

## ABSTRACT

### GENOME WIDE ASSOCIATION STUDY AND GENOMIC HERITABILITY OF ANTI-MULLERIAN HORMONE IN DAIRY HOLSTEIN HEIFERS

By

Muhammad Yasir Nawaz

The objectives of this study were to estimate the genomic heritability of Anti Mullerian hormone (AMH), identify candidate genes associated with AMH production, and establish phenotypic correlations between serum AMH concentrations and parameters of reproductive performance in Holstein heifers. AMH concentrations were determined in 2905 dairy Holstein heifers. Animals were genotyped using the Zoetis 70K SNP Panel. Genotypes were imputed to standard USDA 60,671 bovine SNP set with 54,519 SNP markers remaining after standard editing procedures. A linear mixed model was used to model the random effects of sampling day and genomics on the logarithm of AMH. Results showed that the genomic heritability ( $\pm$ SEM) of AMH was  $0.36\pm 0.03$ . We identified significant associations between AMH and 11 SNP markers on chromosome 11 and one marker on chromosome 20 based on a 5% false discovery rate. Some of the annotated genes in those regions have been previously identified as being important for AMH expression and ovarian function. There was no strong evidence of any association between conventional reproductive performance measures of dairy heifers and their serum AMH concentration. It seems that these associations should be studied in later parities as these heifers continue to mature. Nevertheless, the high heritability of AMH and a well-established association of AMH with super ovulatory response may make AMH a biomarker to genetically select cattle for larger gonads, more follicles and better response to superovulation.