



Conclusions

A substantial amount of genetic variation was discovered within and surrounding the collagenous lectin genes of horses and cattle:

- 4559 SNVs in horses were identified, 74 % of which were not present in dbSNP.
- 5439 SNVs in cattle were identified, however, the better characterization of the genome in this species meant only 122 were novel.

Conclusions

- Variation tended to be lowest in coding regions, but this was not significantly different from the distant upstream (5 - 50 kb), upstream, introns, or downstream regions for either species.
- The *FCN* genes of both cattle and horses had a significantly higher variant density as compared to the remaining gene targets. Whether this represents increased evolutionary need for variation in the FCN proteins is unknown.
- A coding mutation similar to a known deleterious mutation in humans and pigs was found in equine *MBL1*.

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