

Genome wide association mapping in multiple EU cow populations

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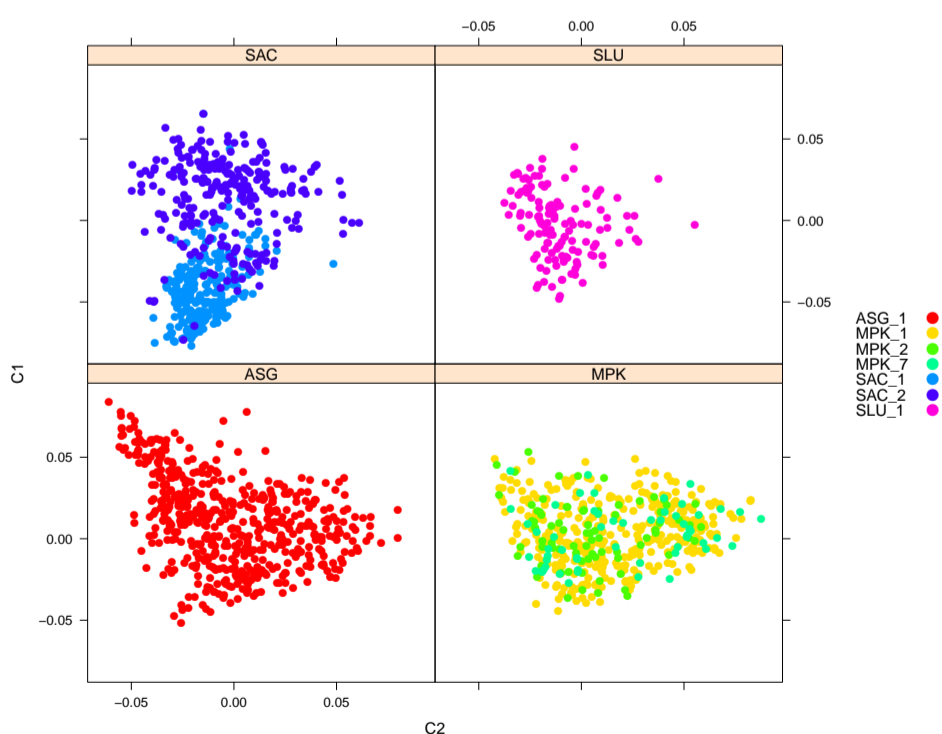
Summary

RobustMilk aims to "develop new useful and practical technologies to allow dairy farmers and the dairy industry to refocus their selection decisions to include additional traits such as milk quality and dairy cow robustness". As part of the project data and DNA samples were combined from 2,000 cows in research herds in 4 different countries. Combining these datasets for genome wide association analysis was investigated and associations were estimated along the genome using 50k genotypes for production and robustness traits.

Question

Does the combination of data collected over 3 decades in multiple cow populations from 4 different European countries increase power of association analysis, or does it just add noise ?

Cow populations

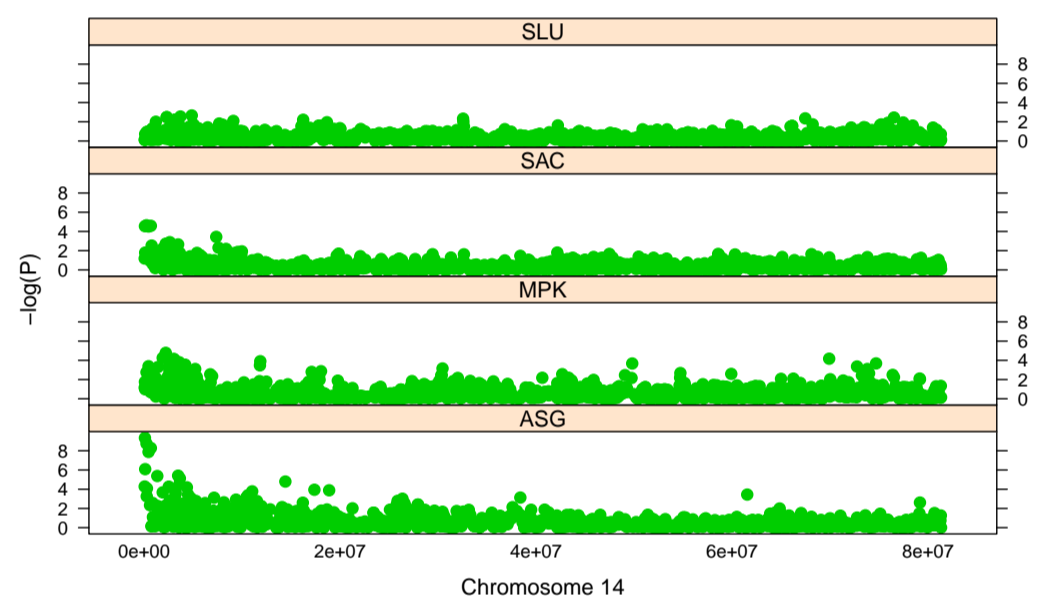


- 1,933 cows born 1980-2007
- 7 Herds in 4 Countries
- 72,008 test-day Records

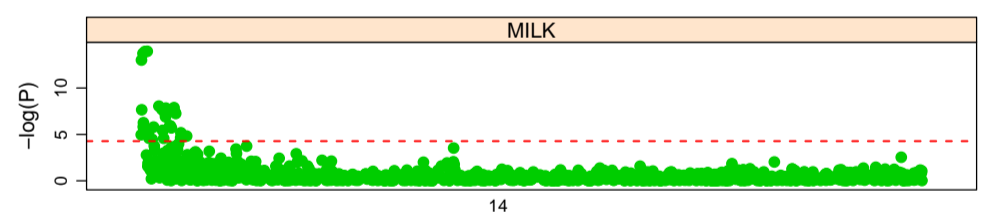
Conclusions

- Combination of data from varied sources increases power to detect genes
- Combining populations is an important approach to investigate cow specific traits

Single population results



Across population results



Whole Genome Association analyses

