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1-1-2008

Letter to the Editor

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Johnson, Rodger K., "Letter to the Editor" (2008). *Faculty Papers and Publications in Animal Science.* Paper 525.
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Letter to the editor

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J. Anim. Sci. 2008. 86:1036–1037
doi:10.2527/jas.2008-0849

I am a co-author of papers published in the *Journal of Animal Science* by Moeller et al. (2004) and Serenius et al. (2006) that report data from the National Pork Producers Council Maternal Line Evaluation project (**MLE**). In his letter to the editor, DeBuse (2007) claims that the authors of these papers misrepresented the line submitted by Newsham Hybrids (USA) Inc. (**NH**; Colorado Springs, CO) to the MLE. Below are the facts, as I know them, regarding the design and implementation of the MLE.

The MLE tested crossbred females that represented maternal lines available to producers. It was designed to detect differences between lines for longevity traits, with probabilities of type 1 and type 2 errors of 0.05 and 0.75, respectively, requiring 531 females per line. The number of sires depended on the effective population size of the nucleus populations. Each participant was required to submit a minimum of 590 gilts per line to assure 531 breeding gilts. To assure that the nucleus populations were materially closed, 90% of the litters born during the last 5 years were required to have a sire that was born within the population, and 90% of the litters were required to have a dam that was born in the population.

Organizations submitted to me 5-generation pedigree files for each nucleus population represented in their gilts. I determined whether the populations met the requirements and the number of sires to be sampled. In August 1996, NH submitted pedigree files for 3 maternal populations, identified as Y, R, and W, representing, respectively, their Yorkshire, Landrace, and Large White lines. They indicated that the sires of the gilts would be either W or R boars. On August 30, 1996, I informed NH by letter that their Y, R, and W populations met the program requirements and that the sampling would be based on a population structure of 62 R and 50 W sires per generation. On August 30, 1996, NH was also informed by phone call that their Y, R, and W populations met the program requirements. I was told then that NH would have an entry comprising gilts by R boars mated with W × Y females and gilts by W boars mated with R × Y females, with approximately 1/2 of each cross. Notes of this conversation are on a copy of the letter sent to NH, and that is in my possession. These 3-way cross gilts expressed 100% heterosis and were considered to be F_1 crosses. The 2 types differed in average genetic makeup by 1/4(R – W), a difference requiring a very large experiment to estimate precisely.

I determined that an entry by R sires required that 32 boars be sampled, an entry by W sires required that 28 boars be sampled, and an entry of R(W × Y) and W(R × Y) gilts be represented by a minimum of 16 R and 14 W boars. On August 30, 1996, in a letter to the National Pork Producers Council, I stated that NH would make 50% R(W × Y) and 50% W(R × Y) gilts and that they would be required to sample a minimum of 16 R and 14 W boars.

Newsham Hybrids submitted 631 segregated, early weaned gilts into the program, 568 of which expressed puberty and entered the MLE. The MLE data were released to the program participants at a meeting (Des Moines, IA, August 31, 1999) before public release of the data, which occurred at a symposium (Des Moines, IA, April 20, 2000). The meeting with participants was attended by representatives of each participating breeding organization. At that meeting, the program design and statistical methods were reviewed, and the results were presented. The line submitted by NH was described as an F_1 female of Large White, Yorkshire, and Landrace lines. As far as I am aware, the NH representative did not offer a correction. Officials of NH also attended the symposium during which the data were released to the public and, to my knowledge, made no comment about the composition of their gilts. The papers published with the MLE data describe the NH line as F_1 crossbred females with Landrace, Large White, and Yorkshire origins that expressed 100% heterosis.

I did not analyze the data and did not see pedigree files for any MLE gilts. On May 23, 2006, I received a file from DeBuse, who claimed it contained parentage records for NH MLE gilts. Sire identification contained a number followed by an R or a W, with approximately 1/2 with each letter. Dam identification comprised a number followed by an X or an A. Newsham Hybrids

did not submit pedigree files for those lines. I have no record or recollection of lines X and A, nor the designations of lines P and P' mentioned in DeBuse's letter to the editor.

Authors of the published papers have been asked by DeBuse to redefine the NH entry as 2 entries and to reanalyze the data. This is not appropriate and cannot be defended scientifically. Newsham Hybrids sampled and submitted the appropriate number of females for 1 entry, and we described it as they officially described it to us. I believe that the results represented the product marketed by NH to their customers.

DeBuse also suggests that only 2-breed crosses are true F_1 crosses. However, many scientists have described multiple-breed crosses as F_1 if they expressed 100% heterosis (e.g., Gregory et al., 1994; Cassady et al., 2002).

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