Large-scale, multibreed genomic evaluation for fertility traits in U.S. dairy cattle using single-step genomic BLUP

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The official U.S. dairy genetic evaluation involves a multistep genomic process, initially estimating pedigree breeding values (e.g., using BLUP), then SNP effects, direct genomic predictions, and genomic breeding values (GEBV) using a selection index. Single-step Genomic BLUP (ssGBLUP) streamlines the computation of GEBV by utilizing all available data in a single run. This study evaluates the official U.S. dairy genetic evaluation's performance for fertility traits employing ssGBLUP and BLUP frameworks. Working with fertility traits is challenging because of low heritability and sparse recording. The pedigree dataset comprises 93 million animals with over 2 million genotypes across all breeds in the Official U.S. multibreed genomic evaluation. Phenotypic records from 1960 to 2023 for Cow Conception Rate (CCR), Early First Calving (EFC), Heifer Conception Rate (HCR), and Daughter Conception Rate (DPR) were analyzed. The four-trait multibreed model integrated Unknown Parent Groups (UPG) and Metafounders (MF) defined by breed, year of birth, and selection pathway, resulting in 417 genetic group definitions. Evaluation methods included bias and dispersion assessments using the Linear Regression method and the Pearson correlation for (G)EBV of each analysis. Validation was performed on Jersey (JE) and Holstein (HO) breeds for CCR and DPR, and the (G)EBV of validation animals for each trait were compared. Genetic trends between ssGBLUP and BLUP with UPG or MF were examined. Bias was identified in evaluations with ssGBLUP and BLUP with UPG or MF. Notably, ssGBLUP

shows better dispersion levels with MF in HO and JE compared to other models. High correlations were observed in ssGBLUP with MF for HO and ssGBLUP with UPG for JE. Genetic trends showed consistency across all models for CCR and DPR, with a decrease in trend from 1960 to 2000 and positive trends between 2000 and 2020, with ssGBLUP MF presenting the smoothest trend. The results underscore the feasibility of ssGBLUP for fertility traits in large datasets, with an emphasis needed for re-evaluating the models to minimize estimation bias.