

ESTIMATE OF GENETIC COMPONENTS OF BIRTH WEIGHT USING MULTI-BREED MODELS WITH PEDIGREE STRUCTURES IN MESTIZO SHEEP

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ABSTRACT - The objectives of this paper were to verify the influence of the multi-breed model and pedigree structure in the estimates of the genetic components to birth weight in a mestizo herd. Using 1234 birth weight records in two ways, one dataset with complete pedigree information (n = 1028) and another with incomplete pedigree information (n = 1234). The pedigree was composed for 10 sires, 366 and 448 dams for complete and incomplete pedigree, respectively. Used for analysis the maximum restricted likelihood method about the animal model, considering the birth weight trait, for a dataset with or not complete pedigree. The direct heritability coefficients in both datasets did not present large difference, 0.06 and 0.09 to best models in the complete and incomplete pedigree, respectively. However, in the incomplete pedigree, the maternal heritability was 0.29. The residual variance, which on the best model of the dataset with complete pedigree presented 0.51 and 0.35 for the best model of the dataset with incomplete pedigree. In conclusion, there was an influence of de multi-breed model only in the dataset with complete pedigree, being the best model that considered the direct and breed effects. In the dataset with incomplete pedigree, the better model was that considered the direct and maternal additive effects. In both datasets, the modeling of contemporary groups as fixed effect presented the best estimates of genetics components to birth weight in this mestizo flock.

KEYWORDS: animal model, direct heterozygosity, maternal heterozygosity, REML, sheep improvement.

ESTIMATIVA DOS COMPONENTES GENÉTICOS PARA O PESO AO NASCER USANDO MODELOS MULTI-RACIAIS COM ESTRUTURAS DE PEDIGREE EM OVINOS MESTIÇOS

RESUMO - O objetivo deste artigo foi verificar a influência de modelos multirraciais e da estrutura do pedigree nas estimativas dos componentes genéticos para peso ao nascer em um rebanho mestiço. Usando 1234 registros de peso ao nascer em dois caminhos, um conjunto de dados com informações de pedigree completa (n=1028) e outro com informações do pedigree incompletas (n=1234). O pedigree foi composto por 10 pais, 366 e 448 mães para o completo e incompleto pedigree, respectivamente. Usou-se para análise o método da máxima verossimilhança restrita sobre um modelo animal, considerando a característica peso ao nascer, para o conjunto de dados com pedigree completo ou não. Os coeficientes de herdabilidade direta em ambos os conjuntos de dados não apresentaram grande diferença, 0,06 e 0,09 para os melhores modelos no completo e incompleto pedigree, respectivamente. No entanto, no com pedigree incompleto, a herdabilidade materna foi de 0,29. A variância residual do melhor modelo do conjunto de dados com pedigree completo foi de 0,51 e 0,35 para o melhor modelo do conjunto com pedigree incompleto. Concluindo, há influência do modelo multirracial apenas no conjunto de dados com pedigree complete, sendo o melhor modelo o que considera os efeitos direto e racial. No conjunto de dados com pedigree incompleto, o melhor modelo foi o que considerou os efeitos aditivos direto e materno. Em ambos os conjuntos, a modelagem do grupo de contemporâneo como um efeito fixo apresentou melhores estimativas dos componentes genéticos para peso ao nascer nesse rebanho mestiço.

Palavras-chave: modelo animal, heterosigiosidade direta, heterosigiosidade materna, REML, melhoramento ovino.

INTRODUCTION

The extensive systems of ovine exploitation have very well-defined bottlenecks; one of them is the calving period. In this, there are several factors that can compromise productive indexes, such as the birth of very light lambs with low viability, which are more susceptible to death by starvation, dehydration, hypothermia and predation (BANCHERO et al., 2012; BINABAJ et al., 2013; HOLLAND et al., 2017). In another extreme, lambs that born with high body weight are more susceptible at

problems as dystocia, which can lead not only the lamb to death (BINABAJ et al., 2013), but also the ewe, a fact that worsens in females of the first calving.

The birth weight, besides being related to survival traits, is often the single registered productive trait (AMARILLO-SILVEIRA et al., 2017). In Brazil, in general, the low level of zootechnical records is a reality, consequently limiting the precision of the estimates of genetic parameters in sheep (AMARILLO-SILVEIRA et al., 2018). However, because it is a trait of economic

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importance, related with the survival and weight at subsequent ages (FORERO et al., 2017), its study is justified, in order to identify the components of the phenotypic variance within of given management system.

In recent years, studies have attempted to identify which is the best to partition the genetic and residual variance for the birth weight trait. Therefore, there is a great variation in the results in detriment of the ovine breed, breeding system, pedigree structure and the number of animals with productive records. Several authors identified better results using different statistical models, considering direct and maternal additive effects (ESKANDARINASAB et al., 2010); direct and maternal additive effects together with the covariance between both (BOUJENANE and DIALLO, 2017; ULUTAS et al., 2013); direct additive and maternal permanent environment effects (AMARILHO-SILVEIRA et al., 2018; MIRHOSEINI et al., 2015); direct additive, maternal additive and maternal permanent environment effects (AGUIRRE et al., 2016; BOUJENANE et al., 2015; SHIOTSUKI et al., 2014) and besides of direct additive, maternal additive and maternal permanent environment effects, also considered the covariance between the additive effects (GHOLIZADEH and GHAFOURI-KESBI, 2015; MANDAL et al., 2015).

In flocks with varied racial composition, there is a requirement in to know as the racial effects affect estimates of genetic variance. However, few studies have explored this issue considering that there is a great influence of this effect in the partition of the phenotypic variance (BROWN et al., 2016; MURPHY et al., 2018). The contemporary groups (CG), is almost a convention among the animal breeding researchers, are considered as a fixed effect. Therefore, some authors have found a better adjustment of data considered the CG how a random effect, mainly in small herds (LEGARRA et al., 2005). This modeling used mainly when there is an insufficient number of animals per CG.

The use of correct statistical modeling will supply estimates more accurate, extremely important to know the structure of the pedigree. Thus, ensuring that the information contained in it is more complete as possible, so that genetic links can be created among the various environmental conditions, such as different contemporary groups, years in evaluation, flocks, etc. (KOSGEY et al., 2006; SAFARI et al., 2005). In this sense, how much larger the data sets, structured and distributed across generations and with a pedigree with enough information, greater will be accuracy, the i.e. closer will be the estimates of the actual breeding values (SAFARI et al., 2007). However, this not always possible in the ovine species, because, besides of to be a species with secondary exploitation tendency, raised in the marginal environments and being often managed in migratory exploitation systems (KOSGEY et al., 2006), the activity come demanding to the research to find alternatives to optimized the application of animal breeding methodologies.

In this sense, expected that multi-breed statistical models be more reliable in the division of the variances among the genetics and environments effects. In addition,

expect to find better estimates modeling of contemporary groups as a random effect due to the small number of animals in some management groups in this flock. However, even attribute the great importance of a complete pedigree, is expected that the inclusion of records of lambs that not present paternal information, in the database with complete pedigree, come contribute with better estimates. Being that in this approach, the number of records submitted to the evaluation will be larger. Thus, the objectives of this paper were to verify the influence of the multi-breed model, modeling of contemporary group and pedigree structure in the estimates of the genetic components to birth weight in a mestizo herd.

MATERIALS AND METHODS

The present study not present implications for submission to ethic commit (Animal Experimentation Ethics Committee - CEEA). The working data were provided by the farmers, that recording the data as a routine of livestock system. A total of 1340 birth records were made available of a maternal base flock the Polwarth breed and paternal the F1 of the Finnish Landrace x East Friesian breeds, of 2012 at 2017, from São João farm, located in the Herval county, Rio Grande do Sul, Brazil, in the geographic coordinates 32°03'21.2"S; 53°18'15.7"W. Such records used to calculate the estimates of genetic components for the birth weight trait.

Of these 1340 birth weight records, excluded were 106 registers due to lack of maternal and paternal information, date of birth, sex and lambing type or being in contemporary groups with less of three individuals. Therefore, the remaining 1234 were used in two ways, one dataset with complete pedigree information (n = 1028) and another with incomplete pedigree information (n = 1234).

The composition of the pedigree file was 10 sires, being for the dataset with complete and incomplete pedigree, respectively, 366 and 448 dams, totalizing 1409 and 1685 animals (progeny, sires, dams, grandsires, and granddads). In the year 2012, when started the zootechnical record of birth weight, lambs born not had the paternal genealogical record, however, decided to use this data as a maternal productive record (used in the dataset with incomplete pedigree). From the 2013 year began the records of the trait referring at Polwarth x F1 (Finnish Landrace x East Friesian) crossbreed, being the products treated like F2. In the year 2014, some F2 females, born in 2013, produced your products (F3), is these children of a ram of Texel breed. Reproduced in 2015 the F2 females born in 2013 and some born in 2014, with the same ram of Texel breed. In 2016, some F2 females put in reproduction with F1 rams and some Polwarth ewes with the Texel ram. In 2017, some F2 females and most F3 females reproduce with a ram of Pool Dorset breed. In addition, some F2 females and the remaining of the F3 females were mated with F1 rams.

Due to these crosses and some retro-crosses (F2 and F3), the breed composition of the individuals born on the farm was considered how random effect, according to the model tested and considered how covariables, in the fixed effects analysis, the maternal and direct

heterozygosity. Thus, sons, and daughters of Polwarth ewes without paternal register and without breed identification considered Half-Blood-Base; sons and daughters of Polwarth ewes without paternal register and with breed identification considered Base; children of Polwarth ewes and of the Texel ram, was considered Base x Texel; children of Polwarth ewes and of the F1 rams, was considered F2; children of F2 Polwarth ewes without paternal register, was considered F2 Half-Blood; sons and daughters of F2 ewes and of the F1 rams, was considered F2 x F1; sons and

daughters of F2 ewes and of the Texel ram, was considered F2 x Texel; children of F2 ewes and of the Pool Dorset ram, was considered F2 x PD; sons and daughters of F3 ewes and of the Pool Dorset ram, was considered F3 X PD and; sons and daughters of F3 ewes and of the F1 rams, was considered F3 x F1.

The maternal and direct heterozygosity calculations were performed with the aim of considered the heterosis effects in the birth weight trait and are given by adapted Equations 1 and 2 of Brown et al. (2016):

$$\text{Maternal heterozygosity} = \sum_n^m (2 \times PRn \times PRm) \times 100 \quad (\text{Equation 1})$$

$$\text{Direct heterozygosity} = \sum_n^m (2 \times PRn \times PRm) \times 100 \quad (\text{Equation 2})$$

Where:

PRn = blood proportion of a specific breed that composes the crossbreed, both in an animal (direct) and your mother (maternal),

PRm = blood proportion of another specific breed that composes the crossbreed and

Σ = sum of the double each multiplication between every breed proportion that compose the animal and/or your mother.

The contemporary groups (CG) were formed per birth season (considering the year and until 45 days of the birth interval), the sex of lambs and the birth type (simple or multiple). In the fixed effects were considered the CG (only in 12 models), the age of mother at calving (eight levels – from one to eight years old), maternal and direct heterozygosity. Was tested the systematics effects influence in the birth weight, using the least square method by

statistical packet Ismeans of R software (R CORE DEVELOPMENT TEAM, 2013). For the dataset with a completed pedigree, there were verified significant effects ($P < 0.05$) for CG, the age of mother at calving and direct heterozygosity (Table 1). For the dataset with incomplete pedigree, every systematics effect tested were significant ($P < 0.05$), results showing in Table 1.

TABLE 1 - Fixed effects analysis for birth weight trait, in crossbred sheep considering two datasets.

Fixed effects	Fixed effects analysis ¹			
	Complete pedigree		Incomplete pedigree	
	Number of levels	Probability	Number of levels	Probability
CG	37	P<0.01	38	P<0.01
Age of months at caving ²	1028	P<0.01	1234	P<0.01
Maternal heterozygosity ²	1028	P=0.373	1234	P<0.01
Direct heterozygosity ²	1028	P<0.01	1234	P<0.01

¹Significative effect ($P \leq 0.05$) by least square test. ²Covariates.

Tested were 24 models to determining the best model for the estimate of genetics parameters. In 12 models the CG was consider as fixed effect and another 12 models, the CG was considered as random effect. The significate

effects analyzed for the least square analysis were included as fixed effects on the statistic models tested. Below is showing the 12 basic statistical models for analysis:

Model I: $y_i = Xb + Zai + ei$

Model II: $y_i = Xb + Zai + Mmi + ei$

Model III: $y_i = Xb + Zai + Wci + ei$

Model IV: $y_i = Xb + Zai + Rri + ei$

Model V: $y_i = Xb + Zai + Mmi + Wci + ei$

Model VI: $y_i = Xb + Zai + Mmi + Rri + ei$

Model VII: $y_i = Xb + Zai + Wci + Rri + ei$

Model VIII: $y_i = Xb + Zai + Mmi + Wci + Rri + ei$

Model IX: $y_i = Xb + Zai + Mmi + ei$, with $COV(a,m) = \sigma_{am}$

Model X: $y_i = Xb + Zai + Mmi + Wci + ei$, with $COV(a,m) = \sigma_{am}$

Model XI: $y_i = Xb + Zai + Mmi + Rri + ei$, with $COV(a,m) = \sigma_{am}$

Model XII: $y_i = Xb + Zai + Mmi + Wci + Rri + ei$, with $COV(a,m) = \sigma_{am}$

Where:

y = one observation on the animal,
 i = sum of the effects of the environment b ; direct additive genetic variance a ; maternal additive genetic variance m ; maternal permanent environment c ; breed composition r ; unknowing, environmental, residual or error effects e ,
 X , Z , M , W , and R = incidence matrices for fixed, direct, maternal and of maternal permanent environment effects, respectively and
 σ_{am} = covariance matrix between direct and maternal effects.

The analyses were performed used the maximum restricted likelihood (REML) method about the animal model, considering the birth weight trait, for each dataset (complete and incomplete pedigree), used the WOMBAT program (MEYER, 2007). The best model was tested using the AIC criterion (AKAIKE, 1992), being calculated of to rank the models of accord with your adjusting data capacity, that how much smaller is AIC values the best is the adjust. The calculation is given by the Equation 3:

$$AIC_i = -2 \log L_i + 2 p_i \quad (\text{Equation 3})$$

Where:

$\log L_i$ = logarithm of the maximum likelihood of the model i , in convergence and

p_i = the number of estimate parameters for each model.

RESULTS AND DISCUSSIONS

In Table 2 showed AIC values for the statistic models for the dataset with complete and incomplete pedigree. For the dataset with a complete pedigree, the model with less AIC value was the model IV (AIC = 529.940), that considered the direct additive and the breed composition effects. In the dataset incomplete pedigree, the model with less AIC value was that considered the direct additive and maternal additive effects (model II) with an AIC value of 544.762.

TABLE 2 - AIC criterion (AIC) of statistic models for the dataset with complete and incomplete pedigree and not considering or considering the CG as a random effect.

Model	Data structure			
	Complete Pedigree		Incomplete Pedigree	
	CGFIX ¹	CGRAN ²	CGFIX	CGRAN
I	534.714	541.254	573.256	583.930
II	535.724	542.104	544.762	553.826
III	536.532	543.076	548.736	558.190
IV	529.940	536.706	575.240	582.978
V	537.810	544.142	598.228	553.476
VI	530.654	537.100	545.578	553.018
VII	531.490	538.104	550.398	557.586
VIII	532.718	539.168	545.492	552.742
IX	536.698	543.388	545.540	554.508
X	538.842	545.514	546.154	554.938
XI	531.786	538.562	546.154	553.758
XII	533.910	540.668	547.020	554.310

¹CGFIX = models that considered the CG as a fixed effect. ²CGRAN = models that considered the CG as a random effect.

In neither dataset, the models that considered the CG as random effect show a good adjust of the data. According to Van Vleck (1987), considering CG as fixed effect removes bias due to an association between effects corresponding to CG and sires or in the case of the present study, of the animals. The same author says that if CG is considered random, then the effective number of children per animal is increased, could be a font of bias because it has not considered the environmental effect in the comparative analysis of animals measured in the same opportunities to express his of genetic merit.

In other studies, the most appropriate model considered the CG as random effect mainly due to the small number of animals in the analysis and/or in the CG (PASCOA et al., 2013). For Babot et al. (2003) the modeling of herd-year-sex to litter size trait in pigs as

random effect improves the predictive ability of the evaluation model. Fitting CG as random effects could solve the problem of forming CG with few individuals, but if mating not done in a way random, this can lead to bias in the prediction of breeding values (LEGARRA et al., 2005). In this sense, this is not applicated in the livestock system, where is sought to mate the best ram with the best ewes.

In the complete pedigree dataset, the best model was that considered the breed composition effect, agreeing with others authors that already found in the multibreed models present the best partitioning of phenotypic variance with estimates of the (co)variance components most accurate (BROWN et al., 2016; MURPHY et al., 2018). This is mainly for considerate the complementary effects among breeds due to crosses, that can influence directly the weight of the lambs' crossbreed, both in the capacity of

development in the uterine environment as in the capacity of crossbreed ewes to provide an adequate environment to growth and development of lambs in the gestational phases. Soon, this theme is worthy of more study, mainly for need meter the magnitude in that direct and maternal heterosis effects contribute to the birth weight trait.

Several studies with pure breed find a great variation in the most suitable model of adjusting. In the Kermani, Afshari and Moghan breeds, the model that better estimate the genetics parameters, for the birth weight trait, was that considered the direct and maternal effects (ESKANDARINASAB et al., 2010; JAFAROGHLI et al., 2010). For the breeds Texel, Merino Bharat, Malpura, Karakul and Makoei the model with better adjusting was the that considered the direct and maternal permanent environment effects (AMARILHO-SLVEIRA et al., 2018; MIRHOSEINI et al., 2015).

Bests adjusting were find used the model that considered the direct and maternal effects and the covariance between both in sheep of the breeds Sardi, Superfine Chinese Merino, Dorper, Arabi and Karayaka (BOUJENANE and DIALLO, 2017; ULUTAS et al., 2013). With sheep of the breeds Santa Inês, D'man, Lori, Mehraban and Morada Nova the genetics parameters were estimated using the model that considered the direct, maternal and maternal permanent environment effects (AGUIRRE et al., 2016; BOUJENANE et al., 2015; SHIOTSUKI et al., 2014).

In sheep of the breeds Baluchi (GHOLIZADEH and GHAFOURI-KESBI, 2015), Columbia, Targhee, Muzaffarnagari, Lori, Dorper and Mehraban (MANDAL et al., 2015; MOHAMMADI et al., 2015; NESER et al., 2011) the genetics parameters were estimated using the model that considered the effects additives (direct and maternal), covariance between they and the maternal permanent environment.

The (co)variance components for Lley breed were estimates for two models, considering, in the first, the effects additives, the covariance between both and the maternal permanent environment effect (CEYHAN et al., 2015). The second model was composed of every previous effect except the covariance between the direct and maternal effects. In the Dorper e, Ile de France breeds, the best model was that considered the maternal and direct effect, the covariance between both and the maternal permanent environment effect (ZISHIRI et al., 2014). However, in the same study, for Merino Landsheep breed, only the direct effect composed the model of best adjusting.

Is very important to test the model which provides better adjust of the data, because of the great variability among several environmental conditions, breeds, and data structure. In this sense, the table 2 showing the (co)variance components and genetic parameters for models that presented better adjusting, in the datasets with pedigree complete and incomplete.

TABLE 3 - (Co)variance components and genetics parameters according to the model to datasets with a complete and incomplete pedigree for the best models and your contrasts (in bold the best model by dataset).

Model	Complete pedigree						
	$^1\sigma_a$	σ_m	σ_r	σ_e	h^2	m^2	r^2
II CGFIX	0.05	0.16	-	0.35	0.09±0.06	0.29±0.05	
IV CGFIX	0.03	-	0.03	0.51	0.06±0.06	-	0.05±0.05
Model	Incomplete pedigree						
	σ_a	σ_m	σ_r	σ_e	h^2	m^2	r^2
II CGFIX	0.05	0.16	-	0.35	0.09±0.06	0.29±0.05	
IV CGFIX	0.03	-	0.03	0.51	0.06±0.06	-	0.05±0.05

$^1\sigma_a$ = direct additive variance, σ_m = maternal additive variance, σ_r = breed composition variance, σ_e = residual variance, h^2 = direct heritability, m^2 = maternal heritability and; r^2 - phenotypic variance attributable to the breed composition.

In both datasets are possible to note that the equivalent model presented the same estimates (Table 2). However, the better models were different among them. This is probably is due not only to the larger data number but also to the higher number of years in the evaluation, on what the evaluation of animals with an incomplete pedigree comprehends data from 2012 at 2017, compared from 2013 at 2017 of the complete pedigree.

Another point of great importance, which may have affected the different models in the adjusting of the data, is that 22% of ewes gave birth in 2012 and in the subsequence years, increasing the number of repetitions of the trait birth weight in the incomplete pedigree. This is very important when desirable estimates are the maternal effects. In this sense, in the dataset complete pedigree, due to smaller maternal information, the partitioning of the

phenotypic variance with breed composition presented more significance.

The direct heritability coefficients in both datasets did not present large difference, 0.06 and 0.09 to best models in the complete and incomplete pedigree, respectively. However, in the incomplete pedigree, the maternal heritability was 0.29. Therefore, the great importance in the use of every phenotypic information is mainly regarding the residual variance, which on the best model of the dataset with complete pedigree presented highest value (0.51 vs 0.35) than the best model of the dataset with incomplete pedigree. Black Sea region in Turkey testing six animal models, the genetics parameters estimate to Karayaka breed were from 0.37 at 0.55 for direct heritability and from 0.09 at 0.21 for maternal heritability. In Superfine Chinese Merino, the direct and maternal

heritability coefficient were, respectively, 0.12 and 0.14 (ULUTAS et al., 2013).

For sheep of Sardi breed in Morocco, the estimates of six animal models ranged to direct heritability from 0.06 at 0.09 and maternal heritability from 0.03 and 0.13 (BOUJENANE and DIALLO, 2017). These authors attributed the lower values of direct and maternal heritability to the likely influence of poor quality of the pasture where these animals were management; result in a large environment influence in the trait expression. In the present study, the environment variance (residual variance) was highest in the dataset with complete pedigree. The difference between the residual variance in datasets can also be attributed to the highest number of phenotype records in the incomplete pedigree dataset, in that the animals born in 2012 added in the evaluation represent about 8% data total evaluated, like this how much more information more accurate is the evaluation (KOSGEY et al., 2006; SAFARI et al., 2007; SOYDAN and ŞAHIN, 2016).

Our results highlight the importance of the breed effect when all pedigree is known, and that this effect can be disregarded, being the maternal effect more important when using data with sire unknown. With these results, it's possible to apply the generated knowledge in the sheep genetic evaluations. In the future, the multibreed model with CG as a fixed effect, with the complete pedigree, will be using in the Brazilian genetics' evaluations.

CONCLUSIONS

There was an influence of de multi-breed model only in the dataset with complete pedigree, being the best model that considered the direct and breed effects.

In the dataset with incomplete pedigree, the better model was that considered the direct and maternal additive effects.

In both datasets, the modeling of contemporary groups as fixed effect presented the best estimates of genetics components to birth weight in this mestizo flock.

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