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Single-step genome-wide association for lameness and BCS in Walloon Holstein dairy cows

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Lameness remains a major welfare problem in dairy cows and is associated with reduced milk yield, increased culling, and impaired reproductive performance. The body condition score (BCS) reflects the body reserves and is a good predictor for health and welfare. Furthermore, a low BCS is known as a risk factor for lameness in dairy cows

Objective

This study aimed to perform genome-wide association studies to identify genomic regions associated with lameness and BCS in Walloon Holstein cows

Data & Method

- ✓ **BCS and lameness records on 12,988 1ST parity Holstein cows in 307 herds**
- ✓ **Lameness recorded on a scale of 1 (no lameness) to 5 (severely lame)**
- ✓ **BCS recorded based on a nine-point unit scale: low values reflecting emaciation and high values corresponding to obesity**
- ✓ **Genotypic data (563,882 SNP) on 4,628 animals (1,591 males)**
- ✓ **Regions of 0.5 Mb accounting for at least 0.50% of the total additive genetic variance were identified**

Results

Table 1: Mean and standard deviation (SD) for BCS and lameness in the first-parity Holstein cows

	Mean	SD
BCS	5.40	0.79
Lameness	1.36	0.66

Table 2: Heritability and genetic correlation of BCS and lameness in the first-parity Holstein cows

	BCS	Lameness
BCS	0.25	-0.19
Lameness		0.02

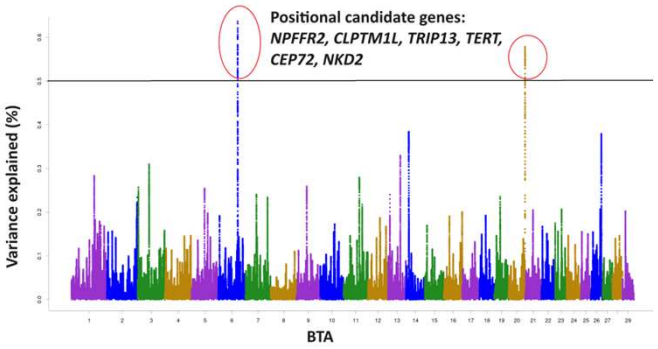

Figure 1: Additive genetic variance explained by windows of 0.50 Mb across chromosomes for BCS in the first-parity Holstein cows

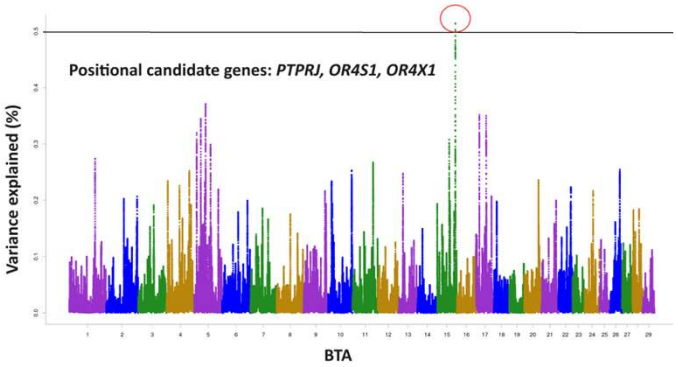

Figure 2: Additive genetic variance explained by windows of 0.50 Mb across chromosomes for lameness in the first-parity Holstein cows

Conclusion

- ➢ **low heritability was estimated for lameness and a moderate heritability was estimated for BCS**
- ➢ **Lameness and BCS are highly polygenic in which many regions across the genome contribute to their genetic variation**
- ➢ **Lower BCS is associated with an increased risk of lameness**

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