

Designing an early selection morphological linear traits index for dressage in the Pura Raza Español horse

M. J. Sánchez-Guerrero^{1†}, I. Cervantes², A. Molina³, J. P. Gutiérrez² and M. Valera¹

¹Departamento de Ciencias Agro-Forestales, Universidad de Sevilla, Ctra. Utrera km 1, 41013 Sevilla, Spain; ²Departamento de Producción Animal, Universidad Complutense de Madrid, Avda. Puerta de Hierro s/n, 28040 Madrid, Spain; ³Departamento de Genética, Universidad de Córdoba, Ctra. Madrid-Cádiz Km.396, 14071 Córdoba, Spain

(Received 1 March 2016; Accepted 17 September 2016; First published online 14 November 2016)

Making a morphological pre-selection of Pura Raza Español horses (PRE) for dressage is a challenging task within its current breeding program. The aim of our research was to design an early genetic selection morphological linear traits index to improve dressage performance, using 26 morphological linear traits and six dressage traits (walk, trot, canter, submission, general impression – partial scores – and total score) as selection criteria. The data set included morphological linear traits of 10 127 PRE (4159 males and 5968 females) collected between 2008 and 2013 (one record per horse) and 19 095 dressage traits of 1545 PRE (1476 males and 69 females; 12.4 records of average) collected between 2004 and 2014. A univariate animal model was applied to predict the breeding values (PBV). A partial least squares regression analysis was used to select the most predictive morphological linear traits PBV on the dressage traits PBV. According to the Wold Criterion, the 13 morphological linear traits (width of head, head–neck junction, upper neck line, neck–body junction, width of chest, angle of shoulder, lateral angle of knee, frontal angle of knee, cannon bone perimeter, length of croup, angle of croup, ischium–stifle distance and lateral hock angle) most closely related to total score PBV, partial scores PBV and gait scores PBV (walk, trot and canter) were selected. A multivariate genetic analysis was performed among the 13 morphological linear traits selected and the six dressage traits to estimate the genetic parameters. After it, the selection index theory was used to compute the expected genetic response using different strategies. The expected genetic response of total score PBV (0.76), partial scores PBV (0.04) and gait scores PBV (0.03) as selection objectives using morphological linear traits PBV as criteria selection were positive, but lower than that obtained using dressage traits PBV (1.80, 0.16 and 0.14 for total score PBV, partial scores PBV and gait scores PBV) or dressage traits PBV and morphological linear traits PBV (2.97, 0.16 and 0.15 for total score PBV, partial scores PBV and gait scores PBV), as selection criteria. This suggests that it is possible to preselect the PRE without dressage traits PBV using as selection criteria the morphological linear traits PBV, but the expected genetic response will be lower.

Keywords: Andalusian horse, conformation, equine, genetic evaluation, linear scoring system

Implications

The Spanish horse industry moves an increasing amount of money being estimated at 0.5% of Spanish Gross National Product. Within this industry, Pura Raza Español horses (PRE) is the most important breed in terms of census and impact on international trade. The growing demand for dressage PRE contrasts with the difficulties in obtaining reliable genetic evaluations. This work aims the selection of the morphological traits more related to functionality, allowing an increase in the reliability of the genetic evaluations, as well as a pre-selection of animals which will be trained for dressage, resulting in savings costs and increasing the genetic progress of the breed.

Introduction

Selecting animals with conformation characteristics which make them excel in sport performance is a major aim of horse breeding programs for the different functional traits (Belloy and Bathe, 1996). In the PRE breeding program, there is an increased interest for horses which demonstrate high performance in sport competitions, especially dressage (Sánchez *et al.*, 2014). Consequently, PRE with superior dressage performances have a greater economic value than other PRE. The main goal of the PRE breeding program is to improve not only the functionality, but also its conformation for sport performance (Sánchez *et al.*, 2016). To accomplish these objectives and obtain data for the genetic evaluations, the PRE were tested in morphological and performance tests.

[†] E-mail: v32sagum@gmail.com

So, a linear assessment methodology was developed and 26 morphological linear traits (LT) have been collected in a systematic way since 2008 (Sánchez *et al.*, 2013). Every year, around 2000 PRE participate in these morphological tests. Besides, young horses (4 to 6 years old) have been tested for dressage traits (DT) since 2004 as part of the PRE breeding program in Spain (around 200 PRE take part each year in this performance test). The high number of PRE with records in morphological tests compared with the low number of participants in dressage could enable us to make a suitable selection by means of LT. The selection of those horses which display adequate morphological qualities for dressage performance would benefit the genetic progress and, therefore it would be possible to screen the animals before undergoing training for dressage (Koenen *et al.*, 1995; Olsson *et al.*, 2008; Ducro *et al.*, 2009). Therefore, the main objective of this work was to study the relationship between LT predicted breeding value (PBV) and DT PBV as a basis for designing an early stage selection index to improve dressage performance, using only LT PBV or both DT PBV and LT PBV together as pre-selection criteria.

Material and methods

Data set

The dressage data set included a total of 19 095 phenotypic performance records that were the DT of one reprise (each DT was composed of five different partial scores (PS): walk, trot, canter (this subset of three PS has been called gait scores; GS) submission, general impression and the average of them called total score; Supplementary Table S1). These performance records belonged to 1545 PRE (1476 males and 69 females; 12.4 records of average) collected between 2004 and 2014 at 469 official dressage tests of young PRE (4 to 6 years old) in Spain. These horses belonged to a total of 572 studs. In these events, the dressage discipline included two dressage tests (two identical reprises), and each consisted of an exercise where the five PS and a TS were given by three judges. Each dressage test (reprise) was evaluated separately by each judge and each one gives a score ranging from 1 to 10 for each DT (in a subjective scale where 1 was the worst and 10 the best). The scores used as DT were the average from the three judges for each DT in each reprise. The TS used was the averaged and rescaled to 1 to 100 points of the five PS.

The morphological data set included morphological linear evaluations from a total of 10 127 horses (4159 males and 5968 females) collected between 2008 and 2013 (one record per horse). There were 687 PRE with both traits; DT and LT, which linked both data sets with 5359 common ancestors. In each morphological linear record, a total of 26 different LT (Table 1) were evaluated, 18 of which were primary traits (directly related with body measurements) and eight of which were secondary traits (not related with objective measurements). All these LT were described in Sánchez *et al.* (2013). The linear assessment was carried out by the 20 appraisers, using a structured score sheet with a scale of nine

Table 1 Basic statistics of the 26 morphological linear traits and the six dressage traits analyzed in the Pura Raza Español horse

	Range	Mean ¹	Mode	CV (%)
Morphological linear traits				
Primary traits				
Length of head	1–9	5.57	5	21.29
Width of head	1–7	3.46	3	18.09
Space between jaws	1–9	4.36	5	30.06
Length of neck	1–9	5.57	6	30.19
Neck–body junction	1–9	4.60	5	27.22
Width of chest	2–9	7.14	7	26.42
Length of back	1–9	4.91	5	36.44
Length of loin	1–9	6.28	7	31.21
Length of shoulder	1–9	5.05	6	34.23
Angle of shoulder	1–9	7.04	7	27.80
Length of forearm	1–9	6.55	6	24.19
Cannon bone perimeter	1–9	5.30	5	21.62
Length of croup	1–9	6.07	6	17.46
Angle of croup	1–9	5.88	7	51.68
Point of hip–stifle distance	1–9	4.34	3	36.83
Ischium–stifle distance	1–9	3.92	4	33.87
Length of buttock	1–9	4.84	5	38.00
Length of leg	1–9	6.16	7	25.30
Secondary traits				
Head–neck junction	1–9	4.83	5	24.10
Upper neck line	1–9	5.23	5	22.82
Dorsal line	1–9	4.72	5	23.61
Lateral angle of knee	1–9	5.15	5	14.76
Frontal angle of knee	1–8	5.34	5	14.82
Rear tendon development	1–9	4.91	5	21.17
Hock from rear	1–9	4.13	4	19.94
Lateral hock angle	1–9	5.08	5	19.35
Dressage traits				
Walk	2–8.7	6.49	6.5	9.31
Trot	4–9.2	6.58	6.5	7.54
Canter	3–8.8	6.64	6.5	7.14
Submission	2–9	6.42	6.5	8.54
General impression	3.5–9	6.55	6.5	7.23
Total score	41–86.2	65.33	65	6.94

¹Any standard error was >0.05.

categories, in which the extremes represented the biological extremes for each trait (Sánchez *et al.*, 2013). These appraisers had been previously trained and tested to select those horses which provided the most accurate ratings in the practical tests (Sánchez *et al.*, 2013) and a mean of two linear scores made by two different appraisers was used in each linear morphological record.

Statistical and genetic analysis

All traits (morphological and performance ones) were first investigated by univariate analyses, to obtain preliminary estimates of variance components and PBV for all the animals in the pedigree, using two univariate animal models: a morphological model described in Sánchez *et al.* (2013) for LT and a dressage model described in Sánchez *et al.* (2014) for DT. The morphologically fitted model included the following systematic effects: age (eight classes: 3, 4, 5, 6, 7, 8,

9, >10 years old, the average age was 5.2 ± 2.38 years old), sex (male or female), geographical region; (1, ..., 49) and combination of appraiser \times event (1, ..., 461). The equation in matrix notation for the morphological model was $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$, and it contained:

$$\begin{pmatrix} \mathbf{u} \\ \mathbf{e} \end{pmatrix} \sim N\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{A}\sigma_u^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_e^2 \end{bmatrix}\right)$$

where \mathbf{y} is the vector of observations, \mathbf{X} the incidence matrix of systematic effects, \mathbf{Z} the incidence matrix of animal genetic effects, \mathbf{b} the vector of systematic effects, \mathbf{u} the vector of direct animal genetic effects, \mathbf{e} the vector of residuals, σ_u^2 the direct genetic variance, σ_e^2 the residual variance, \mathbf{I} an identity matrix, \mathbf{A} the numerator relationship matrix. The dressage-fitted model included the following systematic effects: age (4, 5 and 6 years old, the average age was 4.8 ± 0.77 years old), sex (male or female), stud of birth (1, ..., 572) and event (1, ..., 469). The equation in matrix notation for the dressage model was $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wp} + \mathbf{Qr} + \mathbf{Nm} + \mathbf{e}$, and contained:

$$\begin{pmatrix} \mathbf{u} \\ \mathbf{p} \\ \mathbf{r} \\ \mathbf{m} \\ \mathbf{e} \end{pmatrix} \sim N\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{A}\sigma_u^2 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_p^2 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_r^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_m^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_e^2 \end{bmatrix}\right),$$

where \mathbf{y} is the vector of observations, \mathbf{X} the incidence matrix of systematic effects, \mathbf{Z} the incidence matrix of animal genetic effects, \mathbf{W} the incidence matrix of permanent environmental effects, \mathbf{Q} the incidence matrix of the rider effect, \mathbf{N} the incidence matrix of rider–horse interaction, \mathbf{b} the vector of systematic effects, \mathbf{u} the vector of direct animal genetic effects, \mathbf{p} the vector of permanent environmental effects, \mathbf{r} the vector of rider effects (1, ..., 739), \mathbf{m} the vector of rider–horse interaction effects (1, ..., 2089), \mathbf{e} the vector of residuals, σ_u^2 the direct genetic variance, σ_p^2 the permanent environmental variance, σ_r^2 the rider variance, σ_m^2 the rider–horse interaction variance, σ_e^2 the residual variance, \mathbf{I} an identity matrix, \mathbf{A} the numerator relationship matrix. Pedigree information for genetic evaluation was collected from the PRE official stud-book. At least four generations of all the horses in control were included in the pedigree file, making a total of 37 231 animals.

Selection of the morphological linear traits

The selection of the LT most closely related with DT was performed using the PBV of the 37 231 PRE. A partial least squares procedure (PLS) using the reduced rank regression factorial extraction method was implemented to investigate the relationship between DT PBV as dependent variables and the LT PBV as model effects. It was conducted three times: first, using TS PBV as the dependent variable; second, using PS PBV and third using individual GS (walk, trot and canter) PBV. PLS is a statistical method related to principal components and multiple regression techniques. Unlike the main

components, PLS selects factors of the predictors and of the responses that have maximum covariance, whereas principal components regression effectively selects for maximum variance, subject to orthogonal constraints. In contrast, reduced rank regression selects for as much variation in the predicted responses as possible, effectively ignoring the predictors for the purposes of factor extraction. In reduced rank regression, the Y-weights are the eigenvectors of the covariance matrix of the responses predicted by ordinary least squares regression, and the X-scores are the projections of the Y-scores onto the X space (this technique is also called projection to latent structures). PLS works by extracting one factor at a time, be it the centered and scaled matrix of predictors or the centered and scaled matrix of response values. The PLS method starts with a linear combination of the predictors, which is called a score vector, with its associated weight vector. The specific linear combination is the one that has maximum covariance with some response linear combination (Wold, 1994). It is especially appropriate when the independent variables (regressors) are measured with error (i.e. they are not considered fixed) and correlations or colinearity exists among them.

For trait selection, the Wold Criterion (Wold, 1994) was used after selecting only the 13 LT with a *variable importance for projection* statistic (VIP) greater than one, as a value for the VIP less than one was considered ‘too small.’ VIP summarizes the contribution that a variable makes to the model. If a predictor has a relatively small coefficient (in absolute value) and a small VIP value, then it is a prime candidate for deletion. The LT PBV with the strongest associations according to the Wold criterion (Wold, 1994) were therefore selected. Afterwards, to guarantee that the genetic and phenotypic correlations were consistent, that is to ensure that their covariance matrix was positive and semi-definite, a multivariate analysis including all the LT selected by the PLS procedure and the six DT was also carried out. The multivariate model included 687 PRE with both records and had a pedigree file of 5359 PRE. All the analyses were performed using SAS (SAS Institute Inc., 2005) and VCE v. 6.0.2 software (Groeneveld *et al.*, 2010).

Expected genetic response

The classic selection indices theory (Hazel and Lush, 1943) and its reformulation for the use of PBV (Gutiérrez *et al.*, 2014) were used. Three groups of indices were developed: the first (Type 1), based only on the dressage PBV as selection criteria, the second (Type 2), using only the LT PBV as selection criteria and the third (Type 3), combining DT PBV and the LT PBV as selection criteria. The selection objective traits were the PBV of TS, PS and GS, and nine different genetic indices were therefore designed. The genetic responses using different objectives/criteria were computed and compared. In all cases, all the desired economic weights in the vector \mathbf{p}' were $1/n$, where n is the number of traits considered as selection objectives.

Weights in vector \mathbf{b}' to be used for weighting the PBV on \mathbf{v} were attained by $\mathbf{b}' = \mathbf{p}'\mathbf{C}'\mathbf{G}^{-1}$, where \mathbf{C}' is the covariance matrix between the objectives in vector \mathbf{u} and the PBV used as criteria in vector \mathbf{v} , \mathbf{G} is the (co)variance matrix for the selection objectives \mathbf{u} . PBV were used as independent variables to estimate the genetic response. \mathbf{C}' and \mathbf{G} matrices were obtained from the genetic parameters by assuming all the additive genetic variances to be the unity and therefore using the same, identical genetic scale ($\sigma_{u_1}^2 = \sigma_{u_2}^2 = \sigma_{u_3}^2 \dots = \sigma_{u_n}^2 = 1$) for all of them, where $\sigma_{u_k}^2$ is the additive genetic variance of trait k . Note that the coefficients in \mathbf{b} varied when considering different criteria and/or objectives, and matrices \mathbf{C} and \mathbf{G} also changed. When objective and criteria are the same traits, the (co)variance matrix between the objectives and the criteria \mathbf{C} becomes a genetic additive (co)variance matrix, in which the diagonals are equal to one (Gutiérrez *et al.*, 2014). Off-diagonal elements are the genetic correlations between objectives and criteria, given that $r_{u_k u_l} = \frac{\sigma_{u_k u_l}}{\sqrt{\sigma_{u_k}^2 \sigma_{u_l}^2}}$, where $r_{u_k u_l}$ is the genetic correlation between the traits k and l and $\sigma_{u_k}^2 = 1$ for any trait, thus becoming $\sigma_{u_k u_l} = r_{u_k u_l}$ and \mathbf{C}' :

$$\mathbf{C}' = \text{Var}(\mathbf{u}) = \begin{bmatrix} \sigma_{u_1}^2 & \sigma_{u_1 u_2} & \sigma_{u_1 u_3} & \dots & \sigma_{u_1 u_m} \\ \sigma_{u_2 u_1} & \sigma_{u_2}^2 & \sigma_{u_2 u_3} & \dots & \sigma_{u_2 u_m} \\ \dots & \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \dots & \dots \\ \sigma_{u_m u_1} & \sigma_{u_m u_2} & \sigma_{u_m u_3} & \dots & \sigma_{u_m}^2 \end{bmatrix}$$

$$= \begin{bmatrix} 1 & r_{u_1 u_2} & r_{u_1 u_3} & \dots & r_{u_1 u_m} \\ r_{u_2 u_1} & 1 & r_{u_2 u_3} & \dots & r_{u_2 u_m} \\ \dots & \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \dots & \dots \\ r_{u_m u_1} & r_{u_m u_2} & r_{u_m u_3} & \dots & 1 \end{bmatrix},$$

As \mathbf{G} and \mathbf{C}' are directly dependent on the genetic parameters, these matrices can be derived directly from genetic parameters to build the desired index. When the criteria are not the same, then the \mathbf{C}' matrix is not square, and each element is the genetic correlation between two traits. To compare the genetic indices, the genetic responses for each one have been obtained by weighting, for each of the traits, all those responses obtained in the correlated selected traits including their own direct genetic self-response. Thus, assuming the PBV are not known for certain, and under the assumption stated above about all the additive genetic variances being one, the direct genetic response would be calculated by the selection intensity (i) reduced by the accuracy of the PBV. The correlated response would be the genetic correlation times the selection intensity reduced by the accuracy of the PBV. Assuming that all individuals have the same amount of information, this accuracy is proportional to the square root of heritability of the trait used as a criterion. Gathering this information

into a matrix, the cumulated genetic responses will be obtained by:

$$\mathbf{t} = \mathbf{b}'\mathbf{T}i = \mathbf{b}' \begin{bmatrix} h_1 & h_1 r_{u_1 u_2} & h_1 r_{u_1 u_3} & \dots & h_1 r_{u_1 u_k} \\ h_2 r_{u_2 u_1} & h_2 & h_2 r_{u_2 u_3} & \dots & h_2 r_{u_2 u_k} \\ \dots & \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \dots & \dots \\ h_k r_{u_k u_1} & h_k r_{u_k u_2} & h_k r_{u_k u_3} & \dots & h_k \end{bmatrix} i,$$

where each $\sum \mathbf{t}_{jk}$ is the cumulated genetic response in the trait k . Therefore, genetic responses \mathbf{t} were obtained for each trait when selection was based on indices that weighted the breeding values for the traits of interest. When the criteria are not the same, then objectives \mathbf{T} matrix is not square but each element t_{jk} is the genetic correlation between traits j and k . For the comparison of computed responses, a selection intensity of one was assumed, because this will be a constant, leading to comparable relative results. When there were three or five objectives in the same indices, the global genetic expected response was calculated as the average of all of them. Note that here we are computing genetic responses, but the genetic parameters can be used to set up selection indices as in Martínez *et al.* (2006).

Results

Phenotypic scores

The descriptive statistic in the 26 LT and the six DT analyzed in the PRE population is shown in Table 1. Most of the 26 LT had a mean close to five in the assessed population, although some traits had a mean ranging from 3.5 (width of head) to 7.1 (width of chest) for the primary traits, and from 4.1 (hock from rear) to 5.3 (frontal angle of knee) for the secondary ones. The mode parameter showed that the most common class used in this population ranged from three to seven in primary traits and from four to seven in secondary ones, with all the traits very close to the arithmetic average. In general, the coefficients of variation were high in this study, ranging from 17.5% (length of croup) to 51.7% (angle of croup) for primary traits, and from 14.8% (lateral angle of knee) to 27.2% (neck-body junction) for the secondary ones. In general, therefore, there was an important phenotypic variation for the analyzed traits in this population. All the DT had a mean close to 6.5 and ranged between two and 9.2. The mode was 6.5 for walk, trot, canter, submission and general impression, and consequently 65.0 for the global dressage score. The coefficients of variation were always <9.4.

Selection of morphological linear traits

The LT PBV were chosen according to the PLS procedure (Table 2) and to *Wold Criterion*. The 13 LT with a VIP greater than one were selected. For the PBV of TS, the LT PBV selected were as follows: upper neck line, neck-body junction, width of chest, angle of shoulder, frontal angle of knee, cannon bone perimeter, length of croup, angle of croup, ischium-stifle distance and lateral hock angle. For the PS PBV, the LT PBV selected were as follows: width of head,

Table 2 The weight of the 26 morphological linear traits (as model effects) and the six dressage traits (as dependent variables) in the partial least square model with reduced rank regression factorial extraction method in the Pura Raza Español horse

	Total score	Partial score	Gait score
Morphological linear traits			
Primary traits			
Length of head	0.035	-0.141	-0.091
Width of head	0.063	0.307	0.241
Space between jaws	0.041	0.134	0.089
Length of neck	-0.076	-0.042	-0.028
Neck-body junction	0.137	0.203	0.130
Width of chest	-0.110	-0.121	-0.078
Length of back	-0.003	-0.075	-0.049
Length of loin	-0.051	-0.121	-0.104
Length of shoulder	-0.031	-0.113	-0.093
Angle of shoulder	-0.083	-0.064	-0.041
Length of forearm	-0.017	-0.065	-0.033
Cannon bone perimeter	0.123	0.178	0.111
Length of croup	0.093	0.176	0.137
Angle of croup	-0.093	-0.178	-0.124
Point of hip-stifle distance	0.002	0.054	0.057
Ischium-stifle distance	0.120	0.340	0.267
Length of buttock	-0.006	0.012	0.012
Length of leg	0.025	0.035	0.018
Secondary traits			
Head-neck junction	-0.055	-0.300	-0.236
Upper neck line	0.095	0.297	0.194
Dorsal line	-0.013	0.073	0.057
Lateral angle of knee	0.072	0.212	0.188
Frontal angle of knee	0.126	0.504	0.357
Rear tendon development	-0.006	-0.019	0.004
Hock from rear	-0.002	0.171	0.123
Lateral hock angle	0.184	0.203	0.179
Dressage traits			
Walk		0.385	0.525
Trot		0.477	0.632
Canter		0.428	0.571
Submission		0.472	
General impression		0.468	
Total score	1.000		

head-neck junction, upper neck line, neck-body junction, lateral angle of knee, frontal angle of knee, ischium-stifle distance and lateral hock angle, and finally, for GS PBV, the same LT PBV were chosen, except for neck-body junction.

Genetic parameters of the selected traits

The heritability values (Table 3) were estimated through multivariate analysis of the 13 LT and six DT ranged from 0.12 (ischium-stifle distance) to 0.53 (cannon bone perimeter). The heritability of the DT ranged from 0.21 (walk) to 0.33 (canter). The genetic correlations in absolute value among the LT ranged between 0 (neck-body junction – ischium-stifle distance) and -0.62 (length of croup-lateral hock angle). The genetic correlations among the DT in absolute value ranged between 0.59 (walk-trot) and 1 (general impression – total score) (Table 3). The genetic

correlations between the LT and DT in absolute value ranged between zero (walk and width of head) and 0.46 (canter-angle of shoulder).

Expected genetic responses

The expected genetic response for the TS, PS and GS indices based on early selection for morphology was assessed (Table 4), considering three index groups; the first (Type 1), based only on DT PBV as selection criteria, the second (Type 2), using only the LT PBV as selection criteria and the third (Type 3), combining DT PBV and the LT PBV as selection criteria. When the TS PBV, PS PBV were considered as dependent variables, the maximum expected genetic response was achieved by Type 1 (1.80 and an average response of 0.16, respectively) and the maximum expected genetic response for the GS PBV was achieved by Type 3 (average of 0.15). When only LT PBV were used as criteria (Type 2), a positive response was obtained for all the indices (an average of 0.76, 0.04 and 0.03, respectively), although this was ~25% of the other responses for the other indices. When the PS was analyzed in detail, all the traits (walk, trot, canter, submission and general impression) followed similar patterns. The response was almost the same in the Type 1 and 3 indices (0.12/0.13, 0.15/0.16, 0.17/0.18, 0.18/0.18 and 0.17/0.17, respectively for all analyzed traits) and higher than those in the indices of Type 2 (0.04, 0.04, 0.03, 0.04 and 0.04), with the small exception of the walk, where the percentage rose to nearly one third. Studying the indices which use GS as objective selection in detail, the result was similar to that described above, but the walk response rate of index Type 2 over Type 1 reached 40% (40%, 20% and 18.8% for walk, trot and canter, respectively).

Discussion

Whatever purpose horses are used for, the objective evaluation of conformation and its relation to high sport performance is of great importance (Moore, 2010). There is therefore growing interest in the selection of PRE suitable for sport competitions, especially dressage, the main sports breeding goal for PRE. Currently, the main selection criteria for the functionality in PRE are the dressage scores collected at the dressage tests. To obtain a good selection response for dressage, it is critical to have sufficiently large heritability. The estimated heritability of the DT ranged from 0.21 (walk) to 0.33 (canter). The heritabilities estimated for the gaits found in the recent literature range from 0.08 to 0.38 for walk, 0.16 to 0.50 for trot, 0.25 to 0.48 for canter and 0.18 to 0.32 for TS (Ducro *et al.*, 2007; Posta *et al.*, 2010; Schroderus and Ojala, 2010; Becker *et al.*, 2011 and 2012; Viklund *et al.*, 2011; Vicente *et al.*, 2014), so our results were consistent with the previous results. Previous references to the heritability for submission and general impression have not been found. The estimated heritabilities were therefore considered suitable for genetic evaluations and selection for these performance traits.

However, the base population of selection for this discipline is still very small, as there are very few young horses

Table 3 Genetic correlations (above the diagonal), heritabilities (on the diagonal) and phenotypic correlations (below the diagonal) and their standard error (below its genetic value) between the morphological linear traits and dressage traits analyzed in the Pura Raza Español horse

	WH	HNJ	UNL	NBJ	WC	AS	LAK	FAK	CBP	LC	AC	ISD	LHA	W	T	C	S	GI	TS
WH	0.15	-0.15	0.36	0.12	0.41	-0.37	0.06	0.05	0.28	0.11	-0.03	-0.19	0.16	0.00	-0.20	-0.21	-0.11	-0.18	-0.16
	0.030	0.021	0.061	0.026	0.024	0.069	0.038	0.025	0.015	0.043	0.022	0.067	0.038	0.031	0.022	0.025	0.014	0.021	0.014
HNJ	-0.11	0.44	-0.12	0.21	-0.06	-0.09	0.23	0.25	-0.12	-0.04	0.10	0.09	0.35	-0.12	-0.13	-0.13	-0.13	-0.12	-0.13
	0.040	0.012	0.031	0.068	0.016	0.025	0.073	0.077	0.029	0.020	0.017	0.030	0.048	0.017	0.014	0.013	0.016	0.014	0.013
UNL	0.10	-0.24	0.36	-0.31	0.32	-0.04	0.14	-0.03	0.17	0.10	0.29	-0.08	0.29	0.24	0.06	0.06	0.16	0.12	0.15
	0.036	0.043	0.011	0.056	0.043	0.030	0.045	0.036	0.012	0.038	0.035	0.085	0.047	0.043	0.024	0.027	0.019	0.015	0.011
NBJ	0.03	0.03	-0.08	0.14	0.12	-0.31	-0.04	0.33	0.07	0.01	-0.49	0.00	0.13	-0.22	-0.17	-0.20	-0.29	-0.23	-0.25
	0.038	0.038	0.040	0.026	0.016	0.034	0.030	0.118	0.012	0.025	0.019	0.032	0.015	0.031	0.020	0.020	0.018	0.020	0.020
WC	0.25	0.05	0.12	0.22	0.31	-0.57	-0.18	0.03	0.56	-0.02	0.30	0.13	0.36	-0.20	-0.30	-0.22	-0.10	-0.20	-0.21
	0.033	0.038	0.036	0.034	0.017	0.108	0.067	0.019	0.015	0.050	0.023	0.031	0.028	0.026	0.022	0.020	0.021	0.018	0.014
AS	-0.18	0.02	-0.01	-0.13	-0.21	0.29	0.10	0.12	-0.17	0.16	-0.12	-0.24	-0.19	0.20	0.41	0.46	0.39	0.40	0.41
	0.042	0.038	0.039	0.041	0.042	0.024	0.016	0.017	0.016	0.070	0.030	0.089	0.023	0.043	0.018	0.031	0.026	0.018	0.019
LAK	-0.04	-0.01	0.06	0.06	0.01	0.05	0.22	0.04	-0.06	0.13	-0.32	-0.30	-0.04	0.44	0.20	0.18	0.16	0.24	0.26
	0.042	0.038	0.039	0.041	0.042	0.032	0.034	0.028	0.014	0.020	0.023	0.120	0.024	0.025	0.015	0.027	0.021	0.021	0.021
FAK	-0.01	0.01	-0.06	-0.05	-0.05	0.11	-0.01	0.16	0.22	0.08	-0.31	0.20	0.12	0.10	0.22	0.08	0.12	0.12	0.13
	0.039	0.038	0.040	0.039	0.039	0.036	0.039	0.040	0.051	0.022	0.022	0.027	0.013	0.021	0.017	0.021	0.017	0.013	0.013
CBP	0.26	0.03	0.15	0.01	0.41	-0.04	0.05	-0.07	0.53	0.38	0.36	0.24	0.07	0.21	0.12	0.13	0.24	0.19	0.20
	0.033	0.038	0.036	0.038	0.029	0.039	0.038	0.040	0.013	0.024	0.035	0.031	0.021	0.044	0.022	0.016	0.018	0.013	0.013
LC	0.23	-0.07	0.09	0.13	0.15	-0.07	0.14	0.01	0.29	0.15	-0.30	0.05	-0.62	0.07	-0.01	0.10	0.09	0.07	0.08
	0.034	0.040	0.037	0.036	0.035	0.040	0.036	0.038	0.032	0.039	0.019	0.051	0.067	0.027	0.018	0.021	0.027	0.015	0.012
AC	0.08	0.06	0.11	-0.13	0.20	-0.03	-0.12	0.01	0.13	-0.21	0.25	0.28	0.50	0.14	0.01	0.03	0.18	0.10	0.11
	0.037	0.037	0.036	0.041	0.034	0.039	0.041	0.038	0.036	0.042	0.017	0.067	0.028	0.047	0.024	0.021	0.020	0.017	0.015
ISD	0.07	0.14	0.06	-0.07	0.19	0.05	0.02	0.01	0.15	0.17	0.05	0.12	-0.07	0.22	-0.21	-0.31	-0.15	-0.15	-0.12
	0.037	0.036	0.037	0.040	0.035	0.037	0.038	0.038	0.035	0.035	0.038	0.015	0.045	0.055	0.030	0.026	0.037	0.016	0.015
LHA	0.00	0.08	0.11	0.04	0.40	-0.01	-0.01	-0.03	0.11	-0.17	0.44	0.06	0.35	0.05	-0.04	-0.01	0.10	0.01	0.02
	0.038	0.037	0.036	0.038	0.030	0.039	0.039	0.039	0.036	0.042	0.029	0.037	0.015	0.030	0.019	0.020	0.032	0.013	0.013
W	0.00	-0.04	0.07	-0.04	-0.05	0.05	0.09	0.02	0.07	0.01	0.03	0.03	0.01	0.21	0.59	0.60	0.68	0.73	0.77
	0.038	0.039	0.037	0.039	0.039	0.038	0.037	0.038	0.037	0.038	0.038	0.038	0.038	0.013	0.023	0.025	0.017	0.020	0.017
T	-0.02	-0.04	0.02	-0.03	-0.09	0.11	0.05	0.05	0.04	0.00	0.00	-0.04	-0.01	0.64	0.27	0.92	0.86	0.94	0.93
	0.039	0.039	0.038	0.039	0.040	0.036	0.038	0.038	0.038	0.039	0.038	0.039	0.039	0.023	0.024	0.022	0.009	0.005	0.006
C	-0.03	-0.05	0.02	-0.04	-0.07	0.14	0.05	0.02	0.05	0.02	0.01	-0.06	0.00	0.66	0.81	0.33	0.95	0.97	0.96
	0.039	0.039	0.038	0.039	0.040	0.036	0.038	0.038	0.037	0.038	0.038	0.040	0.039	0.022	0.017	0.026	0.008	0.003	0.004
S	-0.01	-0.05	0.05	-0.06	-0.03	0.12	0.04	0.03	0.10	0.02	0.05	-0.03	0.03	0.66	0.78	0.83	0.31	0.96	0.97
	0.039	0.039	0.037	0.040	0.039	0.036	0.038	0.038	0.036	0.038	0.037	0.039	0.038	0.023	0.018	0.016	0.028	0.006	0.005
GI	-0.02	-0.04	0.04	-0.05	-0.06	0.12	0.06	0.03	0.08	0.02	0.03	-0.03	0.00	0.77	0.87	0.90	0.89	0.30	1.00
	0.039	0.039	0.038	0.039	0.040	0.036	0.037	0.038	0.037	0.038	0.038	0.039	0.038	0.019	0.014	0.012	0.013	0.025	0.002
TS	-0.02	-0.05	0.05	-0.05	-0.06	0.12	0.07	0.03	0.08	0.02	0.03	-0.02	0.01	0.82	0.89	0.91	0.91	0.97	0.30
	0.039	0.039	0.038	0.039	0.040	0.036	0.037	0.038	0.037	0.038	0.038	0.039	0.038	0.017	0.013	0.012	0.012	0.038	0.023

WH = width of head; HNJ = head-neck junction; UNL = upper neck line; NBJ = neck-body junction; WC = width of chest; AS = angle of shoulder; LAK = lateral angle of knee; FAK = frontal angle of knee; CBP = cannon bone perimeter; LC = length of croup; AC = angle of croup; ISD = ischium-stifle distance; LHA = lateral hock angle; W = walk; T = trot; C = Canter; S = submission; GI = general impression; TS = total score.

Table 4 Expected genetic responses for the morphological selection indices related to dressage aptitude in the Pura Raza Español horse

Objective	Index	Selection criteria	Walk	Trot	Canter	Submission	General impression	Total score
			Expected genetic response					
Total score	Type 1 _{TS}	PS						1.80
	Type 2 _{TS}	10 LT						0.76
	Type 3 _{TS}	10 LT + PS						2.97
Partial score	Type 1 _{PS}	PS	0.12	0.15	0.17	0.18	0.17	
	Type 2 _{PS}	8 LT	0.04	0.04	0.03	0.04	0.04	
	Type 3 _{PS}	8 LT + TS	0.13	0.16	0.18	0.18	0.17	
Gait scores	Type 1 _{GS}	GS	0.10	0.15	0.16			
	Type 2 _{GS}	7 LT	0.04	0.03	0.03			
	Type 3 _{GS}	7 LT + TS	0.12	0.15	0.17			

GS = gait score: walk + trot + canter; PS = partial scores: walk + trot + canter + submission + general impression; TS = total scores; 10 LT = upper neck line + neck-body junction + width of chest + angle of shoulder + frontal angle of knee + cannon bone perimeter + length of croup + angle of croup + ischium–stifle distance + lateral hock angle; eight LT = width of head + head–neck junction + upper neck line + neck–body junction + lateral angle of knee + frontal angle of knee + ischium–stifle distance + lateral hock angle; seven LT = width of head + head–neck junction + upper neck line + lateral angle of knee + frontal angle of knee + ischium–stifle distance + lateral hock angle.

taking performance tests due to the high cost that this entails for the breeder. On the other hand, almost all PRE pass a basic morphological test, which is mandatory if a breeder wants to breed with this horse and the cost of these tests is relatively low. The standard procedures in Spanish horse breeding programs, until now, have used only the dressage PBV trait to choose the best PRE for reproduction. So, success in genetic improvement of dressage ability in horses through dressage criteria selection is at present extremely inefficient because most young PRE do not participate in dressage performance tests, because it takes much effort and money to achieve satisfactory results. In the ideal situation, the breeding goal would consist of a single criterion that facilitates the ranking of animals in line with this goal, but with only 155 new PRE a year evaluated in dressage, this is not a realistic scenario. A large number of young animals with good genetics for dressage and with a cheaper mating service (Mantovani *et al.*, 2013) are never evaluated in the performance test, so their potential remains undetected, thus compromising the effectiveness of the PRE selection scheme. However, breeding programs should look ahead to the future, and it would be a positive breakthrough if we could carry out breed improvements in the near future with other variables which are currently collected in most foals. Thus, this situation offers an ideal scenario to provide alternative selection strategies allowing us to improve dressage ability, such as indirect selection by morphological traits.

Using a linear scoring system in horses to refine the morphological trait definitions and increase the objectivity of the trait assessments has been suggested since the late 1980s (Duensing *et al.*, 2014). In the PRE breeding program, the linear scoring system is conceived as a tool for genetic improvement of the animals' functionality. The whole range of scores for the phenotypic LT was used in almost all the traits, as was previously reported in the same breed (Sánchez *et al.*, 2013). The CV was generally high and it is assumable that the morphological differences in the horses were well

reflected with this methodology (Sánchez *et al.*, 2013). It may also be possible to identify indicator traits that are broadly assessable at an early age, thus allowing efficient selection for a durable and competitive riding horse (Duensing *et al.*, 2014). However, the obvious benefits of the descriptive linear scoring system over evaluative assessments have not yet led to its use as an indicator of dressage performance values in horses. It is worth noting that the idea of ideal conformation does not exist, because one conformation trait could be both advantageous for a certain locomotive characteristic and detrimental to others (Back *et al.*, 1996). It should be added that favorable dressage morphology is not the only requirement to obtain good movement abilities, but a minimum level of conformation is certainly needed in certain LT to obtain a good dressage horse. The assessment of a horse's merits by virtue of its conformation is as ancient as man's usage of the species. Conformation traits remain an interesting subject, because they are linked to the morphological aptitudes for performance in the horse most valued by horse breeders (Bakhtiari and Heshmat, 2009). In spite of this, horses will have better chances of receiving high GS under skillful riders, good ambient conditions and training than others with only good morphological conditions.

Because performance in dressage does not depend solely on morphology, a long period of learning and training is required for a horse to achieve the greatest level in dressage, which entails a major economic investment. The search for traits that are indirectly related to dressage performance would allow early assessment of animals; this way, the stud can save resources, which are always limited, and direct their financial resources towards animals that actually have morphological athletic skills. So the main interest of this paper was to assess the possibility of obtaining an indirect selection criterion that allowed a pre-selection of horses to take part in dressage, or which allows us to increase the basis PRE population of selection for dressage – given the high cost entailed in preparing a horse to take the tests, and

consequently the small number of animals involved in the dressage test. Our strategies were therefore to evaluate the addition of morphological traits to the genetic evaluation of a limited number of animals that had DT and to create an early morphological selection index related to dressage aptitude in this breed. This latter strategy would enable the number of animals used for selection to increase significantly, because there are many more PRE with a LT record than those who have DT records. On the other hand, generally, the LT are taken once in the PRE life, which means that a young and an adult PRE would have always identical LT information. Nevertheless, the DT of each PRE may increase over the time, and the older a PRE is, the more accurate the index will be.

The heritabilities of the selected LT analyzed were consistent with LT studied in others breeds (Duensing *et al.*, 2014) and as happened with the DT, they are suitable for use in genetic selection. But, until now, information is scarce on the genetic relationships existing between morphology and dressage ability in horses. The few estimates that have been reported so far point towards a low to medium genetic correlation between morphological traits and performance in dressage events (Koenen *et al.*, 1995; Wallin *et al.*, 2003). Nevertheless, as functional traits in horses are generally measured at a more advanced age, it has been argued that, in spite of the modest genetic correlations that they may have, morphological traits can be used as an early culling criterion when selection is intended to improve dressage performance (Saastamoinen and Barrey, 2000). Nonetheless, the relationship between the LT and the DT has never been addressed before in the PRE and an insufficient knowledge of the influence of conformation on performance can result in inaccurate selection. According to our results, the genetic correlations between DT and LT were of mainly a moderate–low magnitude. These results are similar to the previous studies made with other horse breeds (Koenen *et al.*, 1995; Olsson *et al.*, 2008; Ducro *et al.*, 2009).

Moreover, the importance of the locomotor pattern is related to the fact that for each type of exercise, the horse uses a specific type of locomotion, where its individual characteristics determine the level of performance it can achieve (Leleu *et al.*, 2005), and this would be more evident in young horses, because studying the relationship between morphology traits and dressage performance in young horses has a major advantage: young horses are judged more on the basis of their own gait characteristics than experienced horses (Biau and Barrey, 2004). The greatest challenge in this study was to find a procedure which could take into account the whole relationship among all the morphology and performance traits and to select a small number of traits. In fact, the estimation of variance components in a multivariate analysis with 28 variables leads to many problems and extremely biased estimates are often produced due to the lack of convergence. In these cases, genetic values obtained by univariate analysis are often used. In addition, in our case, the use of PLS regression allows to work out the maximum covariance not only between the dependent and

independent variables, but also among independent traits when its dimension is reduced, so that the potential problem of not taking covariances into consideration among the independent variables is minimized. Although the scale of the problem is quite different in our case, PLS has been used in genomic selection to reduce the number of variables by projecting independent variables onto latent structures. Moser *et al.* (2009) carried out an analysis using five methods to predict the genomic breeding values of dairy bulls from genome-wide SNP markers: Least Squares Regression (FR-LS), Bayesian Regression (Bayes-R), Random Regression Best Linear Unbiased Prediction (RR-BLUP), Partial Least Squares Regression (PLSR) and Nonparametric Support Vector Regression (SVR). The accuracy and bias of the breeding value prediction were calculated using cross-validation of the training set and tested against a test team. The accuracies obtained by Bayes-R, RR-BLUP, PLSR and SVR were very similar, with PLSR and RR-BLUP requiring the least computing time. Colombani *et al.* (2012) used a modification of this methodology for computing sparse matrices with a reference population of 3940 genotyped and phenotyped French Holstein bulls and 39 738 polymorphic SNP markers, concluding that PLS and Sparse PLS were more accurate than pedigree-based BLUP, although they generally provided lower correlations between observed and predicted phenotypes than genomic BLUP.

Holmström (2001) affirmed that the morphological differences between elite and non-selected horses were small but significant for several traits, such as shoulder, pelvis and femur inclinations and shoulder, elbow, stifle and hock joints. Our results show also the angle of shoulder as an important trait, but the angle of pelvis has not shown the same relevance. In Warmblood riding horse Koenen *et al.* (1995) found five morphological traits genetically correlated with dressage ability. Two of them agree with our results in the TS index (angle of shoulder and length of croup) but differed in the length of neck and shoulder, which was not selected in our indices, perhaps due to the relationship among the LT which is taken into consideration in the PLS procedure. According to our results, there were five morphological traits (width of chest, angle of shoulder, cannon bone perimeter, length of croup and ischium–stifle distance) which were different in the PRE selected in studs for dressage purposes to the PRE studs with other purposes. So, these five LT match with the morphological selection carried out during the last years by PRE studs where dressage is the main selection objective (Sánchez *et al.*, 2016).

Based on the relationships among traits, an index has been developed to combine several diverse traits related to the final goal of profitability, because they are dynamic tools that can be adapted to any type of commercial objective. Selection indices have been commonly used for a long time in dairy cows (Miglior *et al.*, 2005), and also studied or implemented in beef (Amer *et al.*, 2001), sheep (Byrne *et al.*, 2010) or alpaca populations (Gutiérrez *et al.*, 2014). The selection index provided a natural connection between the net merit of an animal's genotype and its relationship to profitability.

Given the recognized difficulties in computing realistic economic weights in leisure and/or sport horses, these are not usually computed. In this study, a methodology based on the selection index theory by Hazel and Lush (1943), reformulated to use PBV by Gutiérrez *et al.* (2014), has been developed for the first time in this breed. Each DT was given the same economic weight in the index, to study relative genetic responses starting with genetic parameters such as heritabilities and genetic correlations. In addition, the aggregated genetic response in each trait assessed directly from genetic parameters has been developed for dressage for the first time. Moderate to high heritabilities of LT and a strong relationship among the three indices would make it possible to improve the functionality the next few decades by pre-selecting PRE without DT. Overall, according to our results, the response of a selection index using only LT scores would not be as good as direct selection for performance traits but it is nowadays the only opportunity to apply selection in most PRE and it could be used to pre-select the PRE which will take part in the dressage test. Another possibility to consider in the near future must be the use of functional records in free movement horses (basic gaits – walk, trot and canter). It is known (Becker *et al.*, 2011) that there is a positive genetic correlation between gaits under the rider and gaits in free movement (that can be evaluated even without any training).

The index methodology used here accounts for differences in accuracy depending on the differences in heritability, but ignores possible differences in the amount of information for the different traits, and this is our case, PRE always have only one LT record, while DT records will gradually increase with age. Nevertheless, computation with accuracy correction showed the acceptable genetic responses expected using LT as selection criteria, compared with the current strategies (using only DT as selection criteria). Despite the fact that the use of LT index had a relative lower response, its use could be essential in young animals without any dressage record to carry out an early pre-selection, because at this stage, the animals have LT records but do not have DT records. However, in an old animal, the repeated records of DT would enable us to use only the preferable traits.

In conclusion, the results obtained in this study indicate that both dressage and morphological selection are feasible, given the magnitudes of heritabilities in both types of traits. However, our results also suggest that it is possible to preselect animals to be trained in dressage using LT and perhaps in a near future it could be improved adding the routine use of free movement of these no-training horses into this early evaluation. Nevertheless, the genetic correlations between LT and DT range between 0 and 0.46, and therefore, in the current scenario, a rigorous selection of PRE horses based only on LT might be a gamble, but may prove useful to improve the dressage performance. In a scenario in which there is an equivalent amount of information in the LT and DT groups of traits, the inclusion of LT in the evaluation of PRE appears to have almost no advantages as a pre-selection tool, given the difference in accuracy provided by each type

of characters. In any case, the use of LT allows us to greatly increase the basis of selection (number of animals available for selection) with an acceptable genetic response, thus enabling us to optimize the breeding program in terms of time and money.

Acknowledgements

The authors wish to thank the Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE) for making available the data used in this research.

Supplementary material

To view supplementary material for this article, please visit <https://doi.org/10.1017/S1751731116002214>

References

- Amer PR, Simm G, Keane MG, Diskin MG and Wickham BW 2001. Breeding objectives for beef cattle in Ireland. *Livestock Production Science* 67, 223–239.
- Back W, Schamhardt HC and Barneveld A 1996. The influence of conformation on fore and hind limb kinematics of the trotting Dutch Warmblood horse. *Pferdeheilkunde* 12, 647–650.
- Bakhtiar J and Heshmat G 2009. Estimation of genetic parameters of conformation traits in Iranian Thoroughbred horses. *Livestock Science* 123, 116–120.
- Becker AC, Stock KF and Distl O 2011. Genetic correlations between free movement and movement under rider in performance tests of German Warmblood horses. *Livestock Science* 142, 245–252.
- Becker AC, Stock KF and Distl O 2012. Genetic analyses of new movement traits using detailed evaluations of warmblood foals and mares. *Journal Animal Breeding Genetics* 129, 390–401.
- Belloy E and Bathe AP 1996. The importance of standardising the evaluation of conformation in the horse. *Equine Veterinary Journal* 28, 429–430.
- Biau S and Barrey E 2004. Relationship between stride characteristics and scores in dressage tests. *Pferdeheilkunde* 20, 140–144.
- Byrne TJ, Amer PR, Fennessy PF, Cromie AR, Keady TWJ, Hanrahan JP, McHugh MP and Wickham BW 2010. Breeding objectives for sheep in Ireland: a bio-economic approach. *Livestock Science* 132, 135–144.
- Colombani C, Croiseau P, Fritz S, Guillaume F, Legarra A, Ducrocq V and Robert-Granié C 2012. A comparison of partial least squares (PLS) and sparse PLS regressions in genomic selection in French dairy cattle. *Journal Dairy Science* 95, 2120–2131.
- Ducro BJ, Bovenhuis H and Back W 2009. Heritability of foot conformation and its relationship to sports performance in a Dutch Warmblood horse population. *Equine Veterinary Journal* 41, 139–143.
- Ducro BJ, Koenen EPC, van Tartwijk JMFM and Bovenhuis H 2007. Genetic relations of movement and free-jumping traits with dressage and show-jumping performance in competition of Dutch Warmblood horses. *Livestock Science* 107, 227–234.
- Duensing J, Stock KF and Krieter J 2014. Implementation and prospects of linear profiling in the Warmblood horse. *Journal Equine Veterinary Science* 34, 360–368.
- Groeneveld E, Kovac M and Mielenz N 2010. VCE. User's guide and reference manual version 6.0. Institute of Farm Animal Genetics, Mariensee, Germany.
- Gutiérrez JP, Cervantes I, Pérez-Cabal MA, Burgos A and Morante R 2014. Weighting fibre and morphological traits in a genetic index for an alpaca breeding programme. *Animal* 8, 360–369.
- Hazel L and Lush J 1943. The efficiency of three methods of selection. *Journal of Heredity* 33, 393–399.
- Holmström M 2001. The effects of conformation. In *Equine locomotion* (ed. H Clayton and C Saunders), pp. 281–295. Elsevier Health Sciences, London, United Kingdom.
- Koenen EPC, van Veldhuizen AE and Brascamp EW 1995. Genetic parameters of linear scored conformation traits and their relation to dressage and

- show-jumping performance in the Dutch Warmblood riding horse population. *Livestock Production Science* 43, 85–94.
- Leleu C, Cotrel C and Barrey E 2005. Relationships between biomechanical variables and race performance in French Standardbred trotters. *Livestock Production Science* 92, 39–46.
- Mantovani R, Sartori C and Pigozzi G 2013. Retrospective and statistical analysis of breeding management on the Italian Heavy Draught Horse breed. *Animal* 7, 1053–1059.
- Martinez V, Kause A, Mäntysaari E and Mäki-Tanila A 2006. The use of alternative breeding schemes to enhance genetic improvement in rainbow trout (*Oncorhynchus mykiss*): I. One-stage selection. *Aquaculture* 254, 182–194.
- Miglior F, Muir BL and Van Doormaal BJ 2005. Selection indices in Holstein cattle of various countries. *Journal Dairy Science* 88, 1255–1263.
- Moore J 2010. General biomechanics: the horse as a biological machine. *Journal Equine Veterinary Science* 30, 379–383.
- Moser G, Tier B, Crump RE, Khatkar MS and Raadsma HW 2009. A comparison of five methods to predict genomic breeding values of dairy bulls from genome-wide SNP markers. *Genetic Selection Evolution* 41, 56.
- Olsson E, Näsholm A, Strandberg E and Philipsson J 2008. Use of field records and competition results in genetic evaluation of station performance tested Swedish Warmblood stallions. *Livestock Science* 117, 287–297.
- Posta J, Komlósi I and Mihók S 2010. Genetic parameters of Hungarian sport horse. Mare performance tests. *Animal Science Paper Reports* 28, 373–380.
- Saastamoinen MA and Barrey E 2000. Genetics of conformation, locomotion and physiological traits. In *Genetic horse* (ed. AT Bowling and A Ruvinsky), pp. 439–472. CABI Publ, London, United Kingdom.
- Sánchez MJ, Cervantes I, Valera M and Gutiérrez JP 2014. Modelling genetic evaluation for dressage in Pura Raza Español horses with focus on the rider effect. *Journal Animal Breeding Genetics* 131, 395–402.
- Sánchez MJ, Gómez MD, Molina A and Valera M 2013. Genetic analyses for linear conformation traits in Pura Raza Español horses. *Livestock Science* 157, 57–64.
- Sánchez MJ, Molina A, Gómez MD, Peña F and Valera M 2016. Relationship between morphology and performance: signature of mass-selection in Pura Raza Español horses. *Livestock Science* 185, 148–155.
- SAS Institute Inc 2005. *Sas/statistical users guide for personal computer*. SAS/Genetics TM 9.1.3, Cary, NC, USA.
- Schroderus E and Ojala M 2010. Estimates of genetic parameters for conformation measures and scores in Finnhorse and Standardbred foals. *Journal Animal Breeding Genetics* 127, 395–403.
- Vicente AA, Carolino N, Ralao-Duarte J and Gama LT 2014. Selection for morphology, gaits and functional traits in Lusitano horses: II. Fixed effects, genetic trends and selection in retrospect. *Livestock Science* 164, 13–25.
- Viklund Å, Näsholm A, Strandberg E and Philipsson J 2011. Genetic trends for performance of Swedish Warmblood horses. *Livestock Science* 141, 113–122.
- Wallin L, Strandberg E and Philipsson J 2003. Genetic correlations between field test results of Swedish Warmblood Riding Horses as 4-year-olds and lifetime performance results in dressage and show jumping. *Livestock Production Science* 82, 61–71.
- Wold S 1994. PLS for multivariate linear modeling QSAR: chemometric methods in molecular design. In *Methods and Principles in Medicinal Chemistry* (ed. H van de Waterbeemd), pp. 195–218. VCH, Weinheim, Germany.