Genome-wide association study of residual feed intake in Hereford cattle

Peraza P , Pravia M I , Navajas E A
pperaza@inia.org.uy

Introduction

- Residual Feed Intake (RFI) is a commonly used measure of feed efficiency.
- RFI is include in the breeding program of the Hereford breed in Uruguay.

OBJECTIVE: investigating the genetic background of RFI by genome-wide association studies (GWAS) based on a binational reference population.

Materials and methods

Phenotypes: postweaning RFI 2731 Hereford bulls and steers from Canada and Uruguay

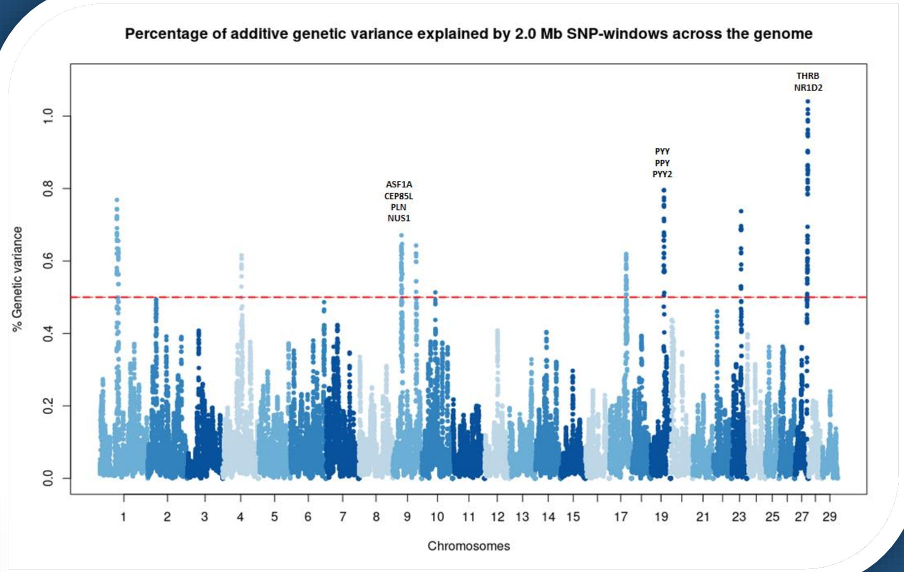
Pedigree: 3 generations of 7068 animals
Genomic: 2603 animals genotyped and imputed to an Illumina 50k array
Number of SNPs: 52.890

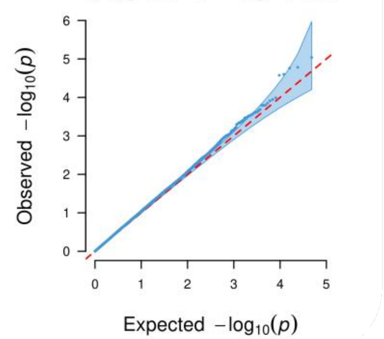
2 approximations used to identify associated genomic regions:
Windows variance and **SNP effects**

Results

Several candidate regions were identified across the genome.

In **BTA9, BTA19, and BTA27** significant genes in relation to RFI trait were identified, such as CEP85L, ASF1A,PLN and NUS1, PYY, PPY and PYY2, and THRB and NR1D2.





- Genomic regions identified harbor genes mostly related to **appetite** (GO:0032098), **feeding behavior** (GO:0007631) and **digestion** (GO:0007586).
- Genes identified with top SNPs effect distribution were enriched in 2 pathways:
  Thyroid hormone (bta04919) and **Cardiac muscle contractions** (bta04260), leading to hypothesis of lipogenesis and lipolysis and cardiovascular overwork.

Conclusions

Genes and metabolic pathways associated with RFI were identified, contributing to a better understanding of the genetic background of feed efficiency with potential benefits for genomic selection.