

Phenotypic and Genetic Evaluation of Morphometric and Dynamic Traits in Mangalarga Horses

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HIGHLIGHTS

Estimated breeding values were obtained for Mangalarga horse traits.

Dynamic traits showed continuous genetic and phenotypic progress over time.

Morphometric traits exhibited stabilization and recent decline.

Cannon bone and movement showed a negative genetic correlation.

Comfort and movement showed a high positive genetic correlation.

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Abstract

Background: Genetic evaluation of morphometric and locomotor traits supports objective selection, avoiding exclusive reliance on subjective methods that may fixate breed traits over functionality or cause undesirable indirect selection.

Aims/objectives: To evaluate genetic and phenotypic parameters for morphometric and dynamic traits in horses of the Mangalarga breed.

Methods: The pedigree included 212,361 animals born between 1919 and 2019. Phenotypic subsets for morphometric and dynamic traits comprised 54,617 and 45,010 horses, respectively, born between 1977 and 2019. Variance components were estimated using an Animal Model via the BLUPF90+ software family.

Results: Phenotypic means $\pm$ SD and heritabilities $\pm$ SD for morphometric traits were withers height (153.86 $\pm$ 4.43 cm; 0.58 $\pm$ 0.01), thoracic perimeter (178.67 $\pm$ 7.97 cm; 0.40 $\pm$ 0.01), and cannon bone perimeter (19.03 $\pm$ 0.96 cm; 0.21 $\pm$ 0.01). Dynamic traits were movement (12.63 $\pm$ 1.45 points; 0.34 $\pm$ 0.01), dynamic limbs (9.03 $\pm$ 1.32 points; 0.26 $\pm$ 0.01), canter (4.23 $\pm$ 0.69 points; 0.22 $\pm$ 0.01), comfort (11.49 $\pm$ 1.14 points; 0.29 $\pm$ 0.02), and total dynamics (38.37 $\pm$ 3.03 points; 0.32 $\pm$ 0.02). Phenotypic correlations ranged from 0.06 $\pm$ 0.01 (cannon bone perimeter and comfort) to 0.87 $\pm$ 0.00 (movement and total dynamics). The weakest genetic correlation was between dynamic limbs and cannon bone perimeter (-0.01 $\pm$ 0.04), and the highest between movement and total dynamics

(0.92 ± 0.01). The strongest negative genetic correlation was between movement and cannon bone perimeter (-0.21 ± 0.04).

Conclusion: Moderate to high heritability estimates demonstrate the selection potential of these traits. However, the genetic antagonism between movement and cannon bone perimeter requires a nuanced approach. These findings provide the breed's first comprehensive breeding values, offering effective tools for the development of selection indexes that weight gait improvement while setting minimum constraints for bone structure.

Keywords: *Animal model; Equine; Gaits; Morphometry; Pedigree*

1. Introduction

The Mangalarga horse breed originated from the search for saddle horses with comfortable gait, suitable for hunting and herding activities. In 1808, with the arrival of the Portuguese royal family in Brazil, the genetic lineage of horses from the Alter Real Stud Farm (Alter do Chão – Portugal) was incorporated into the herd of Fazenda Campo Alegre [1,2]. Through these matings, the breed began to emerge in the southern region of the state of Minas Gerais, later receiving the name Mangalarga [2,3,4]. The aptitude of these animals — characterized by a diagonalized gait with balanced and smooth movements — favored the rapid spread of the breed to the state of São Paulo and neighboring regions [2,5].

In 1928, the equine scholar Paulo de Lima Corrêa launched a project to standardize the animals, establishing the foundations for the breed characterization of the Mangalarga horse. In 1934, the Brazilian Association of Mangalarga Horse Breeders (ABCCRM) was founded. From then on, the association defined the breed standard, promoted efforts to unify the population, and created technical committees in the states of São Paulo and Minas Gerais to register animals in accordance with established criteria [1,2,3].

The Mangalarga is one of the main horse breeds in Brazil and is found throughout the national territory, with higher concentrations in the states of São Paulo and Bahia. According to data from the ABCCRM, 212,361 Mangalarga horses were registered in 2019, making it the fourth most registered breed in the country. Of these, 35,320 horses were considered purebred and active [6].

The breed's distinguishing feature is its natural gait known as “*marcha trotada*” (trot-like march), characterized by a two-beat diagonal bipedal support. This gait presents slight dissociation,

with a minimal suspension time between limb supports, just enough to allow switching. The term “*diagonal march*” is also accepted. The gait must be symmetrical, with overtracking, performed in an elastic, rhythmic, coordinated, and regular manner. There must be a predominance of diagonal bipedal motion over lateral ones, which results in low saddle impact and justifies the term “*marcha trotada*” [3]. Lateral gaits (lateral footfall only), the trot (only diagonal support), and the gaits known as “*marcha picada*” and “*marcha batida*”, typical of other gaited breeds, are not permitted [3,7].

Mangalarga horses are evaluated by ABCCRM-certified technicians in two distinct phases: the first is a provisional registration in the early months of life, and the second is the definitive registration after the horse reaches 36 months of age. The classification is based on a scoring table aligned with the breed standard, divided into categories such as total dynamics (TD), which corresponds to the sum of scores assigned to dynamic traits such as movement (Move), dynamic limbs (DL), canter (CAN), and comfort (Comf). Additionally, morphometric measurements such as withers height (WH), thoracic perimeter (TP), and cannon bone perimeter (CBP) are recorded [3].

The evaluated traits are important phenotypic parameters for selection, especially considering that many horse breeds still do not incorporate genomic tools or genetic values in their breeding programs [8]. The evaluation of TD-related traits and morphometric measures aims to support breeders both in defining breeding animals and selecting individuals to participate in shows and competitions [3,9]. These events play a relevant role in guiding breeders' selection, as performance in competitions is one of the most widely used selection criteria in equine breeding [10]. As a result, award-winning horses tend to produce more offspring [11], with morphofunctional phenotypes being directly associated with success in specific equestrian disciplines [12].

However, success in the sport horse industry is multifactorial, as these characteristics are subject to various environmental influences [13,14]. Therefore, the development of improvement programs based on genetic values is necessary [13,15], especially considering the current insufficiency of studies focused on estimating heritability, genetic trends, and correlations for traits associated with the registration of Mangalarga horses.

The aim of this study was to estimate genetic parameters for morphometric and dynamic traits in Mangalarga horses, with the purpose of providing breeders, technicians, and associations with information to support mating decisions in selection and genetic improvement programs for the breed.

2. Material and methods

2.1. *Ethical approval*

This study utilized zootechnical and pedigree data provided by the ABCCRM and did not involve any experimental manipulation of live animals by the authors; therefore, formal approval from an Animal Care and Use Committee was not required. The use of the database was authorized by the ABCCRM, which collects the information during the official registration process.

2.2. *Animals and Data*

The data used in this study were provided and authorized by the ABCCRM. The database consisted of one complete pedigree file and two phenotypic files. The complete pedigree file comprised 212,361 Mangalarga horses born between 1919 and 2019, of which 58.0% were females, and was used to assess pedigree depth and completeness. The quality of the pedigree file data was assessed using the number of complete equivalent generations traced (Ge), which is widely recognized as one of the most appropriate measures to represent the depth of genealogical information [16]. The pedigree data used in our study showed substantial genealogical depth, with an average of 5.8 Ge. In turn, the completeness of the genealogical information was assessed using the ‘Pedigree Content’ routine implemented in ENDOG v4.8 [17]. The proportion of known ancestors through the different paternal and maternal pathways, up to the fifth generation, was obtained using PediCont, yielding values for parents (93.49% Total, 93.51% ♂, 93.47% ♀), grandparents (92.17% Total, 92.18% ♂, 92.15% ♀), great-grandparents (91.34% Total, 91.38% ♂, 91.31% ♀), great-great-grandparents (89.54% Total, 90.08% ♂, 89.72% ♀), and great-great-great-grandparents (81.05% Total, 87.09% ♂, 80.16% ♀).

Additionally, the pedigree completeness index proposed by MacCluer et al. (1983) [18], calculated for each ancestral generation, was obtained using PedKnow. The index decreased from 0.93 in the first generation to 0.81 in the fifth generation, followed by a marked decline to 0.62, 0.39 and 0.20 in the sixth, seventh and eighth generations, respectively, reaching values close to zero from the eleventh generation onwards (Fig. 1).

The two phenotypic files comprised a morphometric dataset containing 54,617 unique horses and a dynamic-trait dataset containing 45,010 unique horses, all born between 1977 and 2019. The number of non-missing phenotypic records differed among traits because of differences in data availability (Table 1). Among morphometric traits, WH had 54,617 records, whereas Move had the largest number of records among dynamic traits (45,010). The temporal distribution of phenotypic records by birth year is presented in Table S1 (Supplementary Material).

Only animals with a non-missing observation for the trait under analysis were included in the corresponding phenotypic data file. Animals without a record for that trait were not entered as observations with missing phenotypic values. For each analysis, the pedigree included the recorded animals and the ancestors required to construct the trait-specific numerator relationship matrix, traced back to the 11th generation or to the maximum depth available. Consequently, animals with phenotypic records were a subset of the animals in the corresponding pedigree matrix, and these numbers must not be added. For example, the WH analysis comprised 54,617 horses with WH records and 67,732 animals in the corresponding pedigree matrix, of which 13,115 had no own WH record but contributed relationship information.

2.3. *Morphometric and Dynamic traits*

The morphometric traits analyzed were withers height (WH), obtained using a measuring stick and corresponding to the distance from the ground to the horse's withers; thoracic perimeter (TP), and cannon bone perimeter of the forelimb (CBP), both measured with a measuring tape and expressed in centimeters.

The evaluation of dynamic traits includes a set of four traits: movement (Move), dynamic limbs (DL), canter (CAN), and comfort (Comf). Scores are assigned by ABCCRM-certified technicians following a standardized breed protocol. Although these scores are subjective, the technicians undergo regular training and calibration to ensure consistency across evaluators, a common practice in sport horse breeding evaluations. Animals must be ridden, equipped with a saddle, and presented with an appropriate level of riding [3].

The trait Move is assessed during the walk and march, focusing on stride amplitude, as well as the synchronization and quality of the gait, which is technically defined by the absence of dragging or excessively elevated movements. The evaluator looks for relaxed, coordinated, and elastic movements, assigning a total score ranging from 1 to 15 points. In the trait DL, horses are observed from the front and rear during the walk, diagonal march, and canter. The ideal sought is a limb alignment as close as possible to the vertical plane passing through the centers of support and this trait is scored from 1 to 12 points. The trait CAN is evaluated while the horse canters in circles, in both directions, analyzing elasticity, amplitude, and synchronization between forelimbs and hindlimbs; the score ranges from 1 to 5 points.

In the trait Comf, the horse is assessed from the side, front, and rear, while approaching and moving away from the evaluator, in addition to the ridden evaluation, and is scored from 1 to 13 points. Importantly, it is necessary to differentiate this trait from “rideability”. While rideability in sport horses

describes the ease with which a horse can be ridden, emphasizing the reaction to the rider's aids, rein contact, and the absence of conflict behaviors [19,20], the Comf trait in the Mangalarga breed evaluates the biomechanical smoothness of the gait. The assessment focuses on vertical and lateral body movements, head and neck positioning, and willingness to move forward [3]. The total dynamics (TD) trait is obtained by summing the scores for Move, DL, CAN, and Comf, where each horse can achieve a maximum of 45 points [3].

2.4. Analysis methodology

Phenotypic differences between sexes in the eight evaluated traits (morphometric and dynamic) were obtained through non-parametric analyses using the Mann-Whitney U test [21]. This approach was chosen because the data for these traits did not meet the assumption of normality, as determined by the Kolmogorov-Smirnov test. Statistical significance was set at $p < 0.05$.

Analyses were performed to estimate variance components and explore the results for morphometric and dynamic traits. The model included the random effect of contemporary group (CG; stud farm, year of birth, season of birth, and sex), animal additive genetic, and residual effects. To illustrate the data structure, the number of CG levels, the average number of records per group, and the number of animals in the pedigree matrix (traced to the 11^a generation or the maximum depth available) for each trait analysed are detailed in Table 1.

Evaluation dates and evaluator identification at the definitive registration are not present in the dataset. However, the lack of adjustment for 'age at measurement' is mitigated by the ABCCRM's regulation, which requires a minimum age of 36 months for definitive registration evaluations. At this developmental stage, distal bone growth, such as cannon bone circumference, is already physiologically consolidated [22,23], minimizing age-related biases in our estimates.

Regarding the absence of recording dates and evaluator identification, the inclusion of “stud farm”, “year of birth”, and “season” within the contemporary group serves as an important methodological safeguard. The stud farm component was included because it was intended to account partially for the unrecorded environmental effects of management, nutrition, health (sanitary conditions), and training. Given that stud farms typically utilize the same regional technicians for the definitive registration evaluation, this relationship may capture part of the unrecorded evaluator effect, alongside macro-environmental changes and cohort-specific scoring criteria.

Furthermore, estimating the effect of contemporary groups in horse data is generally difficult due to the population structure, where many stud farms register few or only a single animal. This definition resulted in 7,948 to 32,735 contemporary-group levels, with mean group sizes ranging from

1.50 to 1.67 records, depending on the trait. Consequently, many contemporary groups contained only a small number of observations. To overcome this limitation and preserve these records without losing data, the contemporary group was fitted as a random effect, allowing poorly informed group effects to be retained by shrinking them towards the overall population mean. Nevertheless, because evaluation date and evaluator identity were unavailable, the adopted contemporary group should be regarded as a proxy, rather than as a true group of animals evaluated under identical environmental and assessment conditions.

The fixed effect of type of mating was also included, grouped into two classes: natural mating and assisted reproduction (which includes artificial insemination and embryo transfer). All animals had complete records for this effect, requiring no data exclusion and justifying a two-level parametric specification.

Statistical analyses were performed using the BLUPF90+ software family [24]. To obtain the genetic and phenotypic correlations among all evaluated traits, bivariate linear animal models were fitted for all possible pairwise combinations (“all-by-all” approach). However, for reporting the variance components and heritabilities (Table 4), the estimates were extracted specifically from the bivariate models where each trait was paired with withers height (WH). WH was selected as the reference pairing due to its near-complete phenotypic availability (99.99%) in the dataset, which provided high computational stability and consistency of the estimates.

This software family, via Bayesian inference, was used to obtain the posterior distribution of the Estimated Breeding Values (EBVs) and to determine the minimum and maximum values, as well as the 95% Highest Posterior Density (HPD95) intervals. Unlike frequentist approaches that compute reliability from the inverse coefficient matrix, the Bayesian framework assesses the accuracy and uncertainty of each prediction directly through its marginal posterior distribution [25].

The prediction error variance (PEV_i) for each animal was estimated directly from the sample variance of the posterior distribution of the breeding values obtained from the post-burn-in iterations. Individual reliability was then calculated as:

$$REL_i = 1 - \frac{PEV_i}{(1 + F_i)\sigma_a^2}$$

where F_i is the individual inbreeding coefficient and σ_a^2 is the additive genetic variance. Accuracy was subsequently calculated as $ACC_i = \sqrt{REL_i}$ and expressed as a percentage. As highlighted by Aguilar et al. [26], incorporating the inbreeding coefficient in the denominator appropriately scales the theoretical genetic variance for each individual, accounting for the flow of information from relatives and allowing individual accuracies to properly reflect pedigree depth.

To allow comparisons of the relative genetic variability across traits with different units of measurement, the EBVs were additionally scaled by their respective genetic standard deviations (σ_g), derived from the additive genetic variance (σ_a^2) [27]. Estimated Breeding Values are presented in their original units (centimeters and points) to facilitate intuitive interpretation and practical adoption by breeders and technicians, as this is the first study providing genetic values for the Mangalarga breed.

To calculate the genetic trend for the population, the EBVs obtained as solutions from the applied model were utilized. To estimate genetic trends, annual mean EBVs were calculated, for each trait, using all animals with an EBV in the corresponding trait-specific pedigree matrix and born between 1977 and 2019. Therefore, these annual means included both animals with own phenotypic records and pedigree-only animals. Subsequently, a linear regression analysis was applied to these annual means to establish and plot the trend lines. This approach is widely adopted in genetic studies to represent the additive genetic progress of the population [28,29,30]. The results are presented in figures showing the annual means for each trait and their respective linear trend lines.

Additionally, phenotypic trends were calculated separately for each trait using animals with an available phenotypic record. Animals were grouped according to year of birth, and the annual phenotypic mean was calculated for each trait. Birth years ranged from 1977 to 2019 for WH, TP, CBP, Move, DL, and CAN, and from 1988 to 2019 for Comf and TD. Linear regression of the annual phenotypic means on year of birth was subsequently performed, and the regression equations and coefficients of determination (R^2) were used to describe the direction and magnitude of the phenotypic changes over time. The same regression procedure adopted for genetic trends was used here to facilitate direct comparison between phenotypic and genetic changes.

The relative magnitude of the genetic trend in relation to the phenotypic trend was calculated as $(bG/bP) \times 100$, where bG and bP represent the linear regression coefficients of the annual mean EBVs and annual phenotypic means on year of birth, respectively.

3. Results

3.1. Descriptive statistics and sexual dimorphism

Phenotypic morphometric means for WH were 3.2 cm higher in males ($p < 0.001$), suggesting some sexual dimorphism with a superior physical structure compared to females (Table 2). The mode for WH indicated that the most frequent measurement among animals was 155 cm. A total of 789 females, all born before 1989 (1.85% of all females with WH), were identified with a WH below 145.0 cm, the minimum height required for registration after this period.

For TP, females presented average values 3.63 cm higher than males ($p<0.001$). In the case of CBP, a small difference was observed between genders, with males averaging 0.63 cm more than females, which was significant ($p<0.001$). All the morphological traits indicated significant sexual dimorphism in the Mangalarga breed (Table 2).

The mean scores for phenotypic dynamic traits were 12.63 ± 1.45 points (Move), 9.03 ± 1.32 points (DL), 4.23 ± 0.69 points (CAN), 11.49 ± 1.14 points (Comf), and 38.37 ± 3.03 points (TD), all presenting low standard deviations. The mean and mode values were close for traits DL, CAN, Comf, and TD, indicating a concentration of scores around the central value in 4 of the 5 dynamic traits (Table 3). Between genders, significant differences were observed in CAN ($p<0.001$) and Comf ($p=0.006$), with males scoring 0.09 points higher in CAN and 0.07 lower in Comf, compared to females. In the remaining 3 traits (Move, DL and TD), there were no significant phenotypic differences between males and females ($p>0.05$) (Table 3).

3.2. Heritability and Correlations

Regarding morphometric traits (expressed in cm²), analyzed with linear animal models, the additive genetic variances (σ^2_a) ranged from 0.201 (CBP) to 23.520 (TP), contemporary group variances (σ^2_c) from 0.150 (CBP) to 6.784 (TP), and residual variances (σ^2_e) from 0.590 (CBP) to 28.109 (TP). Similarly, for dynamic traits (expressed in points²), the σ^2_a , σ^2_c , and σ^2_e components ranged from 0.100 (CAN) to 2.890 (TD), 0.080 to 0.980, and 0.283 to 5.144, respectively, with CAN exhibiting the minimum and TD the maximum values across all variance sources (Table 4).

The morphometric and dynamic traits provided moderate to high h^2 estimates, with values ranging from 0.213 ± 0.013 (CBP) to 0.578 ± 0.009 (WH) and from 0.215 ± 0.010 (CAN) to 0.337 ± 0.011 (Move), respectively (Table 4).

The genetic correlations among the five dynamic traits ranged from -0.03 ± 0.05 (DL and Move) to 0.92 ± 0.01 (Move and TD). Among the morphometric traits, the values ranged from 0.41 ± 0.03 (TP and CBP) to 0.70 ± 0.02 (TP and WH). Between morphology and dynamics, genetic correlations ranged from -0.21 ± 0.04 (Move and CBP) to 0.29 ± 0.03 (CAN and TP) (Table 5). The trait total dynamics (TD) presented high genetic correlations with 4 of the other 7 traits, all of which are dynamic variables, ranging from 0.57 ± 0.03 (DL) to 0.92 ± 0.01 (Move).

High correlations were observed between Move and Comf (0.62 ± 0.01), and between Comf and CAN (0.53 ± 0.01) (Table 5). The TD trait showed significant phenotypic correlations with all dynamic variables, the highest being with Move (0.87 ± 0.00). Among the morphometric traits, TP and WH also exhibited a high correlation (0.51 ± 0.01).

3.3. *Estimated Breeding Values*

The standardization of the EBVs (EBV_{std}) revealed that the Move (+1.05) and DL (+0.67) traits exhibited the greatest relative genetic progress. Among the morphometric traits, genetic dispersion was lower, indicating a slight reduction in WH (-0.14), while TP showed a more pronounced reduction (-0.51), equivalent in magnitude to that observed in CAN (+0.54), but in the opposite direction (Table S2). When evaluating sexual dimorphism using the original units for all animals included in the trait-specific pedigree matrices (Table 6), the mean estimated breeding values (EBVs) varied for morphometric traits (cm) between sexes, with the smallest and largest EBVs occurring within the same trait (TP), ranging from -2.91 ± 3.26 cm (males) to 2.21 ± 3.46 cm (females). Regarding WH, males on average gained height (0.65 ± 2.77 cm) and females lost size (-0.66 ± 2.96 cm). On the other hand, the CBP was positive and similar for both sexes. Among the dynamic traits, mean EBVs were consistently higher for males. The greatest differences between sexes were observed in Move and DL, with a male superiority of +0.12 and +0.09 points, respectively. The smallest difference between sexes was 0.01 points for Comf. The mean accuracy of EBV predictions ranged from $58.40 \pm 16.55\%$ for Comf to $80.90 \pm 8.08\%$ for WH. Accuracy was consistently higher in males than in females for all traits, with the greatest sex difference observed for TP ($70.85 \pm 9.34\%$ vs. $64.92 \pm 13.27\%$) and the smallest for WH ($82.09 \pm 7.92\%$ vs. $80.58 \pm 8.10\%$) (Table 6).

3.4. *Phenotypic and genetic trends*

Analyzing the genetic trends, the coefficients of determination (R^2) for all traits were high (0.7378 to 0.9840), as indicated in Fig. 2. However, traits displayed distinct non-linear behaviors. The morphometric traits WH, TP, and CBP displayed a distinct pattern; WH presented positive values from 1990 (EBV 0.14) and the highest average EBV in 2001 (2.07 cm). After that, stability and decrease, ending the last year of births (2019) with an average EBV of 1.08 cm. The TP trait presented growth until 2011 (0.09 cm) and was also the first year in which EBV was positive, with the highest annual value in 2015 (0.39 cm), decreasing in the following years, with -0.74 in 2019 (Fig. 2). CBP showed downward genetic trends; starting with a considerable decrease in 1991 (0.14 cm), the EBVs became negative in 2004, stabilizing briefly in 2005 (-0.04 cm) and then showing a slight decrease, with an average EBV of -0.08 cm in 2019 (Fig. 2).

At the dynamic level, the traits presented identical patterns and constant growth, identical between DL and CAN, with the Move trait also close, and the Comf and TD traits showing identical behavior (Fig. 2). The highest averages of dynamic EBV were all observed in the last year of births (2019), with 1.96 (Move), 1.02 (DL), 0.45 (CAN), 0.31 (Comf) and 1.25 (TD) points (Fig. 2).

The phenotypic trends differed among the morphometric traits (Fig. 3). WH and TP showed positive overall trends, with annual increases of 0.1163 cm ($R^2=0.6432$) and 0.1348 cm ($R^2=0.6714$), respectively. For both traits, the annual phenotypic means increased mainly from the late 1980s onwards, followed by relative stabilization and a decline in the most recent birth years. In contrast, CBP exhibited a consistent negative trend, decreasing by 0.0163 cm per year ($R^2=0.7312$) and reaching its lowest annual phenotypic mean in 2019. All dynamic traits showed positive overall phenotypic trends (Fig. 3). TD exhibited the greatest absolute annual increase, corresponding to 0.1310 points per year ($R^2=0.8260$), despite greater fluctuations during the initial years. Among its component traits, Move showed the largest and most consistent increase, corresponding to 0.0531 points per year ($R^2=0.9189$), followed by DL, with an increase of 0.0187 points per year ($R^2=0.8318$). CAN increased more gradually, by 0.0068 points per year ($R^2=0.5599$). Although Comf also showed a positive trend, with an annual increase of 0.0162 points, its lower coefficient of determination ($R^2=0.2846$) reflected greater fluctuations among birth years and a less consistent temporal pattern.

The relative magnitude of the genetic trend in relation to the phenotypic trend varied considerably among traits, corresponding to 93.4% for WH, 94.7% for TP, 31.9% for CBP, 76.6% for Move, 107.5% for DL, 141.2% for CAN, 40.1% for Comf, and 22.1% for TD.

4. Discussion

4.1. Descriptive statistics and sexual dimorphism

The volume of phenotypic records analyzed in this study provided statistical power to evaluate sexual dimorphism in the Mangalarga breed (Tables 2 and 3). As expected by equine biology [31], morphometric traits (WH, TP and CBP), along with CAN and Comf, maintained significant sexual dimorphism ($p<0.05$). However, there were no statistically significant differences between males and females for Move ($p=0.181$), DL ($p=0.127$), and TD ($p=0.402$). This absence of sexual dimorphism in dynamic traits indicates that the ABCCRM evaluators assess movement quality with impartiality. This suggests that, despite structural differences, males and females demonstrate equivalent functional gait performance.

The morphometric traits WH and TP place the Mangalarga horse as taller and more arched than the Mangalarga Marchador, with averages of 149.0 and 150.4 cm for WH and 177.0 and 175.0 cm for TP [32,33]. Similar to the Campolina breed with WH of 153.8 cm and TP of 181.8 cm [34]. Higher values were observed in the Lusitano horse breed, with a WH of 157.8 cm [35], the Sardinian Anglo-Arabian breed, with a WH of 160.8 cm and a TP of 185.9 cm [29] and German Warmblood breeds, with a WH of 167.6 cm and a TP of 190.04 cm [31]. The intermediate stature of the Mangalarga horse is consistent with its heritage and early selection of the breed, with hardy mares of smaller build, and

stallions with superior body structure [1,2]. The significant difference in WH between genders is justified by the sexual dimorphism common among animals and applied to equines [31], as reported in Lusitano [35], Campolina [28] and Anglo-Arabian from Sardinia [29] breeds. The importance of TP in equines is linked to athletic performance, in which animals with deep chests and arched ribs have greater cardiac and pulmonary capacity [32,36,37].

The CBP in Mangalarga presented a higher value compared to Brazilian breeds, such as the Campolina, with 18.96 cm [34] and Mangalarga Marchador, with 18.02 cm [38]. The superiority of bone density suggests that the CBP trait possibly has a higher selection priority in Mangalarga, compared to Campolina and Mangalarga Marchador. However, Almeida et al. [5], studying the same breed as the one in the present study, reported a constant and marked reduction in the phenotypic values of the CBP from females analyzed between 1980 and 2010. This fact, associated with the intense and repetitive exercises characteristic of gaited horses, may increase the risk of fatigue and fractures [39,40]. Therefore, it is essential that selection programs consider CBP as one of the priority traits in the selection criteria, which will be highlighted further below, in the section on breeding values. In an international context, CBP values higher than those of the Mangalarga were observed in the Czech Warmblood [41] and Anglo-Arabian breeds of Sardinia [29], with 20.7 and 20.5 cm, respectively.

Direct comparison of dynamic trait scores is challenging given the different scoring scales for each breed, even when dealing with similar traits (e.g., “marcha trotada” - trotting gait, “marcha picada” - pacing gait, “marcha batida” - beating gait, trot, canter or rideability), which complicates the direct comparison of the values obtained for Move, DL, CAN, Comf, and TD. However, from a quantitative genetic perspective, these traits are comparable to those evaluated in other sport and saddle horse breeds, such as the Mangalarga Marchador [15], Campolina [28], and Warmbloods [19]. This is because, as reported by these authors, they all rely on the subjective assessment of dynamic traits, such as gait quality, elasticity, and biomechanical functionality under saddle, among other similar criteria, evaluated by trained judges during field and registration tests. This structural similarity validates the comparison of their genetic parameters (such as heritabilities and genetic correlations) across breeds.

In a previous study on the Mangalarga breed [42], the authors reported a lower average value for the Move trait (12.01 ± 1.05 points). This is somewhat expected, as the scoring scale used at the time (2006) was limited to 14 points, unlike the present study, with a limit of 15 points (Table 3), which partly justifies the slight difference observed. Ripollés-Lobo et al. [43] reported for the population of young Pura Raza Española horses that males are more successful in basic performance scores, while females score higher in dressage. On the other hand, for Swedish Warmblood horses, males received higher scores in dressage tests [43]. However, most articles investigating gait traits in horses do not

report gender differentiation for score values [10,45,46], as is the case in the present study for the Move and TD traits.

4.2. *Heritability and Correlations*

Variance component partitioning indicated that residual variance (σ^2_e) was the largest source of variation for most traits, particularly for thoracic perimeter (TP), cannon bone perimeter (CBP) and all dynamic traits. Consequently, as reported by Hossein-Zadeh (2021) [47] in a meta-analysis, the dominance of the residual variance over the additive genetic variance (σ^2_a) is an inherent characteristic of historical field data in horses. This substantial residual component naturally reflects environmental heterogeneity, measurement noise, evaluator subjectivity, and missing covariates, such as age at measurement. Although this inherent environmental noise theoretically imposes a limit on the maximum accuracy of Estimated Breeding Values (EBVs) and can introduce background noise in genetic trends, the heritability estimates obtained in this study were of moderate magnitude and in line with those reported for various breeds. Nevertheless, these estimates should be interpreted considering the environmental constraints inherent in the available historical records.

Although the contemporary-group variance accounted for approximately 10–17% of the total phenotypic variance, this finding does not demonstrate that the adopted grouping fully controlled environmental heterogeneity. The small mean number of observations per group implies substantial shrinkage of many contemporary-group solutions towards the population mean, thereby limiting their ability to represent the actual effects of common management and evaluation conditions. Moreover, because year and season of birth were included in the contemporary-group definition, part of the temporal variation may have been absorbed by this effect, whereas residual temporal and evaluator-related variation may remain unaccounted for. Consequently, the estimated genetic trends should be interpreted cautiously as population-level patterns that may still be influenced by incomplete adjustment for temporal, management, and evaluator effects. Furthermore, this same limitation may also have contributed to an overestimation of the heritability estimates.

WH is a trait that frequently exhibits high h^2 estimate, although the exact magnitude depends on the specific segregation of Quantitative Trait Loci (QTLs) within each breed's population. The estimate obtained in the present study (0.58) confirms a substantial additive genetic basis in Mangalarga horses, positioning the breed at a magnitude similar to breeds such as Bardigiano (0.63) [48], Lusitano (0.61) [35] and Pura Raza Española (0.58) [49] and superior to the lower values observed (0.47 to 0.50) in the Mangalarga Marchador [50,51], Belgian Warmblood [52], Campolina [53], and Czech Republic Warmblood Sport breeds [41]. Higher h^2 estimates were reported by Wang et al. [14], Giontella et al.

[29], and Miglior et al. [54] in the Yili (0.72), Sardinian Anglo-Arabian (0.78), and Haflinger (0.79) breeds, respectively.

TP presented high h^2 estimate (0.40) and was consistent with the value reported for the Bardigiano breed (0.41) [48]. Lower h^2 values have been described for the Mangalarga Marchador (0.30 to 0.31) [50,51], while slightly higher estimates were reported for the Warmblood Sport breeds of the Czech Republic (0.46) [41], Anglo-Arabian of Sardinia (0.47) [29] and Pura Raza Española (0.48) [49].

The CBP provided a low to moderate h^2 estimate (0.21), higher than for the Brazilian Campolina breed (0.11) [28] and Pura Raza Menorquina (0.19) [55], and lower than the values described in the Yili breed (0.33) [14], Pura Raza Española (0.35) [49], Czech Warmblood Sport (0.57) [41] and Mangalarga Marchador (from 0.27 to 0.68) [50,51,56]. This variation and some discrepancy between studies reflect that the h^2 estimates for CBP do not demonstrate unanimity in the literature.

The h^2 estimate magnitudes for all morphometric traits reinforce the selection potential of these characteristics in the Mangalarga horse population, reflecting a consolidated genetic basis for body structure in the breed and suggesting that historical phenotypic selection has favored a clearer expression of additive genetic variance, indicating that genetic variability is sufficient to obtain a response to selection. However, it is emphasized that morphometric traits are sensitive to methodology, breed, and age of the animals. Nonetheless, we reinforce that the covariate parameter “age at measurement” should be included in the model whenever available [57], which highlights the need to prioritize the recording of this variable in future data collections in the Mangalarga breed.

The h^2 values for the dynamic traits (Table 4) were of moderate to high magnitudes (0.22 to 0.34), reflecting to be robust when compared with other studies in Brazilian breeds, such as the Campolina [53] with 0.15 for Comf, or even the Mangalarga horse itself [42] with 0.27 for Move. Several sport horses presented h^2 values similar or lower than those obtained in this study for gait characteristics, in breeds such as the Pura Raza Española (0.15 to 0.33) [46,49], Pura Raza Menorquina (0.09 to 0.33) [55] and Dutch Warmblood, with values of 0.12 to 0.22 [58]. Higher h^2 values (0.32 to 0.54) were described for the breeds Belgian Warmblood [52], East Bulgarian [59] and Brazilian Sport Horse [60].

The phenotypic assessment applied by the ABCCRM technicians and evaluated in this study approaches the magnitude of studies that employ more objective methods, such as kinematic video analysis, which tends to reduce environmental variance. Studies with filming under field conditions reported moderate to high h^2 estimates in Lusitano (0.18 to 0.53) [61] and Paso Peruano (0.40 to 0.47) [62]. When the environmental effect was reduced, with all animals evaluated under the same conditions, such as on a treadmill, the h^2 for walk [63] and trot [64] in Pura Raza Española showed

moderate to high values (0.22 to 0.88). The consistency of the results obtained in this study, even considering the subjectivity inherent in the method, suggests that the assessment protocol was effective in capturing the additive genetic variance present in the population.

Despite their effectiveness, subjective scoring systems present limitations, such as the tendency of evaluators not to use the entire scoring scale [65], which can restrict phenotypic variance and hinder genetic gain [42]. In this sense, the adoption of a more descriptive linear scoring system could be a refinement for the selection program [35], increasing h^2 estimates [48]. Mota and Prado [66] in the past suggested scoring horses by linear profiling in the Mangalarga breed; however, the scoring system remains based on the same methodology.

The genetic correlations of morphometric and dynamic traits revealed complex associations and distinct directions (Table 5). WH and TP showed low to moderate positive correlations with gaits (0.08 to 0.29), aligning with studies on the Mangalarga Marchador [56], Pura Raza Española [67], Lusitano [35], Bardigiano [48], and Warmblood Sport Horses [41] that also described positive, albeit low-magnitude, genetic correlations between body measurements (such as height) and movement dynamics. Mota et al. [42] in a study carried out with the Mangalarga breed, obtained a moderate correlation (0.47) between WH and Move.

However, CBP showed null or negative genetic correlations with dynamic traits, highlighting the unfavorable correlation with Move (-0.21). This finding suggests that animals with smaller bone circumference tend to perform better in gait dynamics assessment during the definitive registration, which may explain the historical selection pressure for CBP, favoring dynamics. To manage this trade-off, the breeding program must avoid single-trait selection for gaits and instead apply multi-trait selection criteria that monitor bone structure.

Knowing that form-function in horses is of great importance, this relationship is not universal, and studies conducted on the Pura Raza Española [46] and Campolina [28] reported negative correlations between WH and gait characteristics. Ricard et al. [65] obtained low correlations between WH and performance for several breeds, demonstrating divergences between breed morphometric patterns and equestrian disciplines. The predominantly Iberian base of the Mangalarga [68] and Mangalarga Marchador [69], with a historical selection directed towards a specific functional biotype as a functional population, seems to have strengthened the genetic link between form and function.

It was observed that selection for DL and Move can generate joint gains for CAN quality and Comf, respectively. Furthermore, the high magnitude genetic correlation (0.75) reported between Move and Comf in this study (Table 5) corroborates the findings of Ricard et al. [65] in sport horses, who reported high correlations between gait quality and riding ability.

Phenotypic-morphometric correlations close to the values reported in the present study (Table 5) were observed in Pura Raza Española horse [49], with correlations of 0.44 (WH and CBP), and Czech Warmblood [41], with 0.38 for WH and CBP. Molina et al. [49] also described a similar value (0.37) for CBP and TP. Lower values were reported in Mangalarga Marchador [70] for CBP and TP (0.31), WH and CBP (0.27), and WH and TP (0.40). Novotna et al. [41] also described lower values for CBP and TP (0.22) and WH and TP (0.34).

Phenotypic correlation for TD-like traits (walk, trot, canter, and movement correction) and morphometric measurements was observed in East Bulgarian horses [59], with a value of 0.24, close to the one described for morphometric traits and TD (from 0.13 to 0.27). Similarity was observed between genetic and phenotypic correlations (Table 5), especially for morphometric traits. This proximity suggests a lower influence of environmental factors on the phenotypic expression of WH, TP, and CBP, allowing the underlying genetic relationships to be directly observable in the phenotype. Similar findings were reported in the Mangalarga Marchador breed [70].

In contrast, in the Iranian Thoroughbred [71] and Sardinian Anglo-Arabian [29] breeds, genetic correlations were observed to be much higher than phenotypic correlations. These differences could be attributed to a small database [71] and the nature of selection and management [29], which, by introducing complex environmental correlations, can generate overestimated genetic correlation estimates.

The high similarity between phenotypic and genetic correlations obtained in this study indicates that selection based on phenotypes can be an effective method for correlated genetic progress in the Mangalarga breed. However, although these phenotypic relationships are useful for immediate evaluation, genetic analyses (heritability, correlations, and genetic values) are more effective tools for long-term selection decisions.

4.3. Estimated breeding values

Estimated breeding values (EBVs) are a monitoring tool for selection in breeding programs, allowing for the identification of genetically superior individuals with greater precision, considering not only their phenotype but also that of all their relatives [65]. The distribution of EBVs for morphometric and dynamic traits revealed genetic variability in the Mangalarga horse population, a fundamental prerequisite for successful selection [58]. The range of EBVs obtained is comparable to the Lusitano horse [35], where the evaluation of morphology also demonstrated sufficient additive genetic variance for selection. The existence of genetic variation for gait scores is consistent in the

literature and reported for Brazilian breeds such as Mangalarga Marchador [51,56], Campolina [28], and Brazilian Sport Horse [60], which makes the structuring of genetic evaluation feasible.

The accuracy of EBVs is essential for assessing the confidence associated with individual selection decisions, as it reflects the degree of correspondence between predicted and true breeding values and the likelihood that predictions will remain stable as additional information becomes available [26,72]. In the present study, the moderate-to-high accuracies indicate that the predicted genetic merits already provide useful information for selection, although the lower mean values and greater dispersion observed for Comf and TD require a more cautious interpretation. This pattern is biologically plausible because visually assessed gait traits are subject to environmental and evaluator-related variation, which may reduce the precision of genetic predictions [73].

In Campolina horses, gait scores have also been described as traits with substantial subjectivity, and multivariate approaches were reported to improve the prediction of breeding values, particularly for animals with limited individual information [28,73]. The higher accuracies obtained for WH are consistent with the generally greater objectivity and repeatability of directly measured morphometric traits compared to subjective scoring traits. Therefore, increasing the number of phenotypic records and the amount of information available from relatives should contribute to more stable EBVs in subsequent genetic evaluations.

4.4. Genetic and phenotypic trends

The phenotypic trends indicated that the morphometric development of the Mangalarga population was not uniform across traits (Fig. 3). The overall increases observed for WH and TP are consistent with the temporal changes previously reported in the same breed by Almeida et al. [5]. Between 1970 and 2018, these authors observed increases in WH of 5.1, 3.1, and 2.1 cm in mares, stallions, and geldings, respectively, as well as an increase of 3.3 cm in the TP of stallions. The increase in TP occurred mainly until 2000, followed by stabilization, which is also compatible with the less pronounced changes and subsequent decline observed in the most recent birth years of the present study. Therefore, although the linear trends for WH and TP were positive over the complete period, their recent trajectories suggest that the phenotypic development of body size and thoracic capacity has slowed or changed direction. In contrast, the negative phenotypic trend observed for CBP agrees with the reduction reported by Almeida et al. [5] in Mangalarga mares, whose mean cannon bone perimeter decreased from 19.11 cm in 1980 to 18.77 cm in 2018. As females represented 78.3% of the morphometric dataset in the present study, the overall reduction in CBP may largely reflect the temporal trajectory of the female population. The agreement between studies conducted with partially

overlapping historical records strengthens the evidence that the reduction in cannon bone perimeter represents a persistent phenotypic change in the breed, rather than an isolated fluctuation among birth years.

All dynamic traits showed positive phenotypic trends, indicating a progressive increase in the scores assigned during definitive registration (Fig. 3). This pattern was particularly consistent for Move and TD, whereas the lower coefficient of determination obtained for Comf reflected greater fluctuations among birth years and a less stable phenotypic response. Direct comparisons with other horse populations are limited by differences in the traits and scoring systems used. Nevertheless, Vicente et al. [30] reported moderate phenotypic trends in Lusitano horses, characterized by a slight increase in WH but a decline in the final score, contrasting with the positive evolution observed for all dynamic traits in the Mangalarga population. These authors also concluded that differences among years were predominantly environmental. Accordingly, the positive phenotypic trends observed in the present study may reflect not only selection but also temporal changes in management, training, animal presentation, and evaluation criteria, particularly for subjectively assessed traits. For this reason, their correspondence with the estimated genetic trends must be examined before attributing the observed phenotypic changes specifically to breeding progress.

Genetic trend analysis can indicate the direction and magnitude of genetic progress achieved for traits of interest [74]. Morphometric genetic trends for WH and TP traits (Fig. 2) suggest that the focus of selection has shifted. After decades of pressure to increase animal size (peaks of WH in 2001 and TP in 2014), selection for morphometry first stabilized and then declined in recent years. Vicente et al. [30] also identified stabilization in the genetic trend of WH in Lusitano horses. Similar pattern to the one observed in this study was reported in the Campolina breed, with stability in the WH trend after the year 2000 [53] and a decrease after 2010 [28], suggesting similar selection pressure on the breeds during the same period.

Limb conformation and robustness are phenotypically associated with longevity and athletic lifespan of the horse [75]. In this context, the decline that has occurred since 1992 in the genetic trend for CBP (Fig. 2), despite stabilization since 2005, is a point of attention, since it shows negative values since 2004 and showed a decrease in the last year evaluated (2019). This fact suggests that, possibly unintentionally, guided by the negative genetic correlation between CBP and Move (-0.21), indirect selection for smaller cannon bone circumference may have occurred in favor of gait quality. This trend highlights the importance of monitoring multiple traits to avoid undesirable correlated responses. Specifically, a breeding program for the breed should implement selection indexes that assign weights to dynamic traits while applying independent culling levels or minimum constraints on CBP, ensuring that functional gains do not compromise the necessary bone robustness for athletic longevity.

The genetic trends for dynamic traits were all positive (Fig. 2), with Move, DL, and CAN standing out, showing no stabilization or decline. This indicates that the selection carried out by the association with the breeders has been effective in improving the quality of movement and functionality of the breed. Similar results were observed in the Mangalarga Marchador breed [56], which reported genetic progress for functionality. In contrast, the Campolina breed showed a genetic trend of stability for similar traits [53], suggesting less genetic gain compared to the Mangalarga and Mangalarga Marchador breeds. Although there is a positive genetic correlation between WH and dynamic traits, the genetic trends exhibit different behaviors. While the genetic trend for WH has stabilized, reflecting a stabilizing phenotypic selection to maintain a desirable standard in the breed, the dynamic traits show continuous genetic progress, demonstrating that selection pressure is focused on functional gait improvements.

The linear and upward pattern of the Move trait, coupled with the constant increase in the Comf and TD trend from the end of the 1990s, demonstrates that the scoring criteria in registration and selection, although subjective, have been consistent and efficient in directing the population towards superior genetic merit. The ability to generate genetic progress through subjective scores, if collected systematically and by trained evaluators, is widely documented and its methodology has been validated for breeds such as the Lusitano [30], Brazilian Sport Horse [60] and Pura Raza Española [46]. The trend presented for TD follows a similar pattern to the one described for the Mangalarga breed two decades ago [66], showing that the functional component was an important driver of genetic progress.

When phenotypic and genetic trends were considered together (Figs. 2 and 3), they showed the same overall direction for all evaluated traits. WH and TP increased during most of the study period, followed by stabilization and a decline in the most recent years, whereas CBP showed an overall reduction. Likewise, the positive phenotypic trends observed for Move, DL, CAN, Comf, and TD were accompanied by positive genetic trends. This agreement indicates that genetic selection contributed to the phenotypic changes observed in the Mangalarga population. Nevertheless, the phenotypic trends showed greater fluctuations among birth years, particularly for Comf, whereas the genetic trends were generally more regular. These differences are expected because phenotypic means are also influenced by management, training, environmental conditions, evaluator-related variation, and changes in the animals evaluated over time. Therefore, the observed phenotypic progress cannot be attributed exclusively to genetic improvement, although the parallel trajectories indicate that selection was an important component of the changes achieved in the breed.

The relative magnitude of the genetic trend in relation to the phenotypic trend varied considerably among traits. For WH, TP, and Move, the genetic trend accounted for most of the corresponding phenotypic trend (over 76%), whereas substantially lower values were obtained for

CBP, Comf, and TD. For DL and CAN, the ratios exceeded 100%, indicating that the estimated genetic trend was greater than the observed phenotypic trend. Under the additive relationship in which the phenotypic trend is considered the sum of genetic and environmental trends, this result suggests a negative environmental trend for these traits, which may have partially counteracted the estimated genetic progress. Nevertheless, these ratios should be interpreted as descriptive indicators and not as an exact causal decomposition of the phenotypic changes.

The definition of contemporary groups may have contributed to these results. Contemporary groups were defined using breeder, year of birth, and birth season, but information on test year, test day, test location, rider, trainer, ownership changes, and training condition was unavailable. Consequently, the model may not have fully accounted for environmental conditions operating at the time of evaluation, particularly for subjective and trainable traits that are sensitive to the rider and the horse's training condition [19,73]. Some of these unaccounted effects may therefore have been partially confounded with the additive genetic effect, potentially leading to overestimation of the heritabilities and genetic trends. This limitation should be considered when interpreting the estimates obtained. Future genetic evaluations would benefit from the systematic recording of test date and location, rider, trainer, and other relevant environmental information, allowing the definition of more appropriate contemporary groups and reducing potential bias.

Genetic trend analysis not only quantifies the results of selection practices but also provides information for the continued evaluation and refinement of the ABCCRM assessment framework. The continued estimation and publication of genetic breeding values is fundamental to guiding breeders, with the aim of accelerating genetic gain [76] and, crucially, monitoring and correcting undesirable trends, such as that observed for CBP, ensuring balanced progress for the breed.

Although the morphometric and dynamic traits evaluated in this study represent the current foundation of the ABCCRM, expanding phenotypic data collection is important for the continuous evolution of selection strategies. Future efforts should aim at the systematic recording of additional traits of economic and animal welfare importance, such as health parameters (e.g., incidence of injuries) and athletic longevity. Furthermore, the future incorporation of objective methods, such as computational kinematics for gait analysis, could refine the current subjective evaluations.

5. Conclusion

The estimated genetic trends suggested temporal changes in the genetic merit of the evaluated traits in the Mangalarga population, while the corresponding phenotypic trends showed an overall improvement in gait quality over time. The recent stagnation in height and chest circumference gain,

coupled with the reduction in bone structure and the moderate negative correlation between cannon bone circumference and movement, indicates a transformation of the breed into a lighter animal, increasingly geared towards a saddle horse for sport and leisure activities in the 21st century.

However, these trends should be interpreted cautiously because the small size of the contemporary groups and the absence of evaluation-date, evaluator, and rider/trainer information may have prevented the complete separation of genetic and environmental temporal effects. Still, continuous monitoring of cannon bone circumference is recommended to prevent potential injuries associated with an increasingly lighter bone structure and the traditional gaited and endurance competitions of the breed. Future breeding strategies must adopt selection indexes that weight the estimated breeding values. By establishing minimum constraints for critical structural traits like cannon bone circumference while promoting gait quality, the program can manage genetic antagonisms and ensure balanced, robust, and continuous genetic progress for the Mangalarga horse.

6. References

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7. Tables

Table 1

Number of animals in the complete pedigree database, animals with phenotypic records, contemporary-group levels, and animals included in the trait-specific pedigree matrices used for the genetic evaluation of morphometric and dynamic traits in Mangalarga horse breed in Brazil

Item	Complete pedigree database (n)	Trait							
		Morphometric			Dynamic				
		WH	TP	CBP	Move	DL	CAN	Comf	TD
Males	89,197	11,874	11,870	11,863	9,786	9,773	9,783	3,076	3,063
Females	123,164	42,743	11,763	11,755	35,224	35,175	35,213	9,479	9,430
Total	212,361	54,617	23,633	23,618	45,010	44,948	44,996	12,555	12,493
CG levels (n)	-	32,735	15,775	15,769	27,408	27,351	27,346	7,968	7,948
Records/CG	-	1.67	1.50	1.50	1.65	1.64	1.65	1.58	1.57
Animals in the trait-specific pedigree matrix (n)	-	67,732	39,871	39,857	62,604	62,546	62,597	25,727	25,666
Pedigree-only animals (n)	-	13,115	16,238	16,239	17,594	17,598	17,601	13,172	13,173

CG, Contemporary group; Records/CG, Mean number of records per contemporary group; WH, Withers height; TP, Thoracic perimeter; CBP, Cannon bone perimeter; Move, Movement; DL, Dynamic limbs; CAN, Canter; Comf, Comfort; TD, Total dynamics. The complete pedigree database comprised 212,361 animals. For each trait, animals with phenotypic records were included within the corresponding trait-specific pedigree matrix together with their unphenotyped ancestors; therefore, these numbers represent overlapping, rather than additive, populations.

Table 2

Descriptive statistics of morphometric traits (withers height, thoracic perimeter, and cannon bone perimeter) by sex and overall, for Mangalarga horse breed in Brazil

Trait		$\mu \pm SD$ (cm)			Min	Max	Mode
		Sex	p-value	Overall			
WH, withers height	♂	156.37 $\pm$ 3.71	<0.001	153.86 $\pm$ 4.43	141.0	198.5	155.0
	♀	153.17 $\pm$ 4.36					
TP, thoracic perimeter	♂	176.87 $\pm$ 7.20	<0.001	178.67 $\pm$ 7.97	103.0	232.0	180.0
	♀	180.50 $\pm$ 8.29					
CBP, cannon bone perimeter	♂	19.35 $\pm$ 0.95	<0.001	19.03 $\pm$ 0.96	10.0	30.0	19.0
	♀	18.72 $\pm$ 0.87					

μ , Mean; SD, Standard deviation; Min, Minimum; Max, Maximum; cm, Centimetres; ♂, Males; ♀, Females.

Table 3

Descriptive statistics of dynamic traits (movement, dynamic limbs, canter, comfort, and total dynamics) by sex and overall, for Mangalarga horse breed in Brazil

Trait		$\mu \pm SD$ (points)			Min	Max	Mode
		Sex	p-value	Overall			
Move, movement	♂	12.63 $\pm$ 1.42	0.181	12.63 $\pm$ 1.45	4.50	15	14
	♀	12.63 $\pm$ 1.46					
DL, dynamic limbs	♂	9.07 $\pm$ 1.25	0.127	9.03 $\pm$ 1.32	1.25	12	9
	♀	9.02 $\pm$ 1.34					
CAN, canter	♂	4.30 $\pm$ 0.64	<0.001	4.23 $\pm$ 0.69	0.50	5	5
	♀	4.21 $\pm$ 0.70					
Comf, comfort	♂	11.44 $\pm$ 1.17	0.006	11.49 $\pm$ 1.14	2.50	13	12
	♀	11.51 $\pm$ 1.13					
TD, total dynamics	♂	38.42 $\pm$ 3.04	0.402	38.37 $\pm$ 3.03	22.00	45	40
	♀	38.35 $\pm$ 3.03					

μ , Mean; SD, Standard deviation; Min, Minimum; Max, Maximum; cm, Centimetres; ♂, Males; ♀, Females.

Table 4

Estimates of genetic parameters for morphometric and dynamic traits (withers height, thoracic perimeter, cannon bone perimeter, movement, dynamic limbs, canter, comfort, and total dynamics) in the Mangalarga horse breed in Brazil

Trait	σ^2_a	σ^2_c	σ^2_e	$h^2 \pm SD$
Morphometric				
WH, withers height	9.7074	1.6124	5.4845	0.578 $\pm$ 0.009
TP, thoracic perimeter	23.5200	6.7838	28.1090	0.403 $\pm$ 0.013
CBP, cannon bone perimeter	0.2007	0.1499	0.5899	0.213 $\pm$ 0.013
Dynamic				
Move, movement	0.6526	0.2150	1.0680	0.337 $\pm$ 0.011
DL, dynamic limbs	0.4326	0.2531	1.0004	0.257 $\pm$ 0.010
CAN, canter	0.0996	0.0797	0.2833	0.215 $\pm$ 0.010
Comf, comfort	0.3869	0.1366	0.8207	0.288 $\pm$ 0.021
TD, total dynamics	2.8895	0.9794	5.1444	0.321 $\pm$ 0.020

σ^2_a , Additive genetic variance; σ^2_c , Random variance of CG; σ^2_e , Residual variance; h^2 , Heritability estimate; SD, Standard deviation.

Table 5

Estimates of genetic (above the diagonal) and phenotypic (below the diagonal) correlations among morphometric and dynamic traits (withers height, thoracic perimeter, cannon bone perimeter, movement, dynamic limbs, canter, comfort, and total dynamics) in the Mangalarga horse breed in Brazil

Trait	Trait							
	Morphometric			Dynamic				
	WH	TP	CBP	Move	DL	CAN	Comf	TD
WH		0.70 ± 0.02^a	0.42 ± 0.03^a	0.26 ± 0.02^a	0.10 ± 0.02^a	0.23 ± 0.02^a	0.08 ± 0.04	0.13 ± 0.04^a
TP	0.51 ± 0.01^a		0.41 ± 0.03^a	0.18 ± 0.03^a	0.27 ± 0.03^a	0.29 ± 0.03^a	0.09 ± 0.05	0.22 ± 0.04^a
CBP	0.40 ± 0.01^a	0.36 ± 0.01^a		-0.21 ± 0.04^a	-0.01 ± 0.04	0.12 ± 0.04^a	-0.15 ± 0.06	-0.09 ± 0.05
Move	0.18 ± 0.02^a	0.20 ± 0.01^a	0.07 ± 0.01^a		0.31 ± 0.03^a	0.45 ± 0.02^a	0.75 ± 0.03^a	0.92 ± 0.01^a
DL	0.14 ± 0.01^a	0.26 ± 0.01^a	0.15 ± 0.01^a	0.31 ± 0.01^a		0.25 ± 0.03^a	-0.03 ± 0.05	0.57 ± 0.03^a
CAN	0.21 ± 0.01^a	0.22 ± 0.01^a	0.20 ± 0.01^a	0.48 ± 0.00^a	0.35 ± 0.01^a		0.61 ± 0.04^a	0.68 ± 0.03^a
Comf	0.10 ± 0.01^a	0.16 ± 0.01^a	0.06 ± 0.01^a	0.62 ± 0.01^a	0.09 ± 0.01^a	0.53 ± 0.01^a		0.73 ± 0.02^a
TD	0.19 ± 0.01^a	0.27 ± 0.01^a	0.13 ± 0.01^a	0.87 ± 0.00^a	0.65 ± 0.02^a	0.73 ± 0.01^a	0.77 ± 0.00^a	

WH, Withers height; TP, Thoracic perimeter; CBP, Cannon bone perimeter; Move, Movement; DL, Dynamic limbs; CAN, Canter; Comf, Comfort; TD, Total dynamics; SD, Standard deviation. ^a, Significant correlations at the 0.01 level (2-tailed). Values are presented as correlation estimate $\pm$ SD.

Table 6

Distribution of Estimated Breeding Values and model-based accuracies for animals included in the trait-specific pedigree matrices for morphometric and dynamic traits in the Mangalarga horse breed

Trait	Population	Estimated breeding values					
		Mean $\pm$ SD	Min.	Max.	HPD95	Accuracy (%)	
						Mean $\pm$ SD	HPD95
Morphometric (cm)							
WH, withers height	Overall	-0.42 $\pm$ 2.97	-10.10	14.00	-5.10 to 4.50	80.90 $\pm$ 8.08	66.40 to 87.40
	Males	0.65 $\pm$ 2.77	-9.70	10.90	-3.90 to 5.10	82.09 $\pm$ 7.92	68.50 to 91.60
	Females	-0.66 $\pm$ 2.96	-10.10	14.00	-5.30 to 4.30	80.58 $\pm$ 8.10	65.90 to 86.70
TP, thoracic perimeter	Overall	-2.46 $\pm$ 3.40	-21.60	12.40	-7.50 to 3.60	66.99 $\pm$ 12.37	43.36 to 79.83
	Males	-2.91 $\pm$ 3.26	-21.60	11.00	-7.80 to 2.80	70.85 $\pm$ 9.34	53.66 to 82.33
	Females	2.21 $\pm$ 3.46	-20.90	12.40	-7.30 to 4.00	64.92 $\pm$ 13.27	40.68 to 79.03
CBP, cannon bone perimeter	Overall	0.06 $\pm$ 0.23	-1.10	1.40	-0.30 to 0.40	60.25 $\pm$ 11.87	38.16 to 74.34
	Males	0.11 $\pm$ 0.24	-1.00	1.40	-0.30 to 0.50	63.15 $\pm$ 9.58	48.53 to 76.50
	Females	0.04 $\pm$ 0.22	-1.10	1.10	-0.30 to 0.40	58.69 $\pm$ 12.67	35.40 to 73.51
Dynamic (points)							
Move, movement	Overall	0.85 $\pm$ 0.71	-2.27	3.02	-0.26 to 2.05	70.89 $\pm$ 8.56	55.93 to 80.13
	Males	0.94 $\pm$ 0.71	-1.71	3.02	-0.18 to 2.13	73.17 $\pm$ 8.72	59.17 to 86.39
	Females	0.82 $\pm$ 0.71	-2.27	2.95	-0.28 to 2.03	70.29 $\pm$ 8.42	55.35 to 79.12
DL, dynamic limbs	Overall	0.44 $\pm$ 0.24	-1.58	2.73	-0.33 to 1.24	66.99 $\pm$ 8.54	52.61 to 77.10
	Males	0.51 $\pm$ 0.23	-1.43	2.73	-0.26 to 1.30	69.40 $\pm$ 8.88	56.24 to 83.51
	Females	0.42 $\pm$ 0.24	-1.58	2.38	-0.35 to 1.22	66.35 $\pm$ 8.33	51.94 to 76.03
CAN, canter	Overall	0.17 $\pm$ 0.02	-0.97	1.19	-0.17 to 0.52	65.10 $\pm$ 8.58	50.92 to 75.70
	Males	0.20 $\pm$ 0.02	-0.94	1.19	-0.14 to 0.56	67.56 $\pm$ 8.89	51.68 to 81.87
	Females	0.16 $\pm$ 0.02	-0.97	0.89	-0.18 to 0.51	64.45 $\pm$ 8.36	50.28 to 74.57
Comf, comfort	Overall	0.09 $\pm$ 0.30	-1.67	1.29	-0.39 to 0.63	58.40 $\pm$ 16.55	26.20 to 75.71
	Males	0.10 $\pm$ 0.32	-1.48	1.29	-0.40 to 0.63	61.73 $\pm$ 15.58	29.90 to 79.46
	Females	0.09 $\pm$ 0.30	-1.67	1.10	-0.38 to 0.59	57.41 $\pm$ 16.70	25.18 to 75.05
TD, total dynamics	Overall	0.23 $\pm$ 1.03	-5.40	3.41	-1.42 to 1.98	59.68 $\pm$ 16.86	26.90 to 76.97
	Males	0.27 $\pm$ 1.07	-4.62	3.29	-1.46 to 2.10	62.99 $\pm$ 15.83	30.61 to 80.66
	Females	0.22 $\pm$ 1.01	-5.40	3.41	-1.41 to 1.98	58.69 $\pm$ 17.04	25.79 to 76.39

SD, Standard deviation; Min, Minimum; Max, Maximum; HPD95, 95% highest posterior density; cm, Centimetres. For each trait, the overall, male, and female populations include both animals with own phenotypic records and pedigree-only animals included in the corresponding relationship matrix. The number of animals therefore differs among traits, as reported in Table 1.

8. Figures

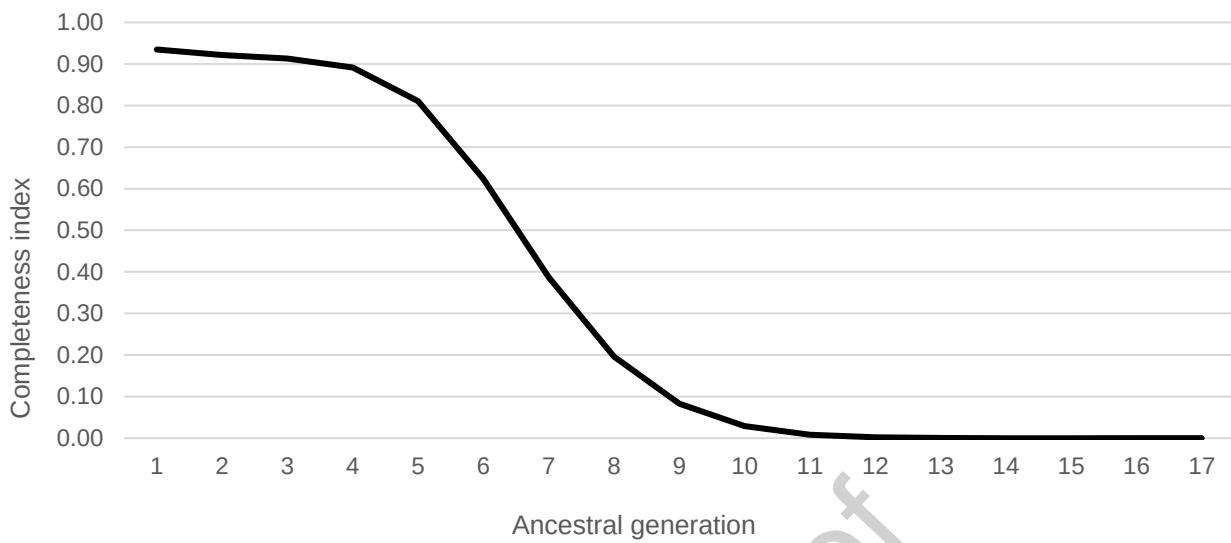


Fig. 1. Pedigree completeness index across 17 ancestral generations, calculated according to MacCluer et al. (1983) in Mangalarga horses.

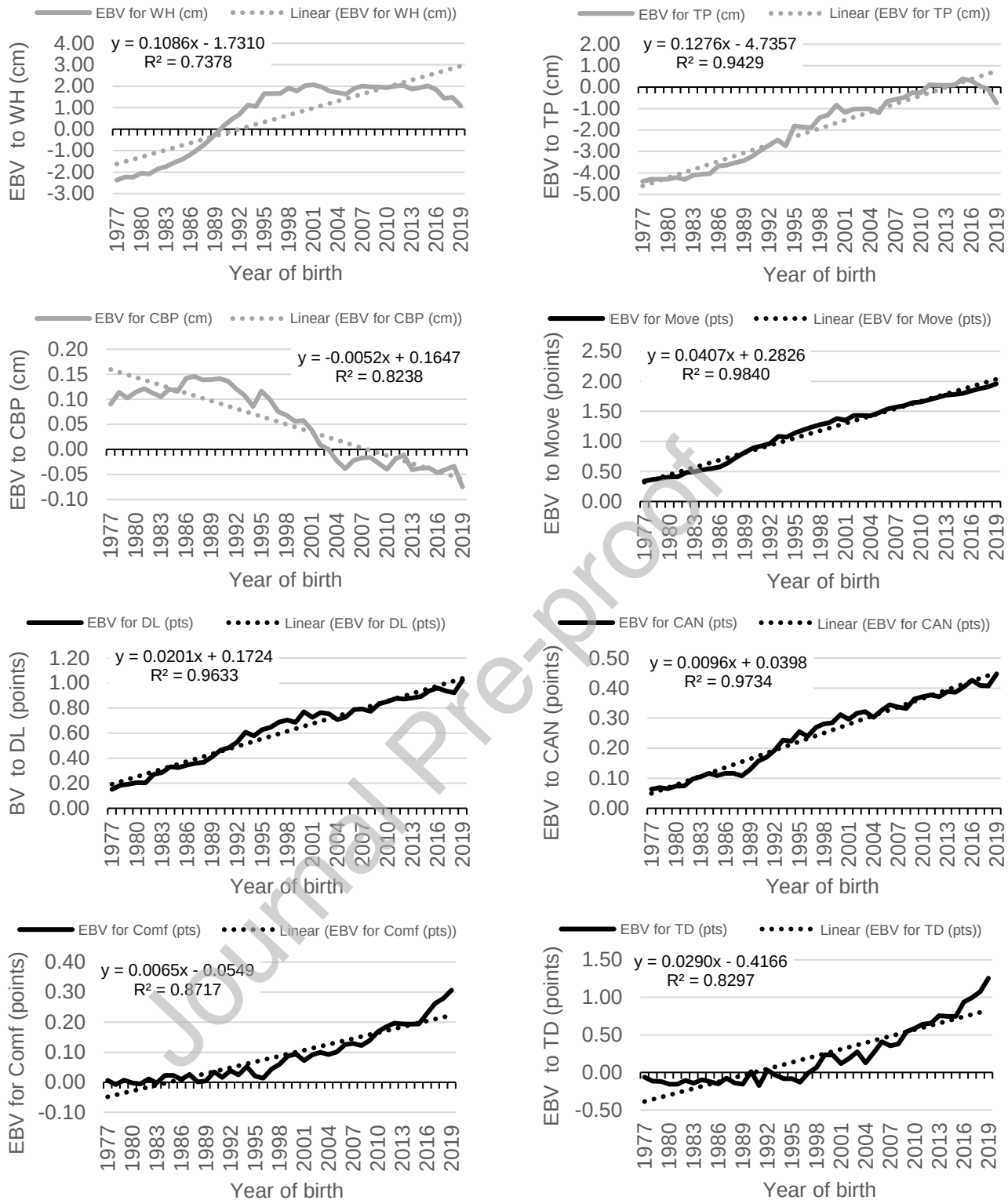


Fig. 2. Genetic trends based on annual mean EBVs for all animals included in the trait-specific pedigree matrix born between 1977 and 2019 for the morphometric traits: withers height (WH), thoracic perimeter (TP), and cannon bone perimeter (CBP); and for the dynamic traits: movement (Move), dynamic limbs (DL), canter (CAN), comfort (Comf), and total dynamics (TD) in the Mangalarga horse breed in Brazil; pts, points.

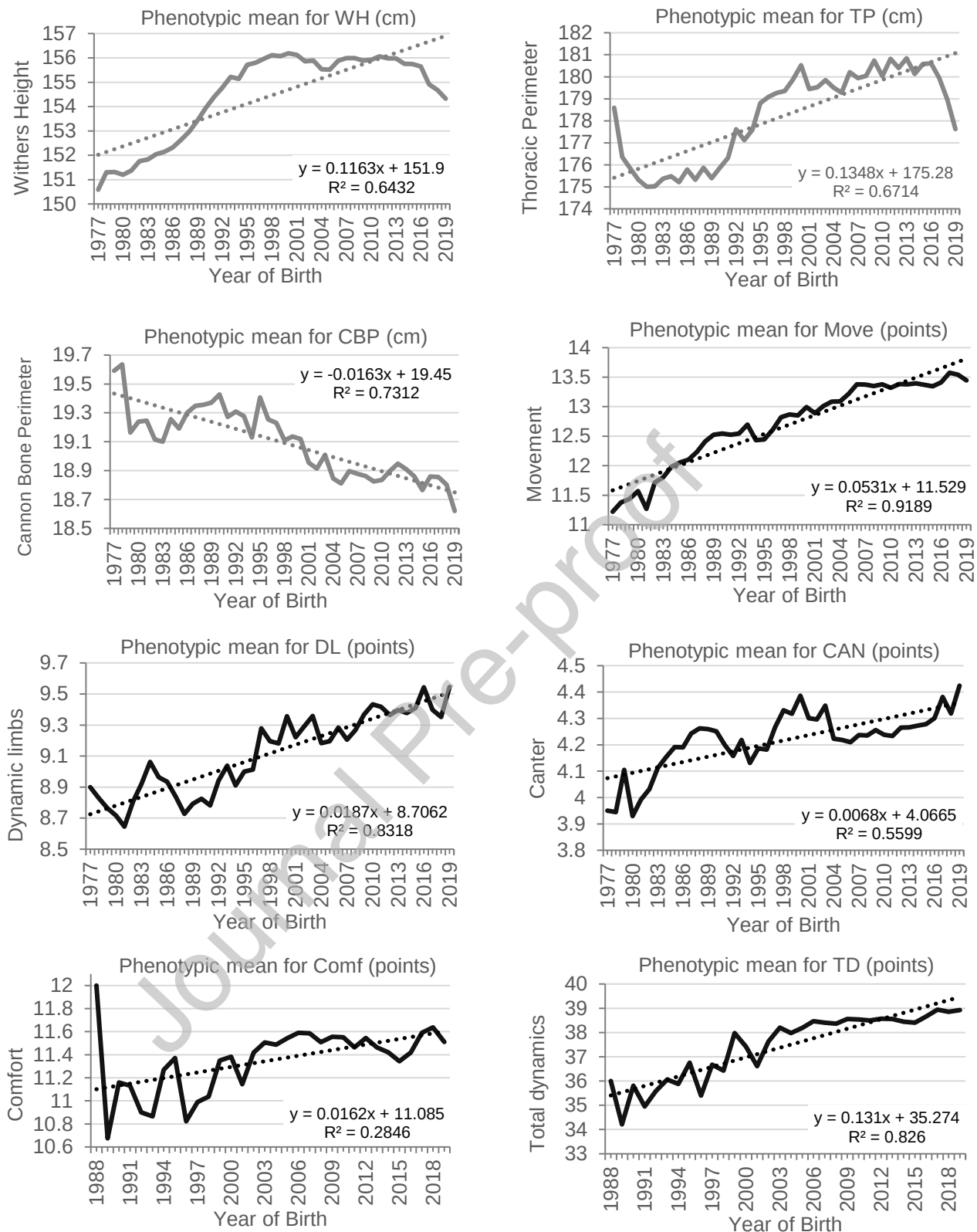


Fig. 3. Phenotypic trends based on annual mean records of animals born between 1977 and 2019 (1988 to 2019 for Comf and TD) for the evaluated morphometric and dynamic traits in the Mangalarga horse breed in Brazil. WH, withers height; TP, thoracic perimeter; CBP, cannon bone perimeter; Move, movement; DL, dynamic limbs; CAN, canter; Comf, comfort; TD, total dynamics.

Ethical Animal Research Statement

Ethical approval was not required for this study, as the research relied exclusively on pre-existing historical data and pedigree records provided by the Brazilian Association of Mangalarga Horse Breeders (ABCCRM). No live animals were handled, manipulated, or subjected to experimental procedures for the purpose of this study.

Declaration of interests

- ☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.
- ☐ The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: