1 *Title:* **Genetic parameters for canalisation analysis of morphological traits**
2 **in the Pura Raza Español horse**

3 *Running title:* Canalisation of PRE horse morphological traits

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15 **Summary:** Measurements from 13 different morphological traits of importance in
16 the Pura Raza Español (PRE) horse were used to estimate genetic and
17 environmental parameters following a heterocedastic model in which data were
18 assigned to stallions. Datasets used ranged from 20,610 (*height at withers*) to
19 48,486 measurements (*length of shoulder*) and the number of animals analysed
20 in the pedigrees varied from 17,662 (*height at withers*) to 23,962 (*dorsal-sternal*
21 *diameter*). Results of heritabilities of the traits varied from 0.09 (*width of chest*
22 and *upper neck line*) to 0.30 (*muscular development*). Further, genetic
23 correlations between traits and their environmental variability were estimated,
24 obtaining values from -0.56 (*muscular development*) to 0.69 (*height at withers*).
25 Also, predicted breeding values for the mean and for the environmental variability
26 were obtained for all horses in the pedigrees, providing individual information
27 about not only the expected phenotypic value of their offspring but also about the
28 expected heterogeneity among them. Results proved the possibility of improving
29 morphological traits and reducing the heterogeneity of offspring at a time by the
30 selection of animals and levels of systematic effects.

31 **Keywords:** *body conformation,* environmental variability, equine.

Introduction

Selection objectives for domestic animals are constantly adapting to major changes in production, the market and society. While some have historically focused on increased production (prolificacy, milk production, birth weight, etc.) others are oriented towards improving functional characteristics. Further, selection programmes also seek to integrate other objectives such as robustness, which is defined as the ability to maintain production potential under a wide variety of environmental conditions, or resilience, which is the maintenance of, or rapid return to, the initial state of performance despite environmental perturbations (Bodin et al., 2010; Iung et al., 2020).The possibility of increasing the robustness of a phenotype against genetic or environmental disturbance is known as canalisation (Bodin et al., 2010). Several papers have demonstrated that environmental variability can be controlled in species such as mice (Formoso-Rafferty et al., 2016; Formoso-Rafferty et al., 2017), rabbit (Garreau et al., 2008) and sheep (SanCristobal-Gaudy et al., 2001) and mainly in production variables, as in the case of birth weight or litter size. Some of these studies involved divergent selection experiments or simulations (Tatliyer et al., 2019). However, studies of canalisation in conformation traits are not very numerous and the bibliography only includes works on fish and cattle (Marjanovic et al., 2016; Neves et al., 2011). In fact, studies in species with long generational intervals are very scarce. In horses, there is one very recent work which addresses the reduction in the variability of horses' rank position in endurance races (Cervantes et al., 2020).

Assuming that genetic heterogeneity of residual variance underlies differences in phenotypic stability, and that a low variance indicates stable performance across environmental factors, residual variance estimates can be employed as an index trait to improve breeding goal uniformity (Iung et al., 2020). The presence of genetic heterogeneity of residual variance suggests that selection can be used to change residual variance based on pedigree information (Sancristobal-Gaudy et al., 1998; Sonesson et al., 2013).

The Pura Raza Español (PRE) horse Studbook comprises around 200,000 individuals in more than 65 countries from all continents (Solé et al. 2018). This

makes it the most important Spanish horse breed and a very important breed in livestock production in economic terms. Furthermore, PRE is one of the hallmarks of Spanish culture and traditions and is the forerunner of other horse breeds (Anaya et al., 2017).

Since its approval in 2004, the PRE breeding programme has aimed both at improving functionality in horse sports, mainly Dressage, and at conformation for sport performance, as the morphology of the horse's body is closely related to performance, and its movements and gaits depend on it (Solé et al. 2013). It has been demonstrated that morphological traits are genetically correlated with certain biokinematic variables at trot and that body conformation is related to a greater or lesser predisposition to Dressage ability, allowing the indirect selection of animals for this discipline (Sánchez-Guerrero et al. 2016a). The body conformation of PRE horses is currently evaluated objectively, through a linear scoring system or quantitative zoometric measurements (Sánchez-Guerrero et al. 2013a).

Due to the great importance that horse morphology presents for PRE breeders, matings are usually planned in order to maintain or improve body conformation, as well as to follow the breed and stud standards. In addition, it is highly desirable for breeders to obtain offspring that present very similar characteristics to their parents and to each other. Hence, the aim of this work was to assess the possibility of using selection to reduce the environmental variability of 13 morphological traits in the PRE horse by selecting the environmental variability genes attributed to the stallions. For this purpose, the genetic parameters and breeding values of the morphological traits were estimated using a canalisation model that assumes heterogeneity of the residual variance for the first time.

Materials and methods

The initial morphological data set analysed in this study comprised records from a total of 111,876 different PRE horses (43,554 males and 68,322 females). Data were obtained from the Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE). Each of these animals had at least one morphological trait measurement collected between 2009 and 2018 in Spain. The number of available records per variable ranged from 20,610 to 48,486. The morphological

96 traits studied included both zoometric measurements and linear scored variables.

97 These traits were selected for being traditionally gathered in basic aptitude tests

98 due to their correlation to Dressage traits (Sánchez-Guerrero et al., 2017).

99 A total of 11 different zoometric measurements were evaluated: *Height at withers*

100 (HaW), *Width of chest* (WoC), *Dorsal-sternal diameter* (DsD), *Buttock-stifle*

101 *distance* (BsD), *Scapular-ischial length* (SiL), *Length of shoulder* (LoS), *Length*

102 *of croup* (LoC), *Length of gaskin* (LoG), *Perimeter of anterior cannon bone*

103 (PoACB), *Perimeter of knee* (PoK) and *Thoracic perimeter* (TP). These variables

104 were measured in centimetres. In addition, 2 linear scored variables evaluated in

105 9 classes were studied: *Upper neck line* (UNL), ranging from class 1 (very poorly

106 marked) to class 9 (very marked) and *Muscular development* (MD), which ranged

107 from class 1 (very little) to class 9 (well developed). All the morphological traits

108 were previously described in works by Sánchez-Guerrero et al. (2013a) and

109 (2016a). The morphological traits are defined in Supporting Information figure 1.

110 The total number of individuals included in the pedigrees analysed (built from the

111 stallions' generation) ranged from 17,662 (height at withers) to 23,962 (dorsal-

112 sternal diameter), depending on the trait analysed. Pedigrees included all data of

113 an animal model: animal (male or female), father and mother. All the generations

114 available were considered (not less than 14 generations). The average number

115 of offspring per stallion with available data that contributed to the estimation was

116 4.78. Table 1 shows the description of the dataset used. Basic statistics were

117 performed using Statistica software 8.0 (Statsoft, Inc., 2007).

118 In this study, a heterocedastic (HE) model developed by San Cristobal-Gaudy et

119 al. (1998) was used. As almost all horses are measured only once on their lives

120 and models require repeated measures per animal, data were assigned to

121 stallions. Theoretically, measurements data could have been assigned equally to

122 dams, but in practice databases would have to be cut, as far fewer broodmares

123 have a sizeable number of offspring. This model assumed that the residual

124 variance is heterogeneous and partially under genetic control. It also assumed

125 that the sampling distribution of data y is Gaussian, as follows:

126
$$y_i = x_i b + z_i s + e^{1/2 (x_i b^* + z_i s^*)} \varepsilon_i$$

4

127

128   where y_i is the measurement of the individual, * indicates the parameters

129   associated with environmental variance, **b** and **b*** are vectors that contain

130   systematic effects and **s** and **s*** are the stallion genetic effects; x_i and z_i are the

131   incidence vectors for systematic and additive genetic effects, respectively; and

132   finally, $\varepsilon_i \sim N(0,1)$. It must be noted that as defined, the direct genetic effects **s**

133   and **s*** are paternal effects that include half of the direct genetic effect of the

134   offspring.

135   The genetic effects **s** and **s*** are distributed together and are assumed to be

136   Gaussian:

137
$$\begin{pmatrix} s \\ s^* \end{pmatrix} \sim N\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \sigma_s^2 & \rho\sigma_s\sigma_{s*} \\ \rho\sigma_s\sigma_{s*} & \sigma_{s*}^2 \end{bmatrix} \otimes \mathbf{A} \right)$$

138

139   where: **A** is the additive genetic relationship matrix; σ_s^2 is the additive genetic

140   variance of the trait; σ_{s*}^2 is the additive genetic variance affecting the

141   environmental variance of the trait; ρ is the coefficient of genetic correlation, and

142    $\otimes$ denotes the Kronecker product.

143   The model applied included offspring sex, with 2 levels (male or female); age,

144   with 8 levels (level 1: ≥3-<4 years old; level 2:≥4-<5 years old; level 3: ≥5-<6

145   years old; level 4: ≥6-<7 years old; level 5: ≥7-<8 years old; level 6: ≥8-<9 years

146   old; level 7: ≥9-<10 years old and level 8: ≥10 years old) and the effect of the

147   interaction between the year-geographical area-season in which the data was

148   recorded, as systematic effects (**b** and **b***), with 338 (HaW) to 543 (LoS) levels.

149   The model was resolved using the GSEVM programme (Ibáñez-Escriche et al.

150   2010). The variance components were obtained by running 500,000 iterations,

151   sampling 1 of each 100 iterations and discarding the first 50,000 as bur-in. This

152   software allows us to define the genetic parameters for mean and environmental

153   variability while providing their correspondent breeding values following this

154   model.

155   The global heritability (h^2) of each of the traits was considered as the mean of the

156   solutions for each of the systematic effects affecting the residual variability.

157   Besides, the heterogeneity of the residual variances also allowed us to obtain

158   specific heritabilities for the different levels of each systematic effect within the

159   variables, by adding to the specific solution for a level the mean of the solutions

160   for each of the rest of the systematic effects affecting the residual variability

161   (Formoso-Rafferty et al., 2017).

162   The genetic coefficient of variation of environmental variability (GCV) was

163   computed as the mean value of the root square of each of the iterations of the

164   posterior distribution of σ^2_{s*} (Hill & Mulder, 2010).

165   **Results**

166   Table 1 shows the number of stallions and records and the mean value of the

167   morphological variables studied in this work. According to the coefficient of

168   variation, WoC was the zoometric measurement that presented the highest

169   variability (10.41% in stallions and 9.64% in offspring), while HaW displayed the

170   lowest CV (2.87% and 3.03%, respectively). Meanwhile, the two linear scored

171   variables (UNL and MD) showed a very similar CV in stallions and offspring

172   (19.83% and 19.80% in the case of UNL vs. 24.00% and 23.37% in MD).

173   The variance components and genetic parameters estimated are shown in Table

174   2. The genetic variances for the variability ranged between 0.05 (TP) and 0.58

175   (HaW). The coefficients of genetic correlation between the traits and their

176   corresponding environmental variability were mainly positive, although they

177   presented a wide range of values: from high and negative (-0.56) in the case of

178   MD, to high and positive (0.71) in the case of TP. Genetic coefficient of variation

179   estimates are also shown in this table. The lowest GCV value was for TP (0.23),

180   while HaW produced the highest value (0.76).

181   Global heritabilities of the traits, estimated for an average scenario of fixed

182   effects, ranged from 0.09 (WoC and UNL) to 0.30 (MD). Heritabilities for the

183   morphological traits in study according to the systematic effect of sex are shown

184   in Figure 1. In all variables, the differences between the effect of gender within

185   the same trait do not surpass 0.08. Nonetheless, it is possible to observe striking

186   discrepancies of heritabilities between genders in some variables. This is the
187   case of PoK and TP, which show differences of 0.05 and 0.07 between males
188   and females, respectively.

189   Heritabilities for the morphological traits as systematic effects according to the 8
190   levels of age are displayed in Figure 2. All of the variables show a fairly stable
191   heritability throughout the life of the animal. However, many of them show the
192   greatest heritabilities in the early stages of life, such as UNL, MD, LoS, LoC and
193   TP in level 1 and DsD in level 2. Conversely, HaW, WoC and BsD have a greater
194   heritability in level 7, which corresponds to the 9 to 10 years old age group. The
195   rest of the traits present the highest values of heritability at level 3 (LoG) and level
196   5 (SiL, PoACB and PoK). Finally, heritabilities according to the interaction year-
197   geographical area-season (results not shown) present an average value of 0.20,
198   with the 50% of them ranging between 0.01 and 0.18.

199   The evolution of mean predicted breeding values (PBV) for the traits and for their
200   variability through years of birth of individuals are shown in Figure 3. The general
201   trend of both predicted breeding values is similar, with an initial rise in values
202   followed by a more accentuated increase from 1991 until the last years of birth.

203

Discussion

205   Horse conformation is of great importance in any breed and is therefore the result
206   of generations of natural and artificial selection. Apart from aesthetic reasons, the
207   relationship between morphology and biokinematics permits the early selection
208   of individuals with a greater predisposition for dressage. This has led to the
209   inclusion of morphological traits in the PRE breeding programme (Sánchez-
210   Guerrero et al., 2016a). Mostly, breeders tend to select horses as breeding
211   animals, especially stallions, due to their interest in obtaining foals with specific,
212   desirable morphological characteristics and following the breed standards, which
213   establish certain limits between which the variables must be included. Despite
214   having genetic tools at their disposal for this purpose, as in the case of PBV,
215   homogeneous offspring is not always possible to achieve. Apart from the distinct
216   genetic breeding values of stallions, there are detectable differences in the

variability of the offspring of a given father compared to others. In fact, some stallions present a high homogeneity among their offspring, while others of similar genetic value present offspring with greater variability. Consequently, selection for environmental variability is of special relevance in equine species (Cervantes et al., 2020). This work aimed to study for the first time the environmental variability in 13 morphological variables related to dressage using a heterogeneity model. Data was assigned to the stallion in order to obtain repeated records for one animal, since it is only possible to select homogeneity when more than one record is collected per animal. Different previous works have demonstrated the suitability of this model (Formoso-Rafferty et al., 2017; Pun et al., 2013). The selection success under this model has already been reported after seven generations of selection (Formoso-Rafferty et al., 2016) and continues being successful after more than 20 generations (Formoso-Rafferty et al., 2020), in which the model is completely comparable to that used here in horses, with the birth weight and its variability assigned to the mother. An alternative to deal with heritability estimates could be considering the traits as different traits by sexes, but in this work a different approach has been implemented. The morphological variables are not exclusively paternal, but also maternal. The choice of attributing data to the stallions meets both the requirements of the model and the fact that males have an average of 4.78 offspring versus 1.61 in females.

Differences in variability were observed between the morphological traits in the coefficient of variation of the dataset of this study (Table 1). For this parameter, the level of variation in the 11 zoometric measurements was low to medium, which is very similar to the CVs obtained in the work of Sánchez-Guerrero et al. (2013b). The CV of the linear scored variables were very similar between them and also match previous studies in this breed. In the traits with higher values of CV, it would be more urgent to use selection in order to reduce the variation, assuming genetic causes.

Additive genetic variance of the residual variance is also a dimensionless factor. The difference between the highest and lowest genetic variances of residual variances (HaW and TP) is noticeable (11.60). We must remember that the additive genetic variance for the variability of a trait could be affected by a scale effect, due to the presence of the additive genetic variance (Tatliyer et al., 2019).

250   One key parameter obtained in this study is genetic correlation, which measures
251   the reciprocity between the genetic variance of the traits and their environmental
252   variability. These correlations determine responses in the mean or the variability
253   when selecting by the additive variance (Tatliyer et al., 2019). Thus, high genetic
254   correlations imply that it is not possible to canalise the traits without major
255   changes in their mean values (Gutiérrez et al., 2006). The sign of the value of the
256   genetic correlation determine the direct or indirect relationship between additive
257   genetic variance and environmental variability, so that a positive one implies that
258   a selection in favour of the mean would be accompanied by a more environmental
259   variability, and thus, a greater heterogeneity. For example, a very high, positive
260   coefficient of genetic correlation, as in the cases of TP and HaW (0.71 and 0.69
261   respectively), would imply that selecting stallions with high PBV values for these
262   variables would also increase the variability and hence produce a more
263   heterogeneous offspring. On the contrary, a negative and high correlation, which
264   is the case of MD, implies the possibility of exerting a selection on the character
265   while reducing the variability of its descendants. The majority of morphological
266   traits present low, positive values, in line with other studies of conformation
267   characters in different species, such as fish or cattle (Marjanovic et al., 2016;
268   Neves et al., 2011). The study by Tatliyer et al. (2019) showed that positive
269   genetic correlations can be partially generated by a scale effect, so that the
270   modification of the mean of a trait would imply a modification in the same sense
271   in the variability. In this way, intermediate values for the genetic correlations
272   between the trait and its variability (0.11 to 0.69) would be attributed to the scale
273   effect.

274   The GCV parameter can be interpreted as a measure of the evolvability (Hill &
275   Mulder, 2010), and thus, high values indicate a good evolutionary adaptability of
276   the traits. Our results indicated GCV estimates from 0.23 (TP) to 0.76 (HaW). All
277   these values are within the range described in previous studies, except in the
278   case of HaW. GCV values higher than 0.69 have been only described in
279   simulation studies and were not considered relevant. Therefore, it can be
280   suspected that the estimation of this variable is not very reliable. This may be due
281   to the fact that measures of HaW follow an asymmetric distribution because of

282 the existence of a greater number of horses dedicated to sports, where there is

283 a greater demand for taller animals (Hill & Mulder, 2010; Tatliyer et al., 2019).

284 The global heritabilities of the traits mostly remain low, under 0.20, although in

285 some traits they had a medium range of values. Most of the global heritabilities

286 obtained in this study are lower than those previously reported in the literature,

287 although some are very similar (Sánchez-Guerrero et al. 2013a, 2016a). The

288 differences among models used could explain these dissimilarities in heritability,

289 as heteroscedastic models assume that records are balanced across the dataset,

290 whereas in the real dataset they are unbalanced (Cervantes et al., 2020).

291 Even though the influence of sex on heritabilities is different between

292 morphological traits, in general, males and females (Figure 1) did not show

293 noticeable differences in heritabilities. PoK and TP are the two traits that stand

294 out of the rest and exhibit a higher heritability in females and males, respectively.

295 PoK is a forelimb perimeter that is of great importance in dressage (Sánchez-

296 Guerrero et al. 2016a), while TP measurements are influenced by pregnancy, as

297 this perimeter grows as the fetus develops, which would explain the greater

298 heritability and stability in stallions. As the selection response is proportional to

299 the heritability, higher heritability results in a greater response (Formoso-Rafferty

300 et al., 2017), and artificial selection for these traits would be more favourable in

301 the gender with higher heritability, namely, in mares in PoK and stallions in TP.

302 The influence of age as a fixed effect on heritabilities of the morphological traits

303 (Figure 2) is not homogeneous either among the variables in study, although they

304 present a similar magnitude. More interestingly, the results demonstrate that

305 there are differences between levels of age within the same trait. Although a

306 horse is considered adult at 4 years old, these differences can be attributed to

307 the fact that zoometric measurements can change with the age of the horse if

308 they are still growing or are affected by aging (Wejer & Lewczuk, 2016).

309 Moreover, these results can be interpreted so that at ages where there exists a

310 greater heritability of the trait, horses express more their genotype than the

311 residual variance: in other words, they are less affected by the environment. This

312 would explain the fact that zoometric measurements of relevant morphological

313 lengths of the horse, such as HaW or WoC, show the highest heritabilities at later

ages, as they may be influenced by different growth precocities which may be stabilised over the years. In addition, the traits with higher heritability, which are therefore less influenced by the environment at early ages, are related to dressage and exercise (e.g., MD). It has been demonstrated that zoometric measurements and physical condition can vary according to the amount of exercise to which the animal is subjected (Sánchez-Guerrero et al., 2019) . As most dressage horses begin training at around 3 or 4 years old and continue over a considerable number of years, their morphology at age level 1 is not affected by exercise as much as at older age levels. In addition, certain diseases affecting the morphology of the horse, such as osteochondrosis or cresty neck, are associated to aging (Sánchez-Guerrero et al. 2016b; Bourebaba et al.,2019).

The work of Formoso-Rafferty et al., 2017 puts forward the possibility of modulating heritability of the traits by selecting the most convenient combination of levels of the systematic effects. Therefore, as the selection response is proportional to heritability, the selection of a morphological trait would be greater if the measurements are registered at the age level at which it presents higher heritabilities. Nowadays, the data for all morphological traits of PRE horses are collected at the same time for obvious practical and economic reasons, when the animals are 3 or more years old. Therefore, the choice of the most important variables for the selection objectives in the PRE Breeding Programme is of major significance in order to establish the ideal age for measuring and selecting the breeding animals. According to our results, for example, the linear conformation score should be carried out at an early age, at the same time as some zoometric measurements are currently taken.

The general trend for both predicted breeding values in the population is initial stability or slight increases, followed by a clear increase in recent years. Horses born around the 2000s present higher average PBVs than older individuals. This can be explained by the fact that these generations encompass the years when the PRE breeding programme was started and a more effective breeding plan has been carried out since then, improving the breeding values of animals. Likewise, mean PBV*s have followed a similar path and variability has increased in turn, with parallel values in morphological traits with positive genetic correlations. The genetic trend in the variability of these traits depends on the

347   genetic correlations with the mean trait and whether this has been selected or
348   not. In addition, the assessment of some zoometric measurements has changed
349   over the breed's history. As a consequence, the environmental variability of
350   morphological traits could be affected by way some variables are collected, such
351   as in the two perimeters and the length of shoulder, whose variability has
352   diminished over the last 20 years, which is when the way animals were measured
353   has been standardized and breeders' interest in certain traits has changed.
354   Finally, these results may be partly justified by a scale effect, which would explain
355   the fact that the increase in the mean values of a trait leads to a rise in its
356   environmental variability in the case of traits that show positive genetic
357   correlations (Tatliyer et al., 2019). In the case of MD, a trait with a high negative
358   genetic correlation, PBV*s tend to decrease as the PBVs rise, as the selection of
359   animals with high genetic values for the mean provide a greater homogeneity in
360   progeny.

361   In conclusion, we found statistical evidence that there is a genetic component for
362   the residual variance, which suggests it would be possible to select for this
363   component. However, not all the traits studied could be modulated in the same
364   way. If the correlation is positive and high, the morphological trait cannot be
365   improved, while environmental sensitivity is lowered. On the contrary, negative
366   correlations will provide the ideal scenario for simultaneously selecting for larger
367   measurements and obtaining a homogeneous offspring. The different
368   heritabilities among the levels of the systematic effects, especially age in terms
369   of practicality, can also provide ideas of how to record performance in order to
370   improve the response to selection. In other words, it is essential to establish the
371   specific age at which measurements should be taken, following the most
372   important selection objectives. Moreover, in the future, the creation of a global
373   index combining predicted breeding values for the traits and for their variability
374   could be used as a new tool for breeders.

375

380 **Conflict of Interest Statement**

381 The authors declare that they have no competing interests.

382

383 **Data Availability Statement**

384 The data that support the findings of this study are available from the Asociación
385 Nacional de Criadores de Caballos de Pura Raza Española (ANCCE).
386 Restrictions apply to the availability of these data, which were used under license
387 for this study. Data are available from the authors with the permission of ANCCE.

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Tables

Table 1: Descriptive statistics of dataset. Number of stallions and records, mean values and standard error of mean (SEM) and coefficient of variation (CV) of their zoometrical measurements, and number of stallions and records, range, quartile range and coefficient of variation (CV) of their linear scored variables.

Zoometrical measurements	Number of stallions	Mean±SEM	C.V. (%)	Number of records[†]	Mean[†]±SEM	C.V. (%)
HaW	5,297	163.97±0.06	2.87	20,610	161.03±0.03	3.03
WoC	7,880	43.00±0.05	10.41	42,203	41.39±0.02	9.64
DsD	7,807	74.72±0.05	5.85	41,759	73.82±0.02	5.63
BsD	5,834	52.68±0.03	4.78	23,782	51.11±0.02	5.54
SiL	7,815	161.47±0.06	3.35	41,862	159.94±0.03	3.41
LoS	8,411	62.28±0.04	5.71	48,486	66.65±0.02	5.83
LoC	5,849	54.36±0.04	5.57	23,823	52.83±0.02	5.85
LoG	5,845	55.28±0.06	7.70	23,790	52.20±0.03	8.38
PoACB	7,871	21.24±0.01	6.24	42,250	20.30±0.01	6.52
PoK	7,818	34.21±0.02	6.36	41,864	32.19±0.01	6.75
TP	7,803	190.53±0.10	4.41	41,743	189.94±0.05	4.92

Linear scored variables	Number of stallions	Range	Quartile range	C.V. (%)	Number of records[†]	Range	Quartile range	C.V. (%)
UNL	5,854	3-9	2.00	19.83	23,818	1-9	2.00	24.00
MD	5,852	2-8	1.00	19.80	23,829	1-9	1.00	23.37

[†]Records correspond to measurements of stallions' offspring. *Height at withers* (HaW), *Width of chest* (WoC), *Dorsal-sternal diameter* (DsD), *Buttock-stifle distance* (BsD), *Scapular-ischial length* (SiL), *Length of shoulder* (LoS), *Length of croup* (LoC), *Length of gaskin* (LoG), *Perimeter of anterior cannon bone* (PoACB), *Perimeter of knee* (PoK), *Thoracic perimeter* (TP), *Upper neck line* (UNL) and *Muscular development* (MD).

Table 2: Additive genetic variances of the mean (σ_s^2) and of the residual variance (σ_{s*}^2) of the traits, global heritabilities estimates of the systematic effects affecting the traits (h^2), coefficient of genetic correlation ($\rho_{a,a*}$), genetic coefficient of variation (GCV) estimates and corresponding SD from posterior marginal distributions.

Trait	σ_s^2 (SD)	σ_{s*}^2 (SD)	h^2 (SD)	$\rho_{s,s*}$ (SD)	GCV (SD)
HaW	6.74 (0.24)	0.58 (0.03)	0.28 (0.04)	0.69 (0.02)	0.76 (0.02)
WoC	1.47 (0.05)	0.20 (0.01)	0.09 (0.01)	-0.11 (0.04)	0.45 (0.02)
DsD	1.51 (0.07)	0.35 (0.02)	0.14 (0.02)	0.14 (0.03)	0.59 (0.02)
BsD	0.54 (0.04)	0.20 (0.02)	0.11 (0.01)	0.18 (0.06)	0.45 (0.02)
SiL	5.87 (0.17)	0.06 (0.01)	0.25 (0.01)	0.54 (0.04)	0.24 (0.01)
LoS	1.72 (0.08)	0.12 (0.01)	0.19 (0.02)	0.11 (0.04)	0.34 (0.01)
LoC	1.13 (0.06)	0.10 (0.02)	0.18 (0.02)	0.37 (0.05)	0.32 (0.02)
LoG	1.26 (0.04)	0.19 (0.02)	0.17 (0.02)	0.19 (0.05)	0.44 (0.02)
PoACB	0.20 (0.01)	0.38 (0.04)	0.17 (0.03)	0.51 (0.03)	0.61 (0.02)
PoK	0.51 (0.02)	0.29 (0.02)	0.21 (0.02)	0.22 (0.03)	0.54 (0.01)
TP	14.65 (0.62)	0.05 (0.01)	0.21 (0.01)	0.71 (0.05)	0.23 (0.02)
UNL (class)	0.10 (0.01)	0.06 (0.01)	0.09 (0.01)	0.25 (0.08)	0.24 (0.02)
MD (class)	0.04 (0.00)	0.29 (0.02)	0.30 (0.19)	-0.56 (0.03)	0.54 (0.02)

Height at withers (HaW), *Width of chest* (WoC), *Dorsal-sternal diameter* (DsD), *Buttock-stifle distance* (BsD), *Scapular-ischial length* (SiL), *Length of shoulder* (LoS), *Length of croup* (LoC), *Length of gaskin* (LoG), *Perimeter of anterior cannon bone* (PoACB), *Perimeter of knee* (PoK), *Thoracic perimeter* (TP), *Upper neck line* (UNL) and *Muscular development* (MD).

Figure Legends

Figure 1: Heritabilities for morphological traits according to sex (male or female) and standard deviation.
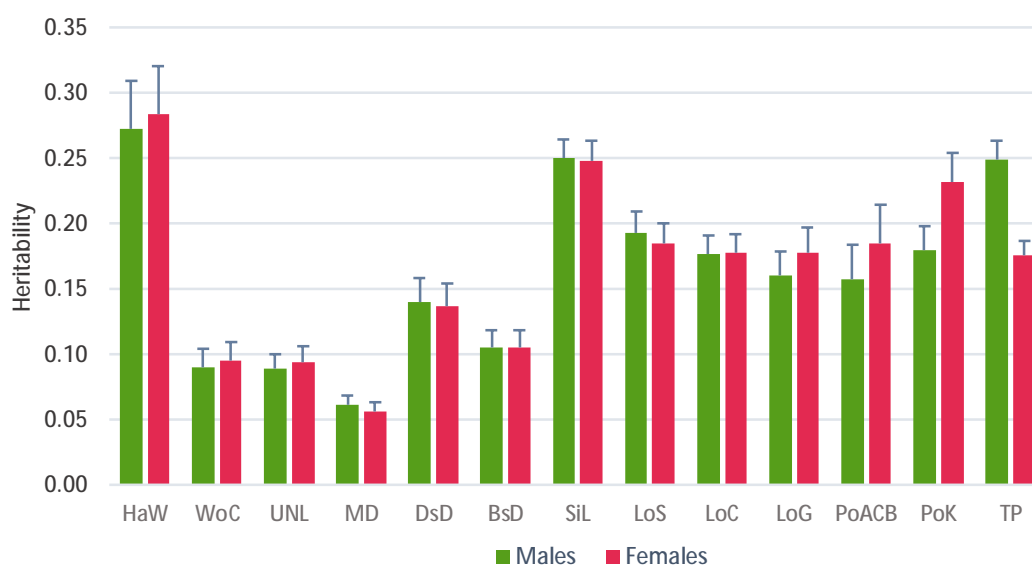
Legend: HaW: Height at withers; WoC: Width of chest; UNL: Upper neck line; MD: Muscular development; DsD: Dorsal-sternal diameter; BsD: Buttock-stifle distance; SiL: Scapular-ischial length; LoS: Length of shoulder; LoC: Length of croup; LoG: Length of gaskin; PoACB: Perimeter of anterior cannon bone; PoK: Perimeter of knee and TP: Thoracic perimeter.

Figure 2: Heritabilities for morphological traits according to age levels.
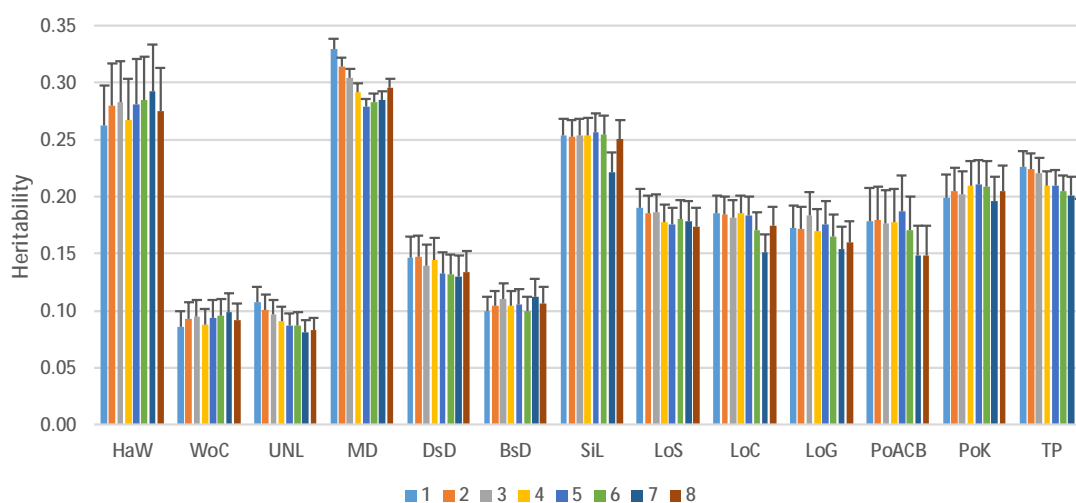
Legend: HaW: Height at withers; WoC: Width of chest; UNL: Upper neck line; MD: Muscular development; DsD: Dorsal-sternal diameter; BsD: Buttock-stifle

distance; SiL: Scapular-ischial length; LoS: Length of shoulder; LoC: Length of croup; LoG: Length of gaskin; PoACB: Perimeter of anterior cannon bone; PoK: Perimeter of knee and TP: Thoracic perimeter. 1: ≥3-<4 years old; 2: ≥4-<5 years old; 3: ≥5-<6 years old; 4: ≥6-<7 years old; 5: ≥7-<8 years old; 6: ≥8-<9 years old; 7: ≥9-<10 years old and 8: ≥10 years old.

Figure 3: Mean predicted breeding values (PBV, primary axis) and mean predicted breeding values for variability of morphological traits in this study (PBV*, secondary axis) across years of birth (abscissa axis).
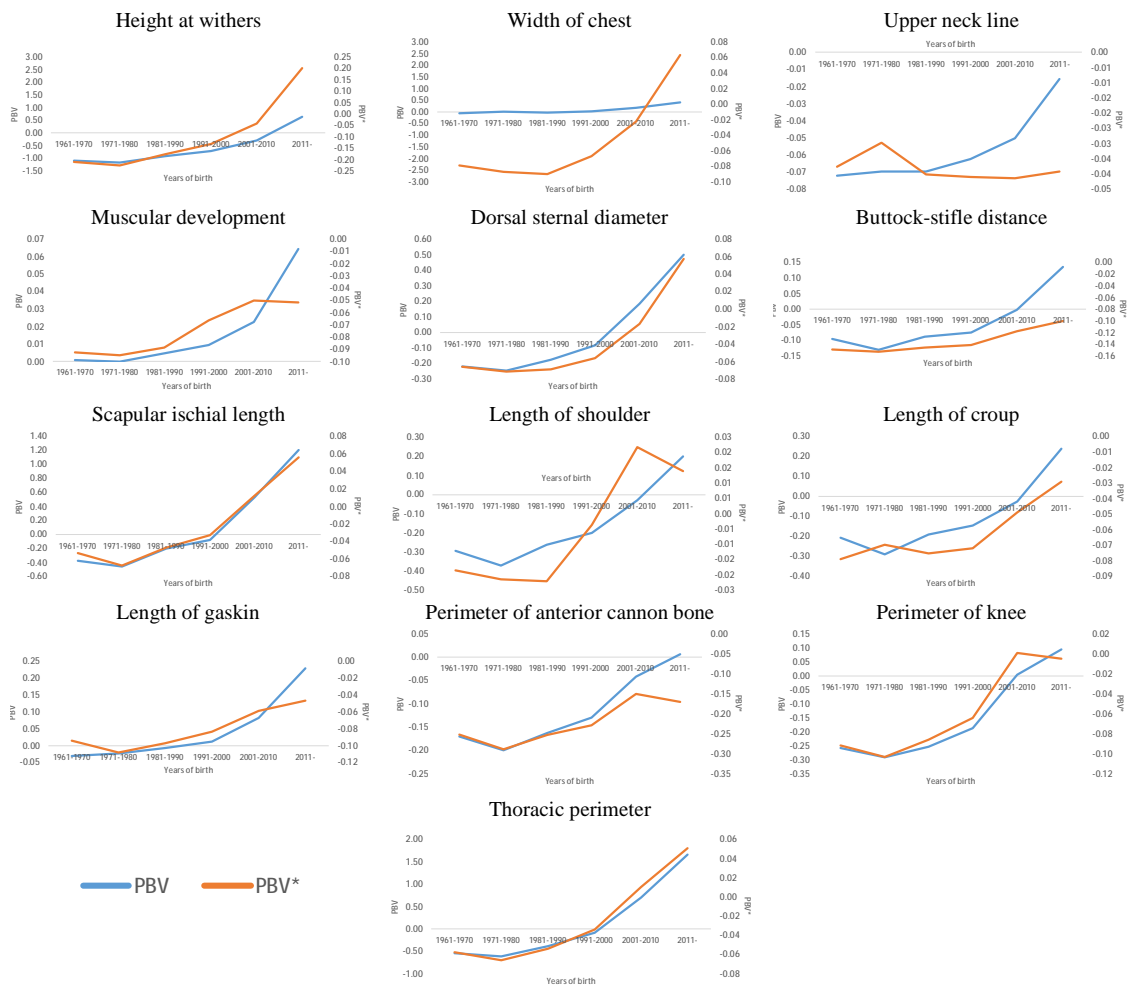
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Title: Representation and description of the morphological traits analysed in PRE horses.

1: Height at withers; 2: Width of chest; 3: Dorsal-sternal diameter; 4: Buttock-stifle distance; 5: Scapular-ischial length; 6: Length of shoulder; 7: Length of croup; 8: Length of gaskin; 9: Perimeter of anterior cannon bone; 10: Perimeter of knee and 11: Thoracic perimeter.

Following the basic aptitude assessment sheet of ANCCE, the zoometrics measurements are described as:

- *Height at withers*: Length of the vertical segment, consisting of the highest point of the withers and the ground where the horse is standing.

- *Width of chest*: Distance between the points of shoulder.

- *Dorsal-sternal diameter:* Length of the straight segment between the highest point of the withers and the sternum along the plane immediately behind the elbow.

- *Buttock-stifle distance:* Distance that links the ventral point of the tuber ischii (point of buttock) and the stifle.

- *Scapular-ischial length:* Distance of the straight segment, between the point of shoulder and the point of buttocks.

- *Length of shoulder:* Straight distance from the highest point of the withers to the point of shoulder.

- *Length of croup:* Length of the straight segment between the most cranial point of the tuber coxae and the most caudal of the tuber ischii.

- *Length of gaskin:* Distance between the stifle and the point of hock.

- *Perimeter of anterior cannon bone:* Perimeter of the upper third of the metacarpal region.

- *Perimeter of knee:* Maximum perimeter of the transversal plane of the carpal bone.

- *Thoracic perimeter:* The reference points are the lowest point of the withers and the sternum along the plane immediately behind the elbow.

Meanwhile, the studied linear scored variables are defined as:

- *Upper neck line*: Caudal view of the width of the upper edge of the neck.

- *Muscular development*: Condition of muscle tone and fat deposits mainly evaluated at the back, loin, croup and buttock.