Diving Deeper into Genomic Relationships

Genomic tools help identify variation among related animals.

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In the May/June issue of *Hereford World*, we discussed expected pedigree relationships among animals and how the biology of inheritance introduces deviations from those assumed relationships that can be characterized with genomic tools. In this article, we will use a simplified example to feature how the addition of a genomic profile provides a more precise understanding of the relationship between four full-sibling calves and how that impacts the estimate of genomic-enhanced expected progeny differences (GE-EPD).

Every calf inherits 50% of its DNA from its sire and the other 50% from its dam. This happens 100% of the time. Therefore, the most accurate estimate of a calf's expected performance, without any additional phenotype or progeny information, is the average of the parents. Using Calving Ease Direct EPD (CED) as an example, Figure 1 highlights the parent average expected performance of four full siblings. If the CED of the sire is +3.5 and the dam is +0.0, then at birth all four full-sib progeny would have a parent average EPD of +1.75. Just like EPDs, the relationship between full-sibling calves is expected to be the parent average, or 50%.

But we know that Mendelian Inheritance creates a shuffle in the DNA that a calf inherits from its parents. In other words, the 50% of DNA that was passed from the sire to calf 1, isn't the same as the 50% of DNA that was passed to Calf 2-4, and so on. This difference in the inherited DNA is what creates variation around the expected 50% relationship of full-sibling progeny outlined in the May article. It is also what creates the performance differences we observe among related cattle. To highlight these differences, Table 1 includes an example of how the random inheritance of three single nucleotide polymorphisms (SNP) changes the CED EPD calculated for each of four full-sib progeny.

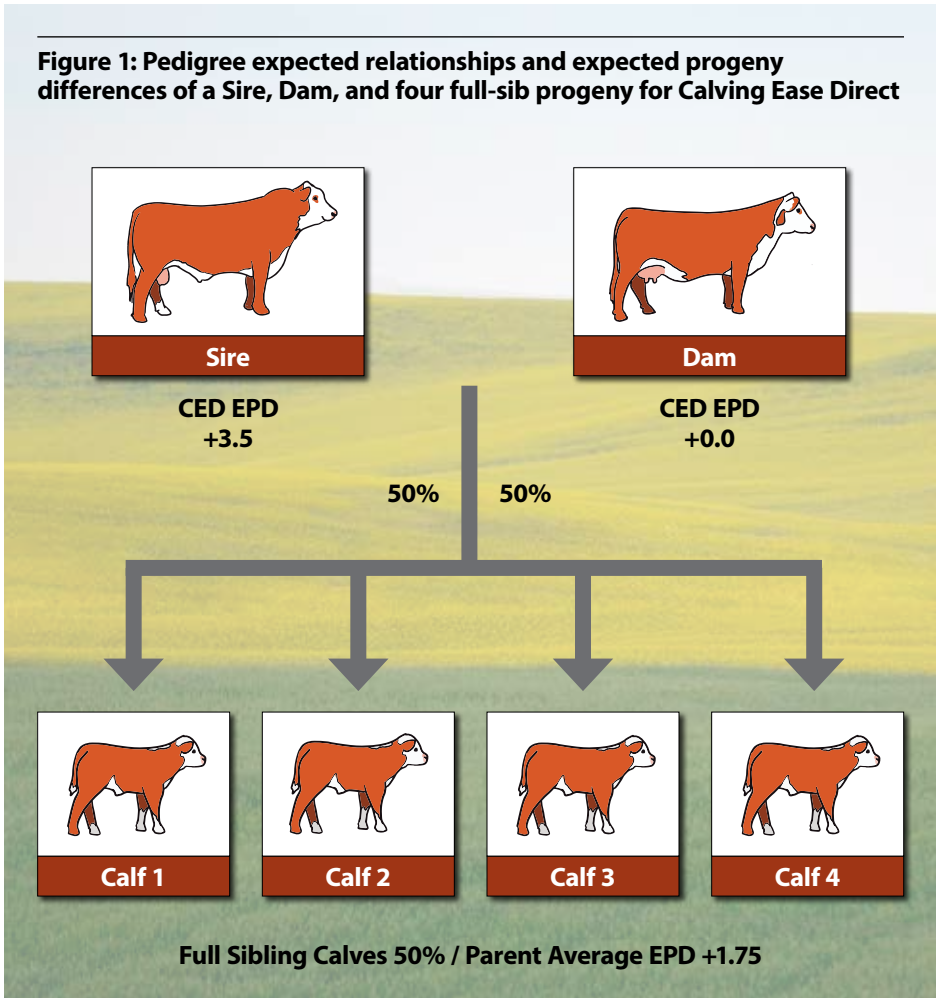

Figure 1: Pedigree expected relationships and expected progeny differences of a Sire, Dam, and four full-sib progeny for Calving Ease Direct

Calculating GE-EPDS

In order to estimate the genetic value of an animal for CED, each SNP within the genetic evaluation is weighted by its predicted effect on the EPD. For this example, you will see that the allelic or 'allele A' effect of SNP 1 is -1.0, SNP 2 is -0.5, and SNP 3 is +2.0 (Table 1). Understanding this relationship between the DNA and the trait of interest, we then need to compare that to how many copies (0, 1, or 2) of allele A each animal has at each SNP. In Table 1, we see that the sire has 0 copies of SNP 1, therefore his value at that location is (0 x -1.0), or 0.0. Extending that principle to SNP 2 and 3, the sire's values are (1 x -0.5), or -0.5 for SNP 2, and (2 x 2.0), or +4.0 for SNP 3. Adding those three values together, we learn that the sire's genomic value for CED is (0.0 – 0.5 + 4.0), or +3.5. Following the same math for the dam, we can calculate her genomic value to be +0.0 for CED.

Without any genomic profile information available for the progeny of this mating, the evaluation's most accurate EPD estimate for the four progeny is the average of the parents, or +1.75. The availability of genomic information provides clarity by replacing the parent average with the exact picture of how many A alleles at each SNP were passed from parent to offspring. In this case, calf 1 inherited the 'winning' combination of markers with a genomic value of +3.0, while calf 4 inherited the 'lesser' of the good markers and only had a genomic value of +0.5. It is important to recognize that, although the genetic values among the four calves vary, the average genomic value does equal the parent average of +1.75.

These figures demonstrate the power of pedigree-based genetic evaluations, the reasoning behind parent average EPDs and the value genomic tools bring to the table. Not only do genomics pick up on the relationship deviations introduced by basic biology, but by doing so they provide a more accurate estimate of the true genomic value of an animal.

Adoption of these tools will allow cattle breeders to gain a more precise understanding of genetic variation in their herds, increasing the accuracy of their selection decisions earlier in each animal's life and accelerating their herd's genetic progress. **HW**

Editor's Note: Jamie Courter is a bovine technical services manager, and J. R. Tait is the director of genetics product development for NEOGEN Genomics.

Table 1: Example of how genetic variation of inheritance among four full-sib calves impacts their genomic value for calving ease direct.

	SNP 1 = -1.0[1]		SNP 2 = -0.5		SNP 3 = +2.0		
Animal	**#Copies[2]**	**Value[3]**	**#Copies**	**Value**	**#Copies**	**Value**	**Genomic Value[4]**
Sire	0	0.0	1	-0.5	2	+4.0	+3.5
Dam	2	-2.0	0	0.0	1	+2.0	0.0
Average	**1**	**-1.0**	**0.5**	**-0.25**	**1.5**	**+3.0**	**+1.75**
Calf 1	1	-1.0	0	0.0	2	+4.0	+3.0
Calf 2	1	-1.0	1	-0.5	2	+4.0	+2.5
Calf 3	1	-1.0	0	0.0	1	+2.0	+1.0
Calf 4	1	-1.0	1	-0.5	1	+2.0	+0.5
Average	**1**	**-1.0**	**0.5**	**-0.25**	**1.5**	**+3.0**	**+1.75**

[1]The number after the SNP indicates the effect of that SNP per allele A on calving ease direct EPD.
[2]Signifies how many copies of allele A (0, 1, or 2) for that SNP that the animal possesses.
[3]The genomic value that animal carries for the SNP indicated. Calculated by multiplying the number of copies of allele A by the SNP effect listed above.
[4]The calculated genomic value of that animal for calving ease direct. Calculated by adding up the values for the three SNP.