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COMPARING METHODS OF SELECTING LITTER SIZE IN RABBITS WHEN DIFFERENT AMOUNT OF INFORMATION IS USED[1]

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SUMMARY

The efficiency of two simplified methods of selecting litter size in rabbits has beer studied. These methods, a family index and a reduced BLUP using only records of twc generations, have been compared with a BLUP, repeatability-animal model that used all records from the foundation until the generation currently selected.

The comparison has been made analyzing correlations between rankings of matings, ratios of coincidence of matings selected to contribute progeny to the next generation, and ratios of response lost when the simplified methods are used.

An analysis of robustness of the methods to changes in genetic parameters was also carried out.

Records of 18 and 14 generations of two lines of rabbits selected for litter size at weaning were used, and the selection process was studied in generation 17, 18 of one line, and 13,14 of the other. The two simplified methods were practically similar in the context of our study, with non overlapping generations and good balance between animals to be selected and fixed effects.

The correlations between rankings of a simplified method and the BLUP using all records ranged between 0.79 and 0.82, the coincidence ratio between 0.62 and 0.90, and the loss ratio between 0 and 0.17, being the average around 0.05-0.06.

The methods of selection revealed themselves as very robust.

Key words: simplified selection, response , litter size, rabbit.

INTRODUCTION

Litter size at birth or weaning have been the traits of choice to select specialized dam lines in meat rabbit production. The methods of selection commonly used are a family index (Matheron and Rouvier, 1977; Baselga *et al.*, 1984) or a BLUP under a repeatability-animal model (Estany *et al.*, 1989). The BLUP used is actually a reduced BLUP that only takes into account the data of the generation to be selected and the previous one, as it is done by the family index. Research work comparing efficiency of a complete BLUP versus a reduced BLUP to select does for litter size revealed that expected losses in genetic gains were almost negligible and less than 12% (Baselga *et al.*, 1985; Estany, 1987). Thus, the use of a reduced BLUP allows to save computer time, what is important in many cases of rabbit breeding, nevertheless computing facilities are fastly increasing with time.

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Currently, prediction of breeding values by BLUP and animal models is quickly expanding to many species involved in livestock production (Carabaño and Alenda, 1990), and the aim of this paper is to compare again the complete BLUP with the reduced BLUP and a family index oftenly used to select litter size in rabbits. The comparisons will be made on the efficiency to select the best matings, nor the best females, analyzing this efficiency in two consecutive generations of two lines of rabbits, that have undergone selection on litter size for a long time.

MATERIALS AND METHODS

Weaning litter size records of two lines of rabbits named A and V are used, including all parities of the does from the foundation of the lines until generation 18 in line A, and generation 14 in line V.

Line A has been selected on a family index (Baselga *et al.*, 1984), and line V on a reduced BLUP (Estany *et al.*, 1989) for litter size at weaning, being the reproduction in non overlapping generations. The family index took into account, to predict breeding values of individuals of the last generation, the own records (if a doe is to be evaluated) and the records of the dam, full sibs and half sibs. The reduced BLUP evaluated individuals of the last generation considering the previous generation as the founding generation. Considered fixed effects were year-season and physiological state of the doe when it became pregnant. Random effects were additive values and permanent non genetic effects of the animals. An heritability of 0.136 and a repeatability of 0.20 (García-Ximénez, 1982) were the parameters used to actually run the family index and the reduced BLUP in order to evaluate the matings.

Progeny of the best matings was selected to make up the next generation. The genetic value of a mating was computed as the average of the breeding values predicted for the male and the doe of the mating. The selection of a generation began when a great part of the females had two parities and then the proportion of matings selected was 0.25 but later, when the majority of females reached its third parity this proportion was 0.33. Thus, we consider two steps in the selection process, the first step with a proportion selected of 0.25 and the last one with 0.33.

Three methods of predicting genetic values of matings are compared in the two steps of selection of generations 17, 18 of line A, and 13, 14 of line V. The methods were the *family index*, the *reduced Blup*, as explained above, and a BLUP on all records (*complete BLUP*) from the foundation of the line to the moment of selecting the progeny of the best matings. To compare the methods four sets of genetic parameters, **TABLE I**, called A, B, C, and D were used. The set A corresponds to the parameters actually used to select. The B and D sets are REML estimates for line A and V respectively, got analyzing the totality of data recorded (Gómez, unpublished). The sets A and B are very like and a different set, the C set, was used in line A, in order to check the robustness of the methods with different parameters. The A, B and C sets were used in line A, and the sets A and D in line V.

TABLE I.- Genetic parameters sets used.

Gen. Param. Set	**A**	**B**	**C**	**D**
h^2	0.136	0.140	0.100	0.064
Repeatability	0.200	0.180	0.180	0.125

The size of the lines was around 120 ♀ and 25 ♂, but **TABLE II** gives the number of animals of the generations involved in the comparison of methods of evaluation, and the number of parities recorded at each one of the two steps of selection.

In order to study the relative efficiency of the methods, comparison will be made between rankings of the matings, the degree of coincidence of the best matings under different methods and genetic parameters will be analyzed and finally, we will compute the losses in predicted genetic value when a simplified method is used instead of a complete BLUP.

TABLE II.- Number of animals and recorded parities at each step of selection in the generations and lines indicated.

Line	**A**		**V**	
Generation	**17**	**18**	**13**	**14**
Number of animals	121♀ 33♂	116♀ 28♂	112♀ 25♂	103♀ 26♂
Recorded parities at first step	224	204	210	204
Recorded parities at last step	374	369	310	349

RESULTS AND DISCUSSION

Comparing the two simplified methods of evaluating matings, **TABLE III** shows that the reduced BLUP and the family index gave the same ordering when the criterion to order the matings was the genetic value predicted by each method.

TABLE III.- Correlations of ranking of matings between a reduced BLUP and a family index in the first and the last steps of selection.

Line	**A**						**V**			
Generation	**17**			**18**			**13**		**14**	
Gen Param[1]	**A**	**B**	**C**	**A**	**B**	**C**	**A**	**D**	**A**	**D**
First	0.99	0.99	0.99	0.98	0.98	0.98	0.99	0.99	0.98	0.97
Last	0.98	0.98	0.99	0.97	0.98	0.98	0.97	0.98	0.98	0.98

[1].- Genetic Parameter Set.

The genetic correlations between rankings were always equal or higher than 0.97. Similar results were obtained by Baselga *et al.* (1985) and by Estany (1987) when the comparison between the methods was made on the basis of rankings and genetic evaluations of individuals instead of matings. The main difference between the family index and the reduced BLUP lies in the fixed effects taken into account by the reduced BLUP and not by the index. These effects seem to be not important to order individuals or matings when the generations non overlap, the animals are housed in the same rabbitry and the females go across the same physiological states. Given the strong similarities between reduced BLUP and family index, hereafter we will discuss only on results of family index.

TABLE IV reports on correlations between rankings of matings at the two steps of selection within method of evaluation. These correlations range between 0.79 and 0.92, being the modal value near 0.85. It means that relevant changes in the order of matings can occur between the first and last step of selection. Consequently it is sensible to select from a lower proportion of matings at the beginning. We must note that the correlations across parameter sets are practically the same, what is a first indication of robustness. Correlation values for complete BLUP and family index are very close in generation 17 of line A and generation 13 of line V. The maximum difference is in generation 18 of line A, being the correlation for BLUP 0.05 higher than for family index. This generation had the minimum ratio parities/females at first step (**TABLE II**).

TABLE IV.- Correlations between ranking of matings at the first and the last steps of selection with a complete BLUP and a family index.

Line	**A**						**V**			
Generation	**17**			**18**			**13**		**14**	
Gen Param[1]	**A**	**B**	**C**	**A**	**B**	**C**	**A**	**D**	**A**	**D**
BLUP	0.86	0.86	0.86	0.85	0.85	0.85	0.90	0.91	0.82	0.83
Fam Index	0.84	0.84	0.84	0.80	0.80	0.79	0.91	0.92	0.85	0.85

[1].- Genetic Parameter Set.

TABLE V.- Comparison between a complete BLUP and a family index at first or last step of selection.

Line		**A**						**V**			
Generation		**17**			**18**			**13**		**14**	
Gen Param[1]		**A**	**B**	**C**	**A**	**B**	**C**	**A**	**D**	**A**	**D**
COR[2]	**First**	0.90	0.91	0.89	0.90	0.90	0.87	0.95	0.92	0.86	0.79
	Last	0.93	0.93	0.91	0.89	0.90	0.87	0.95	0.93	0.90	0.84
CR[3]	**First**	0.63	0.66	0.63	0.81	0.84	0.78	0.86	0.86	0.76	0.62
	Last	0.86	0.86	0.84	0.90	0.90	0.90	0.90	0.88	0.84	0.78
RLR[4]	**First**	0.17	0.14	0.15	0.01	0.02	0.04	0.06	0.07	-0.03	0.08
	Last	0.08	0.07	0.09	0.04	0.04	0.05	0.04	0.06	0.10	0.17

[1].- Genetic Parameter Set.
[2].- Correlations for the ranking of matings.
[3].- Coincidence Ratio of selected matings between both methods.
[4].- Response Loss Ratio using the family index instead of the complete BLUP.

To analyze the loss of efficiency when selection is made on predictions of a family index instead of a complete BLUP, **TABLE V** shows the value of the correlations between rankings of matings got for each method, the ratio of coincidence of matings that produce selected progeny in both methods and the ratio of response lost for using the simplified method. The correlations are always equal or higher at the last step, when there are more information to evaluate, than at the first step of selection. The values are oftenly higher than 0.90. The minimum is 0.79 for generation 14 of line V and the lowest value of heritability. The coincidence ratio range between 0.62 and 0.86 at first step of selection, and between 0.78 and 0.90 at the second. It is due to the higher selected proportion at the last step (Estany, 1987; Baselga *et al.*, 1985) and, probably, to the higher amount of information accumulated at this moment. The relative losses for using the family index were always lower or equal than 0.17, being the average around 0.05-0.06. Similar results were obtained by Baselga *et al.* (1985) and Estany (1987). The loss of efficiency is actually low or negligible.

TABLE VI informs us about how the methods to evaluate genetically the matings are robust to changes in genetic parameters. The three variables computed strongly show that the methods are truly robust (Sales and Hill, 1976).

TABLE VI.- Comparison between the different sets of genetic parameters in a complete BLUP and in a family index at last step of selection.

Line		**A**						**V**	
Generation		**17**			**18**			**13**	**14**
Gen Param[1]		**BA**	**CA**	**CB**	**BA**	**CA**	**CB**	**AD**	**AD**
COR[2]	**Blup**	0.999	0.995	0.992	0.999	0.996	0.993	0.988	0.976
	FInd	0.999	0.995	0.992	0.999	0.996	0.993	0.988	0.976
CR[3]	**Blup**	1.000	0.941	0.941	0.980	1.000	0.980	0.958	0.880
	FInd	1.000	0.941	0.941	0.980	1.000	0.980	0.958	0.880
RLR[4]	**Blup**	0.000	0.006	0.006	0.000	0.000	0.000	0.010	0.032
	FInd	0.000	0.006	0.006	0.000	0.000	0.000	0.010	0.032

[1] .- Genetic Parameter sets compared.

[2] .- Correlations for the ranking of matings.

[3] .- Coincidence ratio of selected matings between both genetic parameter sets.

[4] .- Response loss ratio using the first genetic parameter set instead of the second one.

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