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COMPARISON OF SOME RANDOM REGRESSION MODELS FOR RACING PERFORMANCES OF BRITISH RACING HORSES IN TURKEY

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Abstract

This study was conducted to compare some random regression models applied to Legendre polynomials (L (2.2), L (2.3), L (3.2), L (3.3)) for that run on racing performance in British horses in Turkey. For this purpose, a total of 146850 race time record up to 15 races at different distances of 13625 horse taken from the Jockey Club of Turkey between the years of 2005 and 2016 was used. In this study, the genetic correlations between covariance components, heritabilities and race days for race completion times were estimated by using the DXMRR option in the DFREML statistical package program. The track type, the year and the horse's age, the fixed effect, the track distance were taken as covariates and the breeding value estimates were made. -2logL, Akaike information criterion (AIC), Bayesian information criterion (BIC), Error Variance (RV) and Log likelihood values were used to compare models. Heritabilities (0.24 to 0.28), additive genetic correlations (0.87 to 0.99) and phenotypic correlations (0.22 to 0.55) were estimated by L (2.3) random regression model which had the lowest -2LogL and BIC values. As a result, the L (2.3) model can be used for genetic evaluation and breeding of British racing horses.

Keywords: British horse, Race, Heritability, Additive genetic correlations, Phenotypic correlations

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1. Introduction

Horse racing emerges as a sport and entertainment game where money transfers take place economically in large quantities. Officially, the contribution of the horse races made in every community and culture from the 17th century to the present day to the country's economy is increasing steadily. While horses are bought and sold at very high prices, the high-performing horses in the races are making significant gains to their owners (Cansabuncu Kanman, 2006; Köseman and Şeker, 2016). The performance of horses in races is under the influence of genetic and environmental factors (Köseman and Şeker, 2018). There are differences in performance between both breeds and among the individuals of the same race. British and Arabian horses perform differently at the same distance. This difference is due to the effect of genotype. British horses have become favorite horse races of horse racing due to their physical characteristics and fast running. In addition, the British horse is a breed that maintains its speed at distances that are too long, and has been produced for many years as a symbol of speed and endurance in horse breeders' field (Anonymous, 2018). Therefore, the selection of breeding animals to be allocated is of great importance. The horses that are taken into or out of the sport must be selected according to the highest possible genetic value. However, this is not possible in practice. Generally, selection is made by looking at phenotypes of horses. However, the most reliable estimation of genotypic value is possible with calculations made from phenotypic values (Köseman and Seker, 2018). While the random regression models developed in recent years are used extensively in determining the breeding values for the economic characteristics of different animals (Takma and Akbaş, 2009; Alkan et al., 2012; Onder et al., 2015), there is a growing interest in predicting the breeding values of animals used in horse racing with random regression models (Buxadera and da Mota, 2008). Until today, studies on horse races sufficient work has not been observed for the fitting performance of different ordered Legendre polynomials. In this study, it is aimed to compare the fitting performance of the random regression models applied to the orthogonal Legendre polynomial on the race completion time (min) of British racing horses.

2. Material and Method

In the study, 146850 test day race completion time (sec) records of 13625 British horse raced taken from the Jockey Club of Turkey between 2005 and 2016 were used. Records up to the 15th run of a horse have been used. Some of the animals that were recorded less than two races and some animals whose parents were not reached were excluded from the study. In the study, the race tracks type, the race year and the age of the horse were fixed, and the race tracks distance were taken as covariates.

L (2.2), L (2.3), L (3.2) and L (3.3) models of Legendre polynomial function for additive genetic and permanent environmental effects was estimated by the DXMRR option in the DFREML package program (Meyer, 1997) with the individual model approach using sire and dam pedigree information. The following model was used to apply the random regression model.

$$y = RT_i + Y_j + A_k + \sum_{m=1}^{K_B} \beta_m x_{(m)}(t_{ij}) + \sum_{m=1}^{K_A} \alpha_{jm}\varphi_m(t_{ij}) + \sum_{m=1}^{K_p} P_{jm}\varphi_m(t_{ij}) + e$$

In this model; RT_i: ith race tracks (sand, grass, artificial grass); Y_j: jth race year (2005-2016); A_k: kth horse age (2-18); β_m: mth fixed regression coefficients for horse j; t_{ij}: ith test day of the horse j; $x_{(m)}$ (t_{ij}): mth covariates (race tracks distance: from 800 to 2400, with an increase of 100); α_{jm}: mth additive genetic random regression coefficients for horse j; P_{jm}: mth permanent environmental random regression coefficients for horse j; φ_m: mth polynomial evaluated for the race t_{ij}; K_B, K_A and K_P are the order of fitted fixed, random additive and random permanent regression coefficients; e: random residual effect for y.

-2logL, Akaike information criterion (AIC), Bayesian information criterion (BIC), Error Variance (RV) and Log likelihood values were used to compare random regression models.

3. Results and Discussion

Estimated -2LogL, AIC, BIC and RV values used to compare the random-regression models were given in Table 1. In studied models where the number of parameters ranged from 7 to 13, -2LogL values were changed 529471.7 and 538709.7. The lowest -2logL value was observed in the L (2.3) model. The lowest AIC value was observed in the L (3.3) model while the lowest BIC value was observed in the L (2.3) model. The RV values were found to be similar in these two models L (2.3) and L (3.3). Changes of the maximum log likelihood values in different models were presented in Table 2. Log likelihood changes values were found be significant in L (2.3) and L (3.3) Legendre polynomial models (P<0.05). The highest change was observed in L (2.3) model.

Table 1. Criteria used for comparison of the models

Models	Number of parameters	-2LogL	AIC	BIC	RV
L (2.2)	7	531285.5	513514.4	513583.6	9.75
L (2.3)	10	529471.7	511706.5	511805.5	9.38
L (3.2)	10	538709.7	512051.9	512150.9	9.42
L (3.3)	13	538335.4	511683.6	511812.2	9.38

-2LogL: logarithm of the likelihood function, AIC: Akaike's information criterion, BIC: Bayesian information criterion, RV: residual variance.

Table 2. Maximum log likelihood values and changes in the log likelihoods at the different models

Models	Number of parameters	Log	Changes in Log	Changes in Log	χ^2
L (2.2)	7	-256750.1	-	-	-
L (2.3)	10	-255843.2	906,9*	0.35	7.81
L (3.2)	10	-256015.9	-	-	
L (3.3)	13	-255828.8	187.1*	0.07	7.81

*Significant change (P<0.05)

Log likelihood changes values were found be significant in L (2.3) and L (3.3) Legendre polynomial models (P<0.05). The highest change was observed in L (2.3) model.

The first 3 eigenvalues and ratios (in parentheses) of the predicted additive genetic (co)variance matrices for the Legendre polynomial models are given in Table 3. For additive genetic effect, the first eigenvalues except L (3.2) model account for about 97% of the total variation.

The eigenvalues and ratios (in parentheses) of the predicted permanent environmental (co) variance matrices for the Legendre polynomial models are given in Table 4. The first eigenvalues for Legendre polynomial model belonging to permanent environmental effect account for over 70% of total variation.

Table 3. Eigenvalues of the additive genetic (co)variance matrix and the proportion of total variance (%) estimated from Legendre models.

Models	First	Second	Third
L (2.2)	8.66026 (97,62)	0.211322 (2.38)	-
L (2.3)	8.47599 (97.78)	0.192417 (2.22)	-
L (3.2)	9.26655 (86.15)	1.34219 (12.48)	0.0468867 (1.37)
L (3.3)	8.68255 (97.38)	0.221374 (2.48)	0.0121879 (0.14)

Table 4. Eigenvalues of the permanent environmental (co)variance matrix and the proportion of total variance (%) estimated from Legendre models

Models	First	Second	Third
L (2.2)	4.36048 (79.15)	1.14861 (20.85)	-
L (2.3)	4.56540 (72.93)	1.61273 (25.76)	0.0817904 (1.31)
L (3.2)	4.18318 (87.54)	0.595537 (12.46)	
L (3.3)	4.35628 (71.77)	1.59157 (26.22)	0.122253 (2.01)

Heritabilities for racing order estimated from Legendre polynomials were given in Figure 1. Heritabilities were changed from 0.21 to 0.36. Heritabilities, additive genetic and phenotypic correlations between racing order from L (2.3) models were given in Table 5.

Heritabilities (0.24 to 0.28), additive genetic correlations (0.87 to 0.99) and phenotypic correlations (0.22 to 0.55) were estimated by L (2.3) random regression model which had the lowest -2LogL and BIC values.

Estimated heritabilities from Legendre polynomials except L (3.2) model was found as nearly similar. Buxedera and Mota (2008) similar results were reported for Brazil horses running from 1000 to 1200 meter. But it was found higher than it found by Gómez et al. (2011) for Spanish Trotter horses.

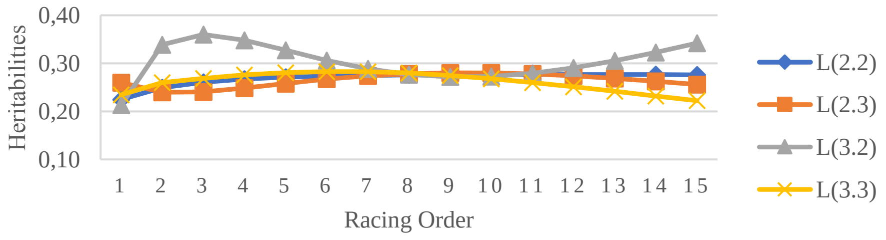

Figure 1. Changes of heritability for racing order estimated from Legendre polynomial models

Table 5. Heritabilities (diagonal), additive genetic (below diagonal) and phenotypic (above diagonal) correlations among race number.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	**0.26**	0.34	0.33	0.33	0.32	0.31	0.30	0.29	0.28	0.27	0.26	0.25	0.24	0.23	0.22
2	0.99	**0.24**	0.43	0.42	0.41	0.40	0.38	0.36	0.34	0.32	0.30	0.28	0.26	0.23	0.22
3	0.97	1.00	**0.24**	0.44	0.44	0.43	0.41	0.39	0.37	0.35	0.33	0.31	0.29	0.27	0.25
4	0.96	0.99	1.00	**0.25**	0.45	0.44	0.43	0.41	0.40	0.38	0.36	0.34	0.33	0.31	0.29
5	0.94	0.98	1.00	1.00	**0.26**	0.45	0.44	0.43	0.42	0.41	0.39	0.38	0.36	0.34	0.33
6	0.93	0.98	0.99	1.00	1.00	**0.27**	0.45	0.44	0.44	0.43	0.42	0.41	0.39	0.38	0.37
7	0.92	0.97	0.99	0.99	1.00	1.00	**0.27**	0.45	0.45	0.45	0.44	0.43	0.42	0.41	0.40
8	0.91	0.96	0.98	0.99	1.00	1.00	1.00	**0.28**	0.46	0.46	0.46	0.45	0.45	0.44	0.43
9	0.91	0.96	0.98	0.99	0.99	1.00	1.00	1.00	**0.28**	0.47	0.47	0.47	0.47	0.47	0.46
10	0.90	0.95	0.98	0.99	0.99	1.00	1.00	1.00	1.00	**0.28**	0.48	0.49	0.49	0.49	0.49
11	0.89	0.95	0.97	0.98	0.99	0.99	1.00	1.00	1.00	1.00	**0.28**	0.50	0.50	0.51	0.51
12	0.89	0.95	0.97	0.98	0.99	0.99	1.00	1.00	1.00	1.00	1.00	**0.27**	0.52	0.52	0.53
13	0.88	0.94	0.97	0.98	0.99	0.99	0.99	1.00	1.00	1.00	1.00	1.00	**0.27**	0.53	0.54
14	0.87	0.94	0.96	0.98	0.99	0.99	0.99	1.00	1.00	1.00	1.00	1.00	1.00	**0.26**	0.55
15	0.87	0.93	0.96	0.97	0.98	0.99	0.99	1.00	1.00	1.00	1.00	1.00	1.00	1.00	**0.26**

4. Conclusions

In conclusion, there is no consensus in literature for British horse about the best order of fit Legendre polynomial models to be used to model of racing order with RRM. So, several RRMs obtained with different Legendre polynomial models have been compared for fitting performance. As a result, the L (2.3) model can be used for genetic evaluation and breeding of British racing horses. Further studies should be conducted with different order Legendre polynomials.

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