

# GENOME-WIDE ASSOCIATION STUDIES OF MILK YIELD AND QUALITY TRAITS IN THE ASSAF SHEEP BREED

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## Introduction

Knowledge of genetic markers associated with milk production traits provides an opportunity to increase the rate of genetic gain using genomic or marker-assisted selection. Within this context, a genome-wide association study (GWAS) using high-density genotyping was carried out to contribute to the knowledge of the genetic basis of milk production traits in the Assaf sheep breed.

## Material and Methods

### Phenotypes

- ✓ 6173 records from 1894 Assaf ewes (Age:2-7 y; 3 flocks) with at least 3 test day records were used for fat (FP), protein (PP), lactose (LP) and total solid percentage (TSP). For milk yield (MY), 2697 records were obtained from 1001 ewes
- ✓ Corrected phenotype values (Repeatability Mixed Model) for the total population for each trait were used for GWAS:

$$y^j(\text{trait}) = \text{Number of lambs born} + \text{HTD} + b(\text{Dim}) + b(\text{Age}) + \text{ewe} + e$$

### Genotypes and GWAS

- ✓ 192 Assaf ewes → *Ovine AgResearch HD (680K)*
- ✓ Plink1.9 and GCTA softwares (FDR correction)
- ✓ Annotation of genes was based on sheep genome assembly Oar\_rambouillet 1.0 (250 kb region on both sides of the significant SNPs)

### Validation

- ✓ KASP genotyping for the SNPs rs419686662 (PP; n = 1839) and rs411200126 (MY; n=1001)
  - ✓ Association analysis (Repeatability Mixed Model; Bonferroni's correction):
- $$y^j(\text{trait}) = \text{SNP} + \text{Number of lambs born} + \text{HTD} + b(\text{Dim}) + b(\text{Age}) + \text{ewe} + e$$

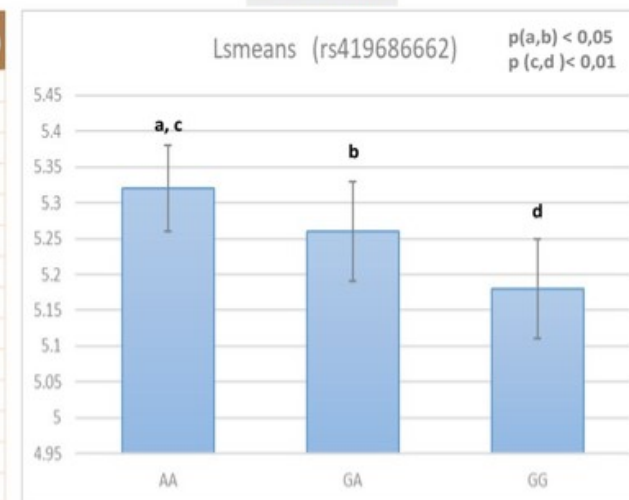
## Results

- ✓ No genome-wide significant results.
- ✓ Two, 6, 3, 15, and 25 significant associated SNPs were found for MY, PP, FP, LP and TSP traits, respectively, at chromosome level (FDR p < 0.1).
- ✓ Validation analysis in the total population confirmed the SNP rs419686662 as markers for PP trait (p < 0.001)

### GWAS

Phenotypes	Significant SNPs	Chromosome	Genes (0.5 Mb)
MY	2	13	<i>CDNF</i>
			<i>HSPA14</i>
			<i>SUV39H2</i>
PP	6	6	<i>MAD2L1</i>
			<i>FGFR2</i>
FP	3	14	---
			---
LP	15	13	<i>FOXE1</i>
			<i>RALGAPB</i>
			<i>SLC32A1</i>
			<i>ESM1</i>
			<i>GLP1R</i>
TSP	25	11	---
			<i>ESM1</i>
			<i>GLP1R</i>

### Validation



## Conclusion

The SNP rs419686662 was involved in the phenotypic variation of the PP trait. This SNP is located close to the *FGFR2* gene that is related to mammary gland development.

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