

Impact of the inclusion of metafounders in the genetic evaluation of morphology in the Pura Raza Español horse

C. Ziadi^{1*}, M. Valera², D. I. Perdomo-González², I. Cervantes³, P. Azor⁴, A. Molina¹

¹Departamento de Genética, Universidad de Córdoba, Edificio Gregor Mendel. Campus de Rabanales. Ctra, Madrid-Cádiz, km 396, 14071 Córdoba.

²Departamento de Agronomía, Escuela Técnica Superior de Ingeniería Agromónica, Universidad de Sevilla, 41013 Sevilla.

³Departamento de Producción Animal, Universidad Complutense de Madrid. Avda. Puerta de Hierro, s/n. Ciudad Universitaria, 28040 Madrid.

⁴Real Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE). Cam. Cortijo del Cuarto, 41014 Sevilla

* Corresponding autor: z72zizic@uco.es

Summary

The genomic era introduced new opportunities to assess relationships between individuals. However, when pedigree and genomic information are used simultaneously, which is the case of single-step genomic REML (ssGREML), defining the genetic base is still a challenge. One alternative to overcome this challenge is to use metafounders, which are pseudo-individuals that describe the genetic relationship between the base population individuals.

The purpose of this study was to evaluate the impact of metafounders on the estimation of breeding values for morphology traits under single-step GREML (ssGREML) in the PRE population.

The dataset consisted of conformation records of 7152 animals and 41,888 animals in the pedigree, provided by the Royal National Association of Spanish Horse Breeders (ANCCE). A total of 2916 animals were genotyped with 61,271 SNPs and included in the analysis. Measurements from five different zoometric traits were analyzed: scapular-ischial length (SiL), length of back (LB), dorso-sternal diameter (DsD), thoracic perimeter (TP), and perimeter of anterior cannon bone (PACB). Three different approaches were studied: pedigree-based model (REML), ssGREML, and ssGREML with metafounders (ssGREMLm). In ssGREMLm, a total of twelve different metafounders based on generation intervals were included for the animals with unknown parents. For the three models, the fixed effects of sex, age, genetic origin and geographical area were considered. All analyses were performed using an animal multivariate model with the GIBBSF90plus v.3.22 software.

Except for LB and TP, estimates of heritabilities were similar for all traits between REML and ssGREML approaches and their values ranged from 0.32 ± 0.028 for DsD to 0.63 ± 0.031 for SiL. When including metafounders, h^2 estimates were greater for all traits than in the other two methodologies and they oscillated between 0.38 ± 0.036 for PACB and 0.69 ± 0.028 for SiL. The addition of metafounders increased heritability for the PRE population because of improved genetic relationships.

The gain in reliability for ssGREML over REML varied between 1.68% for LB and 5.18% for PACB. As expected, the genomic model with metafounders had the greater additional gain over REML (53.05% for LB to 105.62% for PACB) and ssGREML (50.53% for LB to 95.5% for PACB). Our results show the potential of using metafounders to increase reliability of EBVs and GEBVs, and therefore, the rate of genetic gain, even in breeds like the PRE horse, with a deep and very reliable pedigree.

Keywords: conformation, unknown parent groups, metafounders, reliability, horse.