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Genetic Analysis of Subclinical Mastitis Resistance in Early Lactation

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Objectives

- Investigate the genetic variation of subclinical mastitis resistance in early lactation (5 to 30 DIM) in Holstein heifers
- Compare genetic parameters estimated from threshold and linear model

Background and Impact on Dairy Industry

- Subclinical mastitis (SCM) causes economic losses for producers
 - Affects milk production
 - Leads to higher incidence of clinical mastitis and premature culling
- The incidence of SCM in heifers is usually higher during early lactation
- Somatic cell count (SCC) can be used for the diagnosis of SCM
- Threshold to define SCM is highly variable and not uniformly adopted across world

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 only first test-day SCC records from **8,518** Holstein-Friesian heifers from 90 herds between **5 to 30 DIM**
- Six traits were defined as an indicator of SCM based on different threshold (Table 1)
 - > threshold heifers were considered diseased (1)
 - ≤ the threshold heifers were considered healthy (0)

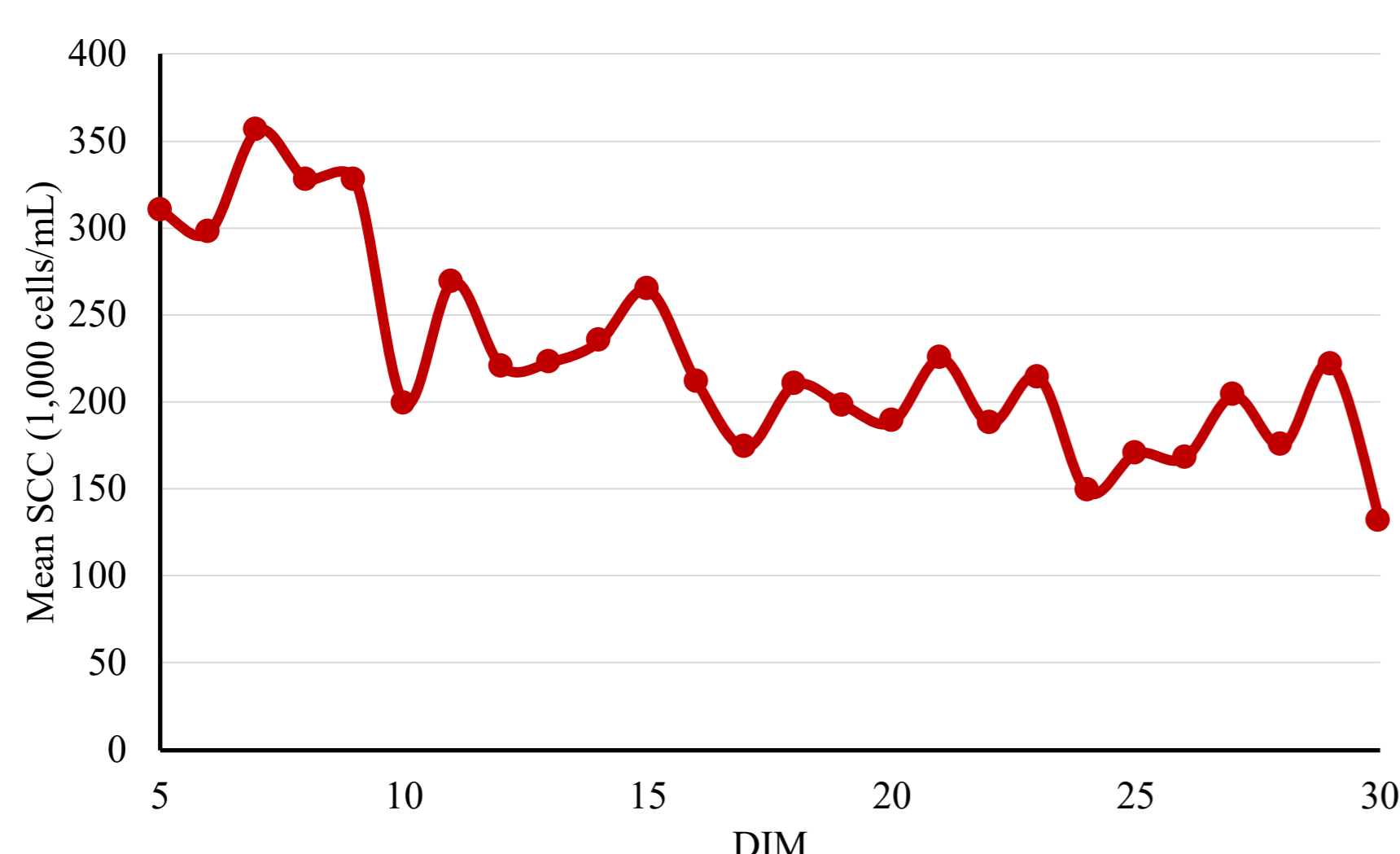
Table 1. Definitions of 6 traits as indicator of SCM

Traits	Threshold
SCM _{150K}	150,000 cells/ml between 5 to 30 DIM
SCM _{200K}	200,000 cells/ml between 5 to 30 DIM
SCM _{250K}	250,000 cells/ml between 5 to 30 DIM
SCM _{400,150K}	400,000 cells/ml between 5 to 10 DIM and 150,000 cells/ml between 11 to 30 DIM
SCM _{400,200K}	400,000 cells/ml between 5 to 10 DIM and 200,000 cells/ml between 11 to 30 DIM
SCM _{400,250K}	400,000 cells/ml between 5 to 10 DIM and 250,000 cells/ml between 11 to 30 DIM

- Genetic parameters were estimated using linear and threshold animal models
- Spearman rank correlation between EBV predicted from linear and threshold model were estimated

Results

Figure 1. Average somatic cell count from 5 to 30 DIM



- Estimated genetic correlation among 6 traits were > 0.90
- Spearman rank correlation between EBV predicted from linear and threshold model were > 0.98

Results

Table 2. Prevalence (%) of SCM from 5 to 30 DIM

Traits	Provinces						Total
	AB	NB	NS	ON	PE	QC	
SCM _{150K}	19.09	23.26	21.77	26.82	27.13	25.84	24.29
SCM _{200K}	14.42	19.03	17.47	20.85	21.06	19.46	18.71
SCM _{250K}	12.01	15.41	14.78	17.02	16.67	15.41	15.20
SCM _{400,150K}	15.42	17.52	17.61	22.07	21.58	20.62	19.61
SCM _{400,200K}	11.96	15.11	14.78	17.94	17.57	16.62	15.85
SCM _{400,250K}	10.38	12.99	12.90	15.00	14.21	14.06	13.40

Table 3. Heritabilities (se) on the underling and observed scale from linear (h^2_{obs-l}) and threshold (h^2_{und} and h^2_{obs-t}) model.

Trait	h^2_{obs-l}	h^2_{und}	h^2_{obs-t}
SCM _{150K}	0.057 (0.018)	0.046 (0.017)	0.024
SCM _{200K}	0.053 (0.017)	0.051 (0.018)	0.025
SCM _{250K}	0.037 (0.015)	0.040 (0.019)	0.017
SCM _{400,150K}	0.051 (0.017)	0.047 (0.018)	0.023
SCM _{400,200K}	0.048 (0.016)	0.047 (0.019)	0.021
SCM _{400,250K}	0.040 (0.015)	0.043 (0.020)	0.017

Figure 2. Percentage of healthy daughters according to the estimated breeding value (EBV) predicted using linear model

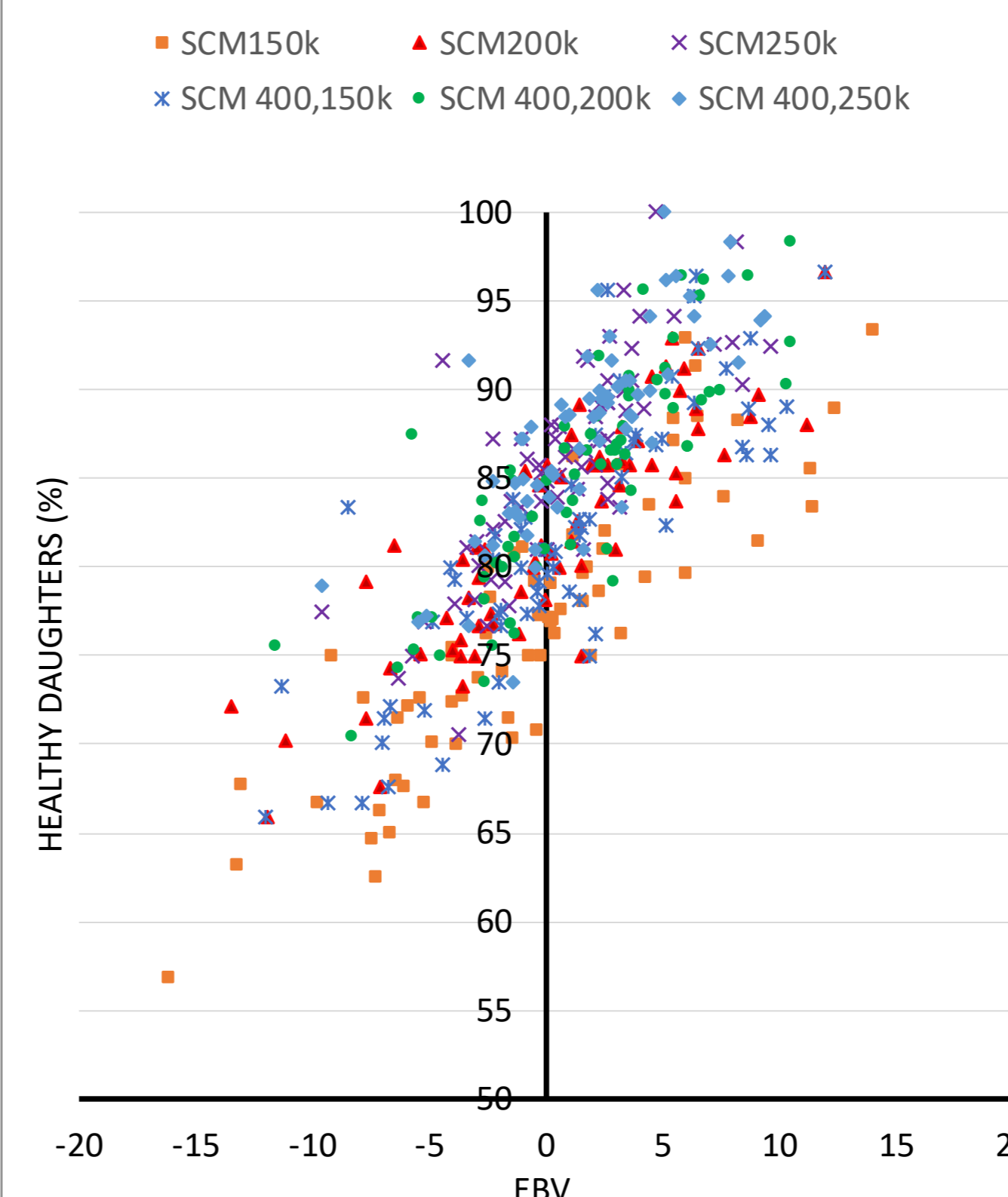
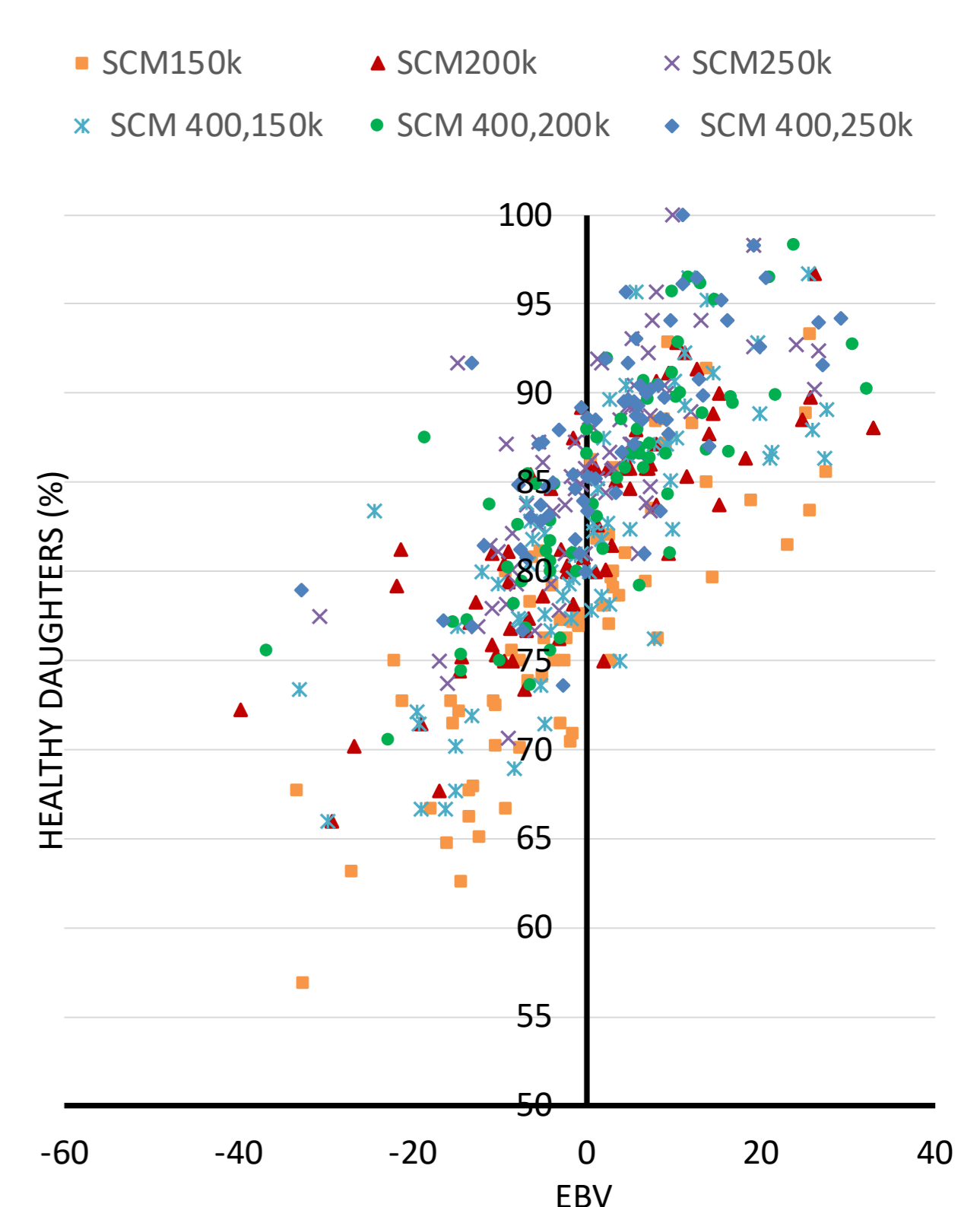


Figure 3. Percentage of healthy daughters according to the estimated breeding value (EBV) predicted using threshold model



Implications

- Estimated genetic parameters will provide insight into genetic variation of heifers associated with SCM in early lactation 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

Conclusions

- Despite the low heritability, there is a exploitable genetic variation in early lactation
- Analyzed 6 traits are genetically similar
- High rank correlation between EBV suggested that there could be no difference in the ranking of sire using threshold versus linear model

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