

Genetic parameters for biometric traits in Mangalarga horses - Parámetros genéticos de caracteres biométricos en caballos Mangalarga

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Resumen

El objetivo del presente estudio fue estimar los parámetros genéticos de caracteres biométricos en caballos de la raza Mangalarga. Los datos fueron proporcionados por el Studbook de la Asociación Brasileña de Criadores de Caballos Mangalarga (ABCCRM) y compuesto por 36.036 registros de alzada a la cruz, 6.906 de la circunferencia del tórax y 6.916 de la circunferencia del hueso frontal de la caña, realizado en caballos nacidos entre enero de 1980 y diciembre de 2003, y comprende 169.228 caballos en la matriz de parentesco. El modelo utilizado para estimar los componentes de la covarianza necesarios para obtener la heredabilidades y las correlaciones incluyen: el efecto aleatorio de los caballos y los efectos fijos de edad, creador y el grupo de contemporáneos, utilizando el programa MTGSAM para las análisis. La media de heredabilidad encontradas oscilaron entre 0,41 (circunferencia del hueso de la caña) a 0,7 (circunferencia torácica) y el correlaciones genéticas y fenotípicas, fueron todos positivos, desde 0,28 a 0,47 y de 0,19 a 0,35, respectivamente.

Palabras claves: caballo, caracteres biométricos, heredabilidad, Mangalarga

Abstract

The aim of the present study was to estimate genetic parameters of biometric traits in Mangalarga horse breed. Data were provided by the Studbook of the Brazilian Association of Mangalarga Horse Breeders (ABCCRM) and comprised 36,036 records of height at withers, 6,906 of circumference of thorax and 6,916 of front cannon bone, realized on horses born between January 1980 and December 2003, comprising 169,228 horses in the relationship matrix. The model used to estimate the components of covariance necessary to obtain the heritabilities and correlations included: the random effect of the horse and the fixed effects of age, breeder and group of contemporaries, using the MTGSAM program for analyses. The mean heritability found ranged from 0.41 (cannon bone circumference) to 0.7 (thoracic circumference) and the genetic and phenotypic correlations were all positive, varying from 0.28 to 0.47 and from 0.19 to 0.35, respectively.

Key words: horse, biometric traits, heritability, Mangalarga

Resumo

O objetivo desse estudo foi estimar parâmetros genéticos de características biométricas em eqüinos da raça Mangalarga. Os dados foram fornecidos pelo Serviço de Registro Genealógico da Associação Brasileira de Criadores de Cavalos da Raça Mangalarga e envolveram 36.036 mensurações de altura, 6.906 de perímetro torácico e 6.916 de circunferência da canela, em eqüinos nascidos entre janeiro de 1980 a dezembro de 2003, totalizando 169.228 animais na matriz de parentesco. O modelo utilizado para estimar os componentes de (co)variância necessários para obtenção das herdabilidades e correlações entre as características estudadas, incluiu o efeito aleatório de animal, além dos efeitos fixos de idade, criador e grupo de contemporâneo, sendo empregado o programa MTGSAM nas análises. As herdabilidades médias encontradas variaram de 0,41 (perímetro de canela) a 0,70 (perímetro torácico) e as correlações genéticas e fenotípicas foram todas positivas e variaram de 0,28 a 0,47 e de 0,19 a 0,35 respectivamente.

Palavras-chave: cavalo, características biométricas, herdabilidade, Mangalarga

Introduction

The Brazilian horse breed Mangalarga, originated from the Iberian horses introduced throughout the colonization process of Brazil, became one of the most important tools in the daily activities of farms in south western Brazil.

However, in the last few decades, agricultural mechanization and the exodus of cattle raising to other regions, as well as a certain urbanization in the use of horses, has made the observation of its functional qualities more difficult, leading to an accentuated valorization of morphology as selection criterion. This tendency is currently under discussion by certain breeders, concerned with the characterization of the breed.

This situation has contributed to the fact that, in spite of being one of the oldest horse breeds in the country, the selection criteria of the Mangalarga have not yet been clearly defined, making planning and the implantation of genetic improvement programs more difficult.

Besides this, the fact that Mangalarga is a horse of varied use; working in cattle farms, racing, endurance, equestrian tourism and non-specialized equestrian sports, makes not only an efficient evaluation of its qualities more difficult, but also the establishment of more precise criteria for the purpose of selection.

Thus, the objective of the present study was to estimate genetic parameters of the biometric traits which have been registered in the Mangalarga breed, a fundamental step for the improved definition of these objectives, consequently contributing to the determination of evaluation strategies and selection programs for this breed.

Material and Methods

The data used in this study were provided by the Studbook of the Brazilian Association of Mangalarga Horse Breeders (ABCCRM) and involved measurements of height at the withers (36,036) and thoracic (6,906) and cannon bone circumferences (6,916), from 1980 to 2003. The minimum age for measuring the horses was three years of age, an occasion when a judge, licensed by the association, realized the measurements. The relationship matrix comprised 169,228 horses.

For the analysis of these traits the following model was used:

$$y = X\beta + Za + e$$

where:

y = vector of observations (height at withers (HW), thoracic circumference (TC) and circumference of front cannon bone (CC))

β = vector of fixed effects age (3 years, 4 years and older than 4 years), breeder (1,223) and group of contemporaries as associated with records in y by X

α = vector of random additive genetic effects as associated with records in y by Z .

X = incidence matrix of fixed effects

Z = incidence matrix of random effects

e = vector of residual effects

The group of contemporaries was formed of horses of the same sex (in the case of height, which is the only trait also measured in females by the ABCCRM), measured by the same judge (28), in the same year and season (January to March, April to June, July to September and October to December).

Like the breeder, these groups contained a minimum of three horses each and totaled 2,053 for HW, 763 for TC and 767 for CC.

The (co)variance components necessary to obtain the heritabilities of the traits were estimated by the software MTGSAM (Multiple-Trait Gibbs Sampler for Animal Models), developed by Van Tassel and Van Vleck (1997), in a one-trait animal model analysis. Posteriorly, with the aim of estimating genetic, phenotypic and environmental correlations between these traits, two-traits analyses were used.

Inferences regarding parameter dispersion were realized from the distributions obtained "a posteriori" via the Gibbs sampler. The Gibbs sample, required for the acquisition of unknown parameters and the reconstruction of the probability density (posterior density) of each parameter, comprised 1,506,000 samples, of which one in every 1,500 were stored for inference after discarding the first 6,000 as the burn-in period, totaling 1,000 samples available for the "a posteriori" distribution description.

The number of discarded samples, the sample interval and the total number of samples were determined in function of the results obtained by the GIBANAL program (Van Kaam, 1998), after a preliminary round of 50,000 samples. For additive and residual genetic variances and covariances, non-informative (flat) "priors" were used.

Heritabilities were estimated by dividing the additive genetic variance (σ_a^2) by the phenotypic variance (σ_p^2) and the correlation from the following expression:

$$r_{12} = \frac{\sigma_{12}}{\sqrt{\sigma_1^2 \times \sigma_2^2}},$$

where:

r_{12} = genetic, phenotypic or environmental correlation between the two traits;

σ_{12} = additive genetic, phenotypic or environmental covariance components between traits;

σ_1^2 and σ_2^2 = additive genetic, phenotypic or environmental variance components of each of the two traits considered.

From the breeding values predicted by the program, the genetic trend was calculated as a linear regression of the mean breeding value of each year over the birth year of the horses. Only horses with registered observations were included in this calculation.

Results and Discussion

The descriptive analysis of the traits considered is shown in Table 1.

Table 1. Descriptive analysis of the biometric traits of the Mangalarga breed

Trait (cm)	Nº Obs.	Mean	C.V.(%)	Mode	Min.	Max.
HW	36,036	153.01	2.82	153	145	170
TC	6,906	175.79	3.80	177	152	201
CC	6,916	19.28	4.53	19	15	23

c.v. = coefficient of variation

The mean height at withers observed (Table 1) was greater than those reported by Jordão and Gouveia (1954) and Mota (1989), also in Mangalarga horses, 149 cm and 150.9 cm respectively. It is possible that part of this increase is the result of gains achieved due to selection and improvements in nutrition, sanitation, etc., since the majority of the data refers to horses born in years after those evaluated by these authors. This mean places the Mangalarga horse in an average height range (between 150 to 160 cm), according Torres and Jardim (1981).

Among the traits studied, height at withers was the one which presented the least variation (C.V. = 2.82%), indicating that Mangalarga horses tend to be more uniform for this biometric trait, a fact also demonstrated by Lage (2001) in horses of the Mangalarga Marchador breed. Coefficients of variation higher than those observed in the present study were reported by Molina et al. (2003), Magnusson and Thafvelin (1980), respectively, in the Andaluz, and Standardbred Trotter breeds. However, McManus et al. (2005), in Campeiro horses, and Sadek et al. (2006), in Arabian horses, found coefficient of variation lower than that observed in the present work (2.1% and 2.2%, respectively).

The mean thoracic circumference observed (Table 1) was much greater than those found by Jordão and Camargo (1950) and Mota (1989), also in Mangalarga horses, 166.5 cm and 172.4 cm respectively, but slightly less than that reported by Lage (2001) in Mangalarga Marchador horses (177 cm). However, in all these studies the coefficient of variation of this trait was very close to the present work (a mean of 3.6%). In other breeds, more distant from the Mangalarga, the same tendency was found: a mean of 3.4%, Miserani et al. (2002); Magnusson and Thafvelin (1980); Molina et al. (1999) and Saastamoinen (1990), respectively for horses of the Pantaneiro, Standardbred Trotter, Andaluz and Finnish breeds.

The mean of the front of circumference cannon bone observed (Table 1) was similar to that reported by Jordão and Camargo (1950) in Mangalarga stallions, but greater than that found by Mota (1989) and Lage (2001), 18.6 and 17.0 cm, respectively. In part, this difference was due to the fact that these authors considered the cannon bone circumference not only of stallions, like in the present study, but also of mares. The greatest variation (C.V. = 4.61%) obtained for this trait, in relation to the remaining biometric traits was also found by these last two authors.

Genetic Parameters

In Table 2, the description of the variation components and heritabilities of the traits evaluated in one-trait analyses is shown.

Table 2 - Means and respective standard deviations (SD), mode, minimum (Min) and maximum (Max) values, and highest "a posteriori" density intervals with 90% probability (HPD90%) and serial correlation (SC) of the genetic (σ^2_a), residual (σ^2_r) and phenotypic (σ^2_p) variances and heritability (h^2) of the traits studied.

Component	Trait	Mean	sd	Mode	Min.	Max.	HPD. 90%
σ^2_a	WH	8.43	0.26	8.35	7.67	9.17	7.95 - 8.90
	TC	36.16	2.21	31.94	24.72	37.92	27.74 - 36.31
	CC	0.27	0.02	0.27	0.20	0.33	0.23 - 0.31
σ^2_r	WH	4.92	0.14	4.91	4.46	5.32	4.65 - 5.18
	TC	11.23	1.29	11.14	7.43	15.16	8.84 - 13.69
	CC	0.38	0.01	0.37	0.33	0.42	0.35 - 0.40
σ^2_p	WH	13.35	0.15	13.31	12.91	13.86	13.04 - 13.62
	TC	43.40	1.21	42.21	39.84	47.44	40.94 - 45.71
	CC	0.65	0.01	0.65	0.61	0.69	0.62 - 0.67
h^2	WH	0.63	0.01	0.63	0.59	0.67	0.60 - 0.65
	TC	0.74	0.03	0.74	0.62	0.84	0.67 - 0.80
	CC	0.41	0.02	0.40	0.34	0.51	0.36 - 0.46

In general, all the traits evaluated presented high heritability estimates, indicating an intense relation between the breeding and phenotypic values of the horses.

Withers Height

The estimated additive genetic variance for height was close to that described by Torzynsk and Szwaczkowski (1999) in different horse breeds (7.1cm²), with a slightly higher residual variance (6.1cm²). In contrast, the additive genetic variance was lower than that reported by Dolvik and Klemetsdal (1999) in Norwegian Trotters, a breed with a mean height close

to that of Mangalarga (151 cm) and whose value reached 12.25 cm², although residual variance was similar (4.54 cm²). Similarly, Costa et al. (1998) estimated a much higher genetic variance in Brazilian ponies (29.1 cm²).

The amplitude of variation observed for height heritability (Table 2) agree with those reported Arnason (1983), Miserani et al. (2002) and Anne (2004) in the Icelandic Toelter, Pantaneira and French Saddle Pony breeds, while higher than those reported by Varo (1965), Evans et al. (1979), Molina et al. (2003) and Dario et al. (2006) and lower than those estimated by Arnason (1980), Mota (1989), McManus et al. (2002), Pretorius et al. (2004) and Dario et al. (2006). These distinctions in values occur in function of the distinct mechanisms of genetic regulation that occur in different breeds (Anne, 2004). The magnitude of heritability (0.63) indicates a considerable possibility of a response if mass selection was applied on this trait.

The genetic trend for height at withers is shown in Figure 1.

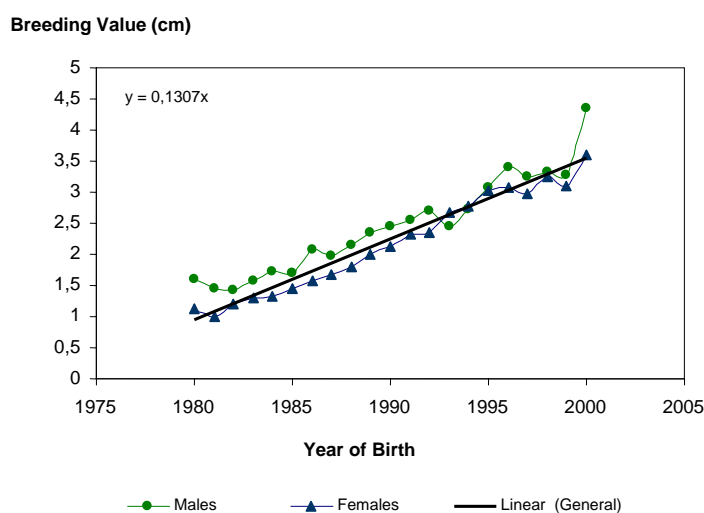


Figure 1. Genetic trends for height at the withers and mean breeding values observed for sex in Mangalarga horses.

This figure shows that the annual rate of genetic response reached 0.1307 cm per year or approximately 1.3 cm per decade, where males generally present a mean breeding value higher than females in the same years. This difference between sex is natural, given that the number of males required for breeding is much smaller, resulting in greater selection pressure, aside from the fact that the ABCCRM requirement of a greater minimum height for stallions (150 cm) than for mares (145 cm) contributes in accentuating this difference.

In relation to the mean of the trait (153 cm), the estimated genetic trend represented an annual change of 0.085%, a value similar (0.08%) to that reported by Costa et al. (2001) in Brazilian ponies, though in the opposite sense, since in this breed breeders seek horses of smaller stature. In

contrast, with respect to phenotypic standard deviation of the trait, the percentage of alteration observed in the present study (3.6%) is substantially greater than found by the these authors (0.97%).

In general, minimal dispersion was found in the breeding values observed in relation to the estimates, with stallions generally presenting greater fluctuation. Greater dispersion in the years of extremes (1980, 1.22 cm; 2000, 3.99 cm) could partially result from a smaller number of observations. In the last few decades, with the reduction in cattle farming in the São Paulo State, the scenario of its most effective use until recently, the ABCCRM sought to guide the selection of the Mangalarga to better conform to the "model universal saddle horse", which, among other things, implied the selection of greater height at the withers. Consequently, the genetic trend has moved in the direction which is favorable to the objectives desired by the association. However, some breeders believe that taller horses present worse quality gaits, which is the reason why studies of this nature should be realized prior to the delineation of genetic improvement programs for this breed, since one of the most illustrious traits of the Mangalarga is its gait.

Thoracic Circumference

Despite the fact that the estimated phenotypic variances (Table 2) were close (45.11 cm^2) to those reported by Dolvik and Klemetsdal (1999), the behavior of genetic and residual variances was the opposite, where the latter was much larger in the same work (32.74 cm^2), with a consequent reduction in heritability. Similarly, Torzynski and Szwaczkowski (1999) found a lower genetic variance (21.51 cm^2) and greater residual variance (41.75 cm^2), than those verified in the present research.

The amplitude of variation in heritability (0.67 to 0.80) agree with observed by Arnason (1980) and Arnason (1983), in horses of the Icelandic Toelter breed (0.71), but higher than those reported by Mota (1999), Dolvik and Klemetsdal (1999), Zechner et al. (2000), Starum and Socha (2002), Molina et al. (2003), Dario et al. (2006) with a mean equal to 0.36, and lower than those estimated by Falcão et al. (2002), McManus et al. (2002) and Miserani et al. (2002), with a mean equal to 0.93.

In general, and particularly in this study, the results indicate that there is sufficient additive genetic variability in this trait and that selection based on the individual phenotype of the horses could effect considerable genetic change in the herd.

The thoracic circumference was the only trait studied in which the mean breeding values were below zero (1980, -0.658 cm to 1988, -0.00587 cm), although the dispersion observed was around that expected, sometimes above (80-84), sometimes below (85-88), it was fairly small in this period (Figure 2). Later, dispersion increased slightly, alternately accentuated in the last two years of the study. Again, a smaller number of observations in 2000 (125 horses) could have contributed to this greater variation, though with more intensity in this case since only males were considered.

The genetic trend for thoracic circumference of Mangalarga males is shown in Figure 2.

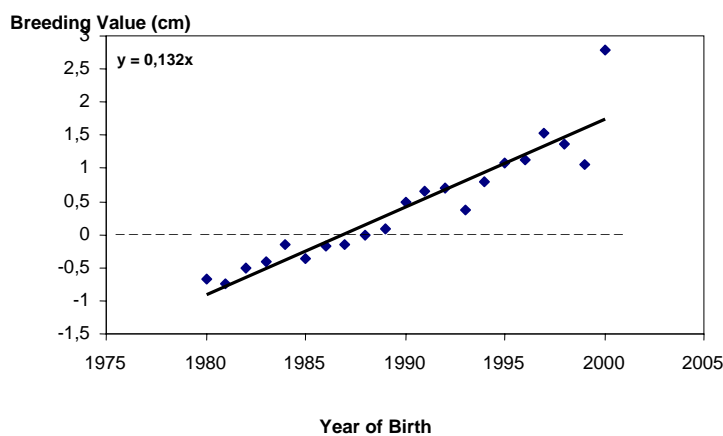


Figure 2. Genetic trend for thoracic circumference of Mangalarga males

In general, a rate of annual genetic response (0.132 cm) similar to height was observed (approx. 1.3 cm per decade), although in relation to the mean of the trait (175.79 cm) and its phenotypic standard deviation (6.59 cm) the values were slightly lower for thoracic circumference (approx. 0.075% and 2.0%, respectively).

Circumference of front cannon bone

Cannon bone circumference was the biometric trait with the lowest estimate of heritability, with a genetic variance (Table 2) similar to that reported by Torzynski and Szwaczkowski (1999) - 0.28. In contrast, the genetic and phenotypic variances were lower than those reported by Dolvik and Klemetsdal (1999) of 0.38 and 0.71, respectively. As in other studies, cannon bone circumference was shown to be a trait with considerable response potential for mass selection, although its genetic gains over time tended to be smaller than those of other biometric traits. Considering the highest "a posteriori" density intervals with 90% probability (HPD90%), the estimates of heritability were close to those reported by Arnason (1983), Mota (1989) and Dario et al. (2006), a mean of 0.42, higher than those found by Varo (1965), Starum and Socha (2002) and Molina et al (2003), a mean of 0.31, and lower than Zechner et al. (2001), Miserani et al (2002) and McManus et al. (2002), a mean equal to 0.54.

The genetic trend for cannon bone circumference in stallions is shown in Figure 3.

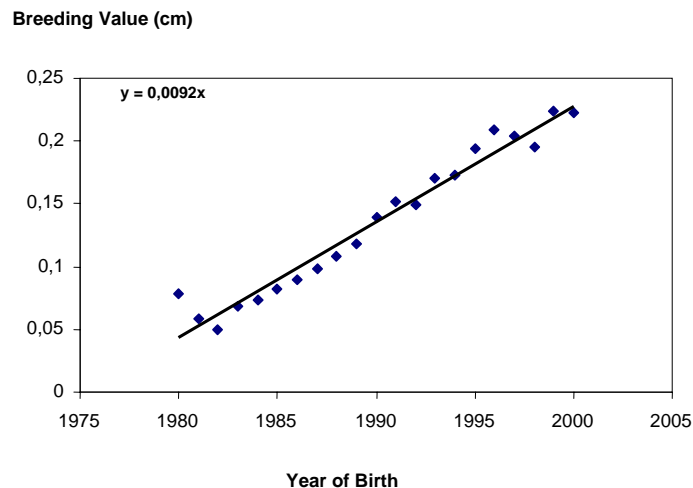


Figure 3. Genetic trend for circumference of front of cannon bone in Mangalarga males

Cannon bone circumference was the trait which showed the smallest dispersion of breeding values observed in relation to those expected (Figure 3). Between 1982 (0.059 cm) and 1989 (0.177 cm) the values observed were lower than those expected, whereas between 1993 (0.169 cm) and 1997 (0.204 cm) the opposite occurred and in the last three years studied, slight oscillations above and below the expected values occurred.

Despite the growth trend of 0.0092 cm/year, this trait showed the lowest annual genetic response rates, in relation to the phenotypic mean and standard deviation, 0.048% and 1.14%, respectively.

As described by Costa (2002) in Mangalarga Marchador horses, it is probable that the large diversity found in the biometric traits studied in the Mangalarga breed is the result of its recent formation, with few generations registered, aside from the introduction of uncontrolled animals originating from other breeds.

Correlations

The estimates of heritability in one-trait analyses (Table 2) were very close to those of two-traits evaluation (Table 3), except for thoracic circumference, where a lower value was found, principally due to a reduction in the additive genetic variance.

Table 3. Heritability estimates (diagonal), genetic (above) and phenotypic (below) correlations of the traits analyzed of Mangalarga breed horses.

	WH	TC	CC
WH	0,63	0,47	0,28
TC.	0,35	0,66	0,29
CC	0,19	0,35	0,41

Of the three associations considered and shown in Figures 4 to 6, in one of them (Figure 4, HW/CC) the genetic correlation was greater than the environmental correlation, suggesting that the association between the action of the same group of genes (pleiotropic effects) is greater than the environmental factors acting on this pair of traits. In contrast, considering the two circumferences (Figure 5, TC/CC) the action of environmental factors was greater and, finally, (Figure 6, HW/TC) the environment and genetics presented similar participation.

All the correlations between the biometric traits were positive, with variables of low to moderate magnitude. Genetically, the greatest association occurred between HW/TC (0.47), a value close to that reported by Zamborlini et al. (1996) in Mangalarga Marchador horses (0.45), but lower than that found by Starum and Socha (2002) and Molina et al (2003) in horses of the Malopolski (0.65) and Andaluz (0.60) breeds.

Similarly, a higher value was found for phenotypic correlation between these two traits (0.47), an estimate similar to that found by Saastamoinen (1990) in Finnish Trotters (0.49) and higher than that found by Zamborlini et al (1996) in Mangalarga Marchadors (0.4) and Falcão et al (2002) in Campeiro horses (0.26) and lower than estimated by Starum and Socha (2002) in Molopolski horses (0.57).

The genetic correlations of CC with HW and TC were very close (0.28 and 0.29) and of low magnitude; the first was lower than reported by Starum and Socha (2002) and Molina et al. (2003), of 0.57 and 0.48, respectively, and higher than described by Zamborlini et al. (1996), of 0.23, and the second lower than all three authors: 0.34; 0.45 and 0.76, respectively. These results indicate that despite the tendency that horses which are genetically superior in CC also tend to be superior in HW and TC, a number of exceptions exist. A similar tendency was observed for the phenotypic correlation between CC and TC, suggesting that horses with thicker cannon tend to have a larger thorax. In contrast, the phenotypic correlation between CC and HW indicates independence between these traits: horses can present larger (or smaller) cannon bone circumferences independent of their stature, taller (or shorter).

Consequently, considering the objective of the ABCCRM is to increase the stature of these horses, selection to alter one of the biometric traits would lead, to a greater or lesser degree, to a concomitant change favorable to the remaining biometric traits of the horses. However, in no case was indirect selection found to proportion a greater genetic gain than direct selection.

Conclusion

Although the considerable heritability estimates have permitted breeders to promote improved genetics in the traits studied, higher annual gains could be achieved if the Mangalarga breeders gave more emphasis to the use of stud horses based on their predicted breeding values, disseminating the alleles responsible for the improvement in these traits in a more organized manner.

Figure 4. Genetic, phenotypic and environmental correlations between withers height (HW) and cannon bone circumference (CC)

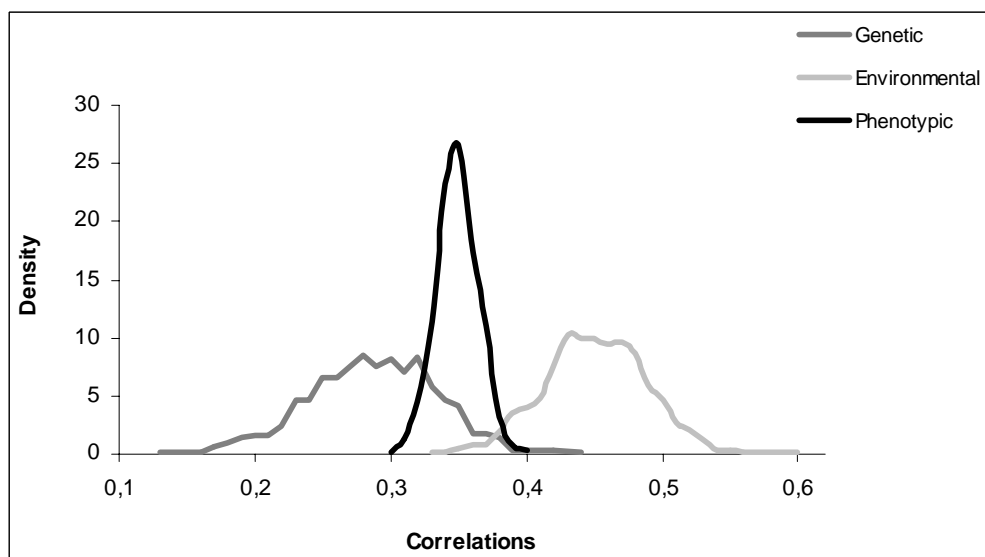
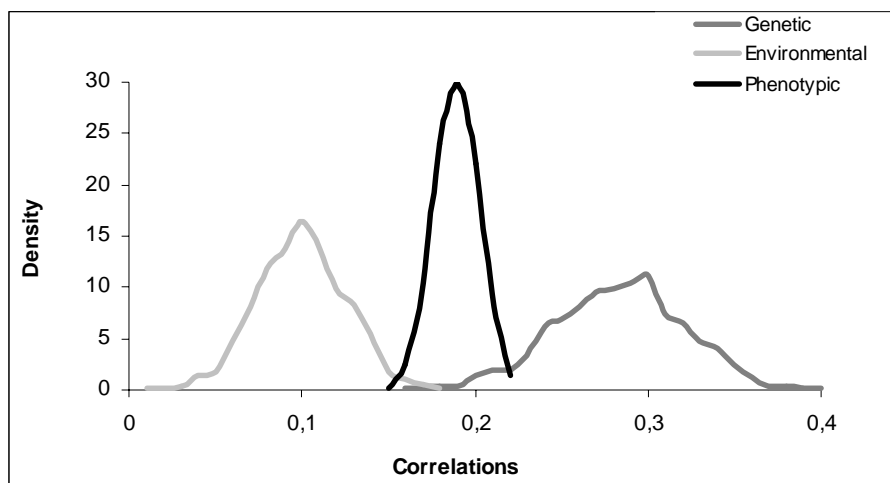


Figure 5. Genetic, phenotypic and environmental correlations between thoracic circumference (TC) and cannon bone circumference (CC)

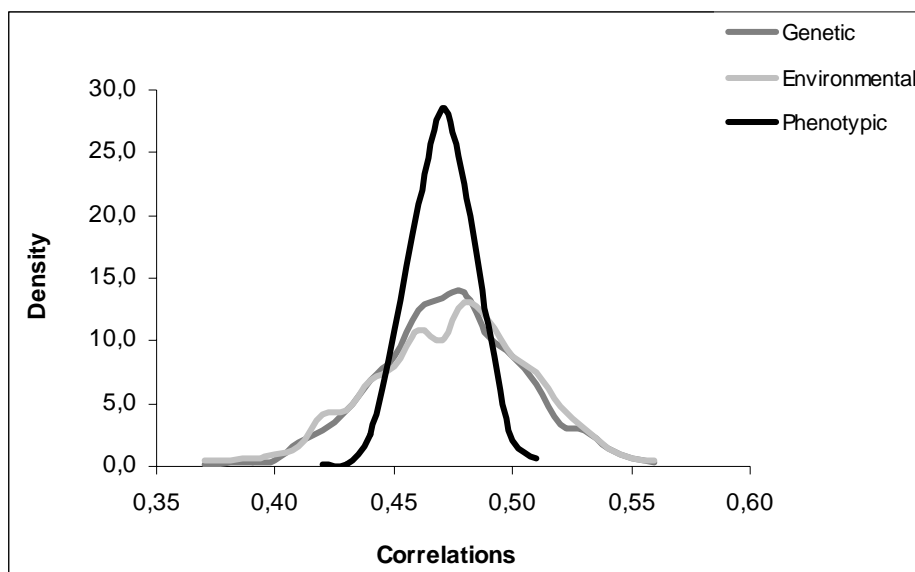


Figure 6. Genetic, phenotypic and environmental correlations between withers height (HW) and thoracic circumference (TC)

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