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Unraveling the genomic architecture of hock conformation defects in Pura Raza Española horses

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Abstract

Conformational traits define a horse's shape and morphology, heavily influencing its functionality, sport performance, health, and appearance, making conformation a critical selection criterion in horse breeding. However, the genomic basis of conformational defects, specifically those affecting the hock, remains largely unexplored. This research aimed to identify the genomic regions associated with hock defects using a large cohort of Pura Raza Española (PRE) horses. A total of 58,930 horses were evaluated for hock angle, with 4,122 genotyped on high- or medium-density arrays. For this purpose, weighed single-step genomic REML analysis methodology was used with the hock evaluation assessed as a continuous variable (lateral view hock defect, LVHD, and rear-view hock defect, RVHD) and divided into two different opposite defects: closed and open and convergent and divergent, respectively (multinomial approach). Some deviation from the optimum hock angle was observed in 49,386 horses, of which 10.1% were evaluated as having a severe or very severe defect. The most prevalent hock defect in the PRE population evaluated was open hock (6.67% considered severe or very severe), while the least prevalent was closed hock (0.2%). The estimated heritability for the continuously evaluated traits was 0.18 for LVHD and 0.25 for RVHD, while the estimated heritability of the traits evaluated with a multinomial approach ranged from 0.25 to 0.42 for open and divergent defects, respectively. A genome-wide association study revealed eight genomic regions associated with hock defects. In these, 17 genes related to musculoskeletal diseases, bone malformations, joint disorders, cartilage defects, or bone fragility were identified. These findings could support the development of selective breeding strategies aimed at reducing conformational defects in the hock of the PRE and related breeds. Furthermore, they provide insight into the genetic and molecular mechanisms involved in the occurrence of conformation defects. However, further studies are needed to shed further light on these conformational defects in the equine species.

Lay Summary

Conformational traits are critical in horse breeding due to their impact on performance, health, and aesthetics. This study investigates the genomic underlying of equine conformation traits, focusing on hock defects in Pura Raza Española horses. For this purpose, a genome-wide association analysis was performed to identify genomic regions associated with hock defects. The findings could contribute to the development of selective breeding strategies aimed at enhancing horse welfare and functionality, as well as potentially reducing the prevalence of conformational defects. In addition, they advance the understanding of genetic factors influencing the musculoskeletal health of horses.

Keywords morphological defects, limbs, GWAS, wssGREML, equine

Abbreviations: ANCCE, Real Asociación Nacional de Criadores de Caballos de Pura Raza Española; Chr, chromosome; CR, call-rate; DAVID, Database for Annotation Visualization and Integrated Discovery software; ECA, *Equus caballus* chromosomes; GEBVs, genomic estimated breeding values; GWAS, genome-wide association study; h^2, heritability; LVHD, lateral view hock defect; OA, osteoarthritis; PRE, Pura Raza Española; QC, quality control; RVHD, rear view hock defect; ssGBLUP, single-step genomic best linear unbiased prediction; ssGREML, single-step genomic restricted maximum likelihood; v.e., variance explained; wssGBLUP, weighted single-step genomic best linear unbiased prediction; wssGREML, weighted single-step genomic restricted maximum likelihood

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Introduction

Conformation is crucial, not only for the animal's appearance and locomotor health but also for its functionality and performance in sport disciplines and fieldwork (Love et al 2006; Ducro et al 2009; Jönsson et al 2014; Sánchez-Guerrero et al 2017; Ripollés-Lobo et al 2023a). Conformational traits, namely external morphological traits, are routinely evaluated during the basic breeding assessment, representing one of the main selection criteria in horse breeding (Sánchez et al 2013; Gmel et al 2018; Viklund and Eriksson 2018). In particular, the hock is a key joint in equine biomechanics, playing a crucial role in mobility, gait quality, endurance, performance, and ultimately in the animal's predisposition to injuries (Welsh et al 2013; Hilla and Distl 2014). This highlights the importance of accurately examining the musculoskeletal characteristics in horse populations and their relationship to functionality, a topic which is arousing increasing interest in most horse breeds (Solé et al 2013; Welsh et al 2013; Kristjansson et al 2016; Gmel et al 2022).

In general, limb diseases and conformation defects appear to be relatively common in horses and constitute one of the main hereditary disorders that weakens performance (Axelsson et al 2001; Love et al 2006; Stock and Distl 2006; Ripollés-Lobo et al 2023b; Ripollés-Lobo et al 2024; Van Cauter et al 2024), consequently affecting stud profitability. These defects are often caused by underlying complex genetic factors, which may be breed-specific or common in certain types of horses (Gmel et al 2019; Ripollés-Lobo et al 2023a). In particular, defects in the hock can manifest in various forms, including angular deformities, alignment issues, and degenerative conditions. Not only are these conformational defects of aesthetic concern, but they also affect the animal's quality of life, limit its athletic ability to perform in various equestrian disciplines, and increase the risk of injury (Van Weeren and Crevier-Denoix 2006; Murray et al 2010).

In the case of the Pura Raza Española (PRE), a breed highly valued for its beauty, agility, and versatility where conformation and aesthetics are key elements, the presence of defects in the hock can have a considerable impact on the animal's market value and its viability in competitions. The PRE horse is a native breed with a current census of 290,407 active horses in over 71 different countries (MAPA 2025). This breed is managed by the Real Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE), which oversees management of the studbook (created in 1912), as well as the breeding program.

Over the last decade, research in equine genomics has advanced significantly, providing powerful tools to understand the inheritance of complex traits. The use of advanced genomic techniques, such as sequencing and genotyping, has revolutionized our understanding of genetic variability in equine breeds, as well as heritable variation in complex traits (Farries et al 2019). In particular, genome-wide association studies (GWAS) have enabled us to identify markers and genomic regions associated with phenotypic traits of interest. The number of GWAS studies focused on conformation traits has been increasing steadily (Frischknecht et al 2016; Sevane et al 2017; Gmel et al 2019; Rosengren et al 2021; Gmel et al 2023; Laseca et al 2025), with traits such as body size and withers height being predominant (Makvandi-Nejad et al 2012; Signer-Hasler et al 2012; Tetens et al 2013; Frischknecht et al 2015; Reich et al 2024). However, to date, there has been little research in the genomic study of conformational defects in limbs. The aim of this study was, therefore, to identify genomic regions associated with hock defects in PRE horses through whole-genome studies. The defects evaluated were studied as a continuous variable (lateral view hock defect [LVHD] and rear-view hock defect [RVHD]) and as independent multinomial variables (closed, open, convergent, and divergent).

Material and methods

Animals and description of traits

A total of 58,930 horses were evaluated for both lateral and rear views of the hock angle during the mandatory PRE morphological assessment, which takes place once in a horse's life at an average age of 4.8 yr before it is officially registered in the PRE studbook. The evaluations were conducted by 12 specially trained veterinary technicians, following the procedures outlined by Sánchez-Guerrero et al (2016), using a linear morphological classification system to assess the hock angle in both views (Ripollés-Lobo et al 2023a).

Regarding the lateral view, defects are defined as closed hock defect, when the horse's leg forms a very closed angle with the shank, and open hock defect, when the horse's leg forms a very open angle with the shank. In contrast, defects related to the direction of the hock from the rear view are defined as convergent hock defects, when a horse's hocks slant inward from the line of aplomb, or divergent hock defects, when they slant outward from the line of aplomb (Ripollés-Lobo et al 2023a) (Figure S1, see online supplementary material for a color version of this figure).

The traits were scored on a nine-level scale ranging from −4 to 4, where 0 indicates the absence of any defect. According to the official ANCCE criteria (ANCCE 2025), any deviation from 0 is considered a conformational defect, with the severity increasing toward the extremes of the scale. To ensure clarity, the severity of these defects is categorized as follows: slight defects are represented by levels −1 and −2 (closed/convergent) and level 1 (open/divergent); severe defects correspond to level −3 (closed/convergent) and level 2 (open/divergent); and very severe defects are indicated by level −4 (closed/convergent) and levels 3 and 4 (open/divergent). This non-symmetric scale reflects the official scoring system used in the PRE studbook for assessing the basic aptitude of breeding horses.

Each hock angle trait was evaluated using two approaches. First, the traits were analyzed as a continuous variable on the observed scale, with scores ranging from −4 to 4 (nine levels), for both lateral view hock defect (LVHD) and rear-view hock defect (RVHD). Second, the hock deviations were modeled by separating the two defect types: LVHD was divided into closed and open deviations, while RVHD was divided into convergent and divergent deviations. Each of these four traits was treated as an independent multinomial variable on an underlying scale, allowing the severity of deviations in each specific direction to be captured. Within this framework, scores were grouped into two ranges (−4 to 0 and 0 to 4) for each defect type, with 0 indicating the absence of deviation. Horses showing one type of defect were considered unaffected for the opposite deviation.

Together, these two approaches provided a comprehensive assessment of hock angle conformation, accounting for both the severity and direction of deviations.

Prevalences were calculated as the percentage of affected animals for each degree relative to the total population evaluated (58,930), including unaffected individuals.

Genotyping

The most representative horses from the population were selected for genotyping based on the low average relatedness between individuals. These animals came from more than 600 different studs, avoiding direct relatives (eg siblings, parent–offspring) to reduce close relatedness. Although no strict numerical threshold was applied, pedigree information was used to prioritize animals with lower average relatedness while also ensuring that the morphological variability of the PRE was represented. Consequently, the average pedigree-based inbreeding and coancestry for this genotyped subset were 0.07 and 0.08, respectively.

Genomic DNA was isolated from blood or hair samples using a DNeasy blood & tissue extraction kit (Qiagen). We used the Affymetrix Axiom Equine 670 K high-density SNP array (Thermofisher) to genotype 2,359 horses, and genotypes were analyzed with the Axiom Analysis Suite 5.0 software following the "Best genotyping practices workflow" with the default parameters (dish quality control [QC] $>$ 0.82 and call-rate [CR] $>$ 0.95). And we used the medium density GGP Equine 70 K array V5 (Neogen) to genotype 1,763 horses. The genotypes were analyzed with a bioinformatics pipeline with GenomeStudio 2.0.5 software, and QC (CR $>$ 0.95) was performed with PLINK v1.9 software (Purcell et al 2007). We then combined the data from both technologies. We retained only the SNPs common to both arrays to have the entire population genotyped with the same number of markers and performed QC of the combined data by applying the filters of CR $>$ 0.95 and minor allele frequencies $>$ 0.01 with PLINK v1.9 software. The final set of markers was 60,136 SNPs distributed over all 32 *Equus caballus* (ECA) chromosomes.

Weighted single-step GREML analysis

In this study, we employed the single-step genomic restricted maximum likelihood (ssGREML) approach to analyze hock defect traits. To analyze LVHD, RVHD, closed, open, convergent and divergent hock traits, an univariate model was employed, following Laseca et al (2024):

$$y = Xb + Za + e \quad (1)$$

where y is the vector of phenotypic observations for the corresponding trait; b is the vector of fixed effects, including sex (male and female), age assessment (young, 3.5 to $<$5 yr old; adult, $\geq$5 yr old), geographical area (Spain, rest of Europe, North America and Mexico, and South and Central America), stud size ($<$3 foals/yr; 3–9 foals/yr; $>$9 foals/yr), proportionality index (height at the withers*100/shoulder-ischial length; $<$98, 98–100, $>$100, and unknown), and inbreeding (calculated using the Endog 4.8 software (Gutiérrez and Goyache 2005); $<$3.125%, 3.125%–6.25%, 6.25%–12.5%, $>$12.5%). a is the vector of random additive genetic effects; e is the vector of random residuals; and X and Z are the incidence matrices of b and a, respectively.

It was assumed that $a \sim N(0, H\sigma_a^2)$ for all traits, $e \sim N(0, I\sigma_e^2)$ for continuous LVHD and RVHD traits, and $e \sim N(0, 1)$ for multinomial closed, open, convergent and divergent defects traits, where σ_a^2 and σ_e^2 represent the additive genetic and residual variances, respectively. The matrix H was constructed following the approach of Aguilar et al (2010), which integrates the numerator relationship matrix (A) with the genomic relationship matrix (G). The inverse of H matrix is expressed as:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

where A represents the pedigree-based relationship matrix for all animals. The renumf90 software (blupf90 suite programs) retained 111,241 informative individuals from the complete PRE studbook pedigree (398,866 horses) to obtain the relationship matrix—specifically, those with phenotypic records (or genotypes) and all their known ancestors (up to 25 generations); A_{22} denotes the pedigree-based relationship matrix for genotyped animals, while G represents the genomic relationship matrix for genotyped animals, constructed according to the method of VanRaden (2008) as follows:

$$G = \frac{ZZ'}{\sum_{i=1}^{n} 2p_i(1-p_i)}$$

where Z represents the centered matrix of SNP genotypes; n represents the total number of SNPs; and p_i denotes the minor allele frequency of the i-th SNP.

Variance components and genomic estimated breeding values (GEBVs) for the hock defect traits were estimated following the approach described by Laseca et al (2025). The Bayesian inference methodology was applied using the Gibbs sampling algorithm in the GIBBSF90+ software (Lourenco et al 2022). Chains of 200,000 samples were used with a burn-in period of 40,000. One sample per 100 was saved to avoid high correlations between consecutive samples. To calculate posterior means and high posterior density intervals, and to check convergence with the Geweke test, a post-Gibbs analysis was performed using the POSTGIBBSf90 software (Tsuruta and Misztal 2006).

The model previously described (equation 1) was likewise employed for weighted single-step genomic REML (WssGREML); however, in this case, the G matrix was constructed using a different approach. Estimates of SNP effects were derived by back-solving GEBVs from ssGREML, following the procedure outlined by Wang et al (2012):

$$\hat{a} = DZ'(ZDZ')^{-1}\hat{u}_g$$

where $\hat{a}$ represents the vector of SNP effects, D represents a diagonal matrix of weights (equal to the identity matrix in the case of ssGREML), Z represents the centered matrix of SNP genotypes, and $\hat{u}_g$ represents the vector of GEBVs for genotyped animals only.

The estimated SNP effects were subsequently employed to compute the individual variance of each SNP effect, as described by (Zhang et al 2010):

$$\sigma^2_{u,i} = 2\widehat{a}^2_i p_i(1-p_i)$$

where p_i denotes the minor allele frequency of the *i*-th SNP. SNP effects and their corresponding variances were computed using the POSTGSF90 software (Aguilar et al 2010). The resulting vector of SNP effect variances was then incorporated as weights in the diagonal matrix D to construct the weighted genomic relationship matrix G (G^*), following the procedure described by Wang et al (2012):

$$G^* = \frac{ZDZ'}{\sum_{i=1}^{N} 2p_i(1-p_i)}$$

GEBVs were re-estimated using the GIBBSF90+ software (Lourenco et al 2022), incorporating SNP-specific weights through the (G^*) matrix within the H matrix. This procedure was implemented iteratively, with the weights updated at each iteration as outlined by Wang et al (2012).

Genome-wide association study

The GWAS was performed by identifying genomic regions of 1 Mb that accounted for more than 1% of the phenotypic variability for each trait. The proportion of genetic variance explained by the *i-th* set of SNPs within a 1 Mb window (*i*-th SNP window) was calculated as described by Wang et al (2012) as:

$$\frac{Var(a_i)}{\sigma^2_a} x\ 100\% = \frac{Var\left(\sum_{j=1}^{x} Z_j\widehat{u}_j\right)}{\sigma^2_a} x\ 100\%$$

where a_i represents the additive genetic value of the *i-th* SNP window composed of consecutive SNPs; σ^2_a denotes the additive genetic variance; Z_j is the vector of gene content for the *j-th* SNP across all individuals; and $\widehat{u}_j$ corresponds to the effect of the *j-th* SNP within the *i-th* window.

The GWAS analysis was performed with the POSTGSF90 software (Aguilar et al 2010), with the 1 Mb overlapping windows option. SNP sets with more than 1% explained additive genetic variance were selected. Manhattan plots were generated with R software.

Functional annotation

We performed functional analysis in significant genomic regions (those explaining more than 1% of additive genetic variance) to identify potential candidate genes related to hock defects. For this we used the Ensembl BioMart tool (Kinsella et al 2011) and the *Equus caballus* reference genome (EquCab3.0. [Beeson et al 2019]). We reported the function of the candidate genes, as well as the metabolic pathways and biological processes involved, using the Database for Annotation Visualization and Integrated Discovery software (DAVID) (Sherman et al 2022), AmiGO 2 (Gene Ontology) software (Carbon et al 2009), and the literature available in public databases.

Results

Prevalence and SNP-based heritability in hock angle defects

Hock angle defects were analyzed as four distinct traits using the two approaches previously described. Regarding the prevalence, 26.02% of the horses (15,335) showed no deviation in the rear view (RVHD), defined as animals scoring 0 for both convergent and divergent defects. In the lateral view (LVHD), 56.52% (33,308) presented no deviation, being free of both closed and open hock defects. These “no deviation” percentages therefore represent aggregated categories, corresponding to animals scoring 0 for both opposing defects within the same view. For animals affected by deviations, prevalence varied markedly by severity. Following the official PRE morphological scoring system, the original nine-level scale was grouped for descriptive purposes into three severity degrees: slight, severe, and very severe. Slight deviations were the most frequent, ranging from 4.42% (divergent) to 65.98% (convergent). In contrast, defects categorized as severe or very severe (combined for analysis) showed much lower prevalences: 0.2% for closed hock, 6.67% for open hock, 1.98% for convergent hock, and 1.61% for divergent hock. Detailed frequencies by defect type and severity level are summarized in Table 1, while additional descriptive statistics for the total and genotyped populations are provided in Tables S1 and S2, respectively.

Estimates of variance components for hock angle defects evaluated from the lateral and rear views are presented in Table 2. Heritability (h^2) estimates obtained using the threshold model ranged from low to moderate, from 0.25 for the open defect to 0.42 for the divergent defect, while those estimated under the linear model were 0.18 for LVHD and 0.25 for RVHD.

Identification of genomic regions associated with hock angle defects

Following the GWAS, genomic regions that explained an additive genetic variance of more than 1% were selected. Eight genomic regions associated with hock defects were identified on seven different chromosomes (ECA1, ECA4, ECA7, ECA10, ECA11, ECA17, and ECA19) (Figure 1 and Table 3). The LVHD trait was associated with three regions, while the individually analyzed closed and open traits were associated with three and one regions, respectively. Interestingly, two regions on ECA17 were associated with LVHD and closed hock defect. Meanwhile, the RVHD trait was associated with two genomic regions, and the individually studied convergent and divergent traits were associated with one and three genomic regions, respectively. Interestingly, the ECA11 region (11:28,631,844-29,622,216) was associated with the LVHD and RVHD, as well as with the convergent and divergent traits studied individually.

To explore the potential functions of genomic regions, their location in the genome was investigated. Sixty-nine genes were found in the eight genomic regions associated with hock defects, as shown in Table 3. Of these, 19 genes were related to different functions and pathways involved in musculoskeletal diseases, cartilage defects, bone malformations, bone and joint fragility, and others.

Table 1 Number of animals per level of deviation and prevalence (%) of the hock angle defects in the Pura Raza Española horses analyzed, depending on the defect level.

Level	−4[a]	−3[b]	−2[c]	−1[c]	0		1[d]	2[e]	3[f]	4[f]
[g]Degree	Very severe	Severe	Slight		Absence		Slight	Severe	Very severe	
Lateral view	**Closed, %**					**Open, %**				
	10 (0.02)	108 (0.18)	2,925 (4.96)	7,314 (12.41)	48,573 (82.42)	43,665 (74.10)	11,333 (19.23)	3,833 (6.50)	87 (0.15)	12 (0.02)
	10 (0.02)	108 (0.18)	10,239 (17.37)		48,573 (82.42)	43,665 (74.10)	11,333 (19.23)	3,833 (6.50)	99 (0.17)	
Rear view	**Convergent, %**					**Divergent, %**				
	104 (0.18)	1,060 (1.80)	10,135 (17.20)	28,744 (48.78)	18,887 (32.04)	55,378 (93.97)	2,602 (4.42)	934 (1.58)	11 (0.02)	5 (0.01)
	104 (0.18)	1,060 (1.80)	38,879 (65.98)		18,887 (32.04)	55,378 (93.97)	2,602 (4.42)	934 (1.58)	16 (0.03)	

[a]Level −4 reflected a very severe close/convergent defect and [f]levels 3 and 4 corresponded to a very severe open/divergent defect. [b]Level −3 represents a severe close/convergent defect and [e]level 2 a severe open/divergent defect. [c]Levels −1 and −2 denote a slightly closed/convergent defect, and [d]level 1 corresponded to a slightly open/divergent hock. [g]Severity degrees (slight, severe, and very severe) represent analytical groupings of the original levels and were applied consistently across closed/open and convergent/divergent defects for descriptive purposes.

Table 2 Genetic parameters and heritability for hock angle defect traits in the Pura Raza Española population evaluated.

	Lateral view			Rear view		
	Closed	Open	LVHD	Convergent	Divergent	RVHD
σ^2_a (SD)	0.38 (0.023)[1]	0.21 (0.013)[1]	0.14 (0.007)	0.12 (0.006)[1]	0.73 (0.054)[1]	0.20 (0.007)
σ^2_e (SD)	0.81 (0.047)[1]	0.66 (0.039)[1]	0.66 (0.006)	0.25 (0.030)[1]	1.02 (0.055)[1]	0.60 (0.006)
σ^2_P (SD)	1.19 (0.052)[1]	0.87 (0.042)[1]	0.79 (0.005)	0.37 (0.029)[1]	1.76 (0.065)[1]	0.81 (0.005)
h^2(SD)	0.32 (0.019)[1]	0.25 (0.016)[1]	0.18 (0.008)	0.32 (0.023)[1]	0.42 (0.024)[1]	0.25 (0.009)

σ^2_a: additive genetic variance; σ^2_e: residual variance; σ^2_P: phenotypic variance.
[1]Underlying scale.

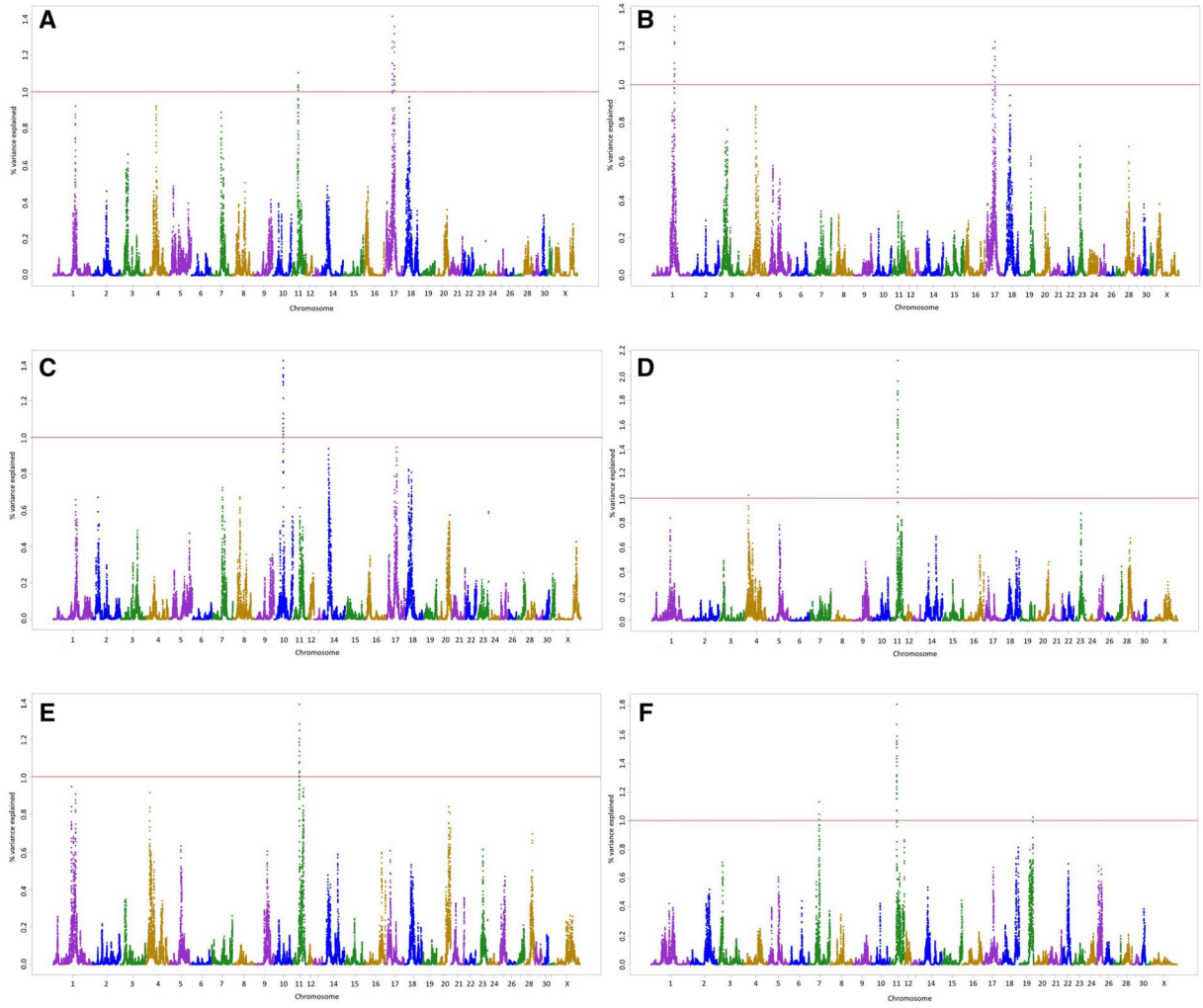

Figure 1 Results of the genome-wide association study for hock conformation defects in genotyped PRE horses. Manhattan plot of the additive genetic variance (y axis) explained by each SNP, calculated using a 1 Mb sliding window, for the analyzed trait. A) Lateral view hock defect. B) Closed hock defect. C) Open hock defect. D) Rear view hock defect. E) Convergent hock defect. F) Divergent hock defect. The red lines indicate the genome-wide significance threshold with an explained variance equal to 1%.

Discussion

Genetic predisposition to certain conformation defects in the limbs and particularly in the hock represents a challenge to breeders and owners, as it affects both the welfare and performance of the horse. In the PRE horse breeding program, one of the main selection criteria is the improvement of conformation and traits related to sporting performance (Sánchez et al 2013; Sánchez-Guerrero et al 2016; Sánchez-Guerrero et al 2017). Although many parameters are involved in selecting an

Table 3 Genomic regions associated with hock defects in Pura Raza Española population accounting for a percentage of variance above 1%.

Trait	Chr	Genomic region, bp	v.e., %	Candidate genes
Closed	1	108,052,754–109,046,228	1.36	*TJP1*[1]*; ENTREP2; APBA2; MCEE*[1]*; MPHOSPH10; FAN1*
RVHD	4	17,659,691–18,611,981	1.02	*TNS3*[1]*; PKD1L1; HUS1; SUN3; UPP1; ABCA13*[1]
Divergent	7	50,454,631–51,447,236	1.13	*ACP5*[1]*; CNN1*[1]*; ELOF1; ECSIT*[1]*; ZNF653; ELAVL3; PRKCSH; RGL3; EPOR*[1]*; SWSAP1; PLPPR2; CCDC159; TMEM205; RAB3D; TSPAN16; DOCK6*[1]*; ANGPTL8; KANK2*[1]*; SPC24*[1]*; LDLR; SMARCA4; YIPF2; CARM1; TMED1; DNM2; QTRT1; ILF3*[1]*; SLC44A2*[1]*; ATG4D; CDKN2D; KRI1; S1PR5; KEAP1; PDE4A*[1]*; CDC37; TYK2*
Open	10	40,539,712–41,516,383	1.42	*HTR1E*[1]*; CGA; ZNF292; GJB7; SMIM8; CFAP206; RARS2; SLC35A1; ORC3; AKIRIN2*
LVHD, RVHD, Convergent, Divergent	11	28,631,844–29,622,216	1.10, 2.12, 1.39, 1.81	*KIF2B*
LVHD, Closed	17	34,742,911–35,601,778	1.41, 1.19	*DIAPH3*[1]*; TDRD3*
LVHD, Closed	17	43,976,369–44,884,257	1.36, 1.23	
Divergent	19	57,663,111–58,661,402	1.02	*LNP1; TOMM70; NIT2; TBC1D23; TMEM30C; CMSS1; FILIP1L; COL8A1*[1]

Chr: chromosome; v.e.: variance explained.
[1]Genes related to biological processes associated with hock conformation defects.

animal for high sporting performance, one of the key factors is the absence of any defect or malformation of the limbs. In the present study, phenotypic data were combined with genomic data in a wssGREML to perform a genome-wide association analysis to identify molecular markers and genomic regions associated with hock defects and to predict genomic predisposition to such defects.

Evaluation of hock defects

The evaluation of hock defects in 58,930 PRE horses revealed that, when the evaluation views were considered as global traits, deviations in the rear view were more prevalent than those in the lateral view when analyzed as continuous variables, regardless of the direction of the defect. When specific defect directions were examined, convergent hock was the most common defect in the population, primarily due to a high incidence of slight deviations. However, when focusing specifically on high-severity levels (severe and very severe), open hock defects showed the highest prevalence (6.67%), while closed hock was the least frequent (0.2%). For slight deviations, convergent hocks were the most observed, whereas divergent deviations were the least frequent. These results agreed with those previously reported by Ripollés-Lobo et al (2023a), where the defect with the highest prevalence in the PRE population studied was the convergent defect. Comparing the prevalence of hock defects in PRE with other breeds revealed distinct, breed-specific patterns. In Swedish Warmblood (SWB) riding horses, Jönsson et al (2014) reported prevalences of 2.6% for large hock angle (analogous to open hock), 8.7% for small hock angle (analogous to closed hock), 9.9% for wide hocks (analogous to divergent), and 1.5% for narrow hocks (analogous to convergent). Although differences in scoring systems and severity thresholds between studies must be considered, these prevalences showed a marked contrast with the PRE population, particularly when focusing on severe and very severe defects. While the SWB showed a higher prevalence of closed hocks (8.7% vs. 0.2% in PRE) and divergent hocks (9.9% vs. 1.61% in PRE), the PRE population exhibited a higher frequency of severe and very severe open hock defects (6.67% vs. 2.6% in SWB) and convergent hock defects (1.98% vs. 1.5% in SWB). These differences suggest that selection pressures or genetic backgrounds influence hock morphology differently in each breed, leading to opposed prevalence patterns for these structural deviations. In jumping Thoroughbred horses, the prevalence was 16% for straight hocks (Mostafa et al 2019), which is similar to our prevalences for closed and open slight deviation. A population of Pura Raza Menorquín (a Spanish horse breed) studied showed a higher frequency for closed hock (62.53%), open (30.61%), and divergent (41.90%) defects than the PRE, except for the convergent hock defect, where the frequency was lower (38.83%) (Ripollés-Lobo et al 2024). These differences between the prevalence of the two

breeds are due to the way the animals with defects are grouped into different categories. In the Pura Raza Menorquín horse, these prevalence values might also reflect selection pressures for specific movements required in the *Doma Menorquina*, although the impact of the data grouping methods must be considered (Ripollés-Lobo et al 2024). It should be noted that the high prevalences in the PRE are due to slight defects (−1 and −2 for closed/convergent and 1 for open/divergent hock defect), which indicates that the breeding program is trying to reduce the prevalence of these defects in the population.

In general, our estimated h^2 on the observed scale were within the same range as most conformation traits described on a linear scale (Gmel et al 2019; Folla et al 2020; Gmel et al 2023). However, the h^2 estimated on the underlying scale (multinomial variable) were higher than those of the linear scale, ranging from 0.25 to 0.42 for open and divergent, respectively. This underlying scaled h^2 is usually higher than the observed h^2 since it is a function of the prevalence of the population evaluated for each defect. The magnitude of the evaluated traits suggests that selecting against hock defects could effectively reduce these defects in the PRE population.

However, comparing the h^2 of different conformational traits between breeds is a complex task, and the scale on which the variables are measured, the different levels scored, as well as whether opposing defects are separated as independent variables must all be considered. In addition, it is necessary to take into account whether the models that evaluate the variables are linear or multinomial, as the estimates with multinomial variables are higher, as well as whether the models for estimating h^2 use genomics or not, and if so, whether they use weighting. Most traits are judged based on the optimum breeding values or evaluated on a specific linear scale within each breed (Rustin et al 2009; Sánchez et al 2013; Duensing et al 2014; Gmel et al 2018). Finally, the different methodologies used should be taken into account: visual assessment, physical examination, static conformation analysis, dynamic movement assessment, gait analysis, image diagnosis, and even computer-assisted modeling (Ripollés-Lobo et al 2024). This results in the comparisons of the evaluated traits differing significantly depending on the breed and the method/model of trait evaluation. A recent study by Ripollés-Lobo et al (2023a), using the REML methodology, reported estimated h^2 values for hock defects in the PRE that were very similar to ours, both on the linear and underlying scales. Remarkably, the h^2 in our study were estimated, including genomics, in evaluation models using an (ssGBLUP) with weighting on SNPs of significance in the H-matrix estimation (wssGBLUP). The ssGBLUP approach assumes the same prior weight for all SNP markers (Legarra et al 2014), but some studies have proved that giving different weights for each SNP can improve the accuracy of prediction (Tiezzi and Maltecca 2015; Zhang et al 2016).

Recently, Reich et al (2024) reported SNP-based h^2 of 0.11 for the hock angulation trait (similar to LVHD in our study) and 0.04 for the hock-back view (similar to RVHD) in German Warmblood horses. In our case, the h^2 for these two traits in the PRE (LVHD and RVHD) were 0.18 and 0.25, respectively. This remarkable difference in the h^2 of the RVHD could be due to the high prevalence of RVHD in the PRE population and the methodology developed to estimate the h^2, since the h^2 reported by Reich et al (2024) were estimated exclusively with genotyped animals and ours were not. In the Franches-Montagnes and Lipizzan horses, the genomic h^2 of the hock was 0.25 (Gmel et al 2019), a value equal to that estimated for the open hock and RVHD in the PRE using the wssGBLUP approach.

On the other hand, when comparing our results to breeds whose h^2 were not estimated with wssGBLUP approach, distinct patterns are observed. In the Swedish Warmblood riding horse, the h^2 for the open hock trait (0.28; large hock angle) was similar to that observed in the PRE (0.25). However, for other traits, the h^2 values were higher in the PRE, such as divergent hocks (0.42 in PRE vs. 0.29 for wide hocks in SWB), while the h^2 for closed hocks was higher in the SWB (0.48; small hock angle) than in the PRE (0.32) (Jönsson et al 2014). In the case of the Pura Raza Menorquin horse, the estimated h^2 were lower (0.16 [open], 0.12 [closed], 0.24 [convergent], and 0.18 [divergent]) (Ripollés-Lobo et al 2024) than those estimated in the PRE population, probably due to the methodology used with genomics and the underlying scale of the h^2, which are higher than the real ones.

Genomic association with hock defects

The GWAS revealed eight significant genome-wide association regions on seven different chromosomes for hock defects in PRE horses, with these regions accounting for a large proportion of the additive genetic variance. Interestingly, the significant region on ECA11 (11: 28,631,844–29,622,216), which was associated with two individually assessed traits (convergent and divergent) and linearly assessed traits (LVHD and RVHD), was the region with the highest explained variance. This seems to point to this region as a possible hotspot for hock defects. However, we did not identify any genes associated with musculoskeletal defects and malformations. In addition, on ECA17, we identified two significant regions that were associated with LVHD and closed defects. Notably, this suggests that there are regions in the genome that are significant for the defect assessed both as a multinomial variable and as a continuous variable. Likewise, there are genomic regions that are significant exclusively when linear scales have been used for defect assessment (LVHD and RVHD). This appears to indicate that there are common genes in hock defects that influence both the defect evaluated as a continuous variable and the specific defect treated as a multinomial variable, while, conversely, there are genes that are specific to a certain defect.

Notably, two of the identified regions have been previously reported as significant in other GWAS. For example, regions on ECA10 (40,539,712–41,516,383) and ECA19 (57,663,111–58,661,402) were previously associated with knee defects in the PRE breed (Laseca et al 2025). These findings suggest that certain genomic regions may serve as hotspots for joint angle conformation traits, offering promising targets for future selection strategies.

In six of the eight significant regions, 17 genes were prioritized for discussion based on a functional criterion, as they are involved in pathways relevant to musculoskeletal diseases, cartilage and ligament defects, bone malformations, and joint fragility. These findings align with the polygenic nature of conformational defects. While other genes were identified, their currently known biological functions do not show a direct link to the traits studied;

nonetheless, the full list of genes located within these regions is provided in Table 3 and Supplementary Material.

To date, to our knowledge, there have been few genomic studies analyzing molecular markers and genomic regions related to morphological defects of the hock in horses (Gmel et al 2019; Reich et al 2024). Therefore, we studied homologies of genes related to limb defects in other species such as humans, mice, and cattle, in addition to horses.

Interestingly, we identified several genes associated with osteoarthritis (OA), a degenerative joint disorder characterized by alterations in subchondral bone and articular cartilage (Coutinho de Almeida et al 2023). Although clinical OA status and OA prevalence were not directly evaluated in this study, the presence of these genes is highly relevant since hock conformation defects are well-known predisposing factors for joint instability, abnormal mechanical loading, and subsequent joint degeneration. These genes were located on ECA1 (*TJP1*), ECA7 (*ILF3* and *SLC44A2*), and ECA19 (*COL8A1*). The *TJP1* (*tight junction protein 1*) gene (Zhang et al 2024) and the *COL8A1* (*collagen type VIII alpha 1 chain*) gene (Fang et al 2019) were identified as potential biomarkers for OA. Additionally, a GWAS study in OA patients revealed that the *SLC44A2* (*solute carrier family 44 member 2*) gene was differentially expressed in subchondral bone and cartilage, while the *ILF3* (*interleukin enhancer binding factor 3*) gene was expressed in articular cartilage (Coutinho de Almeida et al 2023). In equines, chronic joint stress caused by poor hock angulation often leads to the development of bone spavin (hock OA). Therefore, the identification of OA-related genes in our significant regions suggests that the genetic basis for hock conformation is intrinsically linked to the structural integrity and long-term health of the joint tissues.

The identification of genes associated with bone tissue cells is highly relevant, as the morphological development and angulation of the hock joint (high-load joint) depend on the balance of bone modeling and remodeling processes. We identified genes involved in the regulation of osteoclasts (primary mediators of bone resorption) and osteoblasts (responsible for synthesizing the bone matrix), such as the *TNS3 (tensin 3*) gene on ECA4 and the *PDE4A (phosphodiesterase 4A*), *ECSIT (ECSIT signaling integrator*), *CNN1* (*calponin 1)*, and *EPOR* (*erythropoietin receptor*) genes on ECA7. For instance, TNS3 is a known regulator of bone resorption Touaitahuata et al (2016) while the *PDE4A* gene is differentially expressed in bone affected by OA (Hopwood et al 2007) and in osteoblastic cells (Nomura-Furuwatari et al 2008), as is the *ECSIT* gene, which is expressed in osteoblasts, osteocytes, and osteoclasts (Lin et al 2022). In addition, Su et al (2013) showed that the overexpression of *CNN1* in osteoblasts significantly reduced bone mass by inhibiting osteoblast migration and proliferation, promoting osteoclastogenesis. Finally, the *EPOR* gene is essential in osteoprogenitors for regulating osteoblast function and osteoblast-mediated osteoclastogenesis (Rauner et al 2021). Variations in these cellular activities during the growth of the tarsal bones can alter their final structure and joint alignment, directly contributing to the conformational defects observed in this study.

Interestingly, genes on ECA7 (*SPC24; SPC24 component of NDC80 kinetochore complex*) and ECA17 (*DIAPH3; diaphanous-related formin 3*) were identified as potential therapeutic targets for osteosarcoma (Li et al 2020; Zhang et al 2021).

Similarly, various genes (*MCEE, ABCA13, ACP5, DOCK6, KANK2, HTR1E*) were identified in connection with musculoskeletal diseases, joint disorders, and limb abnormalities. The *MCEE* (*methylmalonyl-CoA epimerase*) gene, located on ECA1, is associated with joint disorders and was proposed as a potential diagnostic biomarker in rheumatoid arthritis, a common autoimmune disease affecting the synovial membrane of joints, leading to persistent inflammation, joint deterioration, and loss of function (Guo et al 2023). The *ABCA13* (*ATP binding cassette subfamily A member 13*) gene, located on ECA4, has been associated with osteogenesis imperfecta in male Holstein calves, also known as brittle bone disease, which causes bone fragility, deformities, and joint laxity (Zhang et al 2020). As for the *ACP5* (*acid phosphatase 5, tartrate-resistant*) gene, located on ECA7, it is known to cause a recessive skeletal dysplasia (Hong et al 2018). Another gene located on ECA7, *DOCK6* (*dedicator of cytokinesis 6*), is linked to a rare hereditary disorder in humans characterized by a combination of congenital limb abnormalities and associated skeletal malformations, particularly in hands and feet (Alzahem et al 2020). Interestingly, the *KANK2* (*KN motif and ankyrin repeat domains 2*) gene, also located on ECA7, has been associated with the risk of degenerative suspensory ligament desmitis in various horse breeds (Momen et al 2022), causing scarring and rupture of suspensory ligament fibers in multiple limbs. Finally, the *HTR1E* (*5-hydroxytryptamine receptor 1E*) gene, located on ECA10, was associated with osteoporosis risk by performing a GWAS for musculoskeletal traits (Karasik et al 2012).

Conclusion

This study has revealed several genomic regions associated with hock conformation defects in the PRE horse. In addition, it has been shown that there are significant regions for several defects, as well as significant regions exclusive to one type of defect. These findings suggest that there are common molecular mechanisms involved in hock defects in general and specific molecular mechanisms for certain types of defects. In addition, the weighted single-step GREML showed that the hock defects studied have moderate h^2 and warrant inclusion in the selection process. If used as selection criteria in the PRE breeding program, they could therefore contribute to the eradication of the main limb conformation defects that reduce the animal's economic value by reducing its beauty, hindering the animal's sporting development or even making animals unsuitable for sport and causing significant economic losses in studs. These findings not only provide information on genomic variation and candidate genes involved in the genetic and molecular mechanisms involved in the development of limb conformation defects but also facilitate the selection of individuals with better conformation. The integration of genomics is crucial for developing breeding programs that will decrease the incidence of hock defects, promote performance in the PRE and improve the quality of horses in the future by applying more precise selection strategies in PRE breeding. However, further genomic studies are needed to understand these conformational defects better in the equine species.

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Author contributions

Nora Laseca (Data curation, Formal analysis, Investigation, Methodology, Writing—original draft, Writing—review & editing), Antonio Molina (Conceptualization, Investigation, Methodology, Resources, Supervision, Writing—review & editing), Chiraz Ziadi (Formal analysis, Methodology, Writing—review & editing), Davinia I. Pérdomo-Gonzalez (Data curation, Writing—review & editing), and Mercedes Valera (Conceptualization, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Writing—review & editing)

Supplementary data

Supplementary data are available at *Journal of Animal Science* online.

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Data availability

The dataset was deposited in an official repository (https://doi.org/10.5281/zenodo.17607369).

References

Aguilar I et al. 2010. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J Dairy Sci. 93:743–752. https://doi.org/10.3168/jds.2009-2730

Alzahem T, Alsalamah AK, Mura M, Alsulaiman SM. 2020. A novel variant in DOCK6 gene associated with Adams–Oliver syndrome type 2. Ophthalmic Genet. 41:377–380. https://doi.org/10.1080/13816810.2020.1776339

ANCCE. 2025. PRE stud-book. Basic reproduction approval certificate. Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE), Seville, Spain. Available at: https://www.lgancce.com/Documentacion/Normativa/LG/ficha_valoracion_aptitud_basica_en.pdf (Accessed September 22, 2025).

Axelsson M et al. 2001. Risk factors associated with hindlimb lameness and degenerative joint disease in the distal tarsus of Icelandic horses. Equine Vet J. 33:84–90. https://doi.org/10.2746/042516401776767502

Beeson SK, Schaefer RJ, Mason VC, McCue ME. 2019. Robust remapping of equine SNP array coordinates to EquCab3. Anim Genet. 50:114–115. https://doi.org/10.1111/age.12745

Carbon S et al.; the AmiGO Hub, the Web Presence Working Group. 2009. AmiGO: online access to ontology and annotation data. Bioinformatics (Oxford, England). 25:288–289. https://doi.org/10.1093/bioinformatics/btn615

Coutinho de Almeida R et al. 2023. Allelic expression imbalance in articular cartilage and subchondral bone refined genome-wide association signals in osteoarthritis. Rheumatology (Oxford). 62:1669–1676. https://doi.org/10.1093/rheumatology/keac498

Ducro BJ, Gorissen B, van Eldik P, Back W. 2009. Influence of foot conformation on duration of competitive life in a Dutch Warmblood horse population. Equine Vet J. 41:144–148. https://doi.org/10.2746/042516408X363800

Duensing J, Stock KF, Krieter J. 2014. Implementation and prospects of linear profiling in the Warmblood horse. J Equine Vet Sci. 34:360–368. https://doi.org/10.1016/j.jevs.2013.09.002

Fang Y et al. 2019. Aberrantly hydroxymethylated differentially expressed genes and the associated protein pathways in osteoarthritis. PeerJ 7:e6425. https://doi.org/10.7717/peerj.6425

Farries G et al. 2019. Expression quantitative trait loci in equine skeletal muscle reveals heritable variation in metabolism and the training responsive transcriptome. Front Genet. 10:1215. https://doi.org/10.3389/fgene.2019.01215

Folla F, Sartori C, Mancin E, Pigozzi G, Mantovani R. 2020. Genetic parameters of linear type traits scored at 30 months in Italian heavy draught horse. Animals. 10:1099. https://doi.org/10.3390/ani10061099

Frischknecht M et al. 2015. A non-synonymous HMGA2 variant decreases height in Shetland ponies and other small horses. PLoS One. 10:e0140749. https://doi.org/10.1371/journal.pone.0140749

Frischknecht M, Signer-Hasler H, Leeb T, Rieder S, Neuditschko M. 2016. Genome-wide association studies based on sequence-derived genotypes reveal new QTL associated with conformation and performance traits in the Franches–Montagnes horse breed. Anim Genet. 47:227–229. https://doi.org/10.1111/age.12406

Gmel A, Brem G, Neuditschko M. 2023. New genomic insights into the conformation of Lipizzan horses. Sci Rep. 13:8990. https://doi.org/10.1038/s41598-023-36272-4

Gmel A, Druml T, Portele K, von Niederhäusern R, Neuditschko M. 2018. Repeatability, reproducibility and consistency of horse shape data and its association with linearly described conformation traits in Franches-Montagnes stallions. PLoS One. 13:e0202931. https://doi.org/10.1371/journal.pone.0202931

Gmel A, Druml T, von Niederhäusern R, Leeb T, Neuditschko M. 2019. Genome-wide association studies based on equine joint angle measurements reveal new QTL affecting the conformation of horses. Genes (Basel). 10:370. https://doi.org/10.3390/genes10050370

Gmel AI, Burren A, Neuditschko M. 2022. Estimates of genetic parameters for shape space data in Franches-Montagnes horses. Animals (Basel). 12:2186. https://doi.org/10.3390/ani12172186

Guo Z et al. 2023. Identification and validation of metabolism-related genes signature and immune infiltration landscape of rheumatoid arthritis based on machine learning. Aging (Albany NY). 15: 3807–3825. https://doi.org/10.18632/aging.204714

Gutiérrez J, Goyache F. 2005. A note on ENDOG: a computer program for analysing pedigree information. J Anim Breed Genet. 122:172–176. https://doi.org/10.1111/j.1439-0388.2005.00512.x

Hilla D, Distl O. 2014. Genetic parameters for osteoarthrosis, radiographic changes of the navicular bone and sidebone, and their correlation with osteochondrosis and osteochondral fragments in Hanoverian warmblood horses. Livest Sci. 169: 19–26. https://doi.org/10.1016/j.livsci.2014.09.015

Hong SW, Huh K-H, Lee JK, Kang J-H. 2018. Craniofacial anomalies associated with spondyloenchondrodysplasia: two case reports. Medicine (Baltimore). 97:e13644., https://doi.org/10.1097/MD.0000000000013644

Hopwood B, Tsykin A, Findlay DM, Fazzalari NL. 2007. Microarray gene expression profiling of osteoarthritic bone suggests altered bone remodelling, WNT and transforming growth factor-β/bone morphogenic protein signalling. Arthritis Res Ther. 9:R100. https://doi.org/10.1186/ar2301

Jönsson L et al. 2014. Conformation traits and their genetic and phenotypic associations with health status in young Swedish warmblood riding horses. Livest Sci. 163:12–25. https://doi.org/10.1016/j.livsci.2014.02.010

Karasik D et al. 2012. Genome-wide association of an integrated osteoporosis-related phenotype: is there evidence for pleiotropic genes? J Bone Miner Res. 27:319–330. https://doi.org/10.1002/jbmr.563

Kinsella RJ et al. 2011. Ensembl BioMarts: a hub for data retrieval across taxonomic space. Database (Oxford). 2011:bar030. https://doi.org/10.1093/database/bar030

Kristjansson T et al. 2016. Association of conformation and riding ability in Icelandic horses. Livest Sci. 189:91–101. https://doi.org/10.1016/j.livsci.2016.05.010

Laseca N et al. 2024. Exploring the genetic landscape of vitiligo in the Pura Raza Español horse: a genomic perspective. Animals. 14:2420.

Laseca N et al. 2025. Genetic and genomic insights into morphological knee defects in Pura Raza Española horses. Ital J Anim Sci. 24:1999–2012. https://doi.org/10.1080/1828051X.2025.2556264

Legarra A, Christensen OF, Aguilar I, Misztal I. 2014. Single step, a general approach for genomic selection. Livest Sci. 166:54–65. https://doi.org/10.1016/j.livsci.2014.04.029

Li Q, Liang J, Chen B. 2020. Identification of CDCA8, DSN1 and BIRC5 in regulating cell cycle and apoptosis in osteosarcoma using bioinformatics and cell biology. Technol Cancer Res Treat. 19: 1533033820965605. https://doi.org/10.1177/1533033820965605

Lin C et al. 2022. Impaired mitochondrial oxidative metabolism in skeletal progenitor cells leads to musculoskeletal disintegration. Nat Commun. 13:6869. https://doi.org/10.1038/s41467-022-34694-8

Lourenco D et al. 2022. Recent updates in the BLUPF90 software suite, Proceedings of 12th World Congress on Genetics Applied to Livestock Production (WCGALP). Wageningen Academic Publishers. p. 1530–1533.

Love S et al. 2006. Prevalence, heritability and significance of musculoskeletal conformational traits in Thoroughbred yearlings. Equine Vet J. 38:597–603. https://doi.org/10.2746/042516406X159016

Makvandi-Nejad S et al. 2012. Four loci explain 83% of size variation in the Horse. PLoS One. 7:e39929. https://doi.org/10.1371/journal.pone.0039929

MAPA. 2025. MAPA (Ministerio de Agricultura, Pesca y Alimentación). Sistema Nacional de Información de Razas Ganaderas (ARCA). Explotación de Datos Censales. https://servicio.mapama.gob.es/arca/flujos.html?_flowId=explotaDatosCensosRazaExcel-flow&isMapa=1

Momen M et al. 2022. Selection signature analyses and genome--wide association reveal genomic hotspot regions that reflect differences between breeds of horse with contrasting risk of degenerative suspensory ligament desmitis. G3 (Bethesda). 12:jkac179. https://doi.org/10.1093/g3journal/jkac179

Mostafa MB, Senna NA, Abu-Seida AM, Elemmawy YM. 2019. Evaluation of abnormal limb conformation in jumping thoroughbred horses. J Hellenic Vet Med Soc. 70:1533–1540. https://doi.org/10.12681/jhvms.20859

Murray RC, Walters JM, Snart H, Dyson SJ, Parkin TDH. 2010. Identification of risk factors for lameness in dressage horses. Vet J. 184:27–36. https://doi.org/10.1016/j.tvjl.2009.03.020

Nomura-Furuwatari C et al. 2008. Expression profiles of phosphodiesterase 4D splicing variants in osteoblastic cells. J Bone Miner Metab. 26:152–158. https://doi.org/10.1007/s00774-007-0803-7

Purcell S et al. 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet. 81:559–575. https://doi.org/10.1086/519795

Rauner M et al. 2021. Epo/EpoR signaling in osteoprogenitor cells is essential for bone homeostasis and Epo-induced bone loss. Bone Res. 9:42. https://doi.org/10.1038/s41413-021-00157-x

Reich P et al. 2024. Genomic analyses of withers height and linear conformation traits in German Warmblood horses using imputed sequence-level genotypes. Genet Sel Evol. 56:45. https://doi.org/10.1186/s12711-024-00914-6

Ripollés-Lobo M, Perdomo-González DI, Azor PJ, Valera M. 2023a. Evaluation of potential effects and genetic parameters in conformational limb defects in Pura Raza Española horses. Ital J Anim Sci. 22:407–417. https://doi.org/10.1080/1828051X.2023.2206419

Ripollés-Lobo M, Perdomo-González DI, Azor PJ, Valera M. 2023b. Orthopedic diseases in the Pura Raza Española horse: the prevalence and genetic parameters of angular hoof deviations. Animals (Basel). 13:3471. https://doi.org/10.3390/ani13223471

Ripollés-Lobo M, Perdomo-González DI, Valera M, Gómez MD. 2024. Conformational defects in the limbs of Menorca purebred horses and their relationship to functionality. Animals (Basel). 14:1071. https://doi.org/10.3390/ani14071071

Rosengren MK et al. 2021. A QTL for conformation of back and croup influences lateral gait quality in Icelandic horses. BMC Genomics. 22:267. https://doi.org/10.1186/s12864-021-07454-z

Rustin M, Janssens S, Buys N, Gengler N. 2009. Multi-trait animal model estimation of genetic parameters for linear type and gait traits in the Belgian warmblood horse. J Anim Breed Genet. 126:378–386. https://doi.org/10.1111/j.1439-0388.2008.00798.x

Sánchez-Guerrero MJ, Cervantes I, Molina A, Gutiérrez JP, Valera M. 2017. Designing an early selection morphological linear traits index for dressage in the Pura Raza Español horse. Animal. 11: 948–957. https://doi.org/10.1017/S1751731116002214

Sánchez-Guerrero MJ, Molina A, Gómez MD, Peña F, Valera M. 2016. Relationship between morphology and performance: signature of mass-selection in Pura Raza Español horse. Livest Sci. 185:148–155. https://doi.org/10.1016/j.livsci.2016.01.003

Sánchez MJ, Gómez MD, Molina A, Valera M. 2013. Genetic analyses for linear conformation traits in Pura Raza Español horses. Livest Sci. 157:57–64. https://doi.org/10.1016/j.livsci.2013.07.010

Sevane N, Dunner S, Boado A, Cañon J. 2017. Polymorphisms in ten candidate genes are associated with conformational and locomotive traits in Spanish Purebred horses. J Appl Genet. 58:355–361. https://doi.org/10.1007/s13353-016-0385-y

Sherman BT et al. 2022. DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update). Nucleic Acids Res. 50:W216–W221. https://doi.org/10.1093/nar/gkac194

Signer-Hasler H et al. 2012. A genome-wide association study reveals loci influencing height and other conformation traits in horses. PLoS One. 7:e37282. https://doi.org/10.1371/journal.pone.0037282

Solé M, Gómez MD, Galisteo AM, Santos R, Valera M. 2013. Kinematic characterization of the Menorca horse at the walk and the trot: influence of hind limb pastern angle. J Equine Vet Sci. 33:726–732. https://doi.org/10.1016/j.jevs.2012.12.002

Stock KF, Distl O. 2006. Genetic correlations between conformation traits and radiographic findings in the limbs of German Warmblood riding horses. Genet Sel Evol. 38:657–671. https://doi.org/10.1186/1297-9686-38-6-657

Su N et al. 2013. Overexpression of H1 calponin in osteoblast lineage cells leads to a decrease in bone mass by disrupting osteoblast function and promoting osteoclast formation. J Bone Miner Res. 28:660–671. https://doi.org/10.1002/jbmr.1778

Tetens J, Widmann P, Kühn C, Thaller G. 2013. A genome-wide association study indicates/as a candidate locus for withers height in German Warmblood horses. Anim Genet. 44: 467–471. https://doi.org/10.1111/age.12031

Tiezzi F, Maltecca C. 2015. Accounting for trait architecture in genomic predictions of US Holstein cattle using a weighted realized relationship matrix. Genet Sel Evol. 47:24. https://doi.org/10.1186/s12711-015-0100-1

Touaitahuata H et al. 2016. Tensin 3 is a new partner of Dock5 that controls osteoclast podosome organization and activity. J Cell Sci. 129:3449–3461. https://doi.org/10.1242/jcs.184622

Tsuruta S, Misztal I. 2006. THRGIBBS1F90 for estimation of variance components with threshold-linear models. *Proc. 8th World Congr. Genet. Appl. Livest. Prod.*, August 13–18, 2006, Belo Horizonte, MG, Brazil.

Van Cauter R, Caudron I, Lejeune J-P, Rousset A, Serteyn D. 2024. Distal sagittal forelimb conformation in young Walloon horses: radiographic assessment and its relationship with osteochondral fragments. PLoS One. 19:e0311965. https://doi.org/10.1371/journal.pone.0311965

Van Weeren PR, Crevier-Denoix N. 2006. Equine conformation: clues to performance and soundness? Equine Vet J. 38: 591–596. https://doi.org/10.2746/042516406X159007

VanRaden PM. 2008. Efficient methods to compute genomic predictions. J Dairy Sci. 91:4414–4423. https://doi.org/10.3168/jds.2007-0980

Viklund Å, Eriksson S. 2018. Genetic analyses of linear profiling data on 3-year-old Swedish Warmblood horses. J Anim Breed Genet. 135:62–72. https://doi.org/10.1111/jbg.12311

Wang H, Misztal I, Aguilar I, Legarra A, Muir WM. 2012. Genome-wide association mapping including phenotypes from relatives without genotypes. Genet Res (Camb). 94: 73–83. https://doi.org/10.1017/S0016672312000274

Welsh CE et al. 2013. Preliminary genetic analyses of important musculoskeletal conditions of Thoroughbred racehorses in Hong Kong. Vet J. 198:611–615. https://doi.org/10.1016/j.tvjl.2013.05.002

Zhang W, Wei C, Wang L. 2024. Identification of key lncRNAs, circRNAs, and mRNAs in osteoarthritis via bioinformatics analysis. Mol Biotechnol. 66:1660–1672. https://doi.org/10.1007/s12033-023-00790-3

Zhang X et al. 2020. Osteogenesis imperfecta in a male Holstein calf associated with a possible oligogenic origin. Vet Q. 40: 58–67. https://doi.org/10.1080/01652176.2020.1721611

Zhang X, Lourenco D, Aguilar I, Legarra A, Misztal I. 2016. Weighting strategies for single-step genomic BLUP: an iterative approach for accurate calculation of GEBV and GWAS. Front Genet. 7:151. https://doi.org/10.3389/fgene.2016.00151

Zhang Z et al. 2021. Diaphanous related formin 3 knockdown suppresses cell proliferation and metastasis of osteosarcoma cells. Discov Oncol. 12:20. https://doi.org/10.1007/s12672-021-00415-8

Zhang Z et al. 2010. Best linear unbiased prediction of genomic breeding values using a trait-specific marker-derived relationship matrix. PLoS One. 5:e12648. https://doi.org/10.1371/journal.pone.0012648

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https://doi.org/10.1093/jas/skag116
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