

Genomics and footrot resistance – where are we?

S Mucha, L Bunker, J Conington

SRUC, West Mains Road, Edinburgh, EH9 3JG, Scotland

Email: Joanne.Conington@sruc.ac.uk

Introduction

Lameness caused by footrot is endemic in UK sheep costing £24M annually.

Management control strategies are effective but continually need to be implemented and are labour-intensive.

Genomic information to better predict more resistant sheep to footrot, will improve animal health and welfare and reduce costs associated with managing the disease.



Methods

Footrot scores from each hoof from 4,695 ewes and lambs for undertaken from performance-recorded Texel sheep in 17 flocks across the UK over 2 years.

Breeding values (EBVs) for footrot from these animals were estimated and de-regressed to eliminate bias from different number of relatives contributing to the EBV.

Blood samples from each animal were used to extract DNA and 'SNP chip' technology was used with 50K separate 'gene variants' matched with the footrot data, for 336 ewes.

Genome-Wide Association analysis was performed using multi-locus mixed model algorithm (Segura et al., 2012¹)

Results

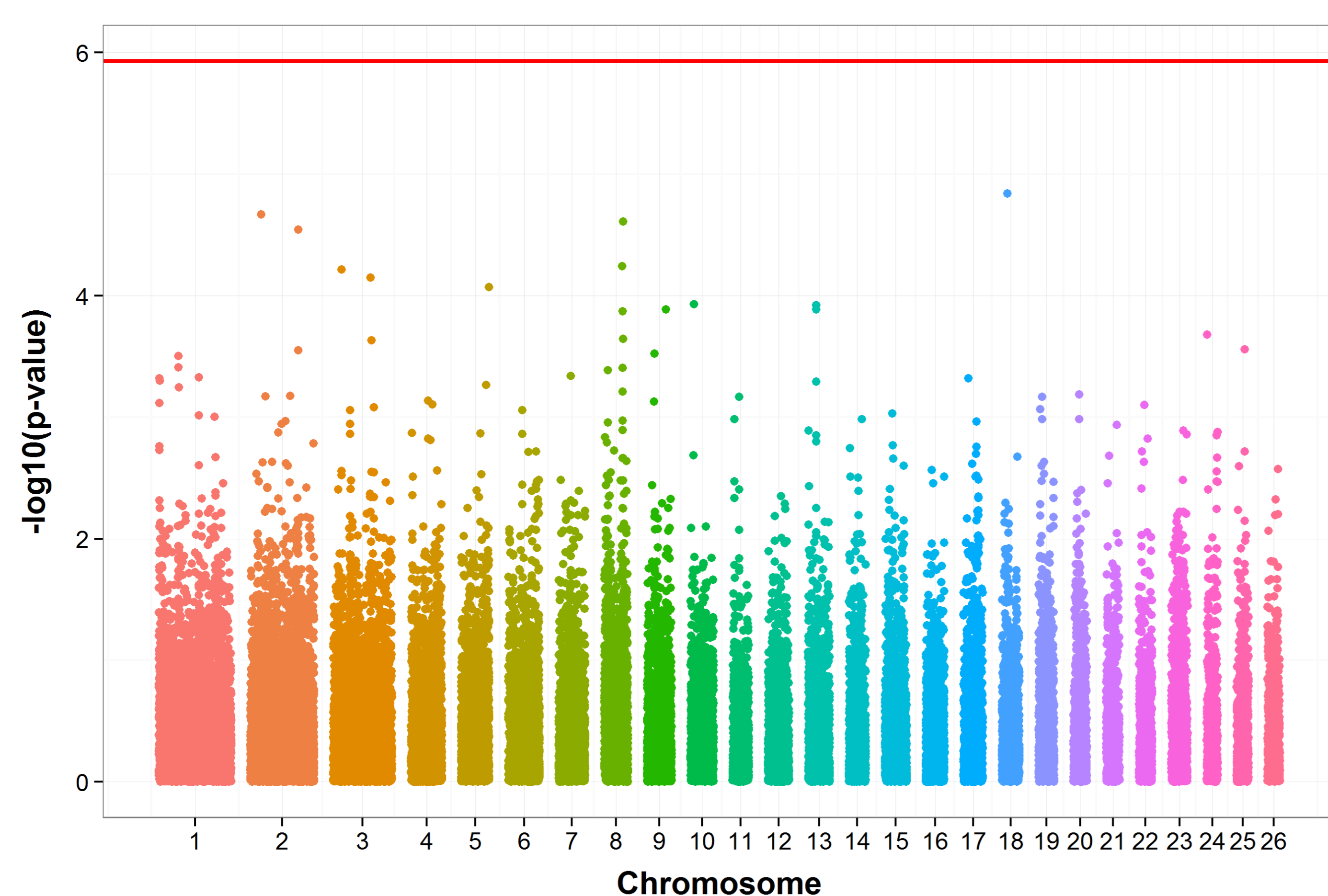


Figure 1: Manhattan plot showing each chromosome coloured differently and the significance of the association between footrot and SNPs. Higher points (above around 4) are significant at the chromosome level. Wider bars indicate that there are more SNPs, (which in turn, is related to the length of the chromosome).



Significant SNPs were located on Chromosomes 8 and 18, with suggestive SNPs on Chromosome 2.

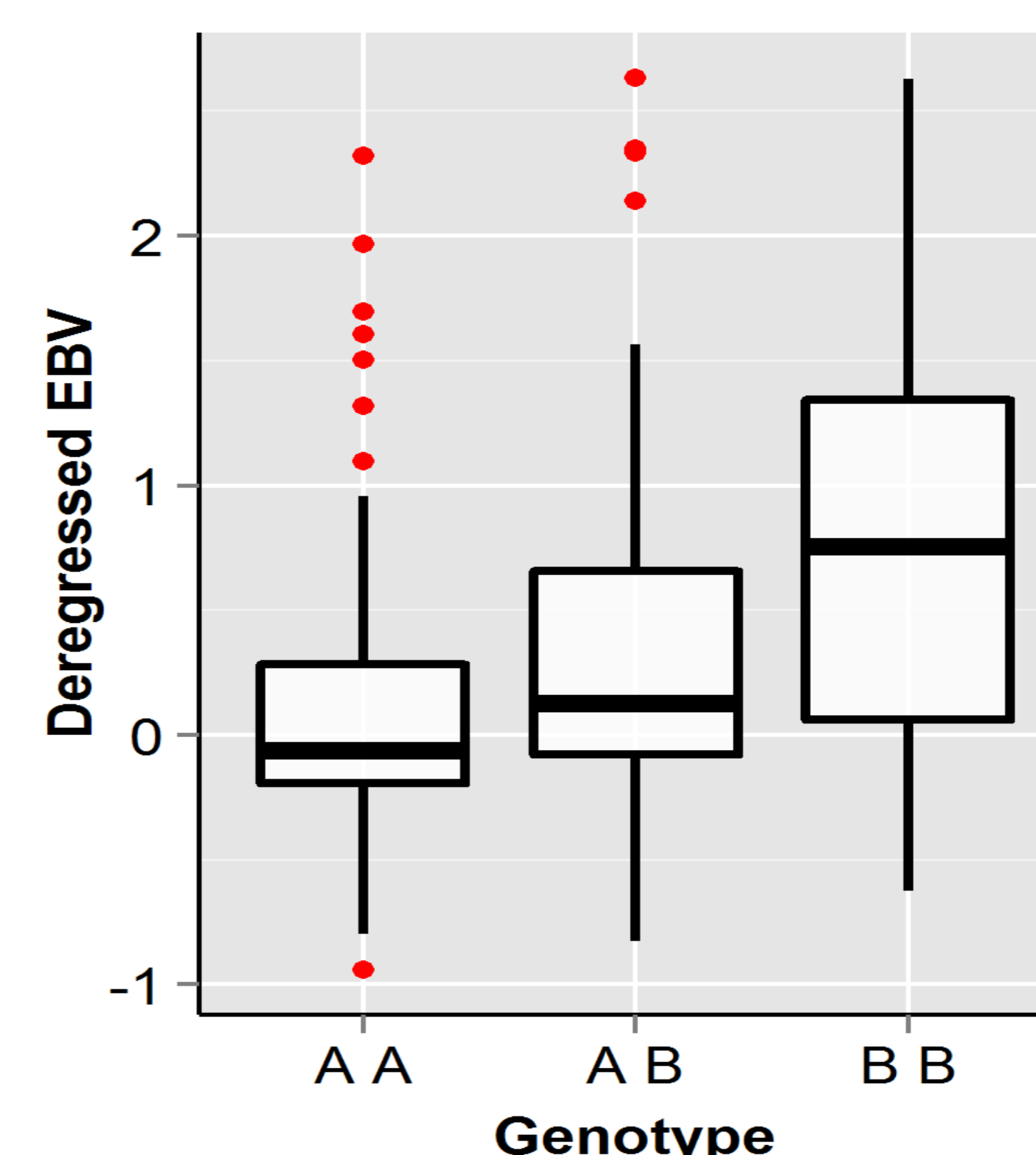


Figure 2: Example of SNP OAR2_198741802.1. This SNP is associated with a gene related to protein coding. Animals with genotype BB have significantly higher (poorer) footrot scores compared to genotype AA or AB. (The interpretation is that 50% of the animals are within the box, with the thicker, horizontal line being the median value. The vertical lines indicate the range outside the middle 50%. Red dots are individual animals with extreme scores).

Conclusions

There exist some genomic regions that confer greater footrot susceptibility

This is the first study to associate genomic information to footrot.

Results will aid genomic selection and health screening in sheep.

Acknowledgements

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¹ Segura, V., B.J. Vilhjálmsson, A. Platt, A. Korte, Ü. Seren, Q. Long, and M. Nordborg. 2012. *Nat. Genet.* 44:825–30).