

Genomic Relationships

Understanding genomic relationships improves prediction accuracy.

By **Jamie Courter**, Ph.D., and **J. R. Tait**, Ph.D.

Each of these three pieces of information is used in genetic evaluation systems to produce expected progeny differences (EPDs): 1) variations in performance of individual animals from their contemporaries; 2) variations in performance of progeny; and 3) expected relationships between those individual animals based on their pedigree relationship.

Then, we add genomics to create a genomic-enhanced EPD (GE-EPD), which increases the accuracy of the trait prediction. The added accuracy is partly due to genomic relationships.

Shared genes

Just as EPDs are “expected” and not “known,” the same is true for relationships within a pedigree. Expected relationships used for evaluation purposes are the average, or most commonly observed, relationship between animals. It is certain that a calf inherits half of its

DNA from the sire and half from the dam. However, because the inheritance is a random assortment of chromosomes, the true relationships between other animals may equal the predictions, or they may be different. In fact, there are more than 1 billion possible combinations of chromosomes in a single sperm cell, and the same in an egg. The benefit of genomics is that they can tell us the actual relationships that exist between animals, rather than an assumed average.

As an example, Figure 1 provides expected relationships between Calf 1 and others within the pedigree. The pedigree-expected relationship between full-sib calves is that they share 50% of their DNA with each other. While this belief is often correct, there is variability around that expectation. Although quite rare, variability can range from 0 to 100%.

A real-world example of the observed relationships among a population of more than 15,000

full-sib chickens is presented in Figure 2. There appears to be a slight shift below the expected 50% (0.50) relationship, but most animals are close to the pedigree estimate for full sibs. The takeaway is that there is a noticeable amount of variability around the expected relationship, which is possible and does exist in these groups of animals. Many times, full-sibs are genetically quite similar, but occasionally, they can be quite diverse.

The extension of this concept also applies to the grandparent generation relationships between calves. The pedigree-expected relationship between Calf 1 and the four grandparents is 25%, since each parent inherits 50% of its DNA from a grandparent, and passes 50% to its progeny (50% of 50% is 25%). But again, since each sperm or egg is a random assortment of chromosomes from the grandparent generation, there is variability within those predictions.

The intention of this article is not to read like a large math problem, but to show gratitude for the power of the genetic evaluations, which were based on expected pedigree relationships and highlight how the biology of inheritance introduces deviations from those assumptions which can be characterized with genomic profile tools. Cattle breeders who leverage these tools allow more precise understanding of relationships among animals, increasing the accuracy of the genetic prediction and accelerating their genetic progress. **HW**

Editor’s Note: Jamie Courter is beef product manager and J. R. Tait is the director of genetics product development for NEOGEN Genomics.

Figure 2: Distribution of genomic relationships for 15,748 full sib genomic-tested chickens

Adapted from: Lourenco et al. (Genet Sel Evol 47, 56, 2015)

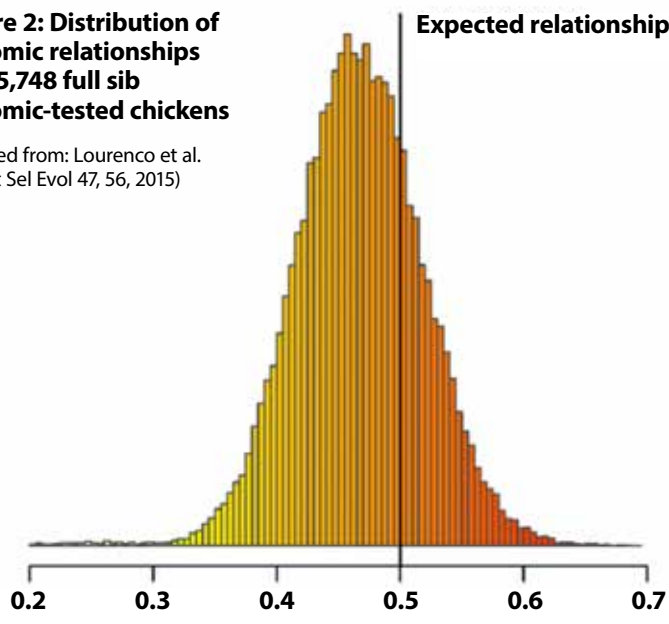


Figure 1: Pedigree expected relationship among grandparents, parents, half and full siblings in relation to Calf 1

