHOPS047-1	3	1
19NEHOPS051-1/PI 635242	4	0
19NEHOPS052-12/19NEHOPS047-1	4	0
19NEHOPS052-12/19NEHOPS052-17	5	0
19NEHOPS052-12/19NEHOPS052-6	8	4
19NEHOPS052-15/19NEHOPS052-17	4	0
19NEHOPS053-16/19NEHOPS052-11	19	8
19NEHOPS053-18/19NEHOPS046-1	29	10
19NEHOPS053-18/19NEHOPS053-8	1	0
19NEHOPS054-16/19NEHOPS054-14	2	0
19NEHOPS054-6/19NEHOPS054-4	5	0
19NEHOPS054-9/19NEHOPS053-3	2	0
19NEHOPS056-12/20NEHOPS094-2	1	0
19NEHOPS056-142/19NEHOPS056-110	1	0
19NEHOPS056-146/19NEHOPS046-1	11	3

Continued next page.

Table 2.4 continued.

Breeding population[a]	Number of progeny observations[b]	
	PRs[c] & FT[d]	ALP[e] & COH[f]
19NEHOPS056-19/19NEHOPS056-83	8	3
19NEHOPS056-25/19NEHOPS056-2	6	1
19NEHOPS058-43/19NEHOPS052-14	5	1
19NEHOPS059-208/19NEHOPS049-12	1	0
19NEHOPS059-217/19NEHOPS059-178	7	2
19NEHOPS059-224/19NEHOPS049-4	5	0
19NEHOPS059-61/19NEHOPS059-46	5	1
19NEHOPS059-94/19NEHOPS059-93	6	2
19NEHOPS105-1/19NEHOPS052-11	12	1
20NEHOPS061-5/20NEHOPS077-1	1	0
20NEHOPS072-2/19NEHOPS045-1	1	0
20NEHOPS074-8/20NEHOPS074-5	1	0
20NEHOPS077-15/20NEHOPS080-9	2	0
20NEHOPS078-11/20NEHOPS078-8	2	0
20NEHOPS093-14/20NEHOPS093-12	15	2
20NEHOPS093-5/20NEHOPS093-6	3	1
20NEHOPS095-17/20NEHOPS096-3	4	1
20NEHOPS095-2/20NEHOPS096-3	3	2
20NEHOPS096-1/20NEHOPS095-8	2	0
20NEHOPS104-2/19NEHOPS052-17	19	2
Arp/18NEHOPS031	70	8
Arp/19NEHOPS056-144	9	1
Arp/PI 635246	40	7
Arp/PI 635458	11	0
Chinook/PI 635246	4	0
Columbus/18NEHOPS026	14	1
Galena/PI 635242	2	0
Galena/PI 635246	1	0
Galena/PI 635287	2	0
Glacier/18NEHOPS026	11	2
Glacier/PI 635246	1	0
Sorachi Ace/19NEHOPS052-11	3	0
Sorachi Ace/19NEHOPS052-5	9	2
Sorachi Ace/19NEHOPS053-8	2	0
Sorachi Ace/PI 635242	5	5
Sorachi Ace/PI 635246	21	13
Sorachi Ace/PI 635287	19	4
Sorachi Ace/PI 635403	24	2

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Table 2.4 Continued.

[a] Breeding populations consisted of crosses between public elite cultivars, wild hops, USDA accessions, and genotypes developed at the University of Nebraska-Lincoln.
[b] Total number of observations, which includes unique progeny genotypes and replicates, assessed from 2019 to 2021 for the PRs and FT, and from 2020 to 2021 for ALP & COH.
[c] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.
[d] Documented as the week the first flowers on an individual plant fully opened.
[e] Concentration of alpha acid content (mg/g of fresh hops).
[f] Concentration of cohumulone content (mg/g of fresh hops).

Table 2.5. The number of hop (*Humulus lupulus* L.) progeny observations assessed for 53 maternal genotypes for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) in the linear mixed model analysis based upon Henderson's Best Linear Unbiased Predictors (BLUPs).

Maternal genotype[a]	Accession type[ab]	Number of progeny observations[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
18NEHOPS005	Unknown	21	3
18NEHOPS007	Unknown	2	0
18NEHOPS008	Unknown	1	0
18NEHOPS009	Unknown	32	3
18NEHOPS014	Unknown	4	0
19NEHOPS041-13	Progeny genotype	4	1
19NEHOPS041-25	Progeny genotype	5	1
19NEHOPS041-29	Progeny genotype	1	0
19NEHOPS041-39	Progeny genotype	9	0
19NEHOPS042-1	Progeny genotype	2	0
19NEHOPS043-1	Progeny genotype	21	1
19NEHOPS045-2	Progeny genotype	7	0
19NEHOPS048-11	Progeny genotype	4	0
19NEHOPS048-4	Progeny genotype	21	6
19NEHOPS050-1	Progeny genotype	3	0
19NEHOPS051-1	Progeny genotype	4	0
19NEHOPS052-12	Progeny genotype	17	5
19NEHOPS052-15	Progeny genotype	4	0
19NEHOPS053-16	Progeny genotype	19	8
19NEHOPS053-18	Progeny genotype	30	10
19NEHOPS054-16	Progeny genotype	2	0
19NEHOPS054-6	Progeny genotype	5	0
19NEHOPS054-9	Progeny genotype	2	0
19NEHOPS056-12	Progeny genotype	1	0
19NEHOPS056-142	Progeny genotype	1	0
19NEHOPS056-146	Progeny genotype	11	3
19NEHOPS056-19	Progeny genotype	8	3
19NEHOPS056-25	Progeny genotype	6	1
19NEHOPS058-43	Progeny genotype	5	1
19NEHOPS059-208	Progeny genotype	1	0
19NEHOPS059-217	Progeny genotype	5	2
19NEHOPS059-224	Progeny genotype	5	0
19NEHOPS059-227	Progeny genotype	2	0
19NEHOPS059-61	Progeny genotype	5	1

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Table 2.5 continued.

Maternal genotype	Accession type[ab]	Number of progeny observations[c]	
		PRs[d] & FT[e]	ALP[f] & COH[g]
19NEHOPS059-94	Progeny genotype	6	2
19NEHOPS105-1	Progeny genotype	12	1
20NEHOPS061-5	Progeny genotype	1	0
20NEHOPS072-2	Progeny genotype	1	0
20NEHOPS074-8	Progeny genotype	1	0
20NEHOPS077-15	Progeny genotype	2	0
20NEHOPS078-11	Progeny genotype	2	0
20NEHOPS093-14	Progeny genotype	15	2
20NEHOPS093-5	Progeny genotype	3	1
20NEHOPS095-17	Progeny genotype	4	1
20NEHOPS095-2	Progeny genotype	3	2
20NEHOPS096-1	Progeny genotype	2	0
20NEHOPS104-2	Progeny genotype	19	2
Arp	Nebraska wild hop	130	16
Chinook	Public elite cultivar	4	0
Columbus	Public elite cultivar	14	1
Galena	Public elite cultivar	5	0
Glacier	Public elite cultivar	12	2
Sorachi Ace	Public elite cultivar	83	26

[a] Progeny genotypes were developed at the University of Nebraska-Lincoln from 2018 to 2020 from crosses between public elite cultivars, wild hops, USDA accessions, and other progeny genotypes developed at the University of Nebraska-Lincoln.
[b] Unknown genotypes were either public elite cultivars or Nebraska wild hops. They were not spaced appropriately in the maternal nursery, and as a result, they began to grow in the same area.
[c] Total number of observations, which includes unique progeny genotypes and replicates, assessed from 2019 to 2021 for the PRs and FT, and from 2020 to 2021 for ALP & COH.
[d] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.
[e] Documented as the week the first flowers on an individual plant fully opened.
[f] Concentration of alpha acid content (mg/g of fresh hops).
[g] Concentration of cohumulone content (mg/g of fresh hops).

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Table 2.6. The number of hop (*Humulus lupulus* L.) progeny observations assessed for 46 paternal genotypes for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) in the linear mixed model analysis based upon Henderson's Best Linear Unbiased Predictors (BLUPs).

Paternal genotypes	Accession type[a]	Number of progeny observations[b]	
		PRs[c] & FT[d]	ALP[e] & COH[f]
18NEHOPS026	Nebraska wild hop	25	3
18NEHOPS031	Nebraska wild hop	71	8
19NEHOPS041-23	Progeny genotype	10	0
19NEHOPS041-27	Progeny genotype	5	1
19NEHOPS041-34	Progeny genotype	8	1
19NEHOPS045-1	Progeny genotype	1	0
19NEHOPS046-1	Progeny genotype	40	13
19NEHOPS047-1	Progeny genotype	7	1
19NEHOPS048-22	Progeny genotype	21	6
19NEHOPS049-12	Progeny genotype	1	0
19NEHOPS049-4	Progeny genotype	5	0
19NEHOPS052-11	Progeny genotype	36	9
19NEHOPS052-14	Progeny genotype	5	1
19NEHOPS052-17	Progeny genotype	28	2
19NEHOPS052-5	Progeny genotype	9	2
19NEHOPS052-6	Progeny genotype	8	4
19NEHOPS053-3	Progeny genotype	2	0
19NEHOPS053-8	Progeny genotype	3	0
19NEHOPS054-1	Progeny genotype	10	0
19NEHOPS054-14	Progeny genotype	2	0
19NEHOPS054-4	Progeny genotype	5	0
19NEHOPS056-110	Progeny genotype	1	0
19NEHOPS056-144	Progeny genotype	9	1
19NEHOPS056-2	Progeny genotype	6	1
19NEHOPS056-83	Progeny genotype	8	3
19NEHOPS059-178	Progeny genotype	7	2
19NEHOPS059-46	Progeny genotype	5	1
19NEHOPS059-93	Progeny genotype	6	2
20NEHOPS069-2	Progeny genotype	1	0
20NEHOPS069-4	Progeny genotype	1	0
20NEHOPS069-8	Progeny genotype	9	1
20NEHOPS074-5	Progeny genotype	1	0
20NEHOPS077-1	Progeny genotype	1	0

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Table 2.6 continued.

Paternal genotype	Accession type[a]	Number of progeny observations[b]	
		PRs[c] & FT[d]	ALP[e] & COH[f]
20NEHOPS078-8	Progeny genotype	2	0
20NEHOPS080-9	Progeny genotype	2	0
20NEHOPS093-12	Progeny genotype	15	2
20NEHOPS093-6	Progeny genotype	3	1
20NEHOPS094-2	Progeny genotype	1	0
20NEHOPS095-8	Progeny genotype	2	0
20NEHOPS096-3	Progeny genotype	7	3
PI 635242	USDA accession	15	5
PI 635246	USDA accession	82	21
PI 635287	USDA accession	47	5
PI 635403	USDA accession	54	6
PI 635458	USDA accession	1	0
PI 635472	USDA accession	1	0

[a] Progeny genotypes were developed at the University of Nebraska-Lincoln from 2018 to 2020 from crosses between public elite cultivars, wild hops, USDA accessions, and other progeny genotypes developed at the University of Nebraska-Lincoln.
[b] Total number of observations, which includes unique progeny genotypes and replicates, assessed from 2019-2021 for the PRs and FT, and from 2020-2021 for ALP & COH.
[c] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.
[d] Documented as the week the first flowers on an individual plant fully opened.
[e] Concentration of alpha acid content (mg/g of fresh hops).
[f] Concentration of cohumulone content (mg/g of fresh hops).

Table 2.7. Estimated breeding values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) of 53 hop (*Humulus lupulus* L.) maternal genotypes based upon progeny performance[a].

Maternal genotype[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
18NEHOPS005	0.927	-0.005	-0.530	0.592	0.582	0.476
18NEHOPS007	-	-	-0.138	0.291	0.336	0.402
18NEHOPS008	-	-	-0.163	0.307	0.149	0.117
18NEHOPS009	3.827	-0.041	-0.887	0.745	1.021	0.923
18NEHOPS014	-	-	-0.310	0.571	0.428	0.346
19NEHOPS041-13	-0.623	0.015	0.117	0.313	-0.041	-0.235
19NEHOPS041-25	-0.358	-0.007	-0.409	-0.117	0.107	-0.140
19NEHOPS041-29	-	-	-0.003	0.052	-0.174	-0.177
19NEHOPS041-39	-	-	0.982	-1.129	-1.152	-0.961
19NEHOPS042-1	-	-	-0.168	-0.106	0.070	0.001
19NEHOPS043-1	-1.010	-0.017	0.440	-0.242	-0.298	-0.252
19NEHOPS045-2	-	-	0.351	-0.591	-0.539	-0.260
19NEHOPS048-11	-	-	0.485	-0.291	-0.422	-0.346
19NEHOPS048-4	0.585	0.025	-0.594	0.113	0.234	0.179
19NEHOPS050-1	-	-	-0.146	-0.373	-0.364	-0.261
19NEHOPS051-1	-	-	0.445	0.239	-0.177	-0.198
19NEHOPS052-12	-1.307	0.010	-0.010	0.194	0.390	0.506
19NEHOPS052-15	-	-	0.691	-0.587	-0.440	-0.198
19NEHOPS053-16	1.906	-0.017	-0.919	0.393	0.369	0.377
19NEHOPS053-18	0.238	0.025	-0.470	-0.165	0.010	-0.302
19NEHOPS054-16	-	-	-0.168	-0.106	-0.108	-0.301
19NEHOPS054-6	-	-	0.102	-0.545	-0.013	-0.003
19NEHOPS054-9	-	-	-0.168	-0.296	-0.286	-0.150
19NEHOPS056-12	-	-	0.128	0.160	0.252	0.235
19NEHOPS056-142	-	-	-0.003	0.052	0.043	-0.177
19NEHOPS056-146	1.925	-0.005	-0.076	-0.152	-0.201	-0.256
19NEHOPS056-19	-0.970	0.023	0.074	-0.218	-0.226	-0.242
19NEHOPS056-25	0.095	-0.023	-0.106	-0.030	-0.095	-0.096
19NEHOPS058-43	-0.146	-0.013	-0.336	0.181	-0.129	-0.210
19NEHOPS059-208	-	-	0.387	0.052	0.043	0.001
19NEHOPS059-217	0.069	-0.022	-0.336	0.423	0.219	0.205
19NEHOPS059-224	-	-	0.431	0.302	-0.013	-0.106
19NEHOPS059-227	-	-	0.159	-0.106	-0.108	0.001

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Table 2.7 continued.

Maternal genotype[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
19NEHOPS059-61	-0.828	0.026	0.577	0.609	0.455	-0.140
19NEHOPS059-94	-1.302	-0.015	-0.008	0.078	0.009	0.186
19NEHOPS105-1	-0.472	-0.007	-0.134	-0.259	-0.175	-0.181
20NEHOPS061-5	-	-	0.128	-0.309	-0.398	-0.120
20NEHOPS072-2	-	-	0.128	-0.074	-0.181	-0.120
20NEHOPS074-8	-	-	-0.067	-0.309	0.035	0.235
20NEHOPS077-15	-	-	0.213	-0.500	-0.476	-0.204
20NEHOPS078-11	-	-	0.213	-0.120	0.414	-0.053
20NEHOPS093-14	-0.506	0.012	0.356	-0.424	-0.406	-0.263
20NEHOPS093-5	-0.979	0.019	0.416	-0.152	-0.531	-0.397
20NEHOPS095-17	-1.164	0.006	0.568	0.514	-0.308	-0.314
20NEHOPS095-2	-1.038	0.014	-0.005	-0.152	0.225	0.127
20NEHOPS096-1	-	-	0.213	-0.500	-0.298	-0.355
20NEHOPS104-2	-2.259	0.003	-0.068	-0.270	0.137	0.260
Arp	1.050	0.019	-0.037	0.570	0.425	0.155
Chinook	-	-	0.097	0.198	-0.099	-0.117
Columbus	-0.474	0.008	-0.121	0.087	-0.019	0.269
Galena	-	-	-0.258	0.297	0.458	0.794
Glacier	-1.441	-0.029	-0.433	0.362	0.810	0.879
Sorachi Ace	4.256	-0.003	-0.634	0.426	0.457	0.463

[a] Progeny was developed and evaluated at the University of Nebraska-Lincoln. PRs and FT were evaluated from 2019 to 2021. A subset of progeny was evaluated for ALP and COH in 2020 and 2021.
[b] Maternal genotypes consisted of public elite cultivars, local wild hops, and genotypes developed at the University of Nebraska-Lincoln.
[c] Concentration of alpha acid content (mg/g of fresh hops).
[d] Concentration of cohumulone content (mg/g of fresh hops).
[e] Documented as the week the first flowers on an individual plant fully opened.
[f] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

Table 2.8. Estimated breeding values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) of 46 hop (*Humulus lupulus* L.) paternal genotypes based upon progeny performance[a].

Paternal genotype[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
18NEHOPS026	-1.794	0.002	-0.380	0.236	0.432	0.658
18NEHOPS031	-0.254	0.008	0.099	0.757	0.426	0.260
19NEHOPS041-23	-	-	1.003	-0.997	-1.092	-0.925
19NEHOPS041-27	-0.486	-0.016	-0.534	-0.108	0.098	-0.118
19NEHOPS041-34	-0.783	0.012	0.390	0.016	-0.287	-0.364
19NEHOPS045-1	-	-	0.176	-0.070	-0.164	-0.109
19NEHOPS046-1	0.698	0.012	-0.442	-0.182	-0.068	-0.274
19NEHOPS047-1	-0.228	0.006	-0.420	-0.305	-0.221	-0.055
19NEHOPS048-22	0.412	0.023	-0.685	0.108	0.222	0.198
19NEHOPS049-12	-	-	0.489	0.050	0.041	0.008
19NEHOPS049-4	-	-	0.473	0.278	-0.018	-0.089
19NEHOPS052-11	1.422	-0.010	-0.680	0.100	0.087	0.098
19NEHOPS052-14	-0.249	-0.012	-0.428	0.165	-0.126	-0.189
19NEHOPS052-17	-2.603	0.003	0.245	-0.330	-0.039	0.193
19NEHOPS052-5	-0.125	-0.006	-0.081	0.267	-0.099	-0.121
19NEHOPS052-6	-1.685	0.007	-0.184	0.389	0.684	0.653
19NEHOPS053-3	-	-	-0.276	-0.259	-0.250	-0.128
19NEHOPS053-8	-	-	0.611	-0.186	-0.186	-0.354
19NEHOPS054-1	-	-	-0.636	0.193	0.204	0.354
19NEHOPS054-14	-	-	-0.276	-0.088	-0.091	-0.269
19NEHOPS054-4	-	-	0.087	-0.512	-0.018	0.010
19NEHOPS056-110	-	-	-0.042	0.050	0.041	-0.157
19NEHOPS056-144	0.461	0.017	0.128	0.287	0.335	0.224
19NEHOPS056-2	0.021	-0.004	-0.169	-0.030	-0.093	-0.077
19NEHOPS056-83	-1.200	0.020	0.061	-0.216	-0.226	-0.221
19NEHOPS059-178	-0.053	-0.005	-0.271	0.271	0.112	0.182
19NEHOPS059-46	-1.005	0.019	0.625	0.570	0.422	-0.118
19NEHOPS059-93	-1.551	-0.011	-0.055	0.071	0.004	0.194
20NEHOPS069-2	-	-	-0.090	0.136	0.025	0.055
20NEHOPS069-4	-	-	0.176	-0.276	-0.164	-0.109
20NEHOPS069-8	-1.216	-0.009	1.526	-0.627	-0.738	-0.781
20NEHOPS074-5	-	-	-0.090	-0.276	0.025	0.220
20NEHOPS077-1	-	-	0.176	-0.276	-0.354	-0.109
20NEHOPS078-8	-	-	0.278	-0.116	0.361	-0.047

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Table 2.8 continued.

Paternal genotype[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
20NEHOPS080-9	-	-	0.278	-0.458	-0.435	-0.188
20NEHOPS093-12	-0.686	0.010	0.390	-0.430	-0.415	-0.248
20NEHOPS093-6	-1.181	0.014	0.518	-0.149	-0.495	-0.371
20NEHOPS094-2	-	-	0.176	0.136	0.215	0.220
20NEHOPS095-8	-	-	0.278	-0.458	-0.276	-0.329
20NEHOPS096-3	-1.927	0.013	0.475	0.241	-0.095	-0.137
PI 635242	2.585	-0.031	-0.235	0.405	0.362	0.508
PI 635246	3.120	-0.008	-0.840	0.327	0.581	0.440
PI 635287	4.604	-0.024	-0.509	0.488	0.307	0.462
PI 635403	3.704	-0.031	-1.031	0.498	0.709	0.706
PI 635458	-	-	-0.018	0.053	0.129	0.122
PI 635472	-	-	-0.284	0.259	0.129	0.122

[a] Progeny was developed and evaluated at the University of Nebraska-Lincoln. PRs and FT were evaluated from 2019 to 2021. A subset of progeny was evaluated for ALP and COH in 2020 and 2021.
[b] Paternal genotypes consisted of USDA accessions, local wild hops, and genotypes developed at the University of Nebraska-Lincoln.
[c] Concentration of alpha acid content (mg/g of fresh hops).
[d] Concentration of cohumulone content (mg/g of fresh hops).
[e] Documented as the week the first flowers on an individual plant fully opened.
[f] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

Table 2.9. Estimated breeding values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) of 74 hop (*Humulus lupulus* L.) breeding populations based upon progeny performance[a].

Breeding population[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
18NEHOPS005/PI 635246	-	-	-0.181	0.236	0.428	0.351
18NEHOPS005/PI 635287	-0.280	-0.020	-0.263	0.580	0.218	0.267
18NEHOPS005/PI 635403	0.906	-0.017	-0.807	0.216	0.600	0.343
18NEHOPS007/PI 635242	-	-	-0.201	0.235	0.333	0.411
18NEHOPS008/PI 635472	-	-	-0.265	0.255	0.144	0.111
18NEHOPS009/PI 635246	2.104	0.018	-0.766	0.530	1.099	0.849
18NEHOPS009/PI 635403	2.858	-0.016	-0.914	0.592	0.778	0.740
18NEHOPS014/PI 635242	-	-	-0.181	0.417	0.428	0.351
18NEHOPS014/PI 635246	-	-	-0.430	0.235	0.136	0.081
19NEHOPS041-13/19NEHOPS041-34	-0.893	0.017	0.203	0.259	-0.098	-0.291
19NEHOPS041-25/19NEHOPS041-27	-0.600	-0.022	-0.466	0.159	0.055	-0.192
19NEHOPS041-29/19NEHOPS041-23	-	-	0.004	0.032	-0.221	-0.213
19NEHOPS041-39/19NEHOPS041-23	-	-	1.217	1.165	-1.275	-1.057
19NEHOPS042-1/19NEHOPS052-11	-	-	-0.222	0.128	0.040	-0.025
19NEHOPS043-1/19NEHOPS054-1	-	-	-0.535	0.135	0.146	0.299
19NEHOPS043-1/20NEHOPS069-2	-	-	-0.071	0.133	0.017	0.048
19NEHOPS043-1/20NEHOPS069-4	-	-	0.225	0.309	-0.229	-0.150
19NEHOPS043-1/20NEHOPS069-8	-1.321	-0.012	1.656	0.686	-0.861	-0.904
19NEHOPS045-2/PI 635287	-	-	0.463	0.628	-0.634	-0.323
19NEHOPS048-11/19NEHOPS041-34	-	-	0.636	0.321	-0.508	-0.410
19NEHOPS048-4/19NEHOPS048-22	0.056	0.028	-0.577	0.044	0.156	0.117
19NEHOPS050-1/19NEHOPS047-1	-	-	-0.178	0.393	-0.444	-0.316
19NEHOPS051-1/PI 635242	-	-	0.634	0.187	-0.245	-0.251
19NEHOPS052-12/19NEHOPS047-1	-0.378	0.009	-0.304	0.188	-0.084	0.086
19NEHOPS052-12/19NEHOPS052-17	-	-	0.515	0.001	-0.082	0.135
19NEHOPS052-12/19NEHOPS052-6	-1.989	0.010	-0.087	0.346	0.693	0.637
19NEHOPS052-15/19NEHOPS052-17	-	-	0.947	0.611	-0.527	-0.251
19NEHOPS053-16/19NEHOPS052-11	1.378	-0.004	-0.925	0.322	0.296	0.321
19NEHOPS053-18/19NEHOPS046-1	-0.381	0.029	-0.411	0.247	-0.082	-0.356
19NEHOPS053-18/19NEHOPS053-8	-	-	-0.292	0.032	0.025	-0.213
19NEHOPS054-16/19NEHOPS054-14	-	-	-0.222	0.128	-0.157	-0.355
19NEHOPS054-6/19NEHOPS054-4	-	-	0.178	0.575	-0.074	-0.046
19NEHOPS054-9/19NEHOPS053-3	-	-	-0.222	0.309	-0.354	-0.190
19NEHOPS056-12/20NEHOPS094-2	-	-	0.225	0.133	0.262	0.246

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Table 2.9 continued.

Breeding population[b]	Estimated breeding value (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
19NEHOPS056-142/19NEHOPS056-110	-	-	0.004	0.032	0.025	-0.213
19NEHOPS056-146/19NEHOPS046-1	1.613	-0.021	-0.045	0.208	-0.283	-0.324
19NEHOPS056-19/19NEHOPS056-83	-1.463	0.026	0.153	0.269	-0.306	-0.306
19NEHOPS056-25/19NEHOPS056-2	-0.098	-0.004	-0.081	0.079	-0.164	-0.149
19NEHOPS058-43/19NEHOPS052-14	-0.365	-0.016	-0.365	0.129	-0.197	-0.267
19NEHOPS059-208/19NEHOPS049-12	-	-	0.597	0.032	0.025	-0.015
19NEHOPS059-217/19NEHOPS059-178	-0.264	-0.005	-0.177	0.227	0.061	0.129
19NEHOPS059-224/19NEHOPS049-4	-	-	0.584	0.246	-0.074	-0.157
19NEHOPS059-61/19NEHOPS059-46	-1.147	0.028	0.754	0.545	0.426	-0.192
19NEHOPS059-94/19NEHOPS059-93	-1.750	-0.014	0.039	0.026	-0.054	0.150
19NEHOPS105-1/19NEHOPS052-11	-0.726	-0.016	-0.110	0.314	-0.258	-0.246
20NEHOPS061-5/20NEHOPS077-1	-	-	0.225	0.309	-0.475	-0.150
20NEHOPS072-2/19NEHOPS045-1	-	-	0.225	0.088	-0.229	-0.150
20NEHOPS074-8/20NEHOPS074-5	-	-	-0.071	0.309	0.017	0.246
20NEHOPS077-15/20NEHOPS080-9	-	-	0.347	0.507	-0.565	-0.250
20NEHOPS078-11/20NEHOPS078-8	-	-	0.347	0.144	0.421	-0.085
20NEHOPS093-14/20NEHOPS093-12	-0.866	0.014	0.484	0.485	-0.497	-0.333
20NEHOPS093-5/20NEHOPS093-6	-1.286	0.020	0.610	0.183	-0.625	-0.463
20NEHOPS095-17/20NEHOPS096-3	-1.491	0.007	0.790	0.453	-0.386	-0.375
20NEHOPS095-2/20NEHOPS096-3	-1.443	0.016	0.052	0.183	0.198	0.104
20NEHOPS096-1/20NEHOPS095-8	-	-	0.347	0.507	-0.368	-0.415
20NEHOPS104-2/19NEHOPS052-17	-2.766	0.005	0.021	0.336	0.058	0.201
Arp/18NEHOPS031	-0.654	0.011	0.236	0.681	0.328	0.125
Arp/19NEHOPS056-144	0.337	0.025	0.229	0.243	0.307	0.171
Arp/PI 635246	1.325	0.020	-0.512	0.062	0.278	-0.071
Arp/PI 635458	-	-	-0.214	0.321	0.317	0.080
Chinook/PI 635246	-	-	0.140	0.139	-0.162	-0.167
Columbus/18NEHOPS026	-0.728	0.009	-0.095	0.024	-0.098	0.216
Galena/PI 635242	-	-	0.027	0.054	0.136	0.411
Galena/PI 635246	-	-	-0.265	0.033	0.144	0.111
Galena/PI 635287	-	-	-0.409	0.236	0.428	0.682
Glacier/18NEHOPS026	-1.879	-0.004	-0.401	0.299	0.847	0.869
Glacier/PI 635246	-	-	-0.265	0.033	-0.101	0.111
Sorachi Ace/19NEHOPS052-11	-	-	0.194	0.086	-0.444	-0.458
Sorachi Ace/19NEHOPS052-5	-0.336	-0.007	0.032	0.214	-0.181	-0.209
Sorachi Ace/19NEHOPS053-8	-	-	1.149	0.309	-0.354	-0.355

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Table 2.9 Continued.

Breeding population[b]	Estimated breeding values (BLUP)					
	ALP[c]	COH[d]	FT[e]	PRs June[f]	PRs July[f]	PRs August[f]
Sorachi Ace/PI 635242	2.227	-0.036	-0.624	0.129	0.358	0.356
Sorachi Ace/PI 635246	2.731	-0.027	-1.002	0.279	0.677	0.642
Sorachi Ace/PI 635287	5.066	-0.020	-0.625	0.602	0.479	0.558
Sorachi Ace/PI 635403	2.500	-0.031	-0.712	0.206	0.312	0.334

[a] Progeny was developed and evaluated at the University of Nebraska-Lincoln. PRs and FT were evaluated from 2019 to 2021. A subset of progeny was evaluated for ALP and COH in 2020 and 2021.
[b] Breeding populations consisted of crosses between public elite cultivars, wild hops, USDA accessions, and genotypes developed at the University of Nebraska-Lincoln.
[c] Concentration of alpha acid content (mg/g of fresh hops).
[d] Concentration of cohumulone content (mg/g of fresh hops).
[e] Documented as the week the first flowers on an individual plant fully opened.
[f] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

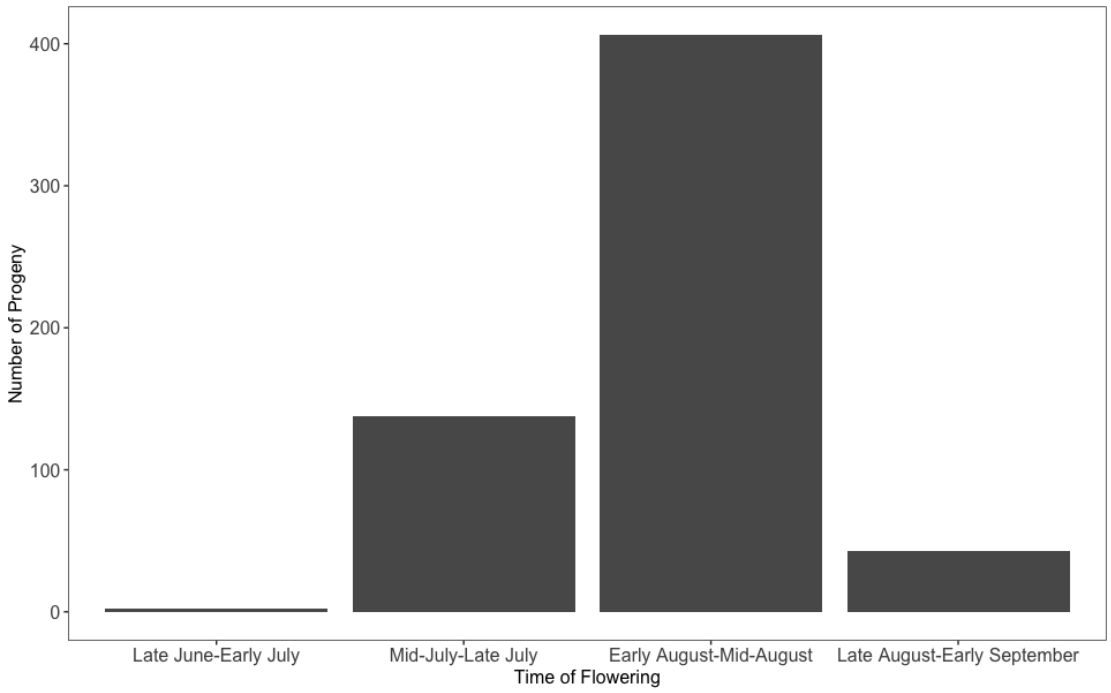

Figure 2.1. Time of flowering (FT) for 589 hop (*Humulus lupulus* L.) progeny genotypes developed and evaluated at the University of Nebraska-Lincoln. FT was evaluated from 2019 to 2021 and was documented as the week the first flowers on an individual plant fully opened. The ideal time for genotypes to flower in Nebraska is mid-June to mid-August.

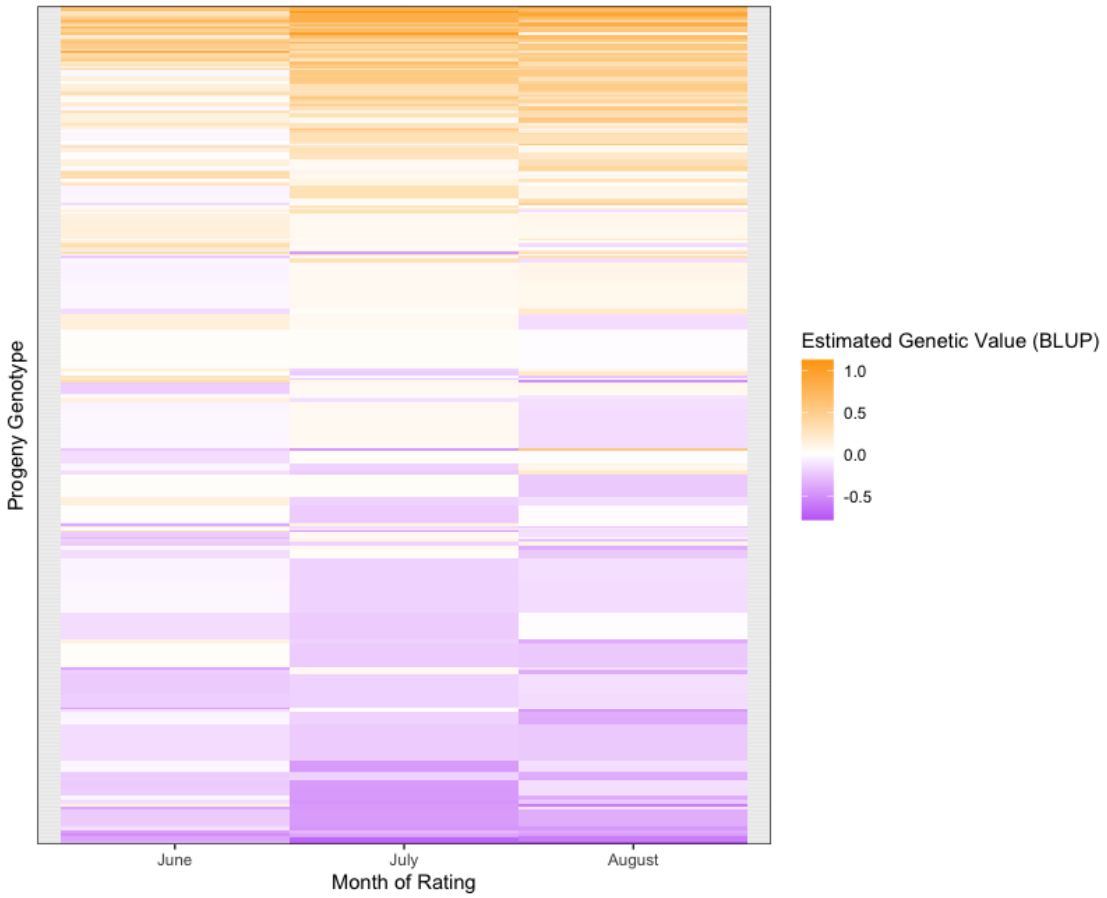

Figure 2.2. Estimated genetic values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs) of 379 hop (*Humulus lupulus* L.) progeny genotypes developed and evaluated at the University of Nebraska-Lincoln. PRs were conducted by rating progeny in the field using a scale from one to five (1 = poor performance, 5 = superior performance). Data for PRs was recorded in June, July, and August from 2019 to 2021.

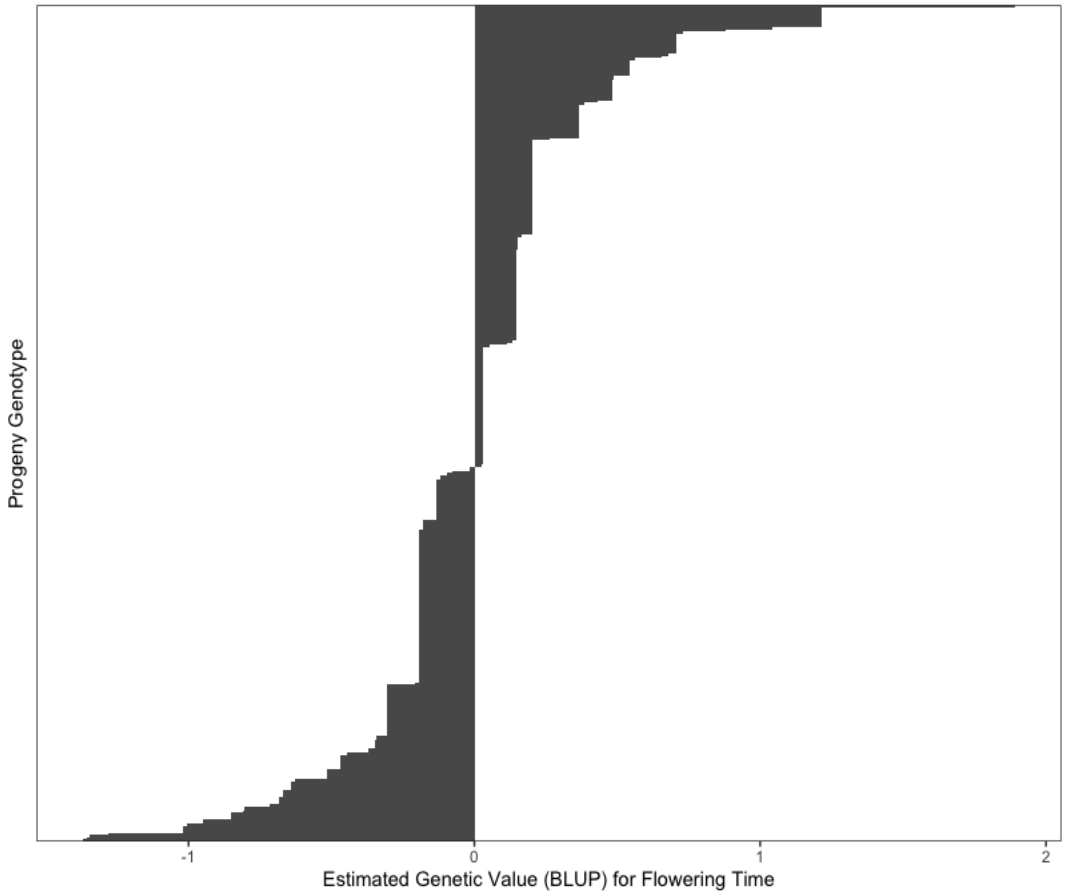

Figure 2.3. Estimated genetic values (Best Linear Unbiased Predictors (BLUPs) for flowering time (FT) of 379 hop (*Humulus lupulus* L.) progeny genotypes develop and evaluated at the University of Nebraska-Lincoln. FT was evaluated from 2019 to 2021 and documented as the week the first flowers on a plant fully opened.

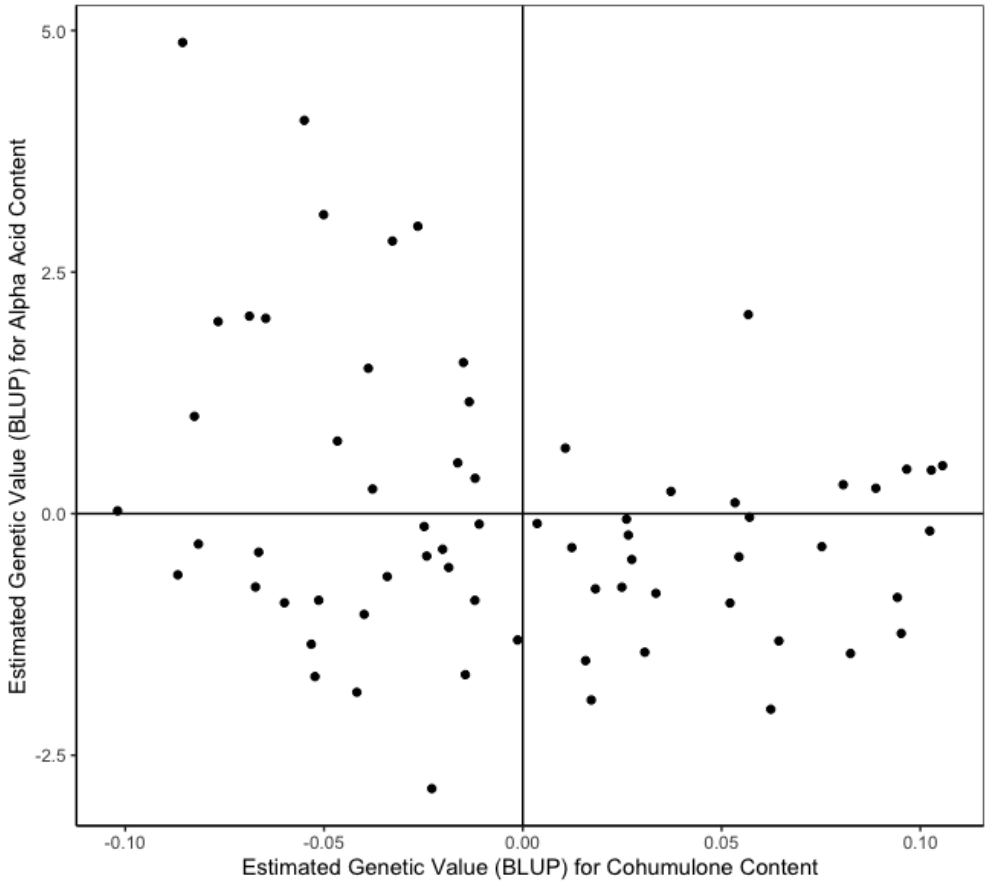

Figure 2.4. Estimated genetic values (Best Linear Unbiased Predictors (BLUPs) for alpha acid content (ALP) and cohumulone content (COH) of 67 hop (*Humulus lupulus* L.) progeny genotypes developed by the University of Nebraska-Lincoln. The concentration (mg/g of fresh cones) of ALP and COH was characterized in 2020 and 2021 by liquid chromatography with tandem mass spectrometry (LC-MS-MS).

Table 2.10. Estimated genetic values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) of 61 female hop (*Humulus lupulus* L.) progeny genotypes developed at the University of Nebraska-Lincoln.

Progeny genotype[a]	Estimated genetic value (BLUP)					
	ALP[b]	COH[c]	FT[d]	PRs June[e]	PRs July[e]	PRs August[e]
19NEHOPS040-3	2.060	0.057	-0.715	0.276	0.832	0.955
19NEHOPS040-5	-	-	-0.192	0.144	0.308	0.073
19NEHOPS041-29	4.876	-0.086	-0.447	0.305	0.127	0.366
19NEHOPS041-39	-1.307	-0.001	-1.369	0.242	0.673	0.327
19NEHOPS041-40	-	-	-0.192	0.322	0.560	0.527
19NEHOPS042-1	-	-	-0.192	0.144	0.056	0.073
19NEHOPS043-1	-	-	-0.121	0.143	0.269	0.422
19NEHOPS045-2	-	-	-0.192	0.144	0.308	0.527
19NEHOPS048-8	0.751	-0.047	-1.020	0.266	0.258	0.426
19NEHOPS049-11	-0.314	-0.082	-1.004	0.773	0.492	0.490
19NEHOPS050-5	-	-	-0.192	0.144	0.056	0.527
19NEHOPS051-1	2.021	-0.065	-0.668	0.114	0.379	0.414
19NEHOPS052-12	4.070	-0.055	-0.668	0.531	0.505	0.889
19NEHOPS052-15	2.974	-0.026	-0.685	0.615	0.832	0.696
19NEHOPS052-7	-	-	-0.192	0.144	0.056	0.300
19NEHOPS053-17	3.094	-0.050	-0.517	0.034	0.115	0.156
19NEHOPS053-18	2.821	-0.033	-1.280	0.635	0.728	0.903
19NEHOPS053-7	-0.896	-0.051	-0.950	0.210	1.131	0.791
19NEHOPS054-16	-	-	-0.192	0.144	0.056	0.073
19NEHOPS054-5	2.044	-0.069	-0.668	0.427	0.379	0.533
19NEHOPS054-9	1.007	-0.083	-0.812	0.010	0.254	0.295
19NEHOPS056-128	0.263	0.089	-0.207	0.193	0.450	0.170
19NEHOPS056-146	1.988	-0.077	-0.950	0.116	0.461	0.472
19NEHOPS059-111	-0.057	0.026	0.113	0.349	0.086	0.020
19NEHOPS059-121	-0.897	-0.012	0.028	0.701	0.845	0.438
19NEHOPS059-140	-	-	-0.192	0.144	0.056	0.073
19NEHOPS059-204	-0.557	-0.019	-0.094	0.635	1.007	0.057
19NEHOPS059-208	-	-	0.728	0.549	0.427	0.519
19NEHOPS059-217	-	-	0.145	0.144	0.056	0.073
19NEHOPS059-74	-	-	0.145	0.322	0.056	0.073
19NEHOPS059-84	-	-	0.055	0.776	0.350	0.260
19NEHOPS105-1	-	-	-0.373	0.143	0.068	0.053
20NEHOPS073-13	0.497	0.106	-0.182	0.266	0.545	0.696
20NEHOPS073-18	0.450	0.103	-0.307	0.024	0.029	0.444

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Table 2.10 continued.

Progeny genotype[a]	Estimated genetic value (BLUP)					
	ALP[b]	COH[c]	FT[d]	PRs June[e]	PRs July[e]	PRs August[e]
20NEHOPS077-1	0.366	-0.012	-0.852	0.499	0.402	0.561
20NEHOPS077-13	1.564	-0.015	-0.685	0.034	0.545	0.291
20NEHOPS077-17	0.255	-0.038	-1.355	0.499	0.258	0.561
20NEHOPS077-19	0.230	0.037	-0.685	0.034	0.402	0.156
20NEHOPS078-16	0.113	0.053	-0.307	0.024	0.282	0.218
20NEHOPS078-33	-2.024	0.062	-1.020	0.150	0.115	0.156
20NEHOPS078-7	-0.108	-0.011	-0.349	0.266	0.258	0.021
20NEHOPS078-9	-0.037	0.057	-0.852	0.034	0.258	0.021
20NEHOPS086-6	-1.239	0.095	0.263	0.601	0.766	0.118
20NEHOPS090-2	-	-	0.656	0.266	0.115	0.021
20NEHOPS091-2	-0.368	-0.020	-0.349	0.382	0.258	0.426
20NEHOPS094-3	0.300	0.081	-0.182	0.499	0.689	0.561
20NEHOPS095-2	-0.761	0.025	0.153	0.499	0.832	0.696
20NEHOPS096-2	-1.686	-0.052	-0.517	0.150	0.689	0.696
20NEHOPS096-5	-0.778	0.018	-0.182	0.382	0.689	0.831
20NEHOPS097-6	-0.439	-0.024	-0.517	0.266	0.258	0.156
20NEHOPS101-1	-1.447	0.082	-0.349	0.034	0.402	0.426
20NEHOPS102-2	-1.848	-0.042	-0.014	0.034	0.115	0.291
20NEHOPS104-2	-2.845	-0.023	-0.517	0.382	0.832	0.831
20NEHOPS104-3	0.460	0.097	-0.076	0.281	0.472	0.621
21NEHOPS109-1	-0.867	0.094	-0.132	0.128	0.309	0.317
21NEHOPS112-20	-1.666	-0.014	-0.806	0.128	0.057	0.544
21NEHOPS113-13	-0.824	0.033	-0.132	0.128	0.309	0.091
21NEHOPS115-4	-	-	0.205	0.128	0.057	0.544
21NEHOPS117-1	-	-	-0.469	0.128	0.057	0.317
21NEHOPS117-2	-1.521	0.016	-0.132	0.307	0.057	0.091
21NEHOPS120-1	-	-	-0.132	0.128	0.057	0.091

[a] Progeny genotypes were developed from 2018 to 2020 from crosses between public elite cultivars, wild hops, USDA accessions, and other progeny genotypes developed at the University of Nebraska-Lincoln. They were evaluated for PRs and FT from 2019 to 2021. A subset of progeny was evaluated for ALP and COH in 2020 and 2021.

[b] Concentration of alpha acid content (mg/g of fresh hops).

[c] Concentration of cohumulone content (mg/g of fresh hops).

[d] Documented as the week the first flowers on an individual plant fully opened.

[e] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

Table 2.11. Estimated genetic values (Best Linear Unbiased Predictors (BLUPs) for performance ratings (PRs) and flowering time (FT) of 23 male hop (*Humulus lupulus* L.) progeny genotypes developed at the University of Nebraska-Lincoln.

Progeny genotype[a]	Estimated genetic value (BLUP)			
	FT[b]	PRs June[c]	PRs July[c]	PRs August[c]
19NEHOPS040-9	-0.192	0.322	0.560	0.300
19NEHOPS041-23	-0.192	0.144	0.308	0.527
19NEHOPS041-34	-0.192	0.144	0.308	0.527
19NEHOPS041-35	-0.192	0.322	0.308	0.300
19NEHOPS041-47	-0.625	0.446	0.672	0.607
19NEHOPS048-22	-0.192	0.144	0.560	0.300
19NEHOPS049-18	0.030	0.381	0.534	0.444
19NEHOPS052-17	0.145	0.144	0.560	0.300
19NEHOPS052-6	-0.121	0.143	0.269	0.237
19NEHOPS053-8	-0.192	0.144	0.056	0.073
19NEHOPS054-10	-0.192	0.144	0.056	0.073
19NEHOPS056-98	-0.192	0.144	0.056	0.073
19NEHOPS058-75	0.145	0.144	0.056	0.073
20NEHOPS069-1	-0.307	0.024	0.029	0.218
20NEHOPS069-7	-1.020	0.499	0.402	0.561
20NEHOPS073-22	-0.852	0.150	0.545	0.426
20NEHOPS076-6	-0.644	0.024	0.282	0.218
20NEHOPS096-3	-0.307	0.024	0.282	0.218
20NEHOPS096-6	-0.307	0.024	0.534	0.444
21NEHOPS110-1	0.205	0.128	0.309	0.317
21NEHOPS112-23	-0.469	0.128	0.057	0.317
21NEHOPS113-14	-0.132	0.128	0.057	0.091
21NEHOPS116-1	-0.132	0.128	0.057	0.091

[a] Progeny genotypes were developed from 2018 to 2020 from crosses between public elite cultivars, wild hops, USDA accessions, and other progeny genotypes developed at the University of Nebraska-Lincoln. They were evaluated for PRs and FT from 2019 to 2021.
[b] Documented as the week the first flowers on an individual plant fully opened.
[c] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

Table 2.12. Heritability estimates[a] for June, July, and August performance ratings (PRs), flowering time (FT), alpha acid content (ALP), and cohumulone content (COH) for hop (*Humulus lupulus* L.).

Trait	Maternal genotype	Paternal genotype	Breeding population	Progeny genotype
PRs June[b]	0.235	0.206	0.221	.179
PRs July[b]	0.217	0.189	0.246	.252
PRs August[b]	0.178	0.165	0.198	.226
FT[c]	0.195	0.265	0.296	.337
ALP[d]	0.252	0.282	0.279	.278
COH[e]	0.191	0.184	0.193	.243

[a] Heritability defined as the ratio of genetic variance to total variance.
[b] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.
[c] Documented as the week the first flowers on an individual plant fully opened.
[d] Concentration of alpha acid content (mg/g of fresh hops).
[e] Concentration of cohumulone content (mg/g of fresh hops).

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Appendix A

Data collected for June, July, and August performance ratings (PRs), flowering time (FT), and gender of 589 (*Humulus lupulus* L.) progeny genotypes evaluated during 2019, 2020, and 2021 at the University of Nebraska-Lincoln East Campus Research Farm.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS037-1	2018	2019	31	1	3	4	5
19NEHOPS037-5	2018	2019	32	2	5	3	2
19NEHOPS040-3	2018	2019	31	1	4	4	5
19NEHOPS040-3	2018	2020	32	1	3	5	5
19NEHOPS040-3	2018	2021	29	1	2	4	3
19NEHOPS040-3	2018	2021	29	1	3	4	5
19NEHOPS040-5	2018	2019	31	1	4	4	3
19NEHOPS040-6	2018	2019	31	2	3	4	4
19NEHOPS040-8	2018	2019	31	1	3	3	2
19NEHOPS040-9	2018	2019	31	2	5	5	4
19NEHOPS041-1	2018	2019	31	1	3	3	3
19NEHOPS041-13	2018	2019	31	1	4	3	2
19NEHOPS041-23	2018	2019	31	2	4	4	5
19NEHOPS041-25	2018	2019	31	1	3	4	4
19NEHOPS041-27	2018	2019	31	2	3	3	3
19NEHOPS041-29	2018	2019	31	1	5	4	5
19NEHOPS041-29	2018	2020	32	1	4	5	5
19NEHOPS041-29	2018	2020	33	1	2	3	3
19NEHOPS041-29	2018	2021	29	1	3	3	3
19NEHOPS041-29	2018	2021	30	3	2	2	3
19NEHOPS041-29	2018	2021	30	1	1	1	1
19NEHOPS041-3	2018	2019	32	1	2	2	2
19NEHOPS041-34	2018	2019	31	2	4	4	5
19NEHOPS041-35	2018	2019	31	2	5	4	4
19NEHOPS041-39	2018	2020	31	1	3	4	3
19NEHOPS041-39	2018	2020	31	1	2	4	4
19NEHOPS041-39	2018	2020	32	1	2	3	3
19NEHOPS041-39	2018	2021	26	3	4	5	4
19NEHOPS041-39	2018	2021	29	1	3	5	4
19NEHOPS041-39	2018	2021	30	1	1	2	2
19NEHOPS041-40	2018	2019	31	1	5	5	5
19NEHOPS041-43	2018	2019	32	2	3	3	3

Continued next page.

Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS041-47	2018	2019	31	2	4	4	4
19NEHOPS041-47	2018	2020	31	2	4	5	5
19NEHOPS042-1	2018	2019	31	1	4	3	3
19NEHOPS043-1	2018	2019	31	1	3	3	3
19NEHOPS043-1	2018	2020	33	1	3	4	5
19NEHOPS044-1	2018	2019	31	1	3	2	3
19NEHOPS045-1	2018	2019	31	2	3	3	4
19NEHOPS045-2	2018	2019	31	1	4	4	5
19NEHOPS046-1	2018	2019	31	2	3	3	3
19NEHOPS047-1	2018	2019	32	2	3	3	4
19NEHOPS047-1	2018	2020	33	2	2	3	4
19NEHOPS048-11	2018	2019	32	1	2	2	1
19NEHOPS048-17	2018	2019	31	1	3	3	2
19NEHOPS048-20	2018	2019	31	1	3	3	2
19NEHOPS048-22	2018	2019	31	2	4	5	4
19NEHOPS048-4	2018	2019	31	1	3	5	5
19NEHOPS048-8	2018	2020	32	1	3	5	5
19NEHOPS048-8	2018	2021	28	1	3	3	4
19NEHOPS048-8	2018	2021	28	1	3	3	3
19NEHOPS048-8	2018	2021	30	1	2	2	2
19NEHOPS049-11	2018	2020	32	1	4	4	4
19NEHOPS049-11	2018	2020	32	1	3	3	3
19NEHOPS049-11	2018	2021	28	1	5	5	5
19NEHOPS049-11	2018	2021	28	1	4	3	4
19NEHOPS049-11	2018	2021	30	1	2	3	2
19NEHOPS049-12	2018	2019	33	2	3	3	2
19NEHOPS049-16	2018	2019	33	2	2	1	2
19NEHOPS049-17	2018	2019	32	2	3	1	2
19NEHOPS049-18	2018	2020	33	2	4	5	5
19NEHOPS049-4	2018	2019	33	2	2	2	2
19NEHOPS050-1	2018	2019	32	1	3	4	2
19NEHOPS050-5	2018	2019	31	1	4	3	5
19NEHOPS051-1	2018	2019	31	1	3	3	3
19NEHOPS051-1	2018	2020	31	1	2	5	4
19NEHOPS051-1	2018	2021	29	1	3	3	3
19NEHOPS051-1	2018	2021	29	1	4	4	5
19NEHOPS051-1	2018	2021	31	1	1	2	2

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS052-10	2018	2019	32	1	2	1	2
19NEHOPS052-11	2018	2019	31	2	3	3	3
19NEHOPS052-12	2018	2019	31	1	3	4	5
19NEHOPS052-12	2018	2020	32	1	3	3	4
19NEHOPS052-12	2018	2021	29	1	5	3	5
19NEHOPS052-12	2018	2021	29	1	3	4	4
19NEHOPS052-12	2018	2021	30	1	3	4	3
19NEHOPS052-14	2018	2019	31	2	3	2	1
19NEHOPS052-15	2018	2020	32	1	3	4	3
19NEHOPS052-15	2018	2021	29	1	5	4	5
19NEHOPS052-15	2018	2021	29	1	4	5	5
19NEHOPS052-15	2018	2021	30	1	2	4	3
19NEHOPS052-17	2018	2019	32	2	4	5	4
19NEHOPS052-2	2018	2019	31	1	4	2	2
19NEHOPS052-20	2018	2019	32	1	2	2	2
19NEHOPS052-5	2018	2019	31	2	3	1	1
19NEHOPS052-6	2018	2019	32	2	3	3	3
19NEHOPS052-6	2018	2020	32	2	3	4	4
19NEHOPS052-7	2018	2019	31	1	4	3	4
19NEHOPS053-1	2018	2019	31	1	1	1	2
19NEHOPS053-10	2018	2019	32	2	3	3	2
19NEHOPS053-16	2018	2019	31	1	3	1	2
19NEHOPS053-17	2018	2020	32	1	1	3	3
19NEHOPS053-17	2018	2021	29	1	4	4	5
19NEHOPS053-17	2018	2021	29	1	2	2	2
19NEHOPS053-17	2018	2021	31	1	2	3	2
19NEHOPS053-18	2018	2019	31	1	5	5	5
19NEHOPS053-18	2018	2020	31	1	3	5	4
19NEHOPS053-18	2018	2020	32	1	4	5	4
19NEHOPS053-18	2018	2020	32	1	3	4	4
19NEHOPS053-18	2018	2021	28	1	3	3	4
19NEHOPS053-18	2018	2021	28	1	2	1	5
19NEHOPS053-18	2018	2021	28	1	3	4	3
19NEHOPS053-19	2018	2019	31	1	3	2	2
19NEHOPS053-2	2018	2019	32	1	2	3	3
19NEHOPS053-3	2018	2019	32	2	2	3	3
19NEHOPS053-7	2018	2019	31	1	3	4	5

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS053-7	2018	2020	32	1	3	5	3
19NEHOPS053-7	2018	2020	32	1	3	4	4
19NEHOPS053-7	2018	2021	28	1	3	5	2
19NEHOPS053-7	2018	2021	29	1	1	5	5
19NEHOPS053-7	2018	2021	29	2	3	4	5
19NEHOPS053-8	2018	2019	31	2	4	3	3
19NEHOPS054-1	2018	2019	31	2	3	3	4
19NEHOPS054-10	2018	2019	31	2	4	3	3
19NEHOPS054-12	2018	2019	32	2	2	1	1
19NEHOPS054-13	2018	2019	32	1	2	1	2
19NEHOPS054-14	2018	2019	31	2	3	3	2
19NEHOPS054-15	2018	2019	31	1	3	5	5
19NEHOPS054-16	2018	2019	31	1	4	3	3
19NEHOPS054-3	2018	2019	32	2	3	3	2
19NEHOPS054-4	2018	2019	31	2	3	3	3
19NEHOPS054-5	2018	2019	31	1	4	4	4
19NEHOPS054-5	2018	2020	33	1	3	4	3
19NEHOPS054-5	2018	2021	28	1	4	3	4
19NEHOPS054-5	2018	2021	29	1	4	4	5
19NEHOPS054-5	2018	2021	30	1	1	2	2
19NEHOPS054-6	2018	2019	31	1	2	2	2
19NEHOPS054-8	2018	2019	31	2	3	3	2
19NEHOPS054-9	2018	2019	32	1	3	2	4
19NEHOPS054-9	2018	2020	32	3	2	3	3
19NEHOPS054-9	2018	2021	28	3	4	4	4
19NEHOPS054-9	2018	2021	29	3	2	5	4
19NEHOPS054-9	2018	2021	29	3	1	2	1
19NEHOPS055-1	2018	2020	34	1	2	3	2
19NEHOPS055-1	2018	2021	32	1	3	2	3
19NEHOPS055-2	2018	2019	31	1	3	2	2
19NEHOPS055-2	2018	2020	32	1	2	3	3
19NEHOPS056-110	2018	2019	31	2	2	3	1
19NEHOPS056-12	2018	2020	33	1	2	2	3
19NEHOPS056-12	2018	2020	34	1	2	3	4
19NEHOPS056-12	2018	2021	31	1	1	3	2
19NEHOPS056-12	2018	2021	31	1	1	4	3
19NEHOPS056-12	2018	2021	31	1	1	3	2

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS056-128	2018	2020	32	1	3	5	4
19NEHOPS056-128	2018	2020	33	1	2	3	3
19NEHOPS056-130	2018	2019	31	2	4	3	2
19NEHOPS056-133	2018	2019	31	1	2	2	2
19NEHOPS056-139	2018	2019	31	1	3	3	2
19NEHOPS056-142	2018	2019	31	1	3	3	2
19NEHOPS056-144	2018	2019	31	2	3	2	1
19NEHOPS056-146	2018	2019	31	1	3	1	2
19NEHOPS056-146	2018	2020	32	1	1	5	5
19NEHOPS056-146	2018	2020	33	1	2	4	4
19NEHOPS056-146	2018	2021	28	1	4	5	3
19NEHOPS056-146	2018	2021	28	1	2	3	4
19NEHOPS056-146	2018	2021	29	1	3	3	3
19NEHOPS056-148	2018	2019	31	1	3	2	2
19NEHOPS056-151	2018	2019	32	2	3	3	3
19NEHOPS056-19	2018	2019	31	1	2	3	3
19NEHOPS056-2	2018	2019	31	2	3	3	2
19NEHOPS056-20	2018	2019	31	1	4	3	2
19NEHOPS056-25	2018	2019	31	1	3	2	3
19NEHOPS056-37	2018	2019	32	2	3	2	2
19NEHOPS056-38	2018	2020	32	1	3	3	3
19NEHOPS056-45	2018	2019	31	1	3	2	2
19NEHOPS056-48	2018	2019	32	2	3	2	2
19NEHOPS056-50	2018	2019	31	1	3	2	2
19NEHOPS056-51	2018	2019	31	1	3	2	2
19NEHOPS056-53	2018	2020	34	1	2	2	3
19NEHOPS056-56	2018	2019	31	1	3	3	2
19NEHOPS056-61	2018	2020	33	1	2	3	2
19NEHOPS056-65	2018	2019	32	2	4	3	2
19NEHOPS056-71	2018	2019	32	2	2	3	3
19NEHOPS056-76	2018	2019	31	2	2	3	1
19NEHOPS056-79	2018	2019	31	1	3	4	4
19NEHOPS056-83	2018	2019	31	2	3	3	2
19NEHOPS056-98	2018	2019	31	2	4	3	3
19NEHOPS057-1	2018	2019	32	1	3	3	3
19NEHOPS058-104	2018	2019	31	1	3	3	2
19NEHOPS058-34	2018	2019	32	2	3	2	2

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS058-43	2018	2019	31	1	3	4	2
19NEHOPS058-50	2018	2019	31	1	3	3	2
19NEHOPS058-52	2018	2019	31	2	3	3	2
19NEHOPS058-75	2018	2019	32	2	4	3	3
19NEHOPS058-8	2018	2019	32	1	3	2	2
19NEHOPS058-83	2018	2019	31	2	3	3	3
19NEHOPS058-96	2018	2019	32	1	5	1	4
19NEHOPS059-103	2018	2019	33	1	3	2	2
19NEHOPS059-103	2018	2020	33	1	3	3	3
19NEHOPS059-111	2018	2019	32	1	4	3	2
19NEHOPS059-111	2018	2020	33	1	3	2	3
19NEHOPS059-111	2018	2020	33	1	3	3	3
19NEHOPS059-111	2018	2020	33	1	2	5	4
19NEHOPS059-111	2018	2020	33	1	2	2	3
19NEHOPS059-118	2018	2019	32	1	3	2	2
19NEHOPS059-12	2018	2019	33	2	5	3	2
19NEHOPS059-120	2018	2019	31	2	3	3	3
19NEHOPS059-121	2018	2020	32	1	4	5	5
19NEHOPS059-121	2018	2020	33	1	3	4	5
19NEHOPS059-121	2018	2020	33	1	3	5	5
19NEHOPS059-121	2018	2020	33	1	3	5	3
19NEHOPS059-121	2018	2020	33	1	2	4	4
19NEHOPS059-121	2018	2021	30	1	4	4	1
19NEHOPS059-121	2018	2021	31	1	3	3	3
19NEHOPS059-121	2018	2021	31	1	3	2	2
19NEHOPS059-124	2018	2019	32	2	3	2	2
19NEHOPS059-140	2018	2019	31	1	4	3	3
19NEHOPS059-160	2018	2019	32	2	4	3	2
19NEHOPS059-161	2018	2019	32	2	1	3	2
19NEHOPS059-162	2018	2020	33	1	2	4	3
19NEHOPS059-162	2018	2021	30	1	2	3	3
19NEHOPS059-162	2018	2021	31	3	3	3	4
19NEHOPS059-162	2018	2021	31	3	1	2	2
19NEHOPS059-165	2018	2019	33	1	2	2	2
19NEHOPS059-173	2018	2019	32	1	4	3	3
19NEHOPS059-173	2018	2020	33	1	4	3	4
19NEHOPS059-173	2018	2020	33	1	2	3	4

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS059-173	2018	2021	30	1	4	2	3
19NEHOPS059-173	2018	2021	31	1	1	4	3
19NEHOPS059-173	2018	2021	31	1	3	2	3
19NEHOPS059-173	2018	2021	34	1	1	2	2
19NEHOPS059-178	2018	2019	32	2	3	2	2
19NEHOPS059-182	2018	2019	32	1	3	2	2
19NEHOPS059-189	2018	2019	31	1	4	3	2
19NEHOPS059-196	2018	2019	31	1	5	1	2
19NEHOPS059-204	2018	2019	32	1	4	4	4
19NEHOPS059-204	2018	2020	33	1	4	5	5
19NEHOPS059-204	2018	2021	29	3	4	4	1
19NEHOPS059-204	2018	2021	30	1	3	5	2
19NEHOPS059-204	2018	2021	31	3	3	4	2
19NEHOPS059-208	2018	2019	33	1	4	3	2
19NEHOPS059-208	2018	2020	32	1	5	5	5
19NEHOPS059-208	2018	2020	33	1	5	4	5
19NEHOPS059-208	2018	2020	33	1	3	3	3
19NEHOPS059-208	2018	2021	31	1	2	4	3
19NEHOPS059-208	2018	2021	32	1	2	3	3
19NEHOPS059-208	2018	2021	34	1	1	2	4
19NEHOPS059-213	2018	2019	31	1	3	3	2
19NEHOPS059-217	2018	2019	32	1	4	3	3
19NEHOPS059-224	2018	2019	33	1	3	3	3
19NEHOPS059-227	2018	2019	32	1	4	2	2
19NEHOPS059-44	2018	2019	32	1	3	1	1
19NEHOPS059-46	2018	2019	33	2	3	2	2
19NEHOPS059-47	2018	2019	32	1	3	3	3
19NEHOPS059-61	2018	2019	33	1	3	3	3
19NEHOPS059-71	2018	2019	32	1	4	2	3
19NEHOPS059-74	2018	2019	32	1	5	3	3
19NEHOPS059-8	2018	2019	33	1	3	4	3
19NEHOPS059-80	2018	2019	32	2	3	3	2
19NEHOPS059-84	2018	2019	32	1	4	4	4
19NEHOPS059-84	2018	2020	33	1	4	4	4
19NEHOPS059-84	2018	2020	33	1	3	3	4
19NEHOPS059-84	2018	2021	29	1	5	3	2
19NEHOPS059-84	2018	2021	31	1	3	3	2

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
19NEHOPS059-84	2018	2021	31	1	3	3	3
19NEHOPS059-92	2018	2019	32	1	3	2	2
19NEHOPS059-93	2018	2019	32	2	3	2	1
19NEHOPS059-94	2018	2019	32	1	4	2	2
19NEHOPS105-1	2018	2019	31	1	3	3	3
19NEHOPS105-1	2018	2020	32	1	3	3	3
20NEHOPS061-11	2019	2020	34	1	2	3	2
20NEHOPS061-15	2019	2020	32	2	2	3	2
20NEHOPS061-16	2019	2020	31	2	2	3	3
20NEHOPS061-2	2019	2020	34	1	2	2	3
20NEHOPS061-4	2019	2020	34	2	1	2	2
20NEHOPS061-5	2019	2020	32	2	1	2	3
20NEHOPS061-7	2019	2020	32	2	2	3	3
20NEHOPS061-8	2019	2020	34	2	1	2	3
20NEHOPS061-9	2019	2020	33	1	2	4	4
20NEHOPS061-9	2019	2021	30	3	2	3	4
20NEHOPS061-9	2019	2021	30	1	1	3	2
20NEHOPS061-9	2019	2021	30	1	1	1	1
20NEHOPS064-3	2019	2020	33	1	2	3	3
20NEHOPS064-3	2019	2021	28	1	4	3	3
20NEHOPS064-3	2019	2021	30	1	3	3	2
20NEHOPS064-3	2019	2021	34	1	2	2	1
20NEHOPS065-1	2019	2020	31	2	2	3	3
20NEHOPS065-2	2019	2020	32	1	2	3	3
20NEHOPS065-2	2019	2021	29	3	3	5	4
20NEHOPS065-2	2019	2021	31	3	1	2	1
20NEHOPS065-3	2019	2020	33	1	1	2	2
20NEHOPS066-2	2019	2020	33	1	2	2	2
20NEHOPS068-6	2019	2020	33	1	1	3	3
20NEHOPS068-8	2019	2020	32	1	2	3	3
20NEHOPS069-1	2019	2020	32	2	2	3	4
20NEHOPS069-2	2019	2020	33	2	1	2	3
20NEHOPS069-3	2019	2020	33	2	1	3	4
20NEHOPS069-4	2019	2020	33	2	1	2	2
20NEHOPS069-6	2019	2020	33	2	2	4	3
20NEHOPS069-7	2019	2020	32	2	2	2	4
20NEHOPS069-7	2019	2021	28	2	4	4	4

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS069-7	2019	2021	29	2	3	3	5
20NEHOPS069-7	2019	2021	29	2	4	5	2
20NEHOPS069-8	2019	2020	33	2	2	3	3
20NEHOPS072-11	2019	2021	30	1	1	2	2
20NEHOPS072-11	2019	2021	31	1	1	1	1
20NEHOPS072-11	2019	2021	31	1	1	3	2
20NEHOPS072-2	2019	2020	33	1	1	2	2
20NEHOPS072-3	2019	2020	33	2	1	2	3
20NEHOPS072-5	2019	2020	35	2	1	2	3
20NEHOPS072-6	2019	2020	34	2	2	2	4
20NEHOPS073-1	2019	2020	33	1	1	3	2
20NEHOPS073-11	2019	2020	33	1	1	3	4
20NEHOPS073-11	2019	2021	28	2	3	2	3
20NEHOPS073-11	2019	2021	30	2	2	3	3
20NEHOPS073-11	2019	2021	31	2	2	2	1
20NEHOPS073-13	2019	2020	33	1	1	3	4
20NEHOPS073-13	2019	2021	30	1	4	4	5
20NEHOPS073-13	2019	2021	30	1	3	3	2
20NEHOPS073-13	2019	2021	30	1	3	5	5
20NEHOPS073-18	2019	2020	32	1	2	3	5
20NEHOPS073-22	2019	2020	32	1	1	2	1
20NEHOPS073-22	2019	2021	28	2	3	4	5
20NEHOPS073-22	2019	2021	29	2	4	5	4
20NEHOPS073-22	2019	2021	30	2	2	4	4
20NEHOPS073-23	2019	2020	33	1	1	2	2
20NEHOPS073-24	2019	2020	33	1	2	3	3
20NEHOPS073-3	2019	2020	34	2	1	3	3
20NEHOPS073-4	2019	2020	33	1	1	2	3
20NEHOPS073-7	2019	2020	31	1	2	3	2
20NEHOPS073-7	2019	2021	28	1	2	2	1
20NEHOPS073-7	2019	2021	28	1	5	4	2
20NEHOPS074-12	2019	2020	33	1	2	2	2
20NEHOPS074-5	2019	2020	34	2	1	2	3
20NEHOPS074-6	2019	2020	35	1	1	2	2
20NEHOPS074-8	2019	2020	34	1	1	2	2
20NEHOPS075-11	2019	2020	33	1	1	1	1
20NEHOPS075-13	2019	2020	32	1	1	2	4

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS075-3	2019	2020	33	1	1	3	2
20NEHOPS076-2	2019	2020	33	1	1	3	3
20NEHOPS076-3	2019	2020	33	1	2	2	3
20NEHOPS076-5	2019	2020	33	2	1	2	3
20NEHOPS076-6	2019	2020	31	2	2	4	4
20NEHOPS077-1	2019	2020	33	1	2	3	3
20NEHOPS077-1	2019	2021	28	1	4	5	5
20NEHOPS077-1	2019	2021	28	1	4	3	5
20NEHOPS077-1	2019	2021	30	1	3	3	2
20NEHOPS077-13	2019	2020	32	1	2	4	4
20NEHOPS077-13	2019	2021	28	1	3	4	4
20NEHOPS077-13	2019	2021	30	1	2	3	3
20NEHOPS077-13	2019	2021	30	1	2	4	2
20NEHOPS077-15	2019	2020	33	1	2	2	2
20NEHOPS077-17	2019	2020	31	1	2	3	3
20NEHOPS077-17	2019	2021	28	1	5	4	4
20NEHOPS077-17	2019	2021	28	1	3	2	5
20NEHOPS077-17	2019	2021	29	1	3	4	3
20NEHOPS077-18	2019	2020	33	1	2	3	3
20NEHOPS077-19	2019	2020	31	1	2	4	3
20NEHOPS077-19	2019	2021	29	1	3	4	2
20NEHOPS077-19	2019	2021	29	1	3	4	4
20NEHOPS077-19	2019	2021	31	1	1	2	3
20NEHOPS077-4	2019	2020	33	1	1	1	2
20NEHOPS078-10	2019	2020	33	1	2	3	3
20NEHOPS078-10	2019	2021	30	1	2	5	3
20NEHOPS078-10	2019	2021	31	1	2	3	2
20NEHOPS078-10	2019	2021	31	1	1	1	1
20NEHOPS078-16	2019	2020	32	1	2	4	4
20NEHOPS078-20	2019	2020	33	1	1	2	1
20NEHOPS078-20	2019	2021	29	1	2	3	2
20NEHOPS078-20	2019	2021	30	1	2	2	3
20NEHOPS078-27	2019	2020	32	2	1	2	2
20NEHOPS078-28	2019	2020	33	1	1	2	2
20NEHOPS078-30	2019	2020	33	1	1	3	3
20NEHOPS078-30	2019	2021	30	1	2	3	1
20NEHOPS078-30	2019	2021	31	1	1	1	3

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS078-30	2019	2021	31	1	1	2	1
20NEHOPS078-31	2019	2020	33	1	2	2	3
20NEHOPS078-33	2019	2020	31	1	2	2	3
20NEHOPS078-33	2019	2021	28	1	3	4	4
20NEHOPS078-33	2019	2021	28	1	3	4	3
20NEHOPS078-33	2019	2021	31	1	2	2	2
20NEHOPS078-5	2019	2020	34	1	1	3	1
20NEHOPS078-7	2019	2020	33	1	3	4	2
20NEHOPS078-7	2019	2021	29	1	2	2	3
20NEHOPS078-7	2019	2021	30	1	4	4	4
20NEHOPS078-7	2019	2021	30	1	2	3	2
20NEHOPS078-8	2019	2020	32	2	1	3	3
20NEHOPS078-9	2019	2020	32	1	1	3	3
20NEHOPS078-9	2019	2021	28	1	3	3	3
20NEHOPS078-9	2019	2021	28	1	3	5	3
20NEHOPS078-9	2019	2021	31	1	2	2	2
20NEHOPS079-1	2019	2020	32	1	2	3	2
20NEHOPS080-7	2019	2020	33	1	1	2	3
20NEHOPS080-9	2019	2020	32	2	1	2	2
20NEHOPS082-5	2019	2020	34	2	1	3	4
20NEHOPS082-7	2019	2020	33	1	1	3	4
20NEHOPS082-7	2019	2021	30	1	1	3	2
20NEHOPS082-7	2019	2021	30	1	1	2	1
20NEHOPS082-7	2019	2021	31	1	2	3	3
20NEHOPS083-2	2019	2020	33	2	1	2	2
20NEHOPS083-4	2019	2020	32	1	2	3	2
20NEHOPS084-1	2019	2020	35	2	1	2	2
20NEHOPS084-2	2019	2020	34	1	2	3	4
20NEHOPS084-2	2019	2021	26	1	2	2	3
20NEHOPS084-2	2019	2021	30	1	3	3	2
20NEHOPS084-2	2019	2021	31	1	2	3	2
20NEHOPS084-3	2019	2020	33	2	2	3	3
20NEHOPS085-7	2019	2020	31	1	2	3	3
20NEHOPS085-8	2019	2020	33	1	2	3	4
20NEHOPS085-8	2019	2021	29	1	3	3	2
20NEHOPS085-8	2019	2021	30	1	3	2	2
20NEHOPS085-8	2019	2021	31	1	2	2	1

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS086-2	2019	2020	35	1	2	2	2
20NEHOPS086-4	2019	2020	35	2	2	3	2
20NEHOPS086-6	2019	2020	33	1	1	3	3
20NEHOPS086-6	2019	2021	31	1	5	5	3
20NEHOPS086-6	2019	2021	31	1	5	5	3
20NEHOPS088-1	2019	2020	33	2	2	3	3
20NEHOPS088-4	2019	2020	34	1	1	2	3
20NEHOPS089-5	2019	2020	35	1	2	3	3
20NEHOPS090-1	2019	2020	33	2	2	2	2
20NEHOPS090-2	2019	2020	34	1	3	4	4
20NEHOPS090-2	2019	2021	31	1	2	3	2
20NEHOPS090-2	2019	2021	31	3	2	2	2
20NEHOPS090-2	2019	2021	32	1	4	3	3
20NEHOPS091-2	2019	2020	32	1	2	3	4
20NEHOPS091-2	2019	2021	29	1	4	3	4
20NEHOPS091-2	2019	2021	30	1	4	4	4
20NEHOPS091-2	2019	2021	31	1	2	3	2
20NEHOPS091-3	2019	2020	32	2	2	3	2
20NEHOPS092-1	2019	2020	33	2	2	3	2
20NEHOPS093-1	2019	2020	32	1	2	2	2
20NEHOPS093-12	2019	2020	32	2	2	3	3
20NEHOPS093-13	2019	2020	34	1	1	3	3
20NEHOPS093-14	2019	2020	33	1	1	2	2
20NEHOPS093-17	2019	2020	33	1	2	3	3
20NEHOPS093-17	2019	2021	28	3	2	3	4
20NEHOPS093-17	2019	2021	30	1	3	3	1
20NEHOPS093-17	2019	2021	34	1	2	2	2
20NEHOPS093-2	2019	2020	33	1	2	2	2
20NEHOPS093-5	2019	2020	33	1	1	2	3
20NEHOPS093-6	2019	2020	32	2	1	3	3
20NEHOPS094-2	2019	2020	33	2	2	3	2
20NEHOPS094-3	2019	2020	33	2	2	3	3
20NEHOPS094-3	2019	2021	29	1	5	5	5
20NEHOPS094-3	2019	2021	30	2	5	5	5
20NEHOPS094-3	2019	2021	31	1	1	3	2
20NEHOPS094-4	2019	2020	33	1	2	3	4
20NEHOPS094-4	2019	2021	31	1	2	3	2

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS094-4	2019	2021	31	1	3	4	3
20NEHOPS094-4	2019	2021	32	1	1	1	2
20NEHOPS095-12	2019	2020	33	1	2	2	2
20NEHOPS095-15	2019	2020	33	1	2	2	3
20NEHOPS095-16	2019	2020	32	2	2	3	3
20NEHOPS095-17	2019	2020	33	1	1	3	5
20NEHOPS095-18	2019	2020	33	1	1	2	2
20NEHOPS095-19	2019	2020	33	1	1	2	2
20NEHOPS095-2	2019	2020	33	1	1	3	5
20NEHOPS095-2	2019	2021	30	1	5	4	3
20NEHOPS095-2	2019	2021	31	1	5	5	5
20NEHOPS095-2	2019	2021	31	1	2	5	3
20NEHOPS095-4	2019	2020	33	2	2	2	3
20NEHOPS095-5	2019	2020	32	2	1	2	4
20NEHOPS095-7	2019	2020	33	1	1	2	2
20NEHOPS095-8	2019	2020	32	2	2	2	4
20NEHOPS096-1	2019	2020	33	1	2	3	3
20NEHOPS096-2	2019	2020	32	1	2	4	5
20NEHOPS096-2	2019	2021	29	1	3	3	3
20NEHOPS096-2	2019	2021	30	1	3	5	5
20NEHOPS096-2	2019	2021	30	1	2	4	3
20NEHOPS096-3	2019	2020	32	2	2	4	4
20NEHOPS096-5	2019	2020	32	1	2	5	5
20NEHOPS096-5	2019	2021	29	1	4	4	5
20NEHOPS096-5	2019	2021	31	1	4	3	3
20NEHOPS096-5	2019	2021	31	1	2	4	4
20NEHOPS096-6	2019	2020	32	2	2	5	5
20NEHOPS097-1	2019	2020	33	1	3	2	3
20NEHOPS097-12	2019	2020	33	1	2	3	2
20NEHOPS097-2	2019	2020	35	1	2	2	2
20NEHOPS097-6	2019	2020	32	1	2	3	3
20NEHOPS097-6	2019	2021	29	1	2	5	3
20NEHOPS097-6	2019	2021	29	1	3	2	3
20NEHOPS097-6	2019	2021	31	1	4	3	3
20NEHOPS097-7	2019	2020	34	1	2	2	2
20NEHOPS097-8	2019	2020	33	2	1	2	3
20NEHOPS098-10	2019	2020	33	1	2	3	3

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
20NEHOPS098-15	2019	2020	34	1	1	1	1
20NEHOPS098-8	2019	2020	33	1	2	2	2
20NEHOPS099-12	2019	2020	36	1	1	1	2
20NEHOPS099-6	2019	2020	35	2	1	3	2
20NEHOPS101-1	2019	2020	33	1	2	3	4
20NEHOPS101-1	2019	2021	29	1	2	4	4
20NEHOPS101-1	2019	2021	30	1	2	3	2
20NEHOPS101-1	2019	2021	30	1	3	4	4
20NEHOPS101-2	2019	2020	33	1	2	2	2
20NEHOPS101-2	2019	2021	31	1	1	2	1
20NEHOPS101-2	2019	2021	31	1	2	1	1
20NEHOPS101-2	2019	2021	32	1	1	1	1
20NEHOPS102-1	2019	2020	33	1	2	2	3
20NEHOPS102-2	2019	2020	33	1	3	4	4
20NEHOPS102-2	2019	2021	30	1	2	3	4
20NEHOPS102-2	2019	2021	30	1	2	3	3
20NEHOPS102-2	2019	2021	31	1	2	2	2
20NEHOPS102-3	2019	2020	33	1	2	3	3
20NEHOPS104-1	2019	2020	35	1	1	3	2
20NEHOPS104-2	2019	2020	32	1	1	4	4
20NEHOPS104-2	2019	2021	28	1	5	5	5
20NEHOPS104-2	2019	2021	30	1	4	4	5
20NEHOPS104-2	2019	2021	31	1	2	4	3
20NEHOPS104-3	2019	2020	33	1	1	3	4
20NEHOPS104-3	2019	2021	30	2	5	5	5
20NEHOPS104-4	2019	2020	33	1	2	3	3
21NEHOPS107-1	2020	2021	31	1	2	5	3
21NEHOPS107-2	2020	2021	31	1	2	3	2
21NEHOPS108-2	2020	2021	31	2	1	2	2
21NEHOPS109-1	2020	2021	30	1	3	4	4
21NEHOPS109-2	2020	2021	30	1	1	2	2
21NEHOPS109-3	2020	2021	31	1	2	4	3
21NEHOPS110-1	2020	2021	31	2	3	4	4
21NEHOPS111-1	2020	2021	31	1	2	2	2
21NEHOPS112-1	2020	2021	30	2	2	3	1
21NEHOPS112-11	2020	2021	32	2	1	2	2
21NEHOPS112-13	2020	2021	30	3	2	4	4

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
21NEHOPS112-14	2020	2021	30	1	2	3	3
21NEHOPS112-15	2020	2021	34	1	1	2	3
21NEHOPS112-18	2020	2021	28	1	2	4	3
21NEHOPS112-19	2020	2021	31	1	2	2	3
21NEHOPS112-20	2020	2021	28	1	3	3	5
21NEHOPS112-21	2020	2021	31	1	2	4	3
21NEHOPS112-22	2020	2021	30	2	2	3	3
21NEHOPS112-23	2020	2021	29	2	3	3	4
21NEHOPS112-24	2020	2021	29	2	2	4	3
21NEHOPS112-25	2020	2021	29	2	2	3	2
21NEHOPS112-3	2020	2021	31	1	2	2	1
21NEHOPS112-4	2020	2021	32	3	1	1	5
21NEHOPS112-5	2020	2021	32	3	2	2	2
21NEHOPS112-7	2020	2021	30	1	3	4	2
21NEHOPS112-8	2020	2021	30	2	2	4	5
21NEHOPS112-9	2020	2021	29	2	2	4	3
21NEHOPS113-10	2020	2021	31	1	1	2	2
21NEHOPS113-11	2020	2021	30	2	2	3	3
21NEHOPS113-12	2020	2021	31	2	2	2	2
21NEHOPS113-13	2020	2021	30	1	3	4	3
21NEHOPS113-14	2020	2021	30	2	3	3	3
21NEHOPS113-15	2020	2021	31	1	2	3	5
21NEHOPS113-18	2020	2021	31	2	1	1	1
21NEHOPS113-19	2020	2021	31	2	1	2	2
21NEHOPS113-20	2020	2021	31	1	1	2	2
21NEHOPS113-21	2020	2021	31	2	2	2	2
21NEHOPS113-3	2020	2021	31	2	1	1	2
21NEHOPS113-4	2020	2021	31	1	2	3	2
21NEHOPS113-5	2020	2021	31	1	2	3	1
21NEHOPS113-6	2020	2021	31	1	2	1	2
21NEHOPS113-8	2020	2021	31	1	2	3	3
21NEHOPS114-2	2020	2021	34	1	2	1	2
21NEHOPS114-3	2020	2021	31	1	2	2	1
21NEHOPS114-4	2020	2021	29	1	2	2	2
21NEHOPS115-1	2020	2021	31	1	2	2	2
21NEHOPS115-2	2020	2021	32	1	2	3	3
21NEHOPS115-3	2020	2021	30	2	2	3	3

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Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
21NEHOPS115-4	2020	2021	31	1	3	3	5
21NEHOPS115-5	2020	2021	31	1	3	3	2
21NEHOPS116-1	2020	2021	30	2	3	3	3
21NEHOPS116-2	2020	2021	31	1	3	2	2
21NEHOPS116-3	2020	2021	34	1	3	2	1
21NEHOPS116-4	2020	2021	30	1	2	3	3
21NEHOPS117-1	2020	2021	29	1	3	3	4
21NEHOPS117-2	2020	2021	30	1	4	3	3
21NEHOPS117-3	2020	2021	36	1	3	1	0
21NEHOPS117-4	2020	2021	31	1	3	2	1
21NEHOPS118-2	2020	2021	31	2	1	2	3
21NEHOPS118-3	2020	2021	31	3	2	3	3
21NEHOPS118-4	2020	2021	31	2	1	2	2
21NEHOPS118-6	2020	2021	34	1	1	1	1
21NEHOPS119-10	2020	2021	34	1	1	1	1
21NEHOPS119-11	2020	2021	31	3	1	1	1
21NEHOPS119-19	2020	2021	31	1	1	2	1
21NEHOPS119-2	2020	2021	31	2	2	2	1
21NEHOPS119-3	2020	2021	33	3	1	3	2
21NEHOPS119-4	2020	2021	34	3	1	2	1
21NEHOPS119-6	2020	2021	34	3	2	1	2
21NEHOPS119-7	2020	2021	31	1	2	2	2
21NEHOPS119-8	2020	2021	32	1	2	2	2
21NEHOPS120-1	2020	2021	30	1	3	3	3
21NEHOPS122-1	2020	2021	30	2	1	3	4
21NEHOPS123-1	2020	2021	31	1	1	1	2
21NEHOPS124-2	2020	2021	31	1	1	3	2
21NEHOPS124-4	2020	2021	31	2	1	1	1
21NEHOPS125-1	2020	2021	31	3	1	1	2
21NEHOPS125-2	2020	2021	31	3	1	2	2
21NEHOPS126-1	2020	2021	32	2	1	2	2
21NEHOPS126-10	2020	2021	32	1	0	1	0
21NEHOPS126-12	2020	2021	34	3	1	1	2
21NEHOPS126-16	2020	2021	31	2	2	2	2
21NEHOPS126-17	2020	2021	31	2	0	0	0
21NEHOPS126-18	2020	2021	31	1	1	1	1
21NEHOPS126-3	2020	2021	34	2	1	1	1

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Appendix A continued.

Progeny genotype[a]	Year developed	Year evaluated	FT[b]	Gender[c]	PRs June[d]	PRs July[d]	PRs Aug.[d]
21NEHOPS126-5	2020	2021	30	2	1	3	3
21NEHOPS126-9	2020	2021	31	1	0	0	0

[a] Includes unique progeny genotypes and their replicates.
[b] Documented as the week number of the year the first flowers on an individual plant fully opened.
[c] Gender was documented numerically, where 1 = Female, 2 = Male, and 3 = Monoecious.
[d] Numeric rating assigned on a scale of one to five, one being the worst score and five being the best score. The ratings were assigned as an aggregate assessment of several traits: downy mildew resistance, vigor, internode length and lateral branch length.

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Appendix B

Data for cohumulone content (COH) and alpha acid content (ALP) of 105 (*Humulus lupulus* L.) progeny genotypes evaluated during 2020 and 2021 at the University of Nebraska-Lincoln East Campus Research Farm.

Progeny genotype[a]	Year developed	Year evaluated	COH[b]	ALP[c]
19NEHOPS040-3	2018	2021	7.181	16.389
19NEHOPS041-29	2018	2021	7.166	26.533
19NEHOPS041-39	2018	2021	1.575	4.262
19NEHOPS048-8	2018	2020	2.623	6.056
19NEHOPS048-8	2018	2020	3.661	11.645
19NEHOPS049-11	2018	2021	2.154	7.838
19NEHOPS051-1	2018	2020	2.296	6.959
19NEHOPS051-1	2018	2020	2.859	7.715
19NEHOPS051-1	2018	2020	3.127	8.470
19NEHOPS051-1	2018	2020	4.380	11.768
19NEHOPS051-1	2018	2021	5.240	17.912
19NEHOPS052-12	2018	2020	2.659	7.303
19NEHOPS052-12	2018	2021	8.579	27.521
19NEHOPS052-15	2018	2020	5.421	13.300
19NEHOPS052-15	2018	2021	5.447	16.479
19NEHOPS053-17	2018	2020	3.158	8.475
19NEHOPS053-17	2018	2021	6.861	21.858
19NEHOPS053-18	2018	2020	2.036	5.115
19NEHOPS053-18	2018	2020	3.326	8.691
19NEHOPS053-18	2018	2020	4.127	9.905
19NEHOPS053-18	2018	2020	4.980	11.767
19NEHOPS053-18	2018	2020	2.992	8.356
19NEHOPS053-18	2018	2021	6.419	19.356
19NEHOPS053-18	2018	2021	6.486	19.753
19NEHOPS053-18	2018	2021	3.125	9.486
19NEHOPS053-7	2018	2020	1.569	4.480
19NEHOPS053-7	2018	2020	2.568	6.219
19NEHOPS053-7	2018	2021	2.203	7.497
19NEHOPS054-5	2018	2021	4.736	16.334
19NEHOPS054-9	2018	2020	3.515	10.748
19NEHOPS056-12	2018	2020	3.026	5.893
19NEHOPS056-128	2018	2020	2.890	5.677

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Appendix B continued.

Progeny genotype[a]	Year developed	Year evaluated	COH[b]	ALP[c]
19NEHOPS056-128	2018	2020	5.218	9.777
19NEHOPS056-146	2018	2020	2.749	8.629
19NEHOPS056-146	2018	2020	5.535	15.737
19NEHOPS056-146	2018	2021	3.059	9.988
19NEHOPS056-38	2018	2020	3.534	6.479
19NEHOPS059-111	2018	2020	3.150	6.917
19NEHOPS059-121	2018	2020	1.483	3.587
19NEHOPS059-121	2018	2020	2.674	6.532
19NEHOPS059-173	2018	2020	3.514	7.350
19NEHOPS059-173	2018	2020	2.368	4.837
19NEHOPS059-204	2018	2020	2.348	5.680
19NEHOPS059-204	2018	2020	2.718	7.397
19NEHOPS059-204	2018	2021	2.669	7.022
20NEHOPS061-9	2019	2021	1.820	6.239
20NEHOPS064-3	2019	2021	2.440	5.640
20NEHOPS065-2	2019	2021	1.798	6.691
20NEHOPS073-1	2019	2020	2.883	6.323
20NEHOPS073-13	2019	2021	5.336	10.761
20NEHOPS073-18	2019	2020	4.774	8.744
20NEHOPS073-22	2019	2020	1.344	3.800
20NEHOPS073-7	2019	2020	3.664	8.178
20NEHOPS073-7	2019	2021	2.648	7.445
20NEHOPS076-2	2019	2020	2.475	5.416
20NEHOPS077-1	2019	2020	4.675	10.863
20NEHOPS077-1	2019	2021	2.345	6.913
20NEHOPS077-13	2019	2020	3.827	9.592
20NEHOPS077-13	2019	2020	3.773	8.845
20NEHOPS077-13	2019	2021	4.702	13.541
20NEHOPS077-17	2019	2020	4.308	11.273
20NEHOPS077-17	2019	2021	1.985	5.995
20NEHOPS077-19	2019	2020	3.726	7.952
20NEHOPS078-10	2019	2020	3.655	9.019
20NEHOPS078-16	2019	2020	3.672	7.531
20NEHOPS078-20	2019	2020	3.581	9.151
20NEHOPS078-20	2019	2021	4.601	12.268
20NEHOPS078-30	2019	2020	0.902	1.957

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Appendix B continued.

Progeny genotype[a]	Year developed	Year evaluated	COH[b]	ALP[c]
20NEHOPS078-33	2019	2020	1.838	3.892
20NEHOPS078-33	2019	2021	1.326	2.886
20NEHOPS078-7	2019	2021	3.075	8.584
20NEHOPS078-9	2019	2020	4.306	8.808
20NEHOPS078-9	2019	2021	3.068	7.116
20NEHOPS084-2	2019	2021	2.903	8.491
20NEHOPS085-8	2019	2021	2.205	7.533
20NEHOPS086-6	2019	2020	1.428	2.660
20NEHOPS091-2	2019	2020	1.861	4.898
20NEHOPS091-2	2019	2021	3.533	9.502
20NEHOPS093-14	2019	2020	4.182	9.564
20NEHOPS093-17	2019	2020	4.748	12.539
20NEHOPS093-2	2019	2020	2.199	7.227
20NEHOPS094-3	2019	2021	4.687	10.050
20NEHOPS095-2	2019	2021	2.496	6.231
20NEHOPS096-2	2019	2021	0.896	2.896
20NEHOPS096-5	2019	2021	2.423	6.169
20NEHOPS097-6	2019	2020	2.708	6.890
20NEHOPS097-6	2019	2021	2.515	7.184
20NEHOPS101-1	2019	2020	3.627	7.328
20NEHOPS101-1	2019	2021	1.012	2.106
20NEHOPS101-2	2019	2020	1.837	4.779
20NEHOPS102-2	2019	2020	2.302	6.309
20NEHOPS102-2	2019	2021	0.434	1.278
20NEHOPS104-2	2019	2020	0.731	1.824
20NEHOPS104-2	2019	2020	1.040	2.672
20NEHOPS104-2	2019	2021	0.995	2.786
20NEHOPS104-3	2019	2020	4.729	8.779
21NEHOPS109-1	2020	2021	2.821	5.847
21NEHOPS109-2	2020	2021	1.691	5.219
21NEHOPS112-20	2020	2021	1.052	2.971
21NEHOPS112-7	2020	2021	0.793	2.025
21NEHOPS113-13	2020	2021	2.465	6.003
21NEHOPS113-4	2020	2021	2.973	7.707
21NEHOPS114-4	2020	2021	1.890	4.227
21NEHOPS117-2	2020	2021	1.361	3.491

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Appendix B continued.

Progeny Genotype[a]	Year developed	Year evaluated	COH[b]	ALP[c]
21NEHOPS119-7	2020	2021	1.265	4.104

[a] Includes unique progeny genotypes and replicates.

[b] Concentration (mg/g of fresh hops).

[c] Concentration (mg/g of fresh hops).