

# Empirical Progeny Equivalent for Genotyped Animals in Multi-breed Beef Cattle Genetic Evaluations Using Single-step Bayesian Regression Model

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### Summary and Implications

The objective of this study was to measure the accuracies of genomic enhanced EPDs of genotyped animals in an international multi-breed beef cattle genetic evaluations using a single-step Bayesian regression model. The average BIF accuracies of genotyped animals with no progeny information were compared to the average BIF accuracies of non-genotyped sires with different number of progenies with observed phenotypes for birth, weaning and yearling weights. The results showed that the BIF accuracy of a genotyped animal is equivalent to the BIF accuracy of a non-genotyped sire with 21, 22 and 10 progenies with observed phenotypes for BW, WW and YW, respectively. These results demonstrate the value of DNA testing of selection candidates for beef cattle breeders across the world.

### Introduction

Genomic profiles provide additional information about the genetic merit of a DNA tested animal and increase the accuracy of EPDs, which are called Genomic Enhanced EPD or GE-EPDs, of selection candidates. In the single-step process, the DNA marker genotypes are directly inserted into the genetic evaluation along with the phenotypes (performance data) and the pedigree.

The single-step Bayesian regression (SS-BR) model benefits from a wider class of variable selection models, while this is a limitation with the single-step GBLUP model. Our previous findings detected a few large-effect quantitative trait loci that explain the majority of additive genetic variations for most growth and carcass traits in ten

US beef cattle breeds. The International Genetic Solutions (IGS), which is a progressive international collaboration between 12 beef breed associations with the largest multi-breed beef database in the world (over 16 million registered animals), decided to take advantage of this knowledge to use the multi-breed SS-BR model for their international genetic evaluations.

### Materials and Methods

A total of 16,061,754 registered animals from 12 collaborative beef breed associations with the pedigree information were available at the IGS database at the time of study. The total number of genotyped animals were 88,999; which were genotyped with different SNP arrays and marker densities. All genotypes were filtered and then imputed to 52,662 high quality markers. The imputation was performed within each breed using FImpute software. After imputation only 2250 highly influential markers (known as MSRP markers) were used for analysis.

We used an extended SS-BR model for multi-breed multi-trait analysis that includes extra polygenic effects on all genotyped and non-genotyped individuals as well as the external EPDs.

### Results and Discussions

In Figure 1 is shown the average BIF accuracies for non-genotyped sires born between 2010 and 2014 (29,525 sires) based on the number of their non-genotyped progenies with observed phenotypes for birth weight (BW), weaning weight (WW) and yearling weight (YW). Figure 1 also shows the average BIF accuracies for genotyped animals born in 2015 and later with no progeny information. These results show that the BIF accuracy of a genotyped animal is equivalent to the BIF accuracy of a non-genotyped sire with 21, 22 and 10 progenies with observed phenotypes for BW, WW and YW, respectively.

These results demonstrate the added value and the empirical observed increase in accuracies of the genomic enhanced EPDs of selection candidate as the result of DNA testing.

Figure 1 – The average BIF accuracy of genotyped animals with no progeny information and non-genotyped sires with different number of progenies with observed phenotypes for birth weight (BW), weaning weight (WW) and yearling weights (YW).

