Single-step genomic evaluation for fertility in Nordic Red dairy cattle

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Joint Nordic (Denmark, Finland, Sweden) genetic evaluations of female fertility traits were updated in 2015. Because the number of genotyped cows has increased considerably in recent years, the fertility model was found to be re-evaluated with genomic information included. The single-step genomic evaluation (ssGBLUP) was based on the same multi-trait multi-lactation animal model and variance components as the routine breeding value evaluation (BLUP). Heifer traits were non-return rate and length of service period. Cow traits in first, second and third parities were non-return rate, length of service period, and days from calving to first insemination. All 11 traits had low heritabilities (0.015-0.04), but moderately high genetic correlations between the parities (0.60-0.88). Phenotypic data contained 4 million animals with records, and pedigree consisted of 5,3 million animals. There were also 315 phantom parent groups (PPG), which were included into the pedigree or both into the pedigree and genomic information using QP-transformation to calculate breeding values directly. Genotypes were available for 23,520 animals. Validity of BLUP and ssGBLUP were studied using regression of deregressed proofs for full data on estimated breeding values (EBV) and genomic enhanced breeding values (GEBV) for reduced data. Both BLUP and ssGBLUP were solved with MiX99-program. With the PPG in the pedigree only, the BLUP and ssGBLUP converged after 3,052 and 29,063 iterations, respectively, while the ssGBLUP with the PPG in both the pedigree and genomic information converged after 2,453 iterations. Genetic trends based on males' EBV and GEBV followed well each other. For EBV, validation reliabilities were 0.16-0.32 and regression coefficients were 0.88-1.14 depending on the trait. The corresponding figures for GEBV were 0.22-0.45 and 0.72-0.99. In conclusion, the joint Nordic fertility evaluation using ssGBLUP was feasible after the genetic groups were correctly accounted. Especially for the cow fertility traits, the ssGBLUP model gave higher validation reliabilities than BLUP.