Validation Of Novel Approach For Estimation Of Bovine Ttransmitting Ability With The Use Of Reporter Gene *DGAT1*- *M.G. Smaragdov,* V.B.Dmitriev, J.G.Turlova, S.I. Loskutov and A.V. Egiazaryan

Introduction

In the 20th century the methods of genetic evaluations of dairy cattle have been steadily improving since computer innovation was applied. The method of "Mother-Daughter" was placed to the method's of Contemporary Comparison and Modified Contemporary Comparison (MCC), and finally, to the BLUP and Animal Model. The main purpose of improvements was to make reliable selection of one bull over another according to the highest transmitting ability of their desirable traits. In the widely used Animal Model, an animal's predicted transmitting ability (PTA) combines information from its own records and records of all its relatives through a weighted average of 1) average of parents' evaluations, 2) half of its yield deviation, and, 3) average across progeny of twice progeny evaluation minus mate's evaluation (VanRaden and Wiggans (1991). Thus, we are dealing with paradigm in accordance with PTA, EBV and Reliability might be sufficiently computed through a mean and variance. Another possible approach, namely Frequentist based on frequencies' value of explanatory parameters was applied. We estimated how many bull's daughters got desirable value of trait (parameter ETAB) instead of daughter yield deviation in Animal Model. The main objective of this study was to calculate bulls' PTA and breeding value by means of frequentist statistics. In support of fidelity and effectiveness of such approach at genetical level the *DGAT1* was used as reporter gene.

Material and methods

The studies were carried out on first-heifers of Black and White breed (n = 65130). They were the daughters of 142 bulls progeny tested. The data recording by "Plinor" Company Limited from 1992 to 2008 were used. According to their data in 1992 cows' milk production was 5500-7500 kg milk yield, 3.73-3.96 milk fat percentage, and 3.15-3.30 milk protein percentage, while in 2008 was 9630-10250 kg, 3.6-3.8%, 2.8-3.1%, respectively. The proposed method is ideally suited to calculate the estimated transmitting ability of the bulls (ETAB) and is based on skewness of distribution of bull's daughters with different values of milk production traits (Fig. 1). The selection differential for a herd or the whole population was fixed, and it was equal to ± 0.5 of phenotype standard deviation for all computations. In addition, each first lactation record (305 d) of cow, taking into consideration the trait-year-herd data was assigned to the following grade ($1 < -0.5\ \sigma$; $-0.5\ \sigma < 2 < 0.5\ \sigma$; $3 > 0.5\ \sigma$). Hence, the distinction between cows in the first and third grade will be 2, 1, and 1of genetical σ for the milk yield, milk fat- and milk protein yield percentage, respectively. Thus, individual bull's transmitted ability can be calculated as ratio of daughters' frequencies at 1 and 3 grades. Unlike to the traditional methods, according to our method the estimated transmitting ability of the bulls was defined as ratio of high - to low – productive daughters according to the formula: $ETAB = \log (P_3 + 1 / P_1 + 1)$; where P_1 – a frequency of the daughters in the 1th grade, P_3 - a frequency of the daughters in the 3d grade.

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Results and discussion

The evaluation of the bull's was made using MCC and ETAB methods at the same 142 bulls. The effect of *DGAT1* gene on milk production traits was estimated by means of MCC method (our unpublished results). The obtained results were compatible with earlier published data in literature. Therefore, for verification of the accuracy of ETAB model the *DGAT1* was used as reporter gene. These data are shown in Table 1. Significant results were confirmed for milk yield, milk fat and protein yield, and milk fat yield percentage. According to the traditional evaluation, the inheritance the 232K allele leads to an increase in milk fat yield and milk fat yield percentage. Consequently, the fraction of cows in the third grade should be higher than in the first one and log (P_3 + 1 / P_1 + 1) value will be positive, as we revealed to be the case for AK bulls (Table 1). According to the traditional evaluation the inheritance of the K232 allele leads to decrease of milk yield. In this case the fraction of cows in the third grade should be less than in the first one and log (P_3 + 1 / P_1 + 1) value will be negative as we also revealed to be the case for AK bulls (Table 1). Thus, ETAB method was suited to track out the inheritance of bulls' K232 allele of *DGAT1* to the daughters. The data obtained by the ETAB method for milk protein yield percentage were not significant but the trend was in much the same way as for the evaluation of bulls by MCC method. As it was shown by MCC method for 142 bulls analyzed, the K232 allele *DGAT1* results in decreasing of milk protein yield, but the data obtained according to the our model were opposite (Table 1). We can propose several explanations for this fact: The first, the estimation of an effect K232 allele on milk protein yield by ETAB model owing to insufficient number of bulls was inexact. The second, the ETAB method reveals not only additive effect of genes but also the dominance and epistasis of genes' alleles inherited from the parents.

Table 1: Transmitted ability of the bulls calculated according to ETAB = log (P_3 + 1 / P_1 + 1) and genotyped at K232A *DGAT1* alleles

Genotype	M	F	P	%F	%P
AK[a]	-0.014±0.004	0.012±0.004	0.013±0.007	0.010±0.004	0.0005±0.006
AA	0.015±0.004	-0.030±0.004	-0.008±0.006	-0.026±0.004	-0.010±0.006
SD[b]	0.8	1.1	0.36	0.86	0.28
SD[c]	0.76	0.13	0.47	1.41	0.44
F-test	27	51	45	32	1.3
P-value	$1\cdot10^{-6}$	$1\cdot10^{-8}$	0.035	$1\cdot10^{-7}$	0.26

M- milk yield; F- milk fat yield; P- milk protein yield; %F- milk fat yield percentage; %P- milk protein yield percentage; [a]- AK and KK bulls are combined; [b] – substitution effect of A to K calculated according to ETAB model expressed in σ scale; [c] - substitution effect of A to K calculated according to MCC model expressed in σ scale.

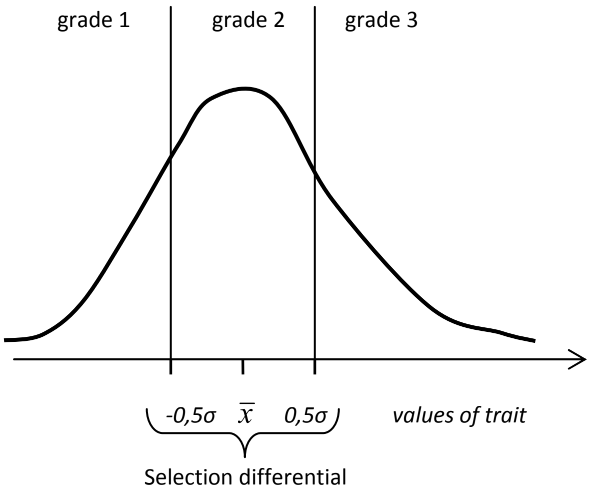

Fig. 1. Distribution of bull's daughters

As we think further experiments are needed to refine these data. The effectiveness of the MCC and ETAB models is difficult to compare because of dissimilarity measured values: milk yield, milk fat yield *etc.* on one side and the proportion of daughters with increased value of the trait to daughters with decreased value of the trait on another side. But, it is possible to compare the effect of K232A alleles on traits expressed in sigma scale (Table 1). As follows from the data in Table 1 the values of SD are similar for two models, except milk fat yield percentage and milk fat yield, i.e. direct effect of K232 allele action on milk fat yield at least (not pleiotropic). These differences may be explained by non-additive interaction *DGAT1* alleles with background genes registered by ETAB model and by information which was loss from the 2d grade cows. Other explanations are also possible.

Conclusion

Thus, with the help of the gene *DGAT1* it was shown that the ETAB method is ideally suited to track out favourable alleles of the genes being under selection.

References

VanRaden,P., Wiggans,G. (1991). J. Dairy Sci., 74:2737-2746.