Genetic parameters for a multiple-trait linear model conception rate evaluation

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Genetic evaluation for female fertility in Finnish, Danish, and Swedish dairy cows has been upgraded to multiple trait animal model evaluation, where heifer and cow fertility up to third parity are considered as four different traits. In next step, non-return rate will be replaced by conception rate (CR). The aim of this study was to estimate required variance components for the implementation of a CR model using outcomes of all available inseminations. A multiple trait multiple parity sire model with 11 traits was used to estimate simultaneously the variance components for CR, interval from first to last service (IFL) and interval from calving to the first service (ICF) in the different parities. Within each lactation the CR observations were treated as repeated observations. The data consisted of Nordic Red dairy cattle heifers and cows (N=101 315) from Swedish milk recording data. The heritabilities of CR were 0.02 in all parities and ranged from 0.02 to 0.05 for the interval traits in different parities. The within-trait genetic correlations between heifer and cow traits varied from 0.4 to 0.7 in CR and in IFL, and were 0.9 or higher among all the cow traits in the later parities. CR are binomial observations with a variance structure depending on the number of repeated trials service period. Proper modeling of CR observations was found to be crucial to avoid biased estimates for heritability and genetic correlations between traits. Female fertility traits are low-heritable and benefit from multiple trait analysis where all available information is used.