Study Of Genotype By Environment Interaction In Meat Type Quails Using Reaction Norms Models Under Residual Variance Heterogeneity Assumption

V.P.S. Felipe[*], B.D. Valente[*], R.R. Wenceslau[*], G.G. Santos[*], L.S. Freitas[*]
and M.A. Silva[*]

Introduction

Protein is one of the most expensive components of meat type quails diet. Therefore, it has a major impact on the cost of breeding selection programs. One way to reduce this cost is by decreasing the crude protein content of the diet used in a selection program. In this scenario, animals would be evaluated in an environment different from the one where they are commercially raised. Genotype by environment interaction (GxE) takes place when individual sensitivities to the same change in the environment are heterogeneous (Falconer & Mackay, 1996). Therefore, if there is GxE for a specific trait, the expected difference between the phenotypes of two subjects may not be the same in two different environments (Kolmodin, 2003). In this context, meat type quails progeny evaluated under diets with different crude protein levels would not exhibit the same performance relative to population mean, possibly resulting in differences in additive genetic effects ranking. In this case, genetic effects prediction should be made under the same nutritional environment where the birds are commercially raised. The study of environmental genetic effects sensitivity can be made via reaction norm (RN) models. RN is defined as the systematic change in mean expression of a phenotype occurring in response to a systematic change in an environmental variable (Jong, 1990). In other words, the expressed phenotype from a subject is considered as a function of the environment. For RN prediction, random regression models are used to represent traits that are expected to change continuously along an environmental gradient. Furthermore, these models allow for heterogeneous residual variance.

The aim of this study was using random regression models assuming heterogeneous residual variance to evaluate the presence of genotype by environment interaction in two lines of meat type quails, for body weight measured at two ages (21 and 35 days of age), under diets containing different levels of crude protein.

Material and methods

Data were from the meat type quail breed program performed at experimental farm of *Universidade Federal de Minas Gerais.* Progeny from 100 sires and 200 hens of each line (EV1 and EV2) were fed with diets containing 24, 26, 28 and 30% of crude protein and 2,900kcal of metabolizable energy. Data consisted of 5,256 measures of body weight at 21 and 35 days of age. Analyses were performed separately for each age x genetic group combination. A single-trait mixed random regression model was applied for each analysis.

---

[*] Federal University of Minas Gerais/UFMG – Department of Animal Science

Fixed regression coefficients were fit for each sex. Additionally, additive genetic random regressions were modeled using Legendre polynomials. Residual variance heterogeneity was considered by dividing the continuous control variable into four classes (24 to 25% of CP, 26 to 27% of CP, 28 to 29% of CP, 30 to 31% of CP). Comparison between models with homogeneous and heterogeneous residual variance was performed using BIC (Bayesian information criterion). The covariance components were estimated using restricted maximum likelihood (REML) methods available in the program Wombat (2006). Covariance functions were used to estimate the additive genetic covariance structure and the direct heritability as a function of crude protein levels and residual variance class. The convergence criterion adopted was $1x10^{-10}$.

Results and discussion

Models that considered residual variance heterogeneity were preferred over models with homogeneous residual variance, according to the values of BIC (Bayesian information criterion). Estimated (co)variance components associated with random regression coefficients and residual classes are described on table 1. The correlation between intercept and linear random regression coefficients were positive for every age and genetic group combination: 0.64 (EV1 – 21 days of age), 0.47 (EV1 – 35 days of age), 0.92 (EV2 – 21 days of age) and 0.98 (EV2 – 35 days of age). It indicates that the slope of the function that describes some genetic effect gets steeper as the predicted value of this genetic effect in the mean crude protein level increases. Additionally, reranking of birds in different environments is expected when the aforementioned correlation is far from 1 (Su et al., 2006).

Table 1. Additive genetic random regression coefficients variances and residual variances for different classes estimated for EV1 and EV2 at 21 and 35 days of age.

	EV1							
	Idade							
	21				**35**			
	b_0		**b_1**		**b_0**		**b_1**	
b_0	99,084		17,799		294,71		41,234	
b_1			7,8899				25,913	
Residual	**CL1**	**CL2**	**CL3**	**CL4**	**CL1**	**CL2**	**CL3**	**CL4**
	177,82	353,69	210,20	60,628	264,73	375,32	279,68	135,46
	EV2							
	Idade							
	21				**35**			
	b_0		**b_1**		**b_0**		**b_1**	
b_0	106,77		21,970		279,35		34,958	
b_1			5,2513				4,5392	
Residual	**CL1**	**CL2**	**CL3**	**CL4**	**CL1**	**CL2**	**CL3**	**CL4**
	137,03	332,23	166,26	89,760	299,09	397,32	315,26	169,80

Direct additive genetic covariance structures as a function of crude protein level in diet, estimated for both genetic groups and ages at evaluation, are presented in figure 1. These structures presented inclination towards greater values of crude protein level. Surface shape of covariance structure was similar for different ages within genetic groups, without considering the scale effect of age. Heterogeneity of variance and covariance values of additive genetic effect for all combinations of genetic group and age were observed.

Heritability estimates are shown in figure 2. There were changes on heritability values for all ages/genetic groups as the crude protein level increases. For both genetic groups, heritability value was greater at 35 days of age so that meat type quails at this age are expected to present greater response to selection with respect to the phenotypic variance, when compared to selection at 21 days of age.

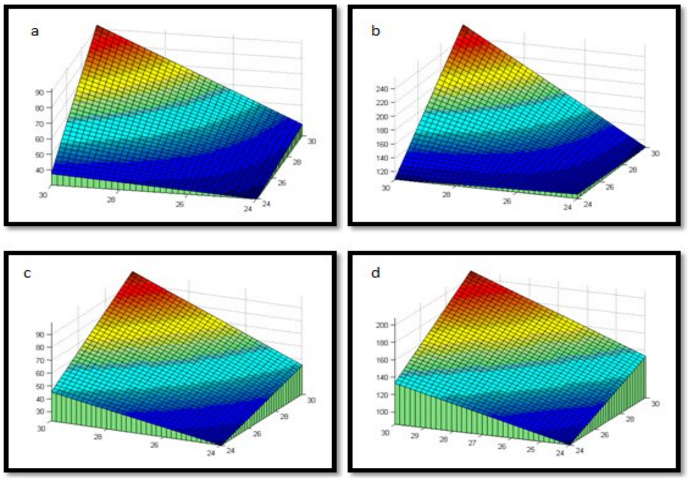

Figure 1. Additive genetic covariance structure (gr²) as a function of diet crude protein level estimated at 21 and 35 days of age for EV1 and EV2 lines (a: EV1-21 days; b: EV1-35 days; c: EV2-21 days and d:EV2-35 days)

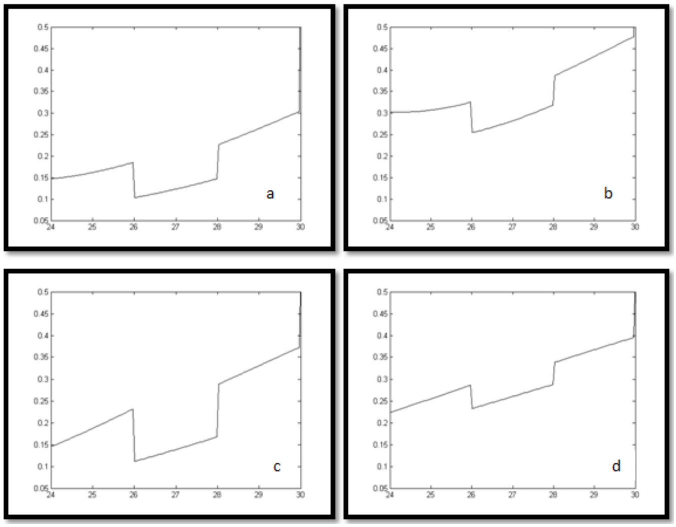

Figure 2. Estimated heritabilities for body weight as a function of diet crude protein level (a: EV1-21 days; b: EV1-35 days; c: EV2-21 days and d:EV2-35 days)

Conclusion

Genotype by environment interaction study should consider heterogeneity of residual variance. Genotype by environment interaction was detected for both lines. Therefore, breeding value prediction for EV1 and EV2 meat type quails should be made under diet with the same crude protein content used for commercially raised birds.

References

FALCONER, D.S.; MACKAY, T.F.C (1996). Introduction to quantitative genetics. 4.ed. London: Longman.

JONG, G. (1990). J. of evol. biol., 3: 447-468

KOLMODIN, R. (2003). Uppsala: Swedish University of Agricultural Sciences,35p. Doctoral thesis. Dep. of Anim. Breed. and Gen., 2003.

MEYER, K. (2006). In: Proc 8th WCGALP, Belo Horizonte. Proceedings... CD-ROM.