



Conclusions

- eQTL analysis identified 298 SNVs associated with altered hepatic expression of 19 innate immune genes in pigs.
- 28 eQTLs were found to be associated with infectious diseases in pigs.
 - Both increased and decreased hepatic expression of innate immune genes was associated with different infectious diseases.
 - These alleles are potential indicators of infectious disease resistance in pigs, and warrant further investigation.

Summary

- There is a substantial degree of variation in the collagenous lectins of livestock, and a larger group of innate immune genes in pigs.
- *In silico* predictive software can help identify potentially interesting variants.
- Some of the identified variants may be useful inclusions on breeding panels, and may contribute to the understanding of infectious disease pathophysiology.

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