Iranian Journal of Applied Animal Science

Genetic Parameters Estimation of Prolificacy Traits under the FecB Introgression Pressure in Afshari Sheep Breed

Research Article

M. Pourtahmasebian Ahrabi[1], M.P. Eskandarinasab[1*] and M. Bagher Zandi Baghcheh Maryam[1]

[1] Department of Animal Science, Faculty of Agriculture, University of Zanjan, Zanjan, Iran

Received on: 3 Jul 2020
Revised on: 15 Sep 2020
Accepted on: 15 Oct 2020
Online Published on: Jun 2021

*Correspondence E-mail: eskandarinasab_m@znu.ac.ir

ABSTRACT

The aim of present research was to estimate genetic parameters and trends of prolificacy traits in Afshari sheep breed under the FecB gene introgression breeding program. In this research, phenotypic data were collected from 2000 to 2015 at the Research Station of University of Zanjan. The reproductive traits include the total number of lambs born (NLB) and number of lambs at weaning (NLW), and composite traits as total litter weight at birth (TLWB) and total ltter weight at weaning (TLWW). The data were analysed using ASReml software according to restricted maximum likelihood (REML) procedure. The fixed model effects parameters were: year, season, age of ewe. Results showed genetic group and number of parturition in the model were significant ($P<0.05$). The direct heritability estimates for NLB, NLW, TLWB and TLWW were 0.08, 0.08, 0.12 and 0.12, before gene introgression and 0.07, 0.10, 0.08 and 0.12 after gene introgression, respectively. The genetic trend of NLB, TLWB, TLWW and NLW from 2000 to 2006 (before gene introgression) were 0.003 ± 0.002 lambs/year, 0.0005 ± 0.003 g/year, 0.010 ± 0.002 g /year and 0.0003 ± 0.003 lambs/year, respectively and 0.055 ± 0.003 lambs/year, 0.04 ± 0.002 g/year, 0.026 ± 0.004 g/year and 0.005 ± 0.005 lambs/year, respectively from 2007 to 2015 (after gene introgressions cheme). Because of gene introgression breeding scheme implementation and parturition of gene carrying ewes in this research station from 2007 to 2015, the genetic trend was positive with a few fluctuations. The results showed that the insertion and stabilization of the FecB gene caused a significant different in the genetic trend of the prolificacy traits.These results suggest that breeding strategy based on transfer major genes such as FecB and cross breeding for genetic improvement of reproduction efficiency is more effective than the classic phenotypic selection.

KEY WORDS Afshari sheep, breeding strategy, FecB gene, genetic trend, reproductive traits, variance components.

INTRODUCTION

Indigenous breeds of any country are considered as national capital and strategic reserves in the economy and prosperity of that country (Esmaeili Fard *et al.* 2019). There are more than 50 million sheep in Iran, including 27 breeds that have adapted to different regions (Zamani *et al.* 2015; Mohammadabadi, 2017).

The Afshari sheep breed is one of the most crucial sheep breeds in Iran for meat production, also well performed in milk production (Karamiyanfili, 2014). The numerous population and distribution area of Afshari sheep is located in Zanjan province. This breed has a high prolificacy between other indigenous sheep breed. Lambing is an essential source of income in all flocks so increasing the fecundity of the Afshari sheep has always been a vital breeding goal (Pourtahmasebian Ahrabi *et al.* 2020).

A crucial biological component in meat production is the reproductive traits (Esmailizadeh *et al.* 2009) so improving reproduction in ewes is a great objective in the sheep industry, partly because of the increased number of lambs or the weight of lambs to be weaning per ewes (Maxa *et al.* 2007; Afolayan *et al.* 2008). The highest income from sheep breeding is generated by lamb production, and its efficiency is possible through reproductive and maternal capacities and lactation production (Latifi *et al.* 2019). Selection program is being implemented to progress meat production in the Afshari sheep breed. Increasing the litter size per ewe is the main objective, but the possible response to the weight of lambs should be considered (Mohammadi *et al.* 2013).

Genetic variance in traits (known traits but also unknown traits of possible future use) should be conserved (Abdoli *et al.* 2019). Therefore, one way to conservation of genetic resources is to focus on reproductive traits improvement of local sheep breed until their breeding would be economically affordable. Thus, reproductive efficiency is an essential factor in the sheep breeds and reproductive traits are one of the most important traits affecting the profitability of Afshari sheep breeding systems because this breed has a good maternal genetic potential to introgression and stabilize the FecB gene (Heidari, 2007). Due to the low heritability of reproductive traits based on research in different breeds are affected not only by additive genetic effects, but also affected by the combination of maternal additive and permanent environmental effects, therefore genetic improvement for these traits is difficult and achievement to genetic progress is slow (Gholizadeh and Ghafouri Kesbi, 2015).

Gene transfer can be a good strategy to introduce new alleles and increase genetic progression (Hospital *et al.* 1992; Latifi *et al.* 2018). Gene transfer involves a set of back crosses between a breed containing the desired alleles and a native breed which leads to an increase in heterozygous sheeps and ultimately a cross between heterozygous individuals leads to the creation of homozygous sheeps to establish desirable alleles (Koudande *et al.* 2000; Valipourkoutanaee *et al.* 2019).

One of the most important factors for the efficiency of the breeding program in improving prolificacy traits is selection whithin population and cross breeding (Latifi *et al.* 2019). Cross breeding includes breed synthesis and gene transfer. Crossbreeding between two or more breeds and interbreeding is called breed synthesis. In general, the goals of breed synthesis include creating high longevity breeds, increasing lambing, increasing growth rate and improving carcass quality (Petrovic *et al.* 2013; Mirzamohammadi *et al.* 2014). In this regard, the first gene itrogression project in Afshari sheep breed was started parturition of carrying ewes in 2007 at the University of Zanjan with the collaboration of Jihad-e-Agriculture Organization of Zanjan province (Sepehri, 2016). The breeding scheme began with the import of Booroola merino semen from New Zealand. This breed is a combination of 75% Romney and 25% Merino that contains the FecB gene associated with the litter size and is located on chromosome 6 in sheep (Karamiyanfili, 2014).

The low heritability of reproductive traits and the desire to produce more lambs per ewe for meat have led to many crossbreeding programs seeking to obtain the benefits of the Booroola gene (Fogarty, 2009; Sepehri, 2016). Booroola Merino sheep carry a major autosomal mutation of the FecB gene which has a significant effect on litter size (Ekiz *et al.* 2005).

It is an additive effect, so one copy of the gene causes an additional lamb born per ewes and two copies inherited from both parents means an extra 1.5 lambs born per ewes (Abdoli *et al.* 2016; Falconer, 1989). Genetic strategies based on improving the profitability of Afshari sheep breed have generally focused on reproduction traits (Ghaffari *et al.* 2009).

Determining the genetic parameters is essential not only to conserve the indigenous breeds, but also to determine the breeding goals and design of genetic breeding programs and well understanding the genetic mechanisms of traits. Estimating the genetic parameters and genetic trends also enables the selection of methods and reveals the roles of genetic and environmental factors such as nutrition, health and reproduction (Mahdavi *et al.* 2014). Genetic improvement of the total number of lambs born (NLB) and number of lambs at weaning (NLW), and composite traits as total litter weight at birth (TLWB) and total ltter weight at weaning (TLWW) traits via selection of best animals as a next generation parents requires the genetic parameters estimation of the traits, so the aim of this study was to estimate the (co)variance components, genetic parameters and genetic trends of basic and composite reproductive traits of Afshari sheep breed with the FecB gene introgression at the university of Zanjan research station.

MATERIALS AND METHODS

In this study, phenotypic data were collected from 2000 to 2015 at the University of Zanjan research station. The number of data for the analyses included 3314 observations. Traits were including the basic traits as NLB and NLW, and TLWB and TLWW and the number of records per traits were 1750, 1669, 929, and 728, respectively.

The variance components of the traits were estimated by restricted maximum likelihood method via ASReml software (Gilmour *et al*. 2000) with the six different animal model as Table 1 and Pedigree was checked with CFC 1.0 software (Sargolzaei and *et al*. 2005). Threshold model was used to analysis the NLB and NLW traits. To perform test of significance ($P<0.05$) between fixed effects using the generilized linear model (GLM) via SAS software (SAS, 2005).

The averages of these traits between the two periods (before the FecB gene introgression and after the FecB gene introgression) were compared by GLM procedure of SAS software. The weaning age was considered as three months at age.

Akaike information criterion (AIC) was used to select the appropriate model by using the following equation:

$$AIC= -2Log\ L+ 2p$$

Where:
Log L: logarithms of the correct function of each model.
p: number of parameters in each model (Dobson, 1991).

Repeatability (r) was calculated as:

$$r= (\sigma^2_a+\sigma^2_{pe}) / \sigma^2_p$$

The parameters for analysis were also estimated by the convergence criterion of 10^{-8}. Annual genetic progress for each trait was calculated by the regression coefficient of ewes breeding values on their birth year. The genetic trend of these traits between the two periods (before the FecB gene introgression and after the FecB gene introgression) were compared by generalized linear model (GLM) procedure of SAS software.

RESULTS AND DISCUSSION

The structure of the data is showed in Table 2. The mean and standard deviation of NLB, TLWB, TLWW and NLW were 1.35 ± 0.57, 4.74 ± 0.75, 36.4 ± 7.10 and 1.36 ± 0.54, respectively before gene intogression and 1.59 ± 0.57, 4.91 ± 0.75, 36.9 ± 7.10 and 1.42 ± 0.54, respectively after gene intogression.

Fixed effecte were the year at 16 levels (2000 to 2015), season at 4 levels, age of ewe at lambing with 5 levels (2, 3, 4, 5 and more than 6 years), genetic group at 5 levels (Pure Afshari, 50% Afshari (F1), 75% Afshari (F2), 87.5% Afshari (F3) and 93.75% Afshari (F4)) and number of parturition at 6 levels were significant ($P<0.05$) for all traits. The effect of interactions between the fixed effects was not significant ($P>0.05$) and it was excluded from the model which corresponded to the results of other studies (Heidari, 2007; Karamiyanfili, 2014).

The estimated of AIC for all traits were presented in Table 3. The lowest AIC value between models as result as best model selection, the models number 6, 2, 6 and 2 were selected as best model for the NLB, TLWW, TLWB and NLW traits, respectively. The estimation of genetic parameters is presented in Table 4. Based on the fitting model, the genetic parameters estimated for NLB, TLWB, TLWW, and NLW traits with model number 6, 2, 6 and 2, respectively. The direct genetic and maternal heritability and permanent ratio for the traits were low to moderate.

Genetic trends have been evaluated annual genetic change in each reproductive trait during the period of 16 years and presented in Table 5 and Figures 1 to 4. Figure 5 showed the phenotypic trend for NLB trait. These figures showed the genetic and phenotypic trends at two periods including before the FecB gene introgression (a, between years from 2000 to 2006) and after the FecB gene introgression (b, between years from 2007 to 2015).

The mean and standard deviation of NLB, TLWB, TLWW and NLW were 1.35 ± 0.57, 4.74 ± 0.75, 36.4 ± 7.10 and 1.36 ± 0.54, respectively before gene intogression and 1.59 ± 0.57, 4.91 ± 0.75, 36.9 ± 7.10 and 1.42 ± 0.54, respectively after gene intogression. Which these parameters are more than the reported result by Mohammadi *et al.* (2012) in Shal sheep and they estimate 1.26 ± 0.36, 1.05 ± 0.48, 5.6 ± 1.73 and 30.51 ± 8.40, respectively. In Baluchi sheep, Jafaroghli *et al.* (2019) reported 1.27 ± 0.44, 5.6 ± 1.66, 28.4 ± 9.22 and 1.28 ± 0.46 for the mean and standard deviation of NLB, TLWB, TLWW and NLW, respectively.

The introgression of FecB gene in Afshari sheep breed increased the average litter size. As shown in Table 2, the average of traits for both scheme including first period (a) and the second period (b) are significantly different ($P<0.05$). Significant mean comparisons between two periods showed that FecB gene transfer and its fixation had a great role to increase the average of all traits.

The coefficients of variation of traits were from 15.56 to 41.13. The coefficient of variation for NLB was 41.13%, shows that NLB was more diverse than the other traits, and indicates the high impact of environmental factors on this trait. The small variation was in TLWB, which is probably due to the small impact of environmental effects on this trait. The reported coefficients of variation of NLB, TLWB and TLWW in Moghani sheep were 29.49, 28.55 and 28.76, respectively (Nayeri, 2013) and it is more divers from this study.

The effects of the year based on climate change, postures of rangelands, breeding management, ewe's breed and feeding lambs has an effect on sheep reproduction performance (Rashidi *et al*. 2008).

Table 1 Details of six different fitted models with or without the covariances

1	$\mathbf{y= Xb + Z_1a + e}$	
2	$\mathbf{y= Xb + Z_1a + Z_3c + e}$	
3	$\mathbf{y= Xb + Z_1a + Z_2m + e}$	$Cov(a,m)=0$
4	$\mathbf{y= Xb + Z_1a + Z_2m + e}$	$Cov(a,m)=A\sigma_{am}$
5	$\mathbf{y= Xb + Z_1a + Z_2m + Z_3c + e}$	$Cov(a,m)=0$
6	$\mathbf{y= Xb + Z_1a + Z_2m + Z_3c + e}$	$Cov(a,m)=A\sigma_{am}$

y: vectors of observations; b: fixed effects; a: direct additive genetic effects; m: maternal additive genetic effect; c: permanent environmental effects of ewes and e: residual random effects, respectively.

X, Z_1, Z_2 and Z_3: design matrices relating the corresponding effects to observations and A: numerator relationship matrix.

Table 2 The descriptive statistics for reproductive traits in Afshari sheep breed in two period of FecB introression program

Traits	**Number of records**	**Average**		**P-value**	**Standard error**	**Range**	**CV (%)**
		Before	After				
NLB (lambs/year)	1750	1.35^b	1.59^a	0.004	0.57	1-4	41.13
TLWB (g/year)	929	4.74^b	4.91^a	0.005	0.75	2.5-17.5	15.56
TLWW (g/year)	728	36.4^b	36.9^a	0.03	7.10	8.55-99.3	19.39
NLW (lambs/year)	1669	1.36^b	1.42^a	0.02	0.54	0-4	38.84

NLB: number of lambs born; TLWB: total litter weight at birth; TLWW: total litter weight at weaning and NLW: number of lambs at weaning.

CV: coefficient of variation.

Table 3 Estimates the akaike information criterion (AIC) in 6 different models

Model	**Traits**			
	NLB (lambs/year)	TLWB (g/year)	TLWW (g/year)	NLW (lambs/year)
Model 1	-570.658	-365.366	10891.44	-965.44
Model 2	28.9858	-443.458	**10843***	**-970.32***
Model 3	-596.668	-445.366	10862.34	-968.11
Model 4	-601.240	-443.696	10862.2	-966.34
Model 5	-605.72	-449.402	10844.63	965.24
Model 6	**-606.75***	**-468.794***	10846.63	969.01

NLB: number of lambs born; TLWB: total litter weight at birth; TLWW: total litter weight at weaning and NLW: number of lambs at weaning.

* ($P<0.05$).

Table 4 Variance components, genetic and phenotypic parameters estiamtion of reproductive traits in Afshari sheep breed

Traits	**NLB**	**TLWB**	**TLWW**	**NLW**
Model	6	6	2	2
σ^2_a	0.021	1.74	1.93	0.06
σ^2_m	0.017	1.47	-	-
σ^2_{pe}	0.026	1.70	1.07	0.02
σ^2_e	0.224	17.51	13.21	0.49
σ^2_p	0.29	22.42	16.21	0.57
h^2	0.07±0.04	0.08±0.02	0.12±0.02	0.10±0.04
m^2	0.06±0.04	0.06±0.01	-	-
c^2	0.09±0.03	0.07±0.03	0.07±0.03	0.03±0.04
r	0.16	0.15	0.18	0.14

NLB: number of lambs born; TLWB: total litter weight at birth; TLWW: total litter weight at weaning and NLW: number of lambs at weaning.

σ^2_a: additive genetic variance; σ^2_m: maternal additive genetic variance; σ^2_{pe}: permanent environmental variance; σ^2_e: residual variance; σ^2_p: phenotypic variance; h^2: direct heritability; m^2: maternal heritability; c^2: ratio of permanent environmental variance on phenotypic variance and r: repeatability.

Table 5 Genetic trend[1] of reproductive traits in Afshari sheep breed

Trait	**Genetic trend ± SE**		**P-value**
	Before	after	
NLB (lambs/year)	$0.003±0.002^b$	$0.055±0.003^a$	0.003
TLWB (g/year)	$0.0005±0.003^b$	$0.04±0.002^a$	0.004
TLWW (g/year)	$0.010±0.002^b$	$0.026±0.004^a$	0.03
NLW (lambs/year)	$0.0003±0.003^b$	$0.005±0.005^a$	0.02

[1] Genetic trend: before the FecB introression program and after the FecB introression program.

NLB: number of lambs born; TLWB: total litter weight at birth; TLWW: total litter weight at weaning and NLW: number of lambs at weaning.

Age of ewe is effective on pre-weaning traits. Lambs born of young ewes are less likely to be weaned than those born of older dams. The significant impact of age of dam effect is probably related to the degree of physical growth, body weight, reproductive system and milk production by the dam for older ewes (Fogarty, 1995). Furthermore, lamb production in dams usually increases until 4 to 5 years of age which it decreases significantly. Thus, lambs from these ewes show a higher growth rate due to adequate nutrition than lambs born of two-year-old dams. Therefore, environmental factors explain a significant part of the diversity in this study.

In general, increased age of the ewe, especially after of four years, improved the TLWB and TLWW traits. Part of these differences is due to maternal effects, lactation and dam behaviour at different ages due to the significant effects of ewes (Zhang *et al.* 2009; Mohammadi *et al.* 2012; Abdoli *et al.* 2019). The heritability for NLB was estimated with 6 different models and estimates 0.02 to 0.11, which model number six was selected as the best model with the lowest AIC. The direct genetic heritability and maternal heritability for this trait were estimated 0.07 and 0.06, respectively, which corresponds to different reported diverse breeds in the range from 0.04 to 0.09 (Rao and Notter, 2000; Nayeri, 2013). Genetic parameters estimation of reproduction traits in different sheep populations has different results and its heritability has been reported in various studies (Safari *et al.* 2005; Hanford *et al.* 2006; Rashidi *et al.* 2011). Heritability for NLB, TLWB, TLWW in Lori Bakhtiari sheep breed were reported 0.10, 0.12 and 0.10, respectively (Vatankhah *et al.* 2008) whereas it was 0.07, 0.08 and 0.12 in this study, also the permanent maternal environments for NLB was estimated was 0.026, which is consistent with the reported parameters in Chaious (0.028), Merino (0.025), Romanov (0.05) and 0.026 in Moghani sheep breeds (Rao and Notter, 2000; Bromley *et al.* 2001; Van wyk *et al.* 2003; Nayeri, 2013).

The estimated heritability of NLB and NLW, and TLWB and TLWW were 0.01, 0.03, 0.06 and 0.18, respectively in Kermani sheep breed (Mokhtari *et al.* 2010). Mohammadi *et al.* (2012) reported the heritability of NLB 0.13 in Shall sheep and Karamiyanfili (2014) reported 0.15 in Afshari sheep. Van wyk *et al.* (2003) estimated the heritability 0.059 for NLB, which is consistent with the results of this study. In Balochi sheep breed, the heritability for the NLB was 0.2 (Mokhtari *et al.* 2010), which is higher than the result of the present study. These differences can be attributed to differences in the various breeds and population sample size as well as applied models for genetic parameter estimations. The heritability for NLW in this study was 0.10. The range of estimated heritability regarding NLB and NLW in the various studies were reported from 0.01 to 0.18 and 0.10 to 0.18, respectively (Rao and Notter, 2000; Hanford *et al.* 2003; Vanimisetti *et al.* 2007; Rashidi *et al.* 2008).

Hanford *et al.* (2003) reported the direct heritability for NLW in Targhee sheep 0.07, which is less than result of the present study. The heritabilty of NLW was 0.02 for Polypay sheep breed (Rao and Notter, 2000) and 0.133 for Dormer sheep breed of south Africa (Van wyk *et al.* 2003), and 0.09 for Moghani sheep breed (Mohammadi *et al.* 2012).

The TLWB is a combination of number of lambs born and weight of lambs in each parity and represents ewe capacity to produce weight of lambs regardless of the number of lambs (Vatankhah *et al.* 2008; Mirzamohammadi *et al.* 2014).

The estimated direct and maternal heritability of TLWB were 0.08 and 0.06, respectively. The range of heritability for this trait was 0.046 to 0.4 and it has been reported in various studies (Van wyk *et al.* 2003; Mokhtari *et al.* 2010; Mohammadi *et al.* 2012). Mokhtari *et al.* (2010), Nayeri (2013), Vatankhah *et al.* (2008) and Karamiyanfili (2014) reported the heritability for TLWB was 0.06, 0.07, 0.10 and 0.14 respectively for Kermani, Moghani, Lori Bakhtiari and Afsharisheep breeds. The permanent maternal environments for TLWB estimated was 0.07, which is consistent with the reported value 0.08 in Shall sheep breed (Mohammadi *et al.* 2012).

The estimated heritability for TLWW was 0.12. In the present study, a higher heritability was estimated for TLWW than the TLWB, which indicates that selection based on total litter weight at weaning rather than total litter weight at birth is more effective. The heritability range of this trait has been reported from 0.025 to 0.17 (Mokhtari *et al.* 2010; Vatankhah *et al.* 2008; Rashidi *et al.* 2011).

The TLWW can be the basis for selection, since this trait represents the total production of an ewe per weight of lamb produced per parity and the estimated heritabilty was 0.12. Matika *et al.* (2003) reported heritability for TLWW equal to the present study (0.12). Mokhtari *et al.* (2010), Vatankhah *et al.* (2008), Mohammadi *et al.* (2012) and Nayeri (2013) reported the heritability for this trait invarious range 0.18, 0.12, 0.11 and 0.14, respectively in kermani, Lori Bakhtiari, Shal and Moghani sheep breeds. The permanent maternal environments (c^2) for TLWW estimated 0.07, which is consistent with the reported value of 0.06 and 0.04 in Shall and Dorset sheep breeds, respectively (Mohammadi *et al.* 2012; Petrovic *et al.* 2013). Increasing lamb production will not be adequate by lamb numbers alone, because the weight of each lamb is not taken into account of lambs, so the weight of lambs weaned per ewe is a complete trait that affected by the fertility of the ewe, the number of lambs born and the performance of the lambs from birth to weaning.

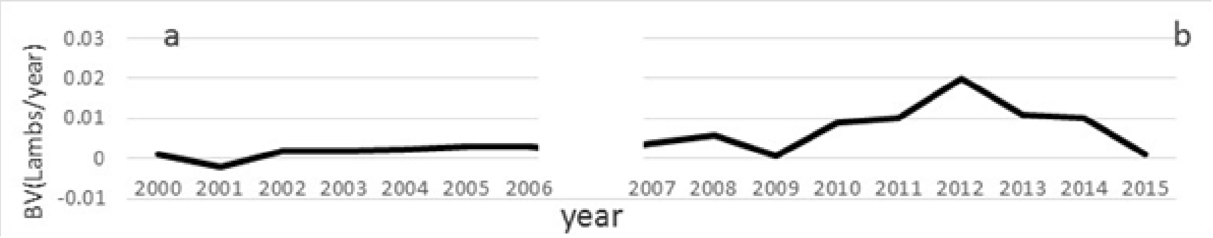

Figure 1 Genetic trend for number of lambs born (NLB) trait before the FecB gene introgression (a) to after the FecB gene introgression (b)

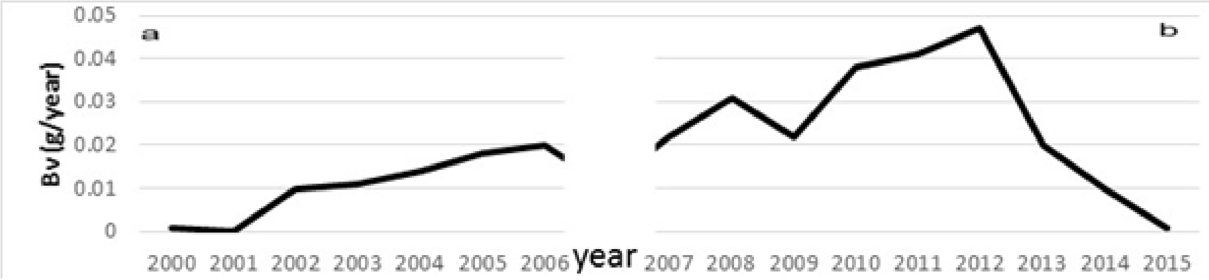

Figure 2 Genetic trend for total litter weight at weaning (TLWW) trait before the FecB gene introgression (a) to after the FecB gene introgression (b)

Figure 3 Genetic trend for number of lambs at weaning (NLW) trait before the FecB gene introgression (a) to after the FecB gene introgression (b)

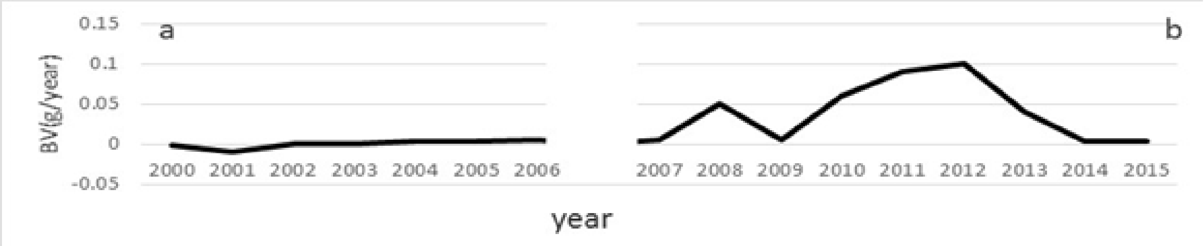

Figure 4 Genetic trend for total litter weight at birth (TLWB) trait before the FecB gene introgression (a) to after the FecB gene introgression (b)

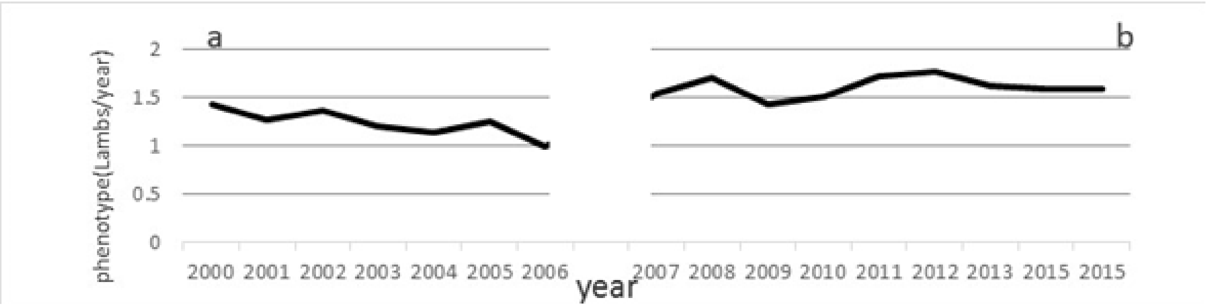

Figure 5 Phenotypic trend for number of lambs born (NLB) trait before the FecB gene introgression (a) to after the FecB gene introgression (b)

Therefore, this trait is the most important factor in specify the production of ewes and also in the economic efficiency of lambs (Abdoli *et al.* 2016).

The repeatability of reproductive traits is low to moderate because of their genetic backgrounds and the nature of these traits. Therefore, in order to increase herd performance, the decision to remove ewes based on a record of reproductive traits had a little accuracy (Mohammadi *et al.* 2013; Pourtahmasebian Ahrabi *et al.* 2020). Estimated repeatability were 0.16, 0.15, 0.18, and 0.14 for NLB, TLWB, TLWW, and NLW respectively. Estimated repeatability of TLWW and NLB were higher than other traits, thus the selection accuracy for these traits would be high via the first NLB record and measures as correlation between performance records in repeated parturition of the ewe, which is agreement with previous studies. Mohammadi *et al.* (2012) reported the repeatability values for NLB, TLWB, TLWW and NLW was 0.17, 0.15, 0.17 and 0.13, respectively in Shall sheep breed. Nayeri (2013) reported the repeatability for NLB, TLWB, TLWW and NLW was 0.13, 0.16, 0.14 and 0.14, respectively in Moghani sheep. Amou Poshte Masari *et al.* (2013) reported 0.02. 0.01, 0.27 and 0.03 in Shall sheep for repeatability of NLB, NLW, TLWB and TLWW, respectively. Karamiyanfili (2014) reported the 0.21, 0.19 and 0.22 for repeatability of TLWB, TLWW and NLW traits respectively. Ekiz *et al.* (2005) estimated 0.124, 0.079, 0.077 and 0.088 for repeatability of NLB, NLW, TLWB and TLWW respectively in Turkish Merino sheep, which is less than the results of the present research. The slight effect of permanent environment can be explained by the negative correlation between litter size and reproduction during reproductive years (Mortazavi *et al.* 2014). If an ewe has a higher number of lambs born per year, stress during pregnancy and lactation lead to decreased litter sizes over the years then the impact of animal permanent environment (Heidari, 2007; Jafaroghli *et al.* 2019).

Genetic trends need to be studied when the goal of measuring breeding programs applied to sheep breeding system over a given period of time (Rashidi *et al.* 2011). The average of estimated breeding values (BV) for NLB, TLWB, TLWW and NLW showed a slightly positive trend (Figures 1 to 4), and demonstrate that those traits had been taken into consideration in the breeding objectives for Afshari sheep breed. The genetic trend of the NLB trait shows that this trait has been improved since the year 2001. Since the introgression of FecB gene scheme in the ewes of university of Zanjan herd in 2007, the trend has been increased. In the year 2009, due to the abortions some of F1 ewes because of intolerance to the injection of the brucellosis vaccine, strong heat stress in Zanjan province in August 2009 and their displayed sensitivity to Agalaxia caused a less genetic trend in this year, although due to the birth of F2 and F3 lambs in 2012 the trend was improved but with the selling of some carrier gene ewes in this herd after 2012, the genetic trend has been declined. Mortazavi *et al.* (2014) reported a genetic trend of NLB trait with 0.016 lambs per year till to 1996 then after this time they reported a negative genetic trend of -0.012 lambs per year for Iranian Black sheep breed. These researchers stated that considerable changes in genetic trends before and after 1996 with lack of a specified breeding strategy for these sheep at Abbas Abad station. Aguirre *et al.* (2017) reported a negative genetic trend for NLB, TLWB and NLW in Brazilian Santaines sheep breed because these traits were not included in the their farm breeding objectives. The genetic trend of NLB, TLWB, TLWW and NLW from 2000 to 2006 (before gene introgression) were 0.003 ± 0.002 lambs/year, 0.0005 ± 0.003 g/year, 0.010 ± 0.002 g/year and 0.0003 ± 0.003 lambs/year, respectively and 0.055 ± 0.003 lambs/year, 0.04 ± 0.002 g/year, 0.026 ± 0.004 g/year and 0.005 ± 0.005 lambs/year, respectively from 2007 to 2015 (after gene introgression scheme). The phenotypic trend from 2000 to 2006 (before gene introgression) for NLB was 1.32 and 1.66 lambs/year from 2007 to 2015 (after gene introgression). Baneh *et al.* (2020) by doing research in Iranblack sheep during 1980 to 2004, reported the genetic trends for NLB, TLWB, TLWW and NLW were 0.010 ± 0.001 (lambs/year), 0.027 ± 0.002 (g/year), -0.004 ± 0.002 (g/year) and 0.010 ± 0.001 (lambs/year), respectively. The genetic trends values of the present research due to the introgression of the FecB gene are higher than the values of recent study. Research has shown that if the goal is to introduce a major gene into native breeds used of traditional gene assisted selection can increase the abundance of the major genes as much as gene assisted genomic selection (Latifi *et al.* 2019). As shown in Table 5, the genetic trend of studied traits for both scheme including first period (a) and the second period (b) are significantly different ($P<0.05$). Significant mean comparisons between two periods showed that FecB gene transfer and its fixation had a great role to increase the genetic trend of all traits. Due to conducted a gene introgression scheme on the Afshari sheep breed of this herd, semen transfers from the foreign country, various management, different recording procedure, elimination and select for commercialization the ewe's carrier FecB gene in 2012 and also because of F1 ewe's abortion in 2009, the genetic trend had a positive value with some fluctuation.

CONCLUSION

Small estimated vluse of heritability and repeatability parameters for NLB, TLWB and NLW indicate that phenoltypic selection for these traits doesn't led the significant genetic improvement of reproductive efficiency in Afshari sheep breed. Therefore, in order to improve these traits, the use of molecular genetics and marker assisted selection such as major genes (FecB) and back crosses between cross breeds of Afshari booroola and Afshari ewes for introre-gression and stabilization the FecB gene is essential to enhancing genetic progression. Of course, consideration of environmental factors is really necessary. However, the high heritability estimates for TLWW compared to other traits studied showed that direct selection based on this trait could be more effective. Nevertheless, the strategy selection based on FecB gene itrogression along with the other traits such as NLB and TLWW can lead more lambs production and it was welcomed by sheep farmers to increase the litter size in their herds.

ACKNOWLEDGEMENT

The author are grateful to the University of Zanjan research station staff and the deputy Animal Science department of Jihad-e-Agriculture Organization of Zanjan province for their cooperation in providing the data and all their collaborations.

REFERENCES

Abdoli R., Zamani P., Mirhoseini S.Z., Ghavihossenzadeh N. and Almasi M. (2019). Genetic parameters and trends for litter size in Markhoz goats. *Rev. Colomb. Sci. Pecu*. **32,** 58-63.

Abdoli R., Zamani P., Mirhoseini S.Z., Ghavihossenzadeh N. and Nadri S. (2016). A review on prolificacy genes in sheep. *J. Rep. Domest. Anim*. **51,** 631-637.

Afolayan R.A., Fogarty N.M., Gilmour A.R., Ingham V.M., Gaunt G.M. and Cummins L.J. (2008). Reproductive performance and genetic parameters in first cross ewes from different maternal genotypes. *J. Anim. Sci*. **86,** 804-814.

Aguirre E.L., Mattos E.C., Eler J.P., BarretoNeto A.D. and Ferraz J.B. (2017). Genetic parameters and genetic trends for reproductive traits of santa Ines sheep kept in extensive environments in Brazil. *J. Anim. Sci. Livest. Prod*. **1,** 1-7.

Amou Poshte Masari H., shadparvar A.A. and Ghavihosseinzadeh N. (2013). Estimation of genetic parameters for reproductive traits in shall sheep. *Trop. Anim. Health Prod*. **45,** 1259-1263.

Baneh H., Ahmadpanah J. and Mohammadi Y. (2020). Genetic analysis of reproductive characteristics in Iran-Black sheep. *Acta Sci. Anim. Sci*. **42,** 23-32.

Bromley C.M., Van Vleck L.D. and Snowder G.D. (2001). Genetic correlations for litter weight weaned with growth, prolificacy, and wool traits in Columbia, Polypay, Rambouillet and Targhee sheep. *J. Anim. Sci*. **79,** 339-346.

Dobson A.J. (1991). An introduction to Generalized Linear Models. Champman and Hall, London, United Kingdom.

Ekiz B., Ozcan M., Yilmaz A. and Ceyhan A. (2005). Estimates of phenotypic and genetic parameters for ewe productivity traits of Turkish Merino (Karacabey Merino) sheep. *Turkish J. Vet. Anim. Sci*. **29,** 557-564.

Esmaeili Fard S.M., Hafezian S.H., Gholizadeh M. and Abdolahi Arpanahi. R. (2019). Gene set enrichment analysis using genome wide association study to identify genes and biological pathways associated with twining in Baluchi sheep. *Anim. Prod. Res*. **8,** 63-80.

Esmailizadeh A.K., Dayani O. and Mohair M.S. (2009). Lambing season and fertility of fat-tailed ewes under an extensive production system are associated with live weight and body condition around mating. *Anim. Prod. Sci*. **49,** 1086-1092.

Falconer D.S. (1989). Introduction to Quantitative Genetics. Longman, London, United Kingdom.

Fogarty N.M. (1995). Genetic parameters for live weight, fat and muscle measurements, wool production and reproduction in sheep. *Anim. Breed*. **63,** 101-143.

Fogarty N.M. (2009). A review of the effects of the Booroola gene (FecB) on sheep production. *Small Rumin. Res*. **85,** 75-84.

Ghaffari M., Nejati Javaremi A. and Rahimi Mianji G. (2009). Lack of polymorphism in the oocyte derived growth factor (*GDF9*) gene in the Shal breed of sheep. *South African J. Anim. Sci*. **39,** 335-360.

Gholizadeh M. and Ghafouri Kesbi F. (2015). Estimation of genetic parameters for growth related traits and evaluating the results of a 27-year selection program in Baluchi sheep. *Small Rumin. Res*. **130,** 8-14.

Gilmour A.R., Bullis B.R., Welham S.J. and Thompson. R. (2000). ASReml Reference Manual. NSW Agriculture Biometric Bulletin. No.3. Orange Agriculture Institute, Orange, Australia.

Hanford K.J., Van Vleck L.D. and Snowder G.D. (2003). Estimates of genetic parameters and genetic change for reproduction, weight and wool characteristics of Targhee sheep. *J. Anim. Sci*. **81,** 630-640.

Hanford K.J., Van Vleck L.D. and Snowder G.D. (2006). Estimates of genetic parameters and genetic trend for reproduction, weight, and wool characteristics of Polypay sheep. *Livest. Sci*. **102,** 72-82.

Heidari L. (2007). Estimation of genetic parameters of growth and reproduction traits in Zandi sheep. MS Thesis. University of Zanjan, Zanjan, Iran.

Hospital F., Chevalet C. and Mulsant P. (1992). Using markers in gene introgression breeding programs. *Genetics*. **132,** 1199-1210.

Jafaroghli M., Safari A., Shadparvar A. and Ghavi Hossein-Zadeh N. (2019). Genetic analysis of ewe productivity traits in Baluchi sheep. *Iranian J. Appl. Anim. Sci*. **9,** 651-657.

Karamiyanfili M. (2014). Study genetic trend of growth and reproductive traits of afshari sheep of zanjan university. MS Thesis. University of Zanjan, Zanjan, Iran.

Koudande O.D., Iraqi F., Thompson P.C., Teale A.J. and Van Arendonk J.A.M. (2000). Strategies to optimize marker assisted introgression of multiple QTL. *Mam. Genome*. **11,** 145-150.

Latifi M., Rashidi A., Abdolahi Arpanahi R. and Razmkabir M. (2019). Comparison of introgression and synthetic breed strategies for litter size trait in sheep using computer simulation. *Res. Anim. Prod*. **10,** 112-119.

Latifi M., Rashidi A., Abdolahi Arpanahi R. and Razmkabir M. (2018). Assessment of classical and genomic selection methods for introgression a major gene in sheep using simulation. *Anim. Sci. J. (Pajouhesh and Sazandegi)*. **124,** 171-182.

Mahdavi M., Nanekarani S. and Hosseini S.D. (2014). Mutation in *BMPR-IB* gene is associated with litter size in Iranian Kalehkoohi sheep. *Anim. Rep. Sci*. **147,** 93-98.

Matika O., Van wyk J.B., Erasmus G.J. and Baker R.L. (2003). Genetic parameter estimatesinSabi sheep. *Livest. Prod. Sci*. **79,** 17-28.

Maxa J., Norberg E., Berg P. and Pederson J. (2007). Genetic parameters for growth traits and litter size in Danish Texel, Shropshire, Oxford Down, and Suffolk. *Small Rumin. Res*. **68,** 312-317.

Mirzamohammadi E., Rashidi A., Vatankhah M. and Jafari M. (2014). Evaluation of inbreeding effects on pre -weaning growth traits and lamb survival in Iran-Black sheep. *Anim. Sci. J. (Pajouhesh and Sazandegi)*. **101,** 62-70.

Mohammadabadi M.R. (2017). Role of clostridium perfringens in pathogenicity of some domestic animals. *J. Adv. Agric*. **7,** 1117-1121.

Mohammadi H., Moradi Shahrebabak M. and Moradi Shahrebabak H. (2012). Estimation of phenotypic and genetic parameters for ewe reproductive traits in shal sheep. *J. Res. Anim. Prod.* **3(6),** 35-45.

Mohammadi H., Moradi Shahrebabak M. and Moradi Shahrebabak H. (2013). Analysis of genetic rrelationship between reproductive traits vs. lamb growth traits in Makooei ewes. *J. Agric. Technol*. **15,** 45-53.

Mokhtari M.S., Rashidi A. and Esmailizadeh A.K. (2010). Estimates of phenotypic and genetic parameters for reproductive traits in Kermani sheep. *Small Rumin. Res*. **88,** 27-31.

Mortazavi S.M., Aslaminejad A.A., Nasiri M.R., Hassanpour K. and Nagusi M. (2014). A comparative study of lamb breeding of Iran black sheep with Arman and Baluchi breeds and study of genetic relationship between lambing traits and mean birth weight of lambs in Iran black breed. *J. Anim. Poult. Res*. **3,** 60-69.

Nayeri F. (2013). Estimation of genetic and phenotypic trend and parameters for reproduction trits of Moghani sheep using threshold and linear model. MS Thesis. University of Zanjan, Zanjan, Iran.

Pourtahmasebian Ahrabi M., Eskandarinasab M.P. and Zandi Baghcheh Maryam M.B. (2020). Estimation of genetic parameters and genetic trend of litter size in under selection flock of Afshari sheep. *Anim. Prod. Res.* **9(2),** 23-35.

Petrovic M.P., Petrovic V.C., Ilic Z.Z., Muslic Z.D.R., Milenkovic M.V., Milosevic B. and Grack D. (2013). Features of the new breed of sheep in Serbia called miss sheep. Reproductive characteristics and body development. *Vet. Med. Zoot*. **64,** 70-75.

Rao S. and Notter D.R. (2000). Genetic analysis of litter size in Targhee, Suffolk and Polypay sheep. *J. Anim. Sci*. **78,** 2113-2120.

Rashidi A., Mokhtari M.S., Esmailizadeh A.K. and AsadiFozi M. (2011). Genetic analysis of ewe productivity traits in Moghani sheep. *Small Rumin. Res*. **96,** 11-24.

Rashidi A., Mokhtari M.S., Safi Jahanshahi A. and Mohammadi Abadi M.R. (2008). Genetic parameter estimates of pre- weaning traits in Kermani sheep. *Small Rumin. Res*. **74,** 165-171.

Safari E., Fogarty N.M. and Gilmour A.R. (2005). A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. *Livest. Prod. Sci*. **92,** 271-289.

Sargolzaei M., Iwaisaki H. and Colleau J.J. (2005). A fast algorithm for computing inbreeding coefficients in large populations. *Anim. Breed. Genet*. **122,** 325-331.

SAS Institute. (2005). SAS®/STAT Software, Release 9.4. SAS Institute, Inc., Cary, NC. USA.

Sepehri R. (2016). Identification of nucleotide polymorphism of some genes associated with fat and their relationship with traits carcasses in Afshari lambs and Brolaramino crossbreds using the Bayesian Method. Ph D. Thesis. University of Tabriz, Tabriz, Iran.

Valipour-Koutanaee O., Farhadi A., Hafezian S.H. and Gholizadeh M. (2019). Molecular and bioinformatics analysis of allelic diversity in *IGFBP2* gene promoter in indigenous Makuee and Lori-Bakhtiari sheep breeds. *Iranian J. Appl. Anim. Sci*. **9,** 283-289.

Van wyk J.B., Fair M.D. and Cloete S.W.P. (2003). Revised models and genetic parameter estimates for production and reproduction traits in the Elsenburg Dormer sheep stud. *South African J. of Anim. Sci*. **33,** 213-222.

Vanimisetti H.B., Notter D.R. and Kuehn L.A. (2007). Genetic (co)variance components for ewe productivity traits in Katahdin sheep. *J. Anim. Sci*. **85,** 60-68.

Vatankhah M., Talebi M.A. and Edriss M.A. (2008). Estimation of genetic parameters for reproductive traits in Lori-Bakhtiari sheep. *Small Rumin. Res*. **74,** 216-220.

Zamani P., Akhondi M. and Mohammadabadi M.R. (2015). Associations of inter-simple sequence repeat loci with predicted breeding values of body weight in sheep. *Small Rumin. Res*. **132,** 123-127.

Zhang C., Chen S., Li X., Xu D., Zhang Y. and Yang L. (2009). Genetic and phenotypic parameter estimates for reproduction traits in the Boer dam. *Livest. Sci*. **125,** 60-65.