Genome-wide association study identifies novel variants associated with host resistance to bovine tuberculosis

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Aims

To further enhance our knowledge of the genetic architecture underlying host resistance to Bovine tuberculosis (bTB) in dairy cattle through determining genetic variants associated with bTB phenotypes.

Data

A population comprised **1,153 Holstein cows** across Northern Ireland: **273 controls and 880 cases** were selected from bTB affected herds and genotyped using Illumina Bovine50 SNP chip.
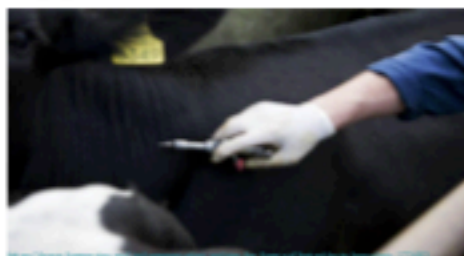
Methods

A. Heritability estimation: A GREML analysis for family data (Zaitlen et al. 2013) using **two** genomic relationship matrixes (GRMs) by GCTA (Yang et al. 2011), was used.

B. Single SNP GWAS and Post GWAS: A Single SNP GWAS analysis using a mixed model containing the **two** GRMs, by GCTA-MLMA (Yang et al. 2014); and a gene analysis using the single SNP GWAS summary statistics by MAGMA (de Leeuw et al. 2015);

C. Regional Heritability Mapping(RHM): To identify genomic regions associated with host resistance to bTB, we preformed the RHM using **three** GRMs (Nagamine et al. 2012).

Results

Heritability estimation

$$h^2_{L\,whole\,genome} = 0.30 \pm 0.06 \qquad h^2_{L\,kinship} = 0.24 \pm 0.06 \qquad h^2_{L\,Total} = 0.54 \pm 0.05$$

Associated variants with host resistance to bTB

✓ Single SNP GWAS analysis detected **six** independent loci.

✓ Gene analysis identified **two** associated genes

✓ RHM demonstrated **thirteen** significant regions.

Figure 1: Manhattan plot of results from Single SNP GWAS in solid circle and RHM with 10-SNP windows in open circle for resistance to bTB. The red horizontal line indicates the adjusted significant threshold level of genome-wide significance at 5% by Bonferroni correction of 1.