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.

Future directions

- Variant validation
  - Biochemical assays
  - NGS techniques
  - Genotyping
- Pathogenesis
  - Role of C

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