Sequence-based GWAS identify genomic regions associated with resistance to gastrointestinal strongyles in Holstein heifers

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Background

Gastrointestinal strongyles (GIS) substantially affect livestock health and productivity, especially during the first grazing season, causing economic losses.

While systematic preventive use of anthelmintics is commonly adopted, genetic selection to reduce parasite load offers a more sustainable alternative. Identifying the genetic basis of resistance is crucial for implementing genomic selection tools.

Materials and Methods

Population: 1,736 Holstein heifers
Precorrected phenotypes (YD):
- ELISA - Level of Ostertagia antibodies (indicator of parasite exposure).
- EPG - Total of GIS eggs per gram of feces (direct measure of parasite excretion).
- Log(EPG) – The EPG was log-transformed to normalize the distribution.
- PEPSI - Serum pepsinogen levels, marker of gastric mucosa lesions, potentially resulting from parasitic infections.

Genotypes:
- SNP-chip data (EuroGMD ~50K SNPs)
- Imputed to sequence level using 1000 Bull Genomes (50K -> HD -> sequence)

Statistical Analysis:
- Linear mixed model (GCTA software)
- Bonferroni correction (red line on the Manhattan plots)
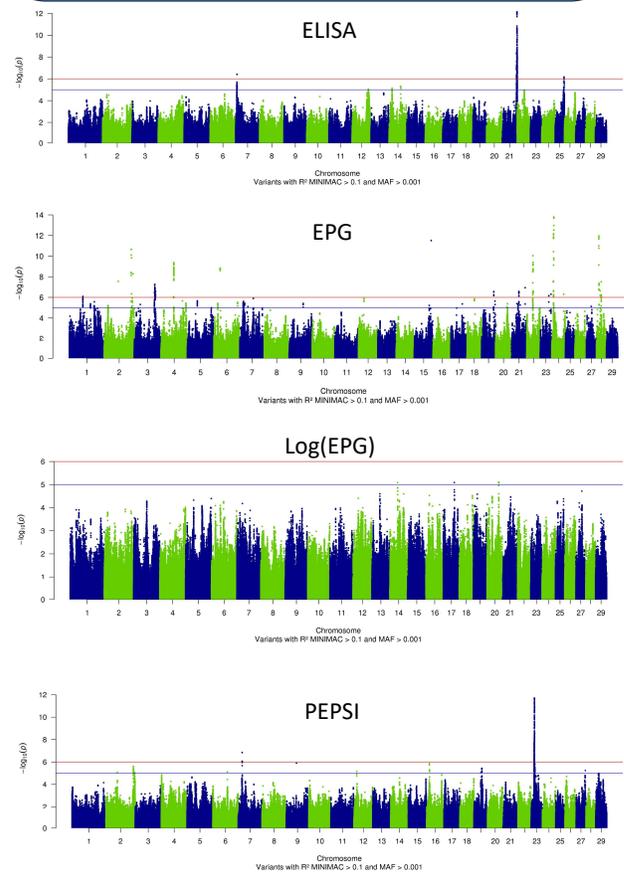
Results

Traits	Genomic h²
ELISA	0.13
EPG	0.07
Log(EPG)	0.12
PEPSI	0.30

Significant QTLs detected:
- BTA21 (ELISA): Near KIF26A, involved in enteric nervous system
- BTA24 (EPG): Near DSEL, candidate under investigation
- BTA23 (PEPSI): Within PGC (Progastricsin), key to gastric mucosa integrity

Objectives

This study (conducted under the GIVERNI project, funded by APIS-GENE) aimed to:
- Identify genomic regions associated with resistance to GIS in Holstein heifers
- Highlight candidate genes involved in immune or gastrointestinal function
- Lay the groundwork for genomic selection targeting parasite resilience

Conclusion

- Identified QTLs suggest involvement of genes related to immunity and gastrointestinal physiology
  - Post-GWAS steps underway
- Results support the feasibility of genomic selection for GIS resistance
  - Results will be confirmed by adding a new animal campaign to enrich the data.
  - Next step: Develop pilot genomic evaluations within the GIVERNI framework