# Southeast Dairy Producer's Check-Off Program

# Research Summary

## In-depth genomic analysis of fertility indicators in Holstein dairy cattle

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## Implications

The incorporation of copy number variations (CNVs) in traditional GBLUP analysis enhanced heritability estimates for fertility traits in dairy cattle. Hence, it is expected that higher heritability estimates lead to better prediction accuracy of genetic merit, boosting genetic trends over the years.

## Methods

Resumption of ovarian cyclicity (CYC), pregnancy after first AI (P1stAI), and days open (DOPN) of 11,489 Holstein cows from 16 herds located in 7 U.S. states (OH, MN, NY, WI, CA, **FL**, and TX) were recorded using a well-defined and standardized phenotyping protocol. Resumption of ovarian cyclicity was assessed via transrectal ultrasonography at 40 ±3 and 54 ±3 DIM with portable ultrasounds and recorded as a binary trait (0 = anovulation, 1 = ovulation), where ovulation was defined as visible corpus luteum on both consecutive ultrasound scans. Pregnancy after first AI was diagnosed by ultrasonography on day 32±3 after AI and reconfirmed at day 60±3 of gestation, also recorded as a binary trait (0 = no, 1 = yes). Days open was defined as the DIM when the cow became pregnant within 305 DIM. For cows that did not become pregnant within 305 DIM, days open were censored when the cow left the herd, died, became "do not breed" or when they completed 305 DIM, whichever came first.

Out of the nearly 12,000 cows, a total of 3,387 Holstein cows have high-density genomic (777,962 SNPs) information. Besides SNPs, 4,113 non-redundant copy number variations (CNVs) were mapped using genomic information of all genotyped cows to assess the contribution of an alternative genomic variant on fertility indicators of a U.S. representative population of Holstein dairy cows.

Traditional SNP-based and alternative SNP+CNV-based models were fitted to in-depth investigate additive genetic variability underlying fertility indicators in Holstein cows. All mapped CNVs were used to build the CNV-derived genomic relationship matrix (CNV_GRM). CNV loci representing deletions showed double deletions, single deletions, and normal states were recoded as 0, 1, and 2, respectively. In contrast, CNV loci representing duplications showed normal state, single duplications, and double duplications were recoded as 0, 1, and 2. Given some CNVs loci presented deletions and duplications, these mixed-CNVs were treated as two distinct CNVs loci, one representing deletions and the other representing duplications. The variance components and heritabilities estimates for CYC, P1stAI, and DOPN were obtained by fitting either only a SNP-derived GRM (SNP_GRM) or jointly SNP_GRM and CNV_GRM in models including the female category and farm-year-season as fixed effects.

## Results

The SNP-based model estimated additive genetic variances of 0.09  0.03 (CYC), 0.10  0.03 (P1stAI), and 305.40  120.94 (DOPN), with heritabilities of 0.08  0.03 (CYC), 0.09  0.03 (P1stAI), and 0.05  0.02 (DOPN). The SNP+CNV model showed complementary additive genetic variances of 0.03  0.02 (CYC), 0.16  0.03 (P1stAI), and 433.39  94.56 (DOPN), leading to higher heritabilities of 0.10  0.03 (CYC), 0.17 0.03 (P1stAI), and 0.12  0.02 (DOPN). These heritability estimates from the SNP+CNV model were 23% (CYC), 95% (P1stAI), and 134% (DOPN) higher than those from the SNP-based model. Therefore, CNVs account for additive genetic variance of fertility traits which cannot be accounted for only by SNPs as genetic markers.

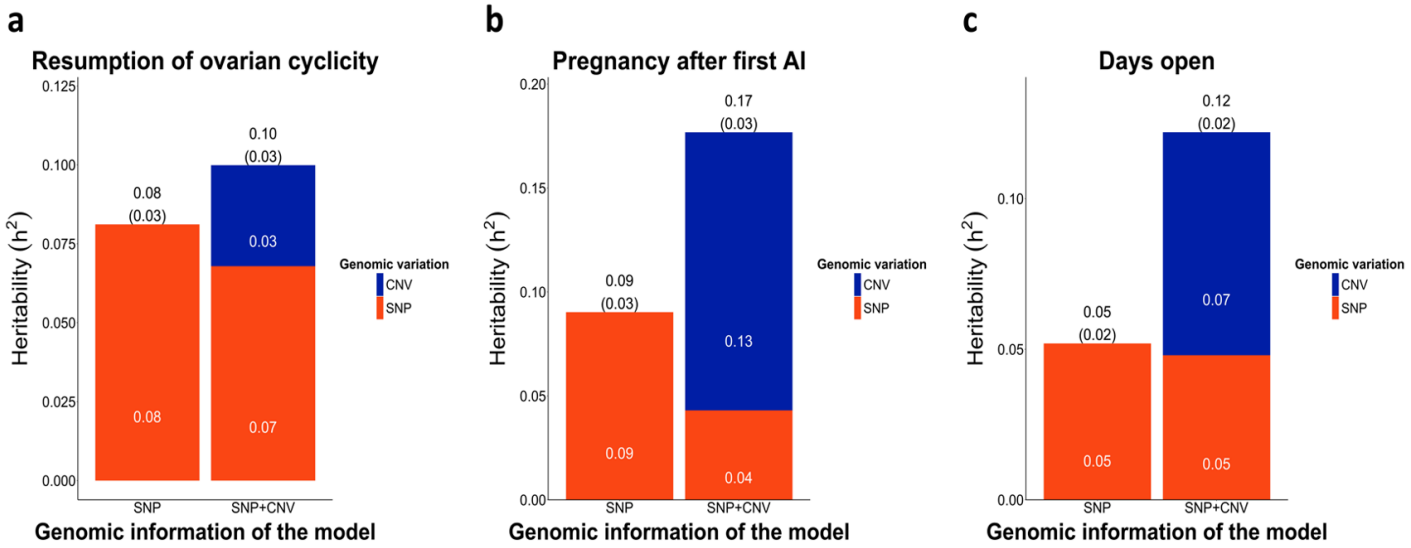


**Figure 1.** Heritability estimates from SNP- and SNP+CNV-based models of fertility indicators in Holstein dairy cows. The y-axis shows the total heritability estimated for resumption of ovarian cyclicity (a), pregnancy after first AI (b), and days open (c) for each model, where the orange and blue fraction represents the proportion of heritability estimates due to SNPs and CNVs, respectively.