A GENE NETWORK DRIVING GENETIC VARIATION IN SHEEP CHEESE QUALITY

Marina, H[1,2]., Gutiérrez-Gil, B[1]., Esteban-Blanco, C[1]., Pelayo, R[1]., Arranz, J.J[1]., Reverter, A[2].

[1]Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, Campus de Vegazana s/n, León 24071, España;

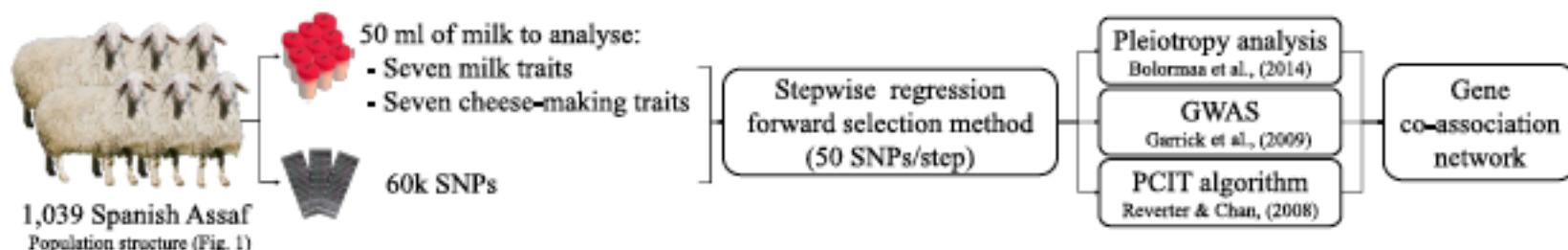[2]CSIRO Agriculture & Food, St Lucia, QLD 4067, Australia; hmarg@unileon.es

INTRODUCTION

Spain holds one of the highest dairy sheep livestock counts in Europe. Almost the entire production of sheep milk is used for cheesemaking. For that reason, the sheep milk coagulation properties are economically important for the dairy industry. Complex traits, as milk and cheese-making characters, are typically influenced by many genomic regions.

OBJETIVE

The study aims to identify candidate genes and their potential regulators related to 14 milk and cheese-making traits, and develop a low density panel of markers that could be used to predict the individual's genetic potential for cheese-making efficiency.

METHODS

1,039 Spanish Assaf
Population structure (Fig. 1)

50 ml of milk to analyse:
- Seven milk traits
- Seven cheese-making traits

60k SNPs

Stepwise regression forward selection method (50 SNPs/step)

Pleiotropy analysis
Bolormaa et al., (2014)

GWAS
Garrick et al., (2009)

PCIT algorithm
Reverter & Chan, (2008)

Gene co-association network

RESULTS

A total of 12,426 SNPs were located in the confidence interval from a gene. The first subset of genes that could explain more than 95% of the genetic variance was composed by 550 genes. After filtering the genes by the number of significant co-association with the transcription and co-transcription factors, the gene co-association network was composed of 374 genes (Fig. 2). This gene-set explain the 76% of the average of the additive genetic variance considering the 14 traits, whereas a random group of this size only explain 15% of the variance.
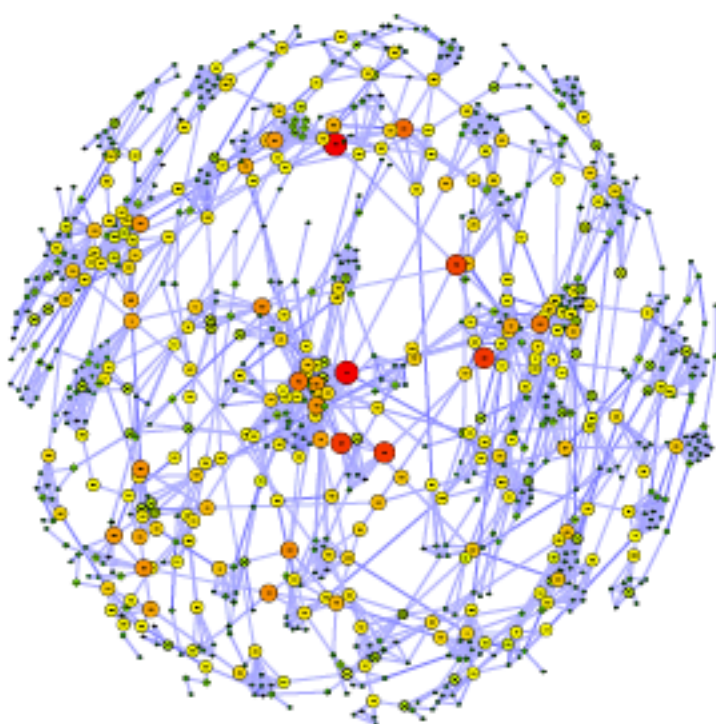

Fig. 1. Pedigromics. This figure shows the genetic relationship (>0.2) among the individuals included in this study. The colour and the size of the nodes are based on the betweenness coefficient (Reverter, 2019).
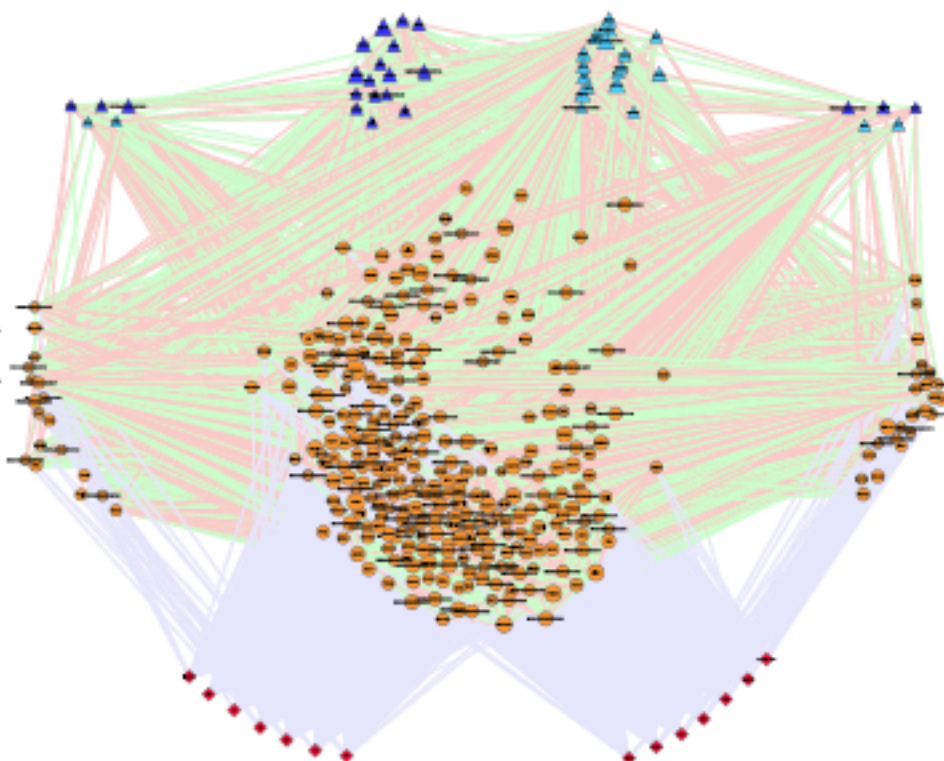
Fig. 2. Co-association network selected by the step-wise procedure. This network includes all the transcription (TF: depicted in dark blue) and co-transcription factors (CF: depicted in light blue) and the rest of genes (depicted in orange), together with the fourteen traits analysed (depicted in red). The edges represent the significant co-association gene-gene (positive or negative) and the significant association gene-trait.

CONCLUSION

Combining the GWAS with the stepwise approach, the PCIT algorithm and the Pleiotropy analysis has allowed to identify a significantly co-associated gene network, composed by potential functional candidate genes and regulators related to several biological processes with a possible influence on the milking synthesis and cheese-making efficiency, which could be used in future programs of genomic selection.

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