

# Empirical Progeny Equivalent of Genotyped Animals in a Multi-breed Beef Cattle Genetic Evaluation Using a 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 evaluation using single-step Bayesian regression model. The average Breed Improvement Federation (BIF) accuracies of genotyped animals with no progeny information compared to the average BIF accuracies of non-genotyped sires with different number of progenies with observed phenotypes. The 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 24 progeny with observed phenotypes for birth, weaning and yearling weights, respectively. The empirical progeny equivalent (PE) for calving ease direct and total maternal were 15 and 3, and it was 18 and 25 for milk and stayability, 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 incorporated 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 significant amounts of additive genetic variation for most growth and carcass traits in ten US beef cattle breeds. The International Genetic Solutions (IGS), which is an 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 single nucleotide polymorphism (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 Mahdi Saatchi Reduced Panel or MSRP markers) were used for analysis.

We used an extended SS-BR model implemented in the BOLT software for multi-breed multi-trait analysis that includes extra polygenic effects for all genotyped and non-genotyped individuals as well as external EPDs derived from non-IGS partner breeds.

### Results and Discussions

Figure 1 shows 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. Figure 1 also shows the average BIF accuracies of genotyped young animals born in 2016 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 24 progeny with observed phenotypes for birth, weaning and yearling weights, respectively (where a horizontal line cross a curve for a specific trait (e.g. red line and blue curve cross each other at the data point corresponding to  $y(\text{accuracy}) = 0.46$  and  $x(\text{progeny}) = 21$  for birth weight). The empirical progeny equivalent (PE) for direct calving ease was 15 and it was only 3 for total maternal calving ease due to few recorded genotypes on cows. The empirical PE for milk and stayability were 18 and 25 progeny, respectively (Figure 1).

These results demonstrate the added values of DNA information to increase the accuracies of genomic enhanced EPDs of selection candidate in an international multi-breed single-step genetic evaluation. To further enhance the benefits of genomic data for more traits, breeders are

strongly encouraged to genotype females with records for sex-limited traits.

**Figure 1 – The average BIF accuracies of GE-EPDs of DNA tested young animals (born in 2016 with no progeny) compared to the non-genotyped sires (born 2010-2014).**

