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Searching for genomic regions associated with conformation traits in the Pura Raza Español horse



N. Laseca^{1*}, C. Ziadi¹, D.I. Perdomo-González², M. Valera², P. Azor³, S. Demyda-Peyrás¹, A. Molina¹



¹Department of Genetics, University of Córdoba, Campus Rabanales, CN-IV KM396, 14014, Córdoba, Spain; ²Department of Agronomy ETSIA, University of Seville, Seville, Spain; ³Royal National Association of Spanish Horse Breeders, ANCCE, Sevilla, Spain. *ge2lagan@uco.com



INTRODUCTION

Conformation is of great importance in equine breeds like the Pura Raza Español (PRE) horse, not only because it reflects the horse's appearance, but also for it's relationship with functionality, especially the classical dressage in this breed.

OBIETIVE

The aim of this study was to determine genomic regions associated with conformation traits and to identify markers associated with 5 zoometric measurements in the PRE horse.

MATERIALS AND METHODS

PHENOTYPES, PEDIGREE AND GENOMIC DATA

- 41.889 PRE animals in the pedigree including ancestors up to 5 generations.
- 2,916 PRE horses were genotyped with the GGP Equine Array V5.
- 61,271 SNPs were used.



- Zoometric records of 7,152 animals from 1,615 studs from 6 countries. Conformation traits:
 - scapular-ischial length (SiL)
 - length of back (LB)

bone (PACB)

- * dorso-sternal diameter (DsD)
- * thoracic perimeter (TP) perimeter of anterior cannon



ASSOCIATION ANALYSIS

Animal single-step REML mixed model

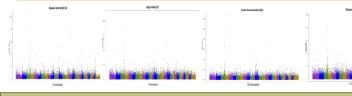
y = Xb + Za + e

BLUPF90+ Software

- y. conformation traits; b: fixed effects: sex, age, coat colour and country of origin of the animal; a: random additive genetic effect; X and Z: incidence matrices relating observations to fixed and random additive genetic effects, respectively; e: residual term.
- ssGREML: pedigree-genomic relationship matrix H

RESULTS

Our results showed 562, 27, 49, 168, and 70 significant SNPs associated with SiL, LB, DsD, TP and PACB, respectively (p-value < 10-6). Furthermore, 17 common significant markers were found for all traits, of which 14 SNPs were located on chromosome 3 and 3 SNPs on chromosome 17.



CONCLUSIONS

In conclusion, although more studies are required to increase the number of animals and the number of zoometric measurements analyzed, our findings indicated that genomic markers associated with conformational traits are in regions on chromosomes 3 and 17.

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