

# Genome-wide association study for daily milk yield in Istrian dairy sheep



M. Špehar<sup>1</sup>, J. Ramljak<sup>2</sup>, A. Kasap<sup>2</sup>

<sup>1</sup>Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia, e-mail: [marija.spehar@hapih.hr](mailto:marija.spehar@hapih.hr)

<sup>2</sup>University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia

## AIM

Identifying associations between genetic markers and traits of economic importance provides practical benefits for the dairy sheep industry facilitating discovery of the underlying genes and mutations

The study aimed to identify genomic regions associated with daily milk yield (DMY)



## MATERIAL

- Istrian breed
- 38,293 test-day records
- 719 genotyped animals (Ovine SNP50 BeadChip)
- QC: SNP and individual genotype call rate > 0.9, MAF > 0.05, autosomal SNPs
- 693 animals and 43,788 SNPs

## METHODS

- Estimation of DMV BVs  
Single step genomic BLUP
- GWAS analysis  
R package 'rrBLUP'
- Four models
  1. without controlling for population structure (PS) or family relatedness
  2. controlling for PS effect
  3. controlling for relatedness
  4. controlling for both PS and relatedness

## RESULTS

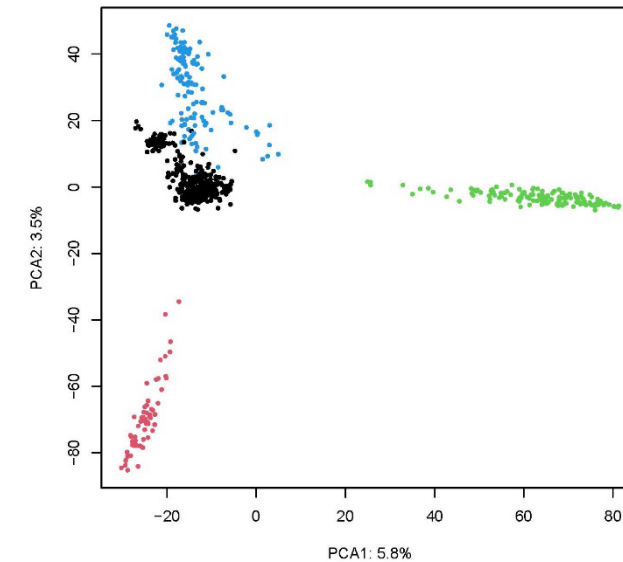


Figure 1. First and second principal component analysis

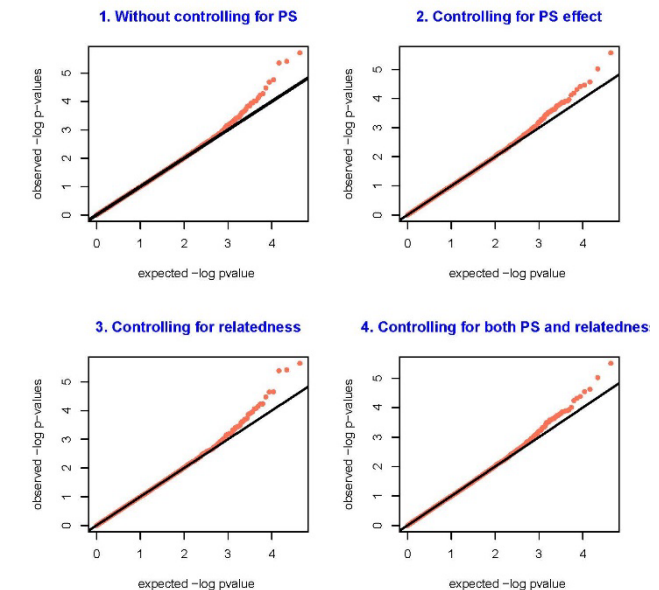


Figure 2. Q-Q plot of the different models for DMV

## RESULTS cont.

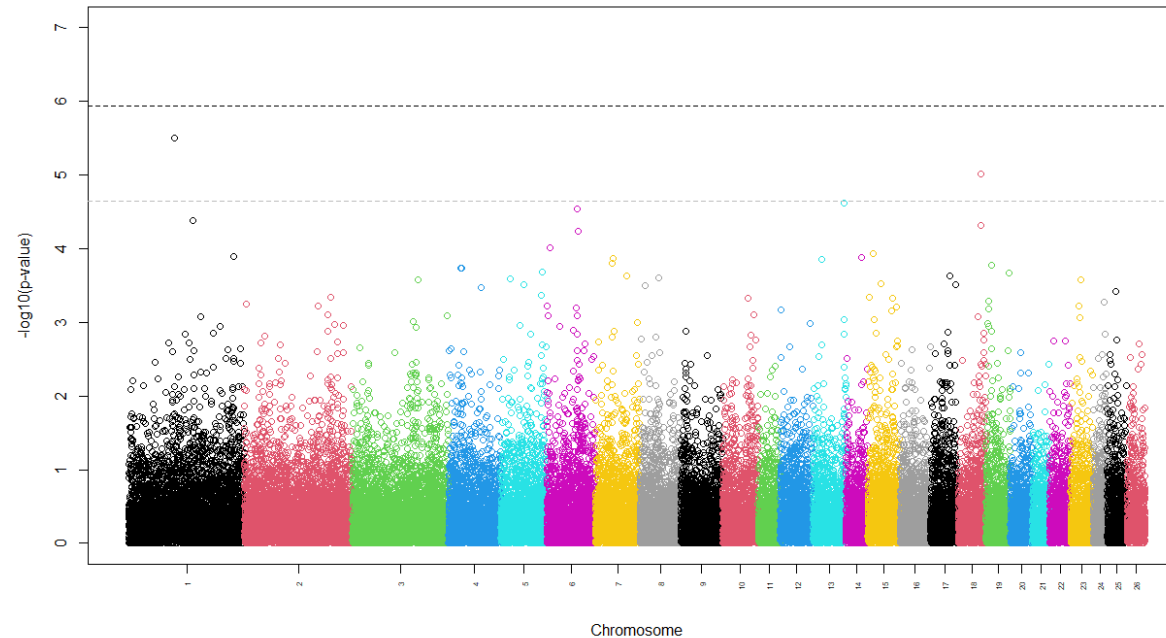


Figure 3. Manhattan plot for DMY (4<sup>th</sup> model)

## CONCLUSION

None of the markers showed significant effect (genome-wide significance threshold) based on the most appropriate model which accounts for population structure and relatedness

Three markers were significant on the suggestive level (chromosomes 1, 13, and 18)