

Single Step:

The Latest Advancement in Genomic Evaluation

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Since 2015, AICA has provided genomically enhanced expected progeny differences (GE-EPD) for Charolais cattle. Using a multi-step approach, based on calibration research from Iowa State University, genomic test results have been combined with pedigree information and performance data, resulting in greater accuracy, especially for young animals. Now AICA will soon transition to a Single Step genomic evaluation. The move is the result of years of research and development to equip Charolais breeders with the most sophisticated, accurate and reliable genetic selection tools available.

What is Single Step?

The key difference between Single Step genomic evaluation and multi-step evaluation is how genetic relationships between animals are determined. With the previous multi-step approach, the relationships between animals are determined by pedigree alone. Pedigree data would dictate all full sibs, for example, would have a genetic relationship to one another of 50%, and the relationship between grandparent and grand-progeny is 25%. These are the correct values on average. However, we know variation exists in these relationships among relatives.

The genomic information identifies differences that the pedigree alone cannot detect. In Single Step evaluation of other breeds, genomic relationships among full-sibs range from as low as 35%, to 65% or higher. Some pairs of flush-mates share over two-thirds of their genetic material, while others share as little as one-third. Through Single Step, genomic relationships among animals are used to improve the accuracy of EPDs for both genotyped and non-genotyped animals.

The methodology works to more fully understand the ancestral source of the DNA of a particular animal. A greater proportion of DNA than expected, 30% or more, may be passed down from the maternal grand-sire (MGS) to an individual grandson or granddaughter, rather than the expected 25%. If the MGS has outstanding growth genetics, then the DNA relationships will drive the associated WW and YW EPDs of the grand-progeny higher. However, if an animal is more genetically related to an individual with low growth genetics, in return, the WW and YW EPDs on that individual will decline. Single Step also recognizes relationships among animals that would appear practically unrelated based on pedigree alone, compared to the average of the animals' parents. Within the breed, many animals share significant

amounts of genetic material passed down from many generations prior. Single Step recognizes these relationships based on DNA markers, and more effectively connects data among animals. Using these genomic relationships, the Single Step methodology results in more accurate genomic values than ever before.

Genomics Updated in Real Time

It is well documented that genomic predictions need to be recalculated regularly as additional data and genotypes are added to the database. Single Step does just that, by updating the genomic information each time the evaluation is run. With Single Step all sources of information – pedigree, performance, progeny data and genomic results – are updated in real time. This is a positive for breeders as the GE-EPDs are not based on outdated information, and when young sires generate their first progeny data, that information is immediately used in the genomic evaluation.

Proven Improvement in Other Breeds

While Single Step will be new to AICA members, a number of other species and beef breeds have successfully used this technology. Most dairy cattle, swine and poultry genetic evaluations use this approach, in many cases using the same University of Georgia software used at AGI. Other US beef breeds such as Beefmaster, Brangus and Santa Gertrudis have used Single Step since the beginning of their genomic evaluations. The American Angus Association successfully transitioned to Single Step in July 2017, followed by the Canadian Angus Association in September 2017. Several beef breeds in Australia and New Zealand have or will soon also use this technology.

It's important to note genomic test results from previously tested animals will be incorporated into the Single Step evaluation, using the same DNA markers used in the multi-step evaluation. Proven sires would be expected to have minimal changes in EPDs after the transition to Single Step, as their EPDs are mostly the result of progeny data. Genomics contribute more heavily to

young animals' EPDs, so those animals would be expected to show more change in EPD values. More variation in EPDs of siblings should be expected, as the evaluation more accurately tracks differences in relatives due to inheritance. As additional data and genotypes are added to the Charolais database, increased accuracy of EPDs on genomically tested animals will result, providing Charolais breeders and their customers the most accurate genetic evaluation possible. 

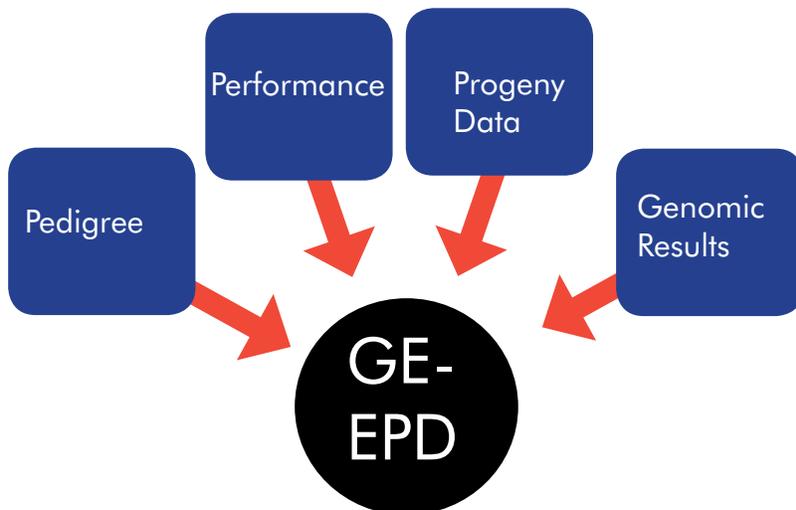


Figure 1. Information contributing to the GE-EPD.