Genetic variance of the prolificacy trait in sheep from North-East Bulgarian Merino breed

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Abstract

The aim of the study was to analyze the overall genetic variance and effects for the prolificacy trait in North-East Bulgarian Merino sheep breed, with distinct participation of the Australian Merino and Booroola breeds in its genotype. The study included 584 pedigrees and 1123 prolificacy records. An animal model was used and the following factors were included in the statistical analysis: year of each lambing, consecutive lambing, year of birth of the animal, regression effect of age in days to the date of lambing. The average value for the prolificacy trait was 1.114 lambs per ewe with typical for the phenotypic variation trait (29.0%). The genetic tendency for prolificacy was negative, depending on the year of birth, and positive on subsequent rearing. Analysis of the variance indicated that the major part of the genetic variance have been described, by the individual characteristics of the animals (0.034 at 0.001 caused by heterosis). The proportion of genetic variance resulting from different breed combination in the genotype was extremely low relative to the individual genetic varians (0.257), which reflected the overall genetic variation. Estimates of additive and non-additive effects by genetic groups did not establish clear distinguishable differences.

Key words: genetic variance, prolificacy, additive and non-additive effects, North-East Bulgarian Merino Sheep, animal model

Introduction

The breeding process for sheep from different productive directions is related to the application of appropriate methods for crossing and breeding schemes to synthesize certain components of high inheritance of desired breeding traits from different breeds and to consolidate them in subsequent generations. Through complex reproductive crossing on the basis of local and with participation mostly of rams from the Caucasian (CA) and Askanian (AS) breeds, in the period 1974–1986, were formed four Bulgarian fine fleece breeds from wool-meat type North-East Bulgarian Merino – (NEBM); Thracian Merino (TM); Karnobat Merino (KM); Danube Merino (DM). In the early 1990s, fine fleece sheep were the largest population (1541000) in Bulgaria. The efforts of the scientific researchers during this period were aimed at increasing the productivity and possibilities for quality improvement of sheep in this direction, both through pure bred breeding and by including the genetic components of the Australian Merino and Booroola breeds. In conducted studies on the effect of applied breeding methods and schemes, Boikovs-

ki (1995), Dimitrov (2001; 2006), Iliev (1999), Slavova (2000), Stefanova (2000), Slavov (2007), Slavov et al. (2008) found different changes, regarding direction, in the genetic variance for the selection subjected traits.

The change in ownership and the economic weight of the produced sheep products in favor of meat and milk has had a major impact on the number of fine-fleece sheep, whose relative share is currently below 1.7%. The gene pool of this sheep population has been greatly altered, genetic structures have been disturbed, new phenotypically similar, composite flocks and uniform lines have been formed within each breed combinations were in different proportions. Breeding programs for their improvement have been replaced by programs for the conservation of the small number of animals left as a purebred part of the population. In 2011, the general "Merinos and Fine Fleece Sheep Breeding Program in Bulgaria for the Period 2011–2020" was approved by the Association for Breeding Merino Sheep Breeding in Bulgaria (ABMSB), and in 2013 they were declared endangered and received subsidies for their conservation and maintenance (Stancheva et al., 2015). According to ABMSB data, in 2018, 5210 sheep were under breeding control, of which 4058 were from the preserved three Bulgarian breeds: North-East Bulgarian Merino - 3686; Thracian Merino – 204 and Karnobat Merino – 168.

Genetic diversity in populations was a basic prerequisite for designing effective genetic improvement and breeding programs for conservation, Gutierrez et al. (2003) and Malhado et al. (2008) stated. On the other hand, researches on the genetic parameters of traits with economic importance have been crucial for genetic evaluation and the selection the best schemes for selection. (Rosati et al., 2002; Safari and Fogarty, 2003; Safari et al., 2005; Ekiz et al., 2005; Vatankhah et al., 2008; Lobo et al., 2009; Rashidi et al., 2011). In these preserving conditions, it has been apparent that the effectiveness of the breeding process in Bulgarian fine fleece sheep will depend on the newly formed genetic diversity and changes in the genetic variance values for the most important productive traits. At this stage, studies of this character haven't been conducted.

The aim of the present study was to analyze the overall genetic variance and effects for the prolificacy trait of sheep from the North-East Bulgarian Merino breed with distinct participation of the Australian Merino and Booroola breeds.

Material and methods

The subject of the study were ewes born in the period 2008–2012, which have a registered productivity based on the prolificacy trait from the main nucleus flock of the North-East Bulgarian Merino breed-Shumen type. The animals were reared in the Agricultural Science Center – Targovishte, a bracnh of the Agricultural Academy system. To improve the quality of the wool and to increase fertility in the period from 1984 to 1994, genetic plasma of the Australian Merino (AM) and Booroola (Bo) breeds was introduced into the herd. It has been established and still exist a genealogical structure and there are currently 7 breeding lines, including purebred NEBM – 2; with a component of Australian Merino – 3 and introduction of the Booroola breed – 2. For more than 30 years, "in-line breeding" has been applied with self-produced rams, using homogeneous selection combined with moderate inbreeding. Ewes were artificially inseminated according to an individual mating plan. Animals were reared on stall-pasture under a semi-intensive scheme. They were inseminated at age of 18 months after the flocks were formed. The breeding process was standard – once a year during the period June–July.

The data for the current research was provided by the Association for Breeding Merinos Sheep in Bulgaria.

Genetic structure of the flock
Based on pedigree book information, pedigrees of 335 sheep were analyzed in terms of the pedigree of the parents and grandparents for each individual up to the 3rd pedigree zone, on the scheme: ♀D(♀(DDDxSDD)x♂(DSDxSSD)) ♂S(♀(DDSxSDS)x♂(DSSxSSS)).

Genotypes have been registered with the participation of: North-East Bulgarian Merino breed (NEBM); Australian Merino (AM); Booroola (Bo) and animals with undetermined origin by one of the direct parents (UP). All available relationships between individuals were established, as a result relation matrix includes 584 individuals (pedigrees), of which 249 were basis and 335 were non-basis. Based on the obtained information, it was found that the genetic structure in the studied flock was formed by 41 genotypes with different breed combinations. There were 315 animals belonging to 33 genotypes with complete pedigree data, and 20 individuals had undetermined origin by one of the direct parents. Depending on blood percentage of the individual breeds in the genotype of each animal, genetic groups in the flock have been identified (Stancheva et al., 2017).

Analysis of the genetic variance and the genetic effects for the prolificacy trait

The total number of registered records for the prolificacy trait of ewes produced from 1st to the 6th lambing was 1123. The data were obtained according to standard methods and guidelines specified in the Instruction for the control of productive traits and the testing of sheep of the Association for Breeding Merino Sheep Breeding in Bulgaria (2008, 2010).

On the basis of analysed information for the breed of parents and ancestors of each sheep was generated a variable with individual information for its genetic origin. This allowed the correct identification of alleles coming from different populations on behalf of Sire or Dam line for the genotype of each animal.

A model based on a common genetic hypothesis was used to determine unaltered variance estimation. The analysis of the present experiment was based on the theoretical expectation that the genetic variance in the studied population was caused by both the additive effect of the individuals and non-additive effects caused by the variation in the different genotypes of the individuals resulting from the crossing of different breeds involved in the formation of pedigrees of every animal.

The statistical analysis is based on an animal model with repeated dimensions of the following characteristics:

$$y = Xb + Zu + e$$

where:

y − Vector of the prolificacy observation of each individual involved in the analysis;

b − Vector of fixed effects (year of each lambing, consecutive lambing, year of birth of the animal, regression effect of age in days to the date of lambing);

u − Random effects vector − genotype expected to evaluate variation caused by non-additive genetic effects (dominant and epistatic), effect of animal with expectation to evaluate variation from additive genetic effect, permanent environmental effect;

e − Random effect of unobserved factors;

X and Z were the corresponding matrices of the variables described.

VCE by Kovac et al. (2008), PEST by Groeneveld et al. (2002) and CBE by Wolf (1996) were used to achieve the above solutions.

Results and discussion

Prolificacy is the main economically significant trait for sheep of all breeds, and according to some authors, the number of lambs born per lambing was more important than the profit generated from the realized lambs (Petrović, 2000). Notter et al. (2000) indicated that fertility also determined the biological performance of sheep in terms of meat, milk and wool productivity. The average value we had obtained for prolificacy was 1.114 lambs from ewe (Table 1) with the specific variation for the trait (29%). Similar values of the animals of the Bulgarian fine fleece breeds have been reported by other researchers. In a study on the phenotypic expression of the main breeding traits for part of the sheep from the fine fleece population in Bulgaria, Tzonev (2014) found similar to our value for the average prolificacy of ewes, produced from 2007 to 2011 (1.119 lambs per ewe) and higher prolificacy

for lambed ewes in 2012 and 2013 – 1.176 and 1.206 lambs born per ewe. For sheep from the Bulgarian fine fleece breeds reared in the institutes of the Agricultural Academy, Stancheva et al. (2015) reported values from 1.070 to 1.180 lambs per ewe in 2012 and from 1.090 to 1.500 lambs per ewe for the sheep produced in 2013. In the reports of ABMSB (2017; 2018), the indicated average sheep prolificacy rate of the fine fleece population was 1.166 lambs per ewe for 2017 and 1.172 lambs for 2018, for the first year animals from Thracian Merino breed had the highest fertility (1.544 lambs), and for the second year, the sheep from the Karnobat Merino breed (1.437 lambs). In both reporting years the sheep from the North-East Bulgarian Merino breed – Shumen type had the lowest biological fertility (1.080 and 1.114 lambs per ewe), but it should be noted here that the animals from Thracian and Karnobat fine fleece breeds were the smallest population from fine fleece breeds, and were reared in only two scientific institutes, and this probably contributes to the full expression of their genetic potential.

It has been known that sheep prolificacy is determined by genetic and non-genetic factors, like age, environmental conditions also had a significant impact on the trait (Rosati et al., 2002; Ekiz et al., 2005; Hanford et al., 2005; 2006; Safari et al., 2005; Vatankhah et al., 2008; Mokhtari et al., 2010; Rashidi et al., 2011; Petrović et al., 2012; Amou Posht-e-Masari et al., 2013; Mohammadabadi and Sattayimokhtari, 2013). Genetic estimates of sheep prolificacy on consecutive lambing were shown in Fig. 1. The results indicate that the number of lambs per ewe are lowest at first lambing – 1.057. At subsequent ages, the value of the trait as a general trend increased (1.104, 1.132, and 1.158 at 2nd, 3rd, and 4th lambing) or remained (1.281 and 1.282 at 5th and 6th lambing, respectively). In contrast to us, Stefanova (2000) found higher average fertility for 1st lambing (1.263 and 1.229) compared to the 2nd lambing (1.120 and 1.180) for the ewes from North-East Bulgarian Merino breed – Shumen type and Dimitrov (2006) for the same flock studied by us, and Stancheva et al. (2015) indicated close values for both ages – 1.230 and 1.260. Higher fertility rate was also reported by Slavov (2007) for the sheep from the North-East Bulgarian Merino breed – (Dobrudzha type) (1.180 and 1.301 lambs of the 1st and 2nd lambing), and Slavova (2000) for the Thracian fine fleece breed (1.182 and 1.398 lambs of the 1st and 2nd lambing), Slavova et al. (2013) and Dimova (2019), which also found increasing of fertility rate from the first to the third lambing and subsequent decrease in the same breed.

Fertility estimates of sheep by the year of there birth indicated a decline in the genetic potential of the sheep (Fig. 2). The highest scores had animals born in 2008 and 2009 (1.163 and 1.117 lambs per ewe), while the estimates of the other three generations are below the average – 1.080, 1.101 and 1.041 lambs born in 2010, 2011 and 2012. Dimitrov (2006) found higher fertility in sheep from the same herd, based on their year of birth (born 1995–2002). The obtained results were most likely due to a narrowing of genetic diversity, long-term selection by phenotype, applied breeding methods of selection under conditions of internal breeding, age structure of the flock and changes in environmental factors in the farm.

The productivity of the sheep, depending on the year of lambing, is shown in Fig. 3. Despite the overall positive trend, the results were multifaceted and correspond to the assumption of change of environmental factors in the farm.

Table 1. General mean for the prolificacy trait, lambs per ewes

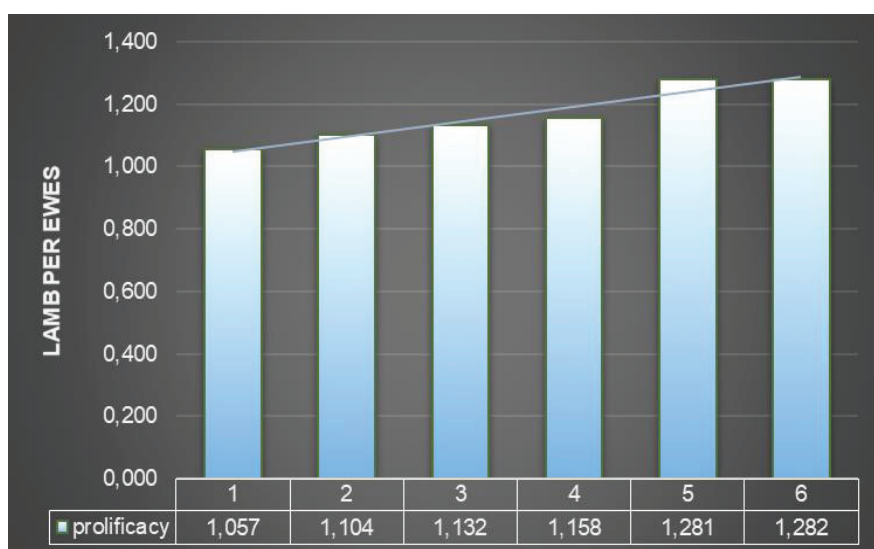| Descriptive statistics	Number
observations	1123
number of base animals	249
number of non-base animals	335
total number of animals	584
min (age of lambing), days	620
max (age of lambing), days	2540
min (lambs per ewes)	1
max (lambs per ewes)	3
mean (lambs per ewes)	1.114
S.D.	0.321
C.V. (%)	29.0

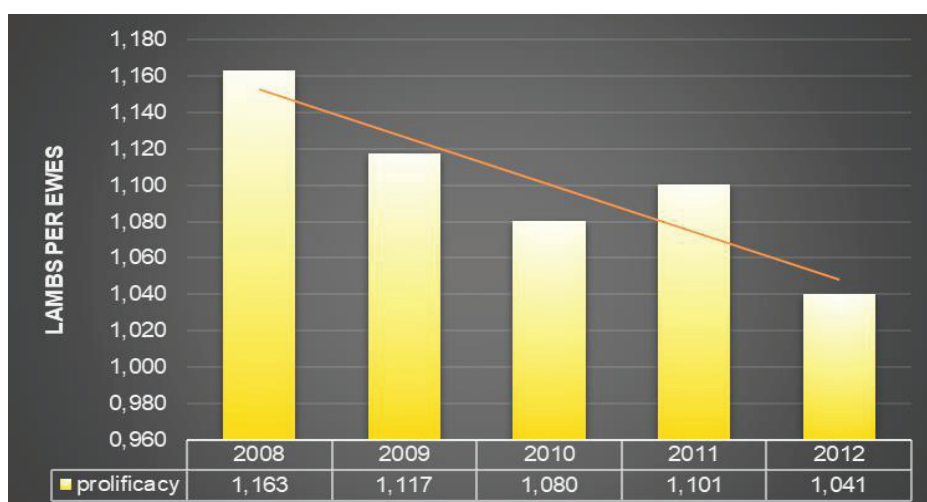**Fig. 1.** Estimates of prolificacy trait by parity of lambing

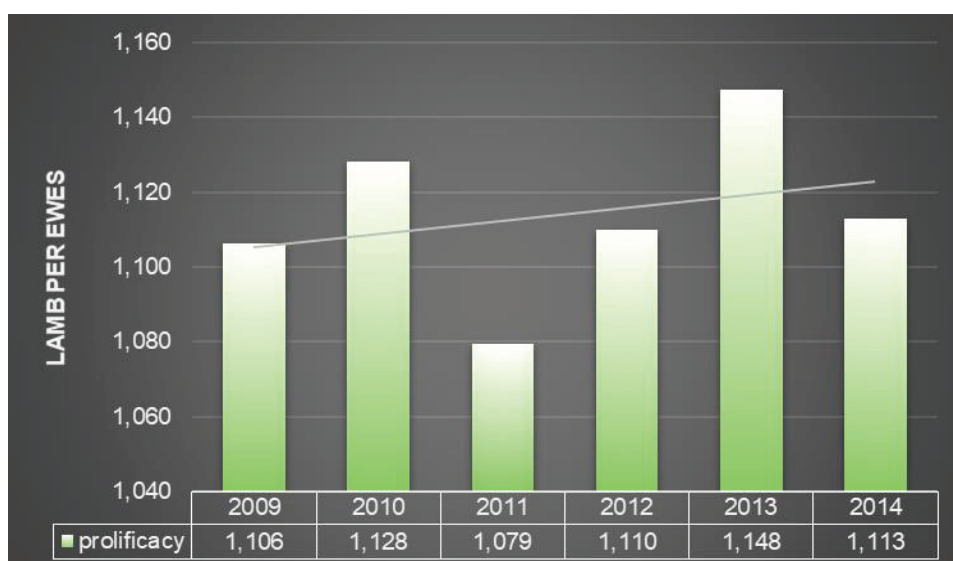**Fig. 2.** Estimates of prolificacy trait by year of birth

Fig. 3. Estimates of prolificacy trait by year of lambing

The highest fertility rate was the lambed ewes in 2010 and 2013 – 1.128 and 1.148 lambs per ewe. Sheep produced in 2012 and 2014 (1.110 and 1.113) were with prolificacy close to the overall average and below the total average were those lambed in 2009 and 2011 (1.106 and 1.079).

The indicated prolificacy values of sheep in the studied flock allowed us to speak out hypothesise that they were also due to the heterogeneity of the genetic variability of the new formed genetic diversity and the specific genetic interactions between the animals, with distinct participation of the separate breeds in the genotype. In the herd structure, purebred animals from North-East Bulgarian Merino sheep breed were 20.3%. Ewes, a product of intra-linear breeding, with a component of AM in the genotype, constitute 59%, with their individual variants distributed within 0.6 to 11.4%. The established overall percentage (7.2%) of the animals from North-East Bulgarian Merino sheep breed with a component of the Booroola breed in the genotype was in the range 0.3 to 3.28%, and individuals whose genotypes were formed with the participation of all three breeds were 7.5% of total (Stancheva et al., 2017). The percentage distribution of sheep from the same flock, born in the years 1995–2002, was in the range of 31.6% for purebreds, 48.8% for those with AM blood and 19.6% for animals from the Booroola breed (Dimitrov, 2006). In the conducted study, the author found that the infusion of blood from the Booroola and AM breeds has led to an increase in the fertility of the sheep of the North-East Bulgarian Merino breed. The highest fertility rates of 1st (1.415) and 2nd (1.375) lambing and with positive deviations (+ 0.156 and + 0.163) were animals from Booroola breed, and sheeps from the AM breed exceeded purebreds by 1.71 % on 1st lambing and 2.87% on 2nd lambing.

The results of the initial variance analysis (Table 2) showed very low levels of genetic variability, which mainly came from the individual ability of the animals – 0.034 at 0.001 for induced from the heterosis variance. This was confirmed by the established proportion of the genetic variance arising from the different breed combination in the genotype (0.002) related to the individual genetic varians (0.257), which reflected the overall genetic variation.

The obtained results did not show great potential for increasing the genetic variance for the fertility trait. Obviously, the heterosis effect of the high prolificacy component of the Booroola breed, introduced more than 25 years ago, was being exhausted and the breeders will have to decide whether to import new genetic plasma or to rely on individual abilities of the animals, improved feeding conditions and organization of the production process.

The estimates of additive genetic effects and non-additive deviations for the fertility trait in the identified genetic groups and genotypes of the smallest count of individuals are summarized in Table 3.

In the purebred genetic group (100% NEBM), a moderate additive effect near the overall average (1.109) and a slight negative non-additive genetic effect (- 0.005) were found.

Ewes with a component of AM are predominant in total and obviously have a significant effect on the fertility trait. In the groups with different levels of participation of the AM breed, the values of additive and epistatic non-additive effect have slight negative and positive deviations (from 1.067 to 1.146 for the first and from - 0.047 to + 0.032 for the second).

At internal breeding with the Booroola breed, a slight positive non-additive genetic effect was

Table 2. Genetic variance and respective ratios for the trait

Source of variation	Variance	Corresponding ratios (h^2)	Standart Error
Residual	0.099	0.743	± 0.013
Animal	0.034	0.257	± 0.013
Genotype	0.001	0.002	± 0.016

Table 3. Estimation of the genetic effects of the different genetic groups

Genetic group	n	Group additive means	Non-additive variance
100% NEBM	68	1.109	- 0.005
87.5% NEBM 12.5% AM	35	1.109	- 0.005
75% NEBM 25% AM	70	1.118	0.004
62.5% NEBM 37.5% AM	56	1.067	- 0.047
50% NEBM 50% AM	37	1.146	0.032
62.5% NEBM 37.5% Bo	14	1.166	0.052
50% NEBM 50% Bo	8	1.039	0.075
75% NEBM 12.5% AM 12.5% Bo	8	1.240	0.126
62.5% NEBM 25% AM 12.5% Bo	5	1.134	0.020
62.5% NEBM 25% Bo 12.5% AM	5	1.150	0.036
50% NEBM 37.5% Bo 12.5% AM	3	0.958	- 0.156
50% NEBM 25% AM 25% Bo	3	1.100	- 0.014
87.5% NEBM 12.5% Bo	2	1.263	0.148
50% NEBM 37.5% AM 12.5% Bo	1	0.956	- 0.158
Unknown pedigree from the side of one of the parents	20	1.147	0.033

observed − + 0.052 (for the group with 37.5% participation from the Bo breed) and + 0.075 (for the group with 50% participation from Bo). However, the established values for additive effects (1.166 and 1.039) and the limited number of these animals give reason to expect that their contribution to increasing fertility will not be significant.

For the more substantially represented groups of animals with participation from the three breeds, the values for the additive and epistatic effects were positive and varies from 1.150 to 1.240 for the first and from + 0.020 to + 0.126 for the second. Their inclusion in the breeding schemes seems to have indicated good combinative ability, but this thesis should not have been favored due to the available exceptions in the groups and in the genotypes of the registered single individuals.

Overall, for the group of animals with unidentified origin by one of the direct parents, the values for the additive and epistatic effects were slightly above the overall average − 1.147 and + 0.033.

Our results corroborate those of Stefanova (2000), Dimitrov (2001, 2006), Slavov (2007) and Slavov et al. (2008), who found that introduced genetic component from Booroola breed has a positive effect on fertility, and the introduction of Australian merino breed has no adverse effect on the same trait for the NEBM breed. However, the performed analyzes have indicated that due to the changed genetic structure and the applied selection schemes, the genetic variability of the fertility trait has greatly reduced. The new formed genetic groups were not clearly differentiated, despite the positive values found for the additive and non-additive genetic effect in animals with Booroola participation in the genotype.

Conclusions

A negative genetic tendency was found for fertility trait, depending on the year of birth of the studied generations, and a positive one in consecutive lambing.

The major part of the genetic variance was described by the individual ability of the animals (0.034 at 0.001) for the heterosis-induced variance. The proportion of genetic variance resulting from different breed combination in the genotype was extremely low relative to the indi-

vidual genetic variance (0.257), which reflected the overall genetic variation.

There were no clearly differentiated differences in estimates of additive and non-additive effects by genetic groups.

Acknowledgements

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