

# Genome-wide genomic and functional association study for workability and calving traits in Holstein cattle

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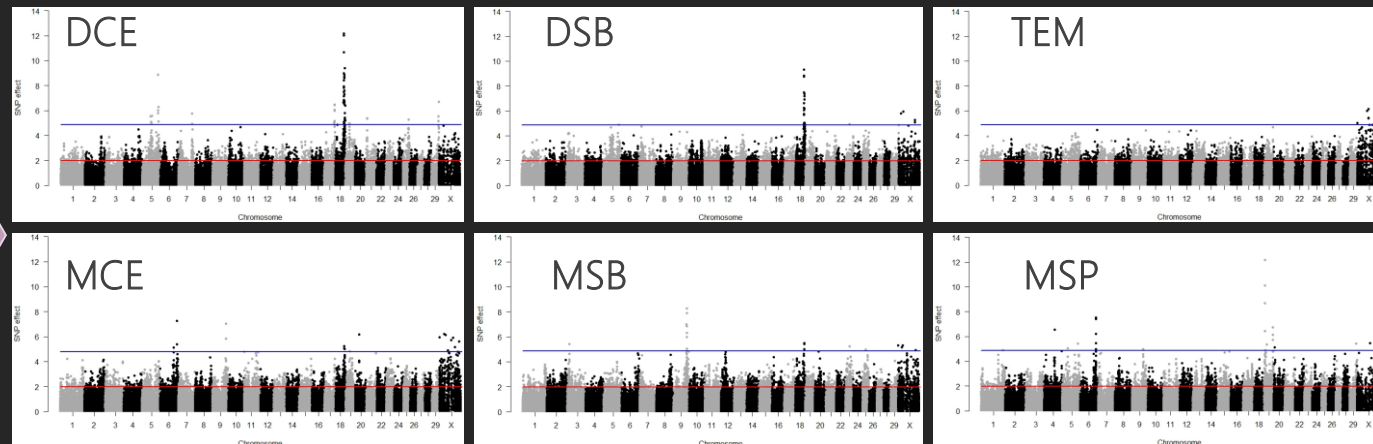
## Bull DRP

- DCE: direct calving ease  
30,603 bulls
- MCE: maternal calving ease  
29,738 bulls
- DSB: direct stillbirth  
24,521 bulls
- MSB: maternal stillbirth  
28,081 bulls
- TEM: temperament  
22,301 bulls
- MSP: milking speed  
28,376 bulls

## Genotypes

- Illumina BovineSNP50  
BeadChip 2 (87% bulls)  
→ 54,609 SNPs
- Illumina BovineSNP50  
BeadChip 1 (12% bulls)
- Other (1% bulls)

$$\text{GWAS} \rightarrow \text{DRP} = \mu + \mathbf{Z}_g \mathbf{g} + \mathbf{Z}_a \mathbf{a} + e$$



$$\mathbf{g} \sim N(\mathbf{0}, \mathbf{I}\sigma_g^2) \text{ random SNP effects, } \mathbf{a} \sim N(\mathbf{0}, \mathbf{A} \cdot 0.4\sigma_a^2) \text{ random polygenic effects}$$

$$\text{KEGG} \rightarrow |\hat{\mathbf{g}}| = \mu^* + \mathbf{Z}_p \mathbf{p} + \varepsilon$$

$$\mathbf{p} \sim N(\mathbf{0}, \mathbf{P}\sigma_g^2) \text{ random KEGG effects}$$
$$\varepsilon \sim N(\mathbf{0}, \mathbf{L}\sigma_\varepsilon^2) \text{ random residual}$$

$\mathbf{P}$  contains % of genes common between 2 KEGG

$\mathbf{L}$  diagonal, "1" for SNP assigned to KEGG / "10" for SNP not assigned to KEGG

MSB	bta05235	PD-L1 expression and PD-1 checkpoint pathway in cancer
	bta04658	Th1 and Th2 cell differentiation
TEM	bta00630	Glyoxylate and dicarboxylate metabolism
	bta00860	Porphyrin metabolism
MSP	bta00280	Valine, leucine and isoleucine degradation

