

GENETICS OF MATERNAL TRAITS IN A NEW SYNTHETIC RABBIT LINE UNDER SELECTION

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ABSTRACT

The study aimed to estimate genetic parameters in a synthetic rabbit line selected for maternal traits and compare different animal model methods, i.e. single (ST) vs. multiple trait (MT) approach to be used to calculate estimated breeding values (EBVs). Data on 4462 kitting belonging to 1151 does were used and classified for different generation (G, 3 levels), month of kitting (M, 12 levels), GxM interaction, parity order (9 levels) and age class within parity (18 levels). Random permanent environment and additive genetic effects were included in Animal Model accounting for a total of 1297 animals. ST and MT approach were used alternatively for 3 traits measured: 1) total number of born, 2) number of born alive and 3) mortality rate up to weaning. ST and MT approaches were compared by using Percentage of Square Biases (PSB), Means Absolute Deviation (MAD), Coefficient of determination (R^2) and correlations between actual values and estimated breeding values (EBVs). Correlation coefficients were calculated between rankings for EBVs obtained with ST or MT method for each variable. The parameters used to compare the models indicated that, despite small differences in term of PSB, MAD or R^2 , the ST animal model could be preferred. However, a general poor R^2 for all methods and variables considered was observed, suggesting the presence of undetermined environmental factors that could influence the overall variability of each trait studied. Moreover, for the mortality rate variable a very huge amount of biases was detected, probably because of the large asymmetry of distribution for this variable. Heritability estimates were similar in both ST and MT approach: low for total number of born (0.075-0.076 for ST and MT, respectively) and number of born alive kits (0.048-0.053 for ST and MT, respectively), and basically zero for the mortality rate up to weaning (0.0004-0.0007 for ST and MT, respectively). Genetic correlations produced by the MT method were generally high (0.61 to 0.97) and in an expected range for the considered variables. The correlation between rankings of animal based on ST or MT EBVs confirmed a considerable similarity between the two methods as regard the EBVs for total number of born or number of born alive kits (correlation between 0.93 and 0.98), but inconsistent for the mortality rate, suggesting the need to avoid such a variable in selection for maternal traits. The easiest ST animal model for total number of born or number of born alive could therefore be used to predict breeding values for selecting maternal line of rabbits.

Key words: Genetic parameters, Maternal traits, Animal models, BLUP, Selection.

INTRODUCTION

The literature about variance components of reproductive traits, indicate very low values for traits such as the number of born alive or the weaned kits (Rochambeau, 1997). Despite fertility traits have low heritability (Blasco *et al.*, 1993) reproductive performance could be improved by including female fertility in a selection program, although the response to selection would be probably low as reported by Garreau *et al.* (2004). In any case, the knowledge of heritability is a key factor in a selection program (Falconer, 1989), allowing the selection of animal on a BLUP basis as implemented in Spain (Argente *et al.*, 1997). Among the different estimation methods proposed to calculate heritability, single (ST) vs. multiple trait (MT) methods have been proposed as alternatives for selection on BLUP. The advantage of MT on ST method has generally been recognized, due to the simultaneous

evaluation of genetic parameters for more than one trait accounting also for genetic correlation among them, despite the more time consuming and computer memory requirements (Schaeffer and Wilton, 1981; Johansson, 1987). The aim of this paper was to study the heritability of reproductive performance in a new synthetic line of rabbit selected for maternal traits, comparing also different animal model methods, i.e. single (ST) vs. multiple trait (MT) approach, to be used to estimate breeding values (EBVs) for selection purpose.

MATERIALS AND METHODS

Data at birth obtained from females rabbits belonging to a synthetic line (CPC-Italy) selected in the North-East of Italy for maternal traits were registered over two years. The total number of born kits, the no. of born alive, the no. of stillbirth and the no. of weaned kits were recorded for each doe belonging to the selection nucleus, located in one single farm in Pinzano al Tagliamento (Pordenone). An overall number of 4462 kitting belonging to 1151 does (i.e. about 4 kitting/doe) were retained. Data analyzed were the total no. of born, the no. of born alive and the percentage of mortality from birth to weaning as respect to the initial no. of kits leaved under each doe. After a preliminary analysis of variance (ANOVA), the fixed effects included in the model were the generation effect (G, 3 contemporary levels taken into account), the month of kitting (M, 12 levels from January to December) and the interaction GxM (36 levels). Other effects retained after ANOVA were the parity order (9 levels, i.e. from nulliparous to a parity order equal of greater than the 8th) and the class of age within parity (i.e., early and late age class for each parity order for a total no. of 18 levels). The permanent environmental effect and the genetic effect were also added in an Animal Model that included a total number of 1297 animals in the pedigree. Genetic parameters were estimated using a REML procedure from the BLUPF90 package (Misztal *et al.*, 2002) both using ST and MT approaches for the 3 traits considered. Residuals for each variable and model were obtained from the solutions for each effect accounted in the analysis and the different estimation methods were compared in terms of Percentage of Square Biases (PSB) and Means Absolute Deviation (MAD). The first parameter gives an evaluation of models on the basis of the amount of biases produced, while the second one allows, other than a the model comparison, a general estimate of the biases produced by each model. These parameters are calculated as follows (Ali and Schaeffer, 1987):

$$PSB = \left(\frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{\sum_{i=1}^n (y_i)^2} \right) \times 100$$

$$MAD = \frac{\sum_{i=1}^n |y_i - \hat{y}_i|}{n}$$

Where, for each variable analyzed:

y_i = Actual value

\hat{y}_i = Predicted value

Moreover, estimation methods were also compared in term of coefficient of determination (R^2) and correlation between actual values and EBVs. The coefficient of determination was calculated as ratio between the variance of predicted values and the sum of variances of predicted and residual. Correlation coefficients were also calculated between the ranks for EBVs obtained for each variable as results of ST or MT analysis. In this case both females with records and males sub-populations were considered separately.

RESULTS AND DISCUSSION

Table 1 reports the comparison between the ST and MT approaches to estimate variance components and subsequent estimates for fixed and random effects in the model. As indicated by Ali and Schaeffer (1987), that first proposed the method of PSB and MAD to compare models, the lower values for both these measures should indicate the best fitting method. At this regard, the ST animal model used exhibited a better fitting both in terms of PSB and MAD than the MT approach, despite the differences observed between methods could be considered generally small.

Table 1: Comparison of different models (ST vs. MT) for each variable considered

Item	Total born		Born alive		% Mortality up to weaning	
	ST	MT	ST	MT	ST	MT
PSB (%)	4.74	4.75	5.59	5.63	64.77	64.82
MAD	1.74	1.74	1.81	1.82	24.73	24.75
R ² (%)	22.72	22.40	18.75	18.68	18.71	18.65
Correlations actual/EBVs (%)	37.43	37.17	32.62	32.20	1.78	3.59

As regard the determination coefficient of the models, a higher value for this parameter was always observed for all variables in the ST approach, still indicating a slightly better fitting of this method in comparison with the MT analysis. Generally speaking, small differences were detected also for the correlation between actual values and correspondent EBVs. However, for this parameter, the ST animal model indicated a better fitting only for the total no. of kits born and the no. of born alive kits. Indeed, for the percentage of mortality up to weaning, the MT method of analysis led to a better response as correlation between actual and EBVs, despite a general very low value for the coefficient (i.e., under 4% in both cases). In spite of this, the main point about these part of the study remain the huge amount of PSB observed for the % of mortality, that indicate as this variable transfer a great amount of biases into the breeding values for animals. Therefore, this should suggest a careful use of such a variable in animal selection. Most probably, the reason for such a reduced capability of mortality incidence to be used as selection variable could be linked with its asymmetrical distribution. Indeed, most observations are of none mortality (i.e., 41%), and almost three out of four observations (75%) are within a range of 30% of mortality from birth to weaning. Therefore, such a distribution results very difficult to be modeled for breeding values estimates. Last, another result that has to be stressed is the generally low value observed for the coefficient of determination that reached at its best 22.7%, indicating a general poor fitting for all methods considered.

Despite the previous results, ST estimates of variance component were performed for all traits measured at kitting and Table 2 reports the results obtained. All heritability estimates resulted very low, and the estimates for the percentage of mortality up to weaning resulted lower than 0.1%, indicating a nadir genetic component for such a trait. As reported by Rochambeau (1997), h^2 estimated in this study was in the expected range for the no. of kit born alive. Indeed, reviewing the topic this author reported general estimates between 5-8%, despite reporting a general feeling among researcher that it could be lower than 1%. However, our study substantiates such a feeling only for the mortality incidence up to weaning that showed a mean heritability of 0.06% combining both ST and MT estimates.

Table 2: Results of single trait genetic analysis for each variable considered in the study

Item	Total born	Born alive	% Mortality up to weaning
Variances:			
- Additive Genetic	0.5130	0.3268	0.2552
- Permanent Environment	0.3805	0.4289	30.9300
- Residual	5.9880	6.0020	679.1000
Heritability (%)	0.075	0.048	0.0004
Repeatability (%)	0.13	0.11	0.0439

All heritability estimates performed with the MT animal model, showed comparable results with the ST analysis, but gave also a general idea about the correlations among the studied traits (Table 3). As expected, the number of total born and the no. of born alive were positively correlated, both as phenotypic (92.3%) and genetic correlations (96.4%). This seems an indirect confirmation that the number of stillborn kits decrease when selection takes place for the prolificacy. Previous studies from Baselga *et al.* (2003) aimed to estimate heterosis for this trait found that stillborn is a variable that accounts for a significant amount of heterosis, suggesting the need to be considered by genetic improvement. However, the present study does not substantiate such result from Spanish researchers. On the other hand, a positive genetic correlation between total born and born alive was found in our study with the incidence of mortality up to weaning (i.e., 61 and 63%), indicating a negative trend in decreasing the no. of weaned kits with the enhancement of the total born or born alive kits. This negative result is probably attributable to the limited amount of milk that a doe can produce after

kitting avoiding a highly negative energy balance and, therefore, fertility problems as a consequence of such a physiological status.

Table 3: Heritability (diagonal) and correlations (genetic above, phenotypic below) obtained with the multiple trait animal model using the 3 variables recorded on does (all values expressed as %)

	Total born	Born alive	% Mortality up to weaning
Total born	0.076	0.97	0.61
Born alive	0.92	0.053	0.62
% Mortality up to weaning	-0.035	-0.06	0.0007

The correlations among the ranking of animals due to their EBVs estimated using alternatively a ST or a MT approach, separated for females with records and males (Table 4), indicated a general good fitting for the number of total born and born alive, while a very low correlation coefficient was produced by ranks obtained in single rather than in MT trait approach, indicating both in females and males sub-population, heavy changes due to the correction made by the program on the basis of the genetic correlation among traits. Indeed, the rank correlation between EBVs for total born and born alive with the mortality rate up to weaning resulted extremely different within method, with the single trait ST animal model that produced a mean correlation of 8% against an almost 98% produced by the MT method. On the other hand, it has to be taken into account the very low heritability observed for the mortality rate, which also could have influenced the results in terms of ranking for EBVs produced under different animal model methods. In general, the low correlation observed between ranks for the incidence of mortality up to weaning, indicate once more the low power of this variable to be used for selection of maternal traits in grandparent lines.

Table 4: Correlation between animal rankings for single vs. multiple trait EBVs estimate for each variable analyzed and for the sub-populations of females and males

Variable	Females with record	Males
Total born	0.98	0.96
Born alive	0.93	0.93
% Mortality up to weaning	0.25	0.24

Conversely, the other correlation coefficients considered in terms of ranking for EBVs obtained with ST or MT methods, with a pattern similar to that reported for females' total no. of born in figure 1, suggested a consistent high relationship between the two animal model methods, with only small changes in the animal rankings in the middle part of the rankings. Indeed, as shown by the Figure 1, only small changes in animals' rank are possible within the first and the last 100 positions.

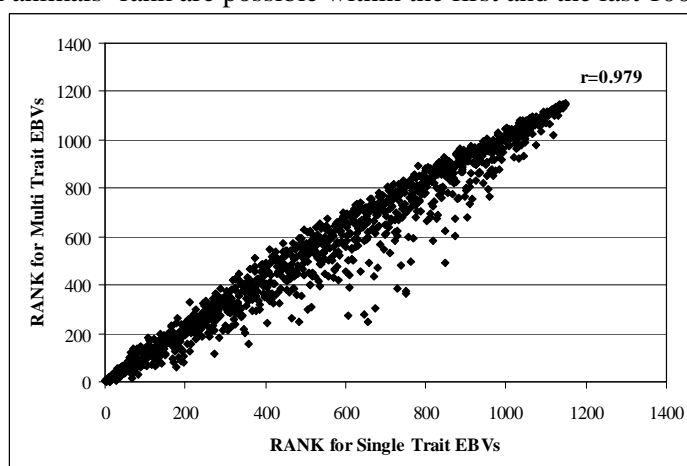


Figure 1: Correlation between the rankings of females with record as results of EBVs obtained with a single or multiple trait animal model for the total no. of born kits

CONCLUSIONS

Results from this study indicated a generally poor R^2 of the model used for fitting fixed and random effects. Moreover, for the mortality rate variable a very huge amount of biases were detected, probably because of the large asymmetry of distribution for this variable. Heritability estimates were similar in ST and MT approaches: generally low for the total no. born and for no. of born alive kits, and basically zero for the mortality up to weaning. Genetic correlations resulted always high between traits studied, and generally speaking in the expected range. The correlation between rankings of animal based on EBVs obtained with ST or MT confirmed a considerable similarity between the two methods as regard the EBVs for total no. of born alive and the born alive kits, but indicated substantial differences between animal model methods for the mortality rate. On the light of the results obtained, we could conclude that the easiest single trait evaluation method for total no. of born or born alive kits could be easily implemented for selection purposes, while the mortality rate up to weaning could be avoided as selection variable.

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