

Heritability Estimates for Intramammary Infection in Canadian Holsteins Heifers

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Mastitis is one of the most common diseases in dairy cattle, which causes heavy economic losses to the dairy farmers. The disease occurs due to udder infection caused by several bacterial species. A group of minor pathogens, non-*aureus* staphylococci (NAS) are the most frequent cause of IMI. Although a good progress has been made in comprehension of genetics of bacteria-specific clinical mastitis, studies involving the genetic analysis of pathogen-specific udder infection are still scarce. Therefore, the objective of this study was to estimate heritabilities for overall and bacteria-specific udder infection in non-clinical heifers. Data and samples were collected over a 2-year interval as part of the Canadian Bovine Mastitis Research Network (CBMRN). The final data set contained 5,084 records from 1,271 clinically healthy heifers in 84 herds. Four traits were considered for the genetic analysis; overall IMI, contagious bacteria, environmental bacteria, and NAS. Data were analyzed at the quarter level using a threshold probit model. Variance components were estimated Gibbs sampling approach with chain length of 100,000 and a burn-in of 200,000 using Blupf90 program. The model included days in milk and age at first calving as fixed effects and herd-sample collection date, animal additive genetic and permanent environmental effects and residuals as random effects. Prevalence of overall udder infections, contagious bacteria, environmental bacteria, and NAS were 47, 6, 14 and 34%, respectively. Heritability estimates ranged between 0.02 (0.01) to 0.07 (0.05) for the four traits.

Implications: Results from this research provides insight into exploitable genetic variation of sires of heifers associated with mastitis in Canadian dairy herds. This knowledge can be used by dairy improvement organizations, the AI industry and dairy farmers to improve genetic resistance to mastitis through genetic selection.