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Genetic Analysis of Udder Infections in Canadian Holsteins

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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 Industry

- 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 National Cohort of Dairy Farms of Canadian Bovine Mastitis and Milk Quality Research Network (CBMQRN) from 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 in 84 herds
- Six traits (binary) 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 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

- The model included DIM and parity as fixed effects and herd-sample collection date, animal additive genetic and permanent environmental effects within and across parity and residuals as random effects

Results

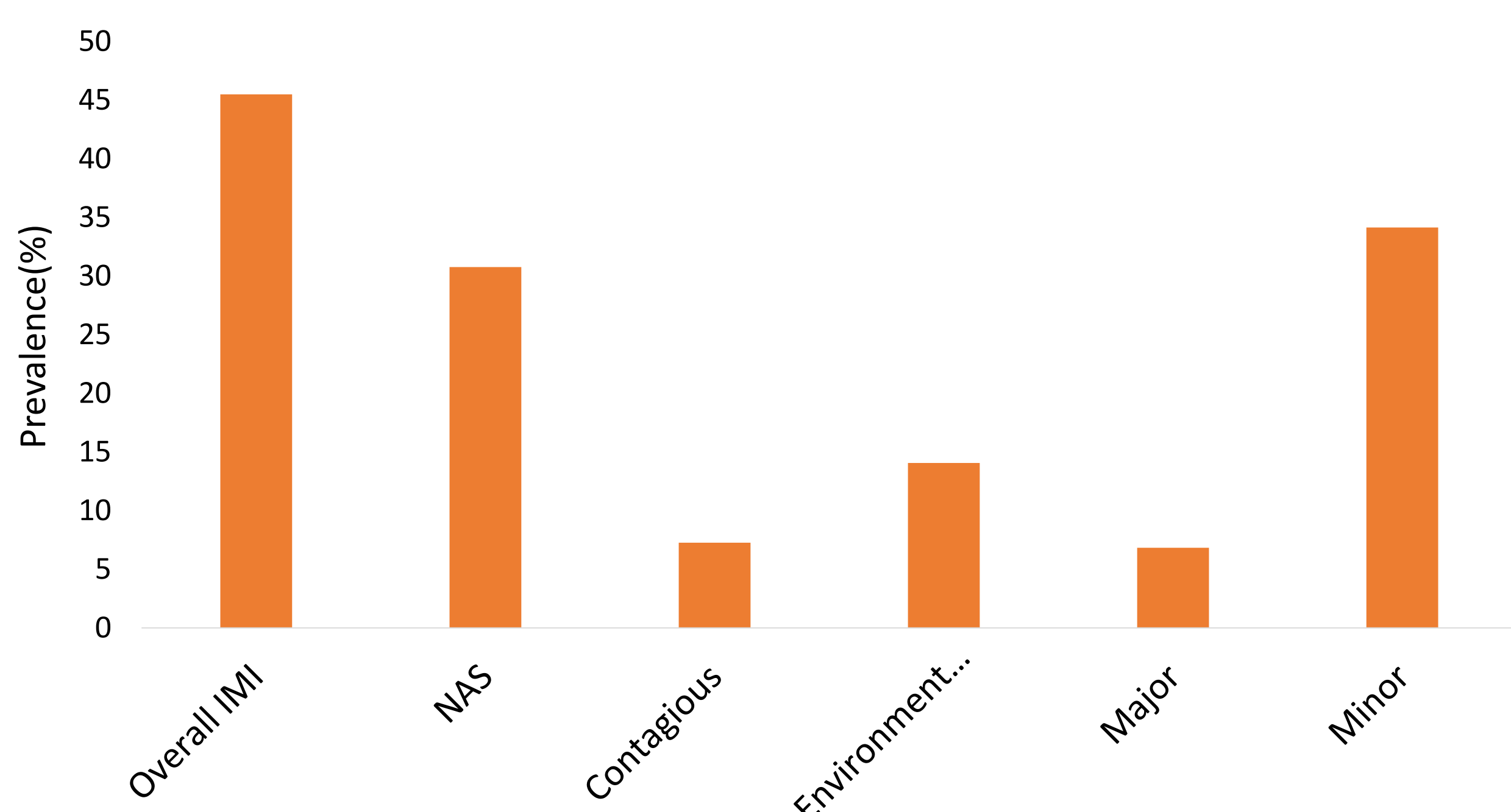


Figure 1. Overall and pathogen-specific quarter-level prevalence

Results

Table 2. Heritability (diagonal) and genetic correlations (above the diagonal) for 6 traits

	IMI	NAS	Contag.	Enviro.	Major	Minor
IMI	0.04 (0.01)	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)
Contag.			0.07 (0.03)	0.69 (0.30)	0.96 (0.06)	0.66 (0.21)
Enviro.				0.01 (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 estimated breeding value (EBV)

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

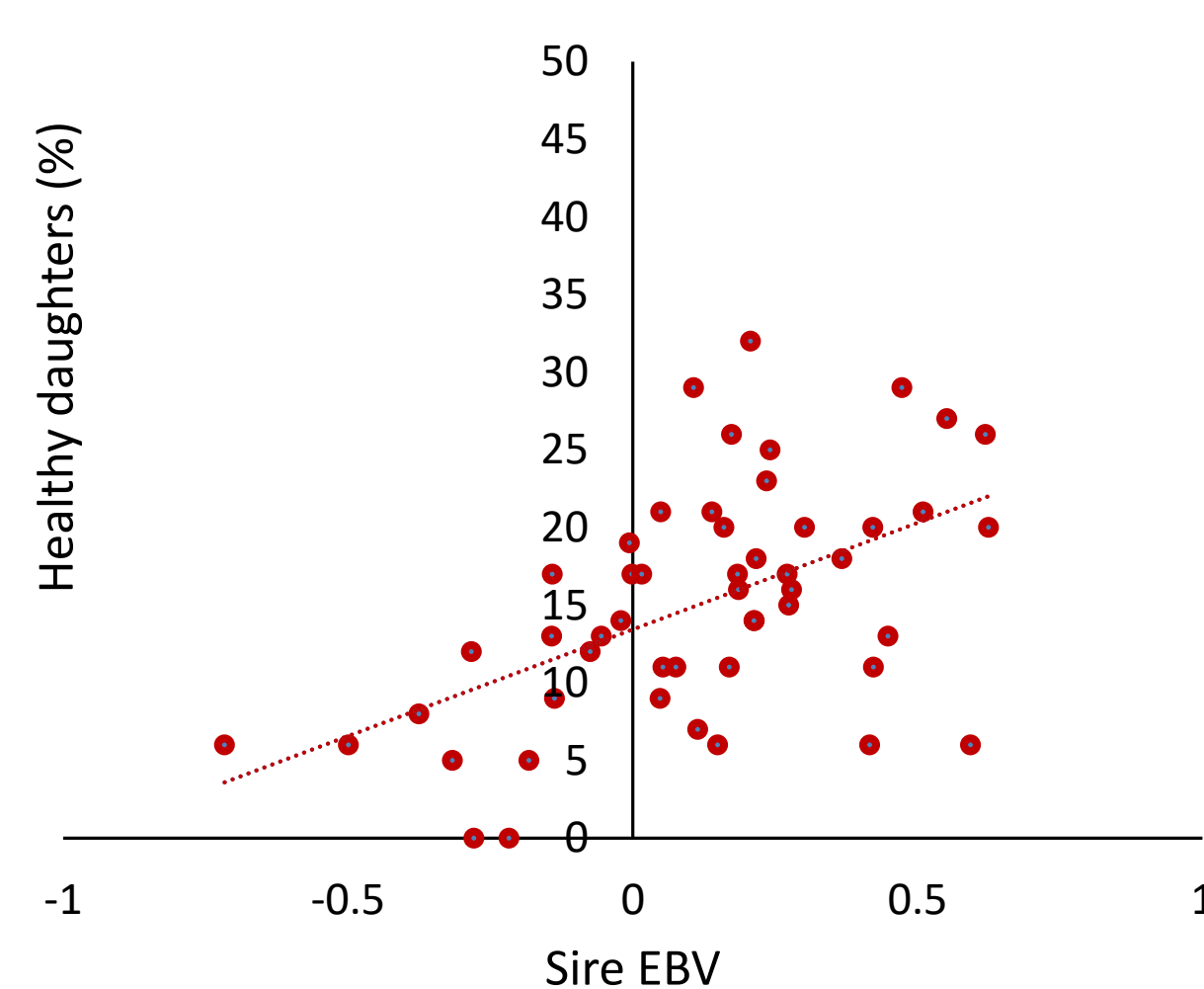


Figure 2. Percentage of healthy daughters according to EBV predicted for overall IMI

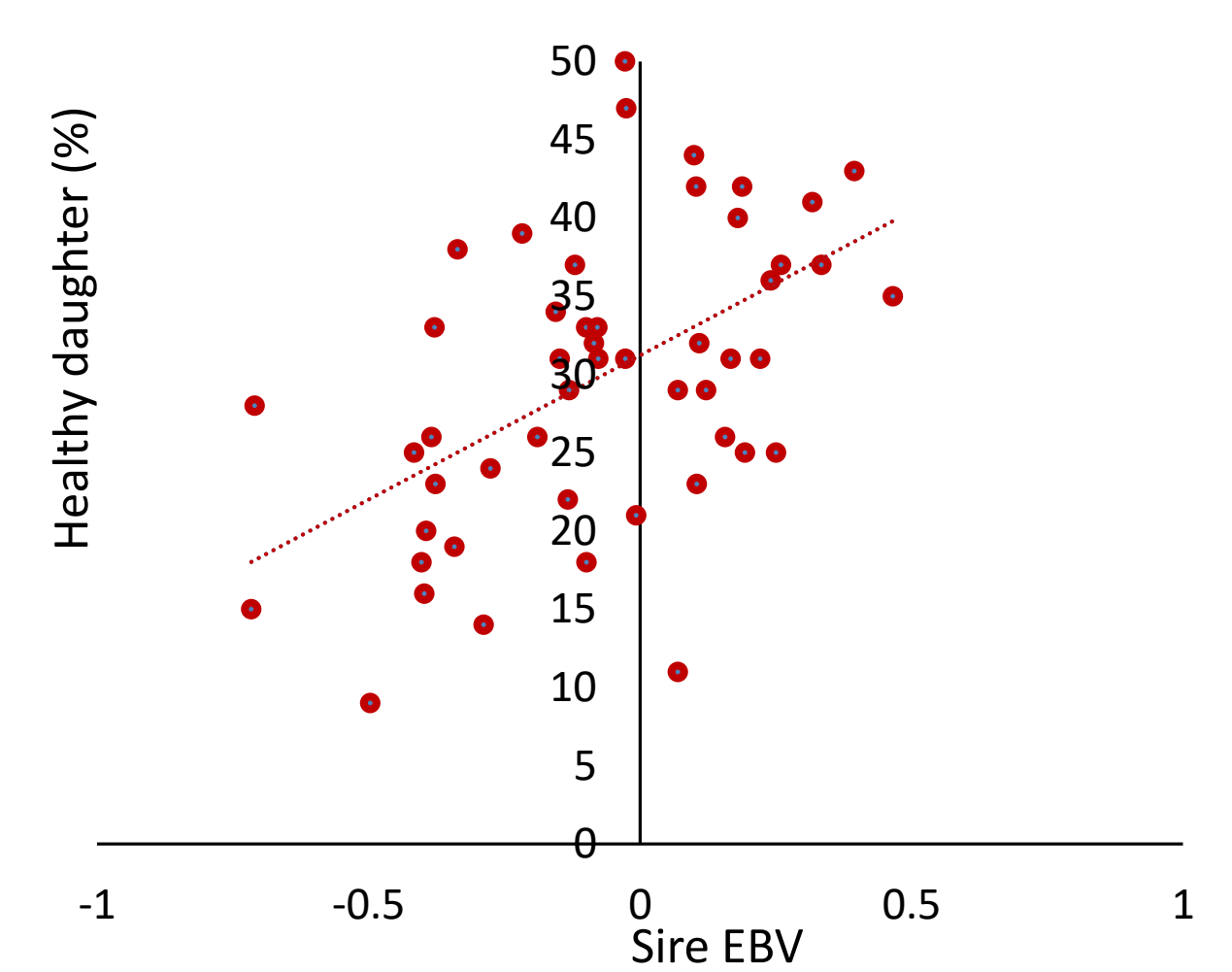


Figure 3. Percentage of healthy daughters according to EBV predicted for NAS pathogen group

Implications

- Estimated genetic parameters will provide insight into genetic variation of udder infections in Canadian dairy herds
- This knowledge can be used by dairy improvement organizations, the AI industry and dairy farmers to improve genetic resistance to udder infections through genetic selection

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 resistance to udder infections

Acknowledgements

- All participating dairy farmers are greatly acknowledged
- Supported by NSERC, Alberta Milk, Westgen Endowment Fund, Dairy Farmers of Canada, BC Dairy, Dairy Farmers of Manitoba, CanWest DHI, and Canadian Dairy Network