

## **ABSTRACT # 30**

### **MULTIBREED GENOMIC EVALUATIONS IN DAIRY CATTLE**

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Multibreed models are currently used in traditional USDA dairy cattle genetic evaluations of yield and health traits, but within-breed models are used in genomic evaluations. Multibreed genomic evaluation models were developed and tested using 19,686 genotyped bulls included in the official August 2009 USDA genomic evaluation. The data were divided into training and validation sets. The training data set were comprised of bulls that were proven (had daughter information) as of November 2004 and totaled 5,331, 1,361, and 506 Holstein, Jersey, and Brown Swiss, respectively. The validation data set had 2,477 Holstein, 410 Jersey, and 182 Brown Swiss bulls that were unproven (no daughter information) in November 2004 and proven by August 2009. A common set of 43,385 single nucleotide polymorphisms (SNP) were used for all breeds. Three methods of multibreed evaluation were investigated. Method 1 estimated SNP effects separately within-breed and was tested by multiple regressions to predict daughter deviations of bulls of another breed. Method 2 estimated a common set of SNP effects from combined genotypes and phenotypes of all breeds. Method 3 solved for correlated SNP effects within each breed estimated jointly using a multitrait model. Multiple regressions were used to test across-breed genomic predicted transmitting ability (GPTA) with within-breed GPTA and parent average (PA). A few effects were significant with method 1, mostly for Jerseys and Holsteins, but estimates were small compared with within-breed GPTA and PA. Across-breed GPTA from method 2 were significant for certain traits in some breeds; correlations between within-breed GPTA and across-breed GPTA ranged between 0.91 and 0.93. Results from method 3 were significant and adjusted coefficient of determinations for protein yield (the only trait tested for method 3) were highest of all methods for all breeds. However, compared with the current within-breed genomic model, method 3 increased the adjusted coefficient of determination by 0.0097, 0.0042, and 0.0017 for Brown Swiss, Jerseys, and Holsteins, respectively.