

Genetic Analysis of Pathogen-Specific Intramammary Infection in Dairy Cows

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Objective

Determine the genetic variation of udder infections in clinically healthy Holsteins for overall and pathogen-specific infections

Background and Impact on Dairy

- Udder infection leads to subclinical and clinical mastitis
 - Affects milk production and causes economic losses
- Several bacterial pathogens causes udder infection
 - Non-aureus staphylococci* (NAS) are the most prevalent cause of udder infections
- Genetic selection against udder infections will aid in controlling mastitis

Materials and Methods

- Data collected over a 2-year period as part of the National Cohort of Dairy Farms from the Canadian Bovine Mastitis and Milk Quality Research Network (CBMQRN), which included 91 Canadian dairy herds across 6 provinces
- The final dataset contained 46,900 quarter-level records (0-400 days in milk; DIM) from 3,382 multiparous Holsteins cows in 84 herds
- Six binary traits (0=not infected, 1=infected; Table 1) were analyzed with probit threshold model using a Markov Chain Monte Carlo (MCMC) Gibbs sampling approach (univariate and bivariate)

Table 1. Pathogens included in analyzed infection traits

Traits	Pathogens
Overall IMI	All pathogens
Contagious pathogens	<i>Staphylococcus aureus</i> , <i>Streptococcus agalactiae</i> , <i>Corynebacterium</i> spp.
NAS	Non-aureus staphylococci
Environmental pathogens	<i>Escherichia coli</i> , <i>Klebsiella</i> spp., <i>Enterobacter</i> spp., <i>Nocardia</i> spp., <i>Prototheca</i> spp., <i>Trueperella pyogenes</i> , <i>Streptococcus uberis</i> , <i>Streptococcus dysgalactiae</i> , <i>Bacillus</i> spp., <i>Streptococcus</i> spp., <i>Serratia</i> spp., <i>Citrobacter</i> spp., <i>Proteus</i> spp., <i>Salmonella</i> spp., <i>Pseudomonas</i> spp., <i>Pasteurella multocida</i>
Major pathogens	<i>Staph. aureus</i> , <i>Strep. agalactiae</i> , <i>Streptococcus</i> spp., <i>Strep. uberis</i> , <i>E. coli</i> , <i>Klebsiella</i> spp., <i>Enterobacter</i> spp., <i>T. pyogenes</i> , <i>Strep. dysgalactiae</i>
Minor pathogens	<i>Corynebacterium</i> spp., non-aureus staphylococci

Results

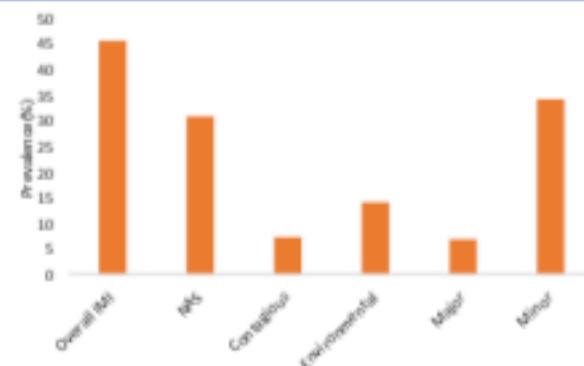


Figure 1. Overall and pathogen-specific quarter-level prevalence

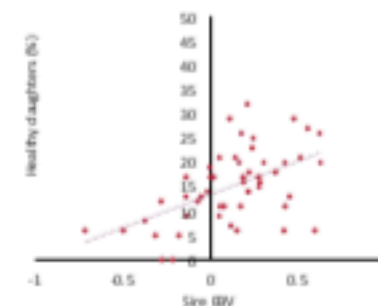


Figure 2. Percentage of healthy daughters according to EBV for overall IMI

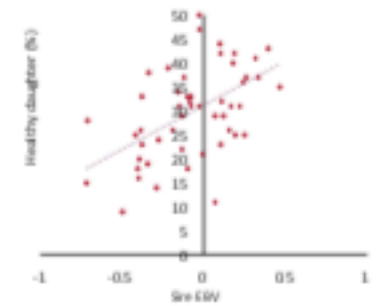


Figure 3. Percentage of healthy daughters according to EBV for NAS pathogen group

Table 2. Heritability (diagonal) and genetic correlations (above the diagonal) for 6 infection traits. Corresponding SE are within brackets

	IMI	NAS	Contag.	Enviro.	Major	Minor
IMI	0.04 (0.08)	0.80 (0.08)	0.83 (0.11)	0.22 (0.24)	0.71 (0.14)	0.91 (0.04)
NAS		0.03 (0.02)	0.35 (0.28)	-	0.21 (0.27)	0.97 (0.01)
Contagious			0.07 (0.03)	0.69 (0.30)	0.96 (0.06)	0.66 (0.21)
Environmental				0.08 (0.01)	0.39 (0.30)	-
Major					0.04 (0.02)	0.35 (0.27)
Minor						0.04 (0.01)

Table 3. Percentage of diseased daughters from all (average), the best (10% decile), and the worst (90% decile) sires [with at least 10 daughters in >5 herds (n = 51)] according to their EBV

Traits	Mean prevalence % (Cow-level)	10% decile (Best sire)	90% decile (worst sire)
IMI	85	80	93
NAS	70	64	82
Contagious	22	14	32
Enviro.	39	29	48
Major	24	16	40
Minor	74	65	85

Conclusions

- Non-aureus staphylococci were the most prevalent cause of udder infections compared to other pathogens
- Heritability of overall and pathogen-specific udder infections was low and ranged between 0.01 to 0.07
- Despite the low heritability, there is an exploitable genetic variation among sires in producing daughters that are more resistance to udder infections

Acknowledgements

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