Genetic parameters of fertility indicators in Holstein

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The goal of this study was to estimate the genetic parameters of fertility indicators in dairy cattle. Measurements from a regional sub-project of 953 Holstein cows from one farm in Texas during 2 calving years were analyzed. Three fertility indicators were evaluated: (1) probability of cycling at day 45 postpartum (Pr_Cyc); (2) probability of disease diagnosis at 45 days postpartum (Pr_Sck); and (3) probability of pregnancy after 2 AIs (Pr_Prg). These indicators were estimated using a logistic model including the covariables of dystocia, retained placenta, body condition score at 7 and 35 days postpartum (BCS7 and BCS35, respectively), and blood β-hydroxybutyrate (BHBA) as an indicator of subclinical ketosis. Univariate sire models, including the effects of contemporary group and lactation number, were used to estimate the genetic parameters of days open (DO), BCS7, BCS35, Pr_Cyc, Pr_Sck, and Pr_Prg. The percentage of cows cycling, diagnosed with a disease, and pregnant after 2 AIs were 69.7%, 14.9%, and 64.6%, respectively. The marginal probabilities indicated that cows diagnosed with dystocia, retained placenta, metritis, and mastitis were 1.7%, 6.0%, 11.4%, and 7.3% and less likely to be cycling than healthy cows, respectively. Cows were 2.7% and 4% less likely to be cycling per unit increases in mucus score at 7 ± 2d after calving and BHBA, respectively. The heritability estimates (and standard errors) for Pr_Cyc, Pr_Sck, Pr_Prg, DO, BCS7, and BCS35 were 0.23(0.15), 0.29(0.17), 0.58(0.19), 0.19(0.13), 0.25(0.16), and 0.25(0.18), respectively. Our results from this sub-project of the grant indicated that the considered fertility traits have an important genetic component and could be used as effective indicators of fertility in breeding and management decisions. These findings, of a regional sub-group of the project, support the foundation premise of the grant that novel fertility indices may be possibly combined as fertility indicators, to be collated with genomic analyses, to improve the accuracy of pregnancy prediction and selection for improved fertility in dairy production.