

## GENETIC ANALYSIS OF EWE PRODUCTIVITY TRAITS IN GHEZEL SHEEP USING LINEAR AND THRESHOLD MODELS

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### ABSTRACT

In this study, the genetic parameters of ewe productivity (reproductive parameter) in Iranian native Ghezel sheep were estimated using six different linear and threshold univariate animal models. The data set consisted of 4173 records from 2420 ewes that were collected since 1992 to 2010 in the breeding centre of Ghezel sheep Station of Miandoab, Western-Azerbaijan province. Based on Akaike's Information Criteria and Deviance Information Criterion, the most appropriate linear and threshold model for each trait was the fourth model (including direct genetics of animal and maternal genetics with non-zero covariance between them). The direct heritability estimates ( $\pm$  standard errors) with linear analysis for conception rate, number of lambs born, number of lambs born alive, number of lambs at weaning, number of lambs born per ewe exposed, number of lambs at weaning per ewe exposed, total litter weight at birth per ewe lambing and total litter weight at weaning per ewe lambing were as  $0.077 \pm 0.02$ ,  $0.074 \pm 0.01$ ,  $0.081 \pm 0.01$ ,  $0.088 \pm 0.02$ ,  $0.028 \pm 0.01$ ,  $0.026 \pm 0.01$ ,  $0.195 \pm 0.02$ ,  $0.193 \pm 0.01$ , respectively. But the estimates resulted from threshold analysis were as  $0.080 \pm 0.02$ ,  $0.079 \pm 0.01$ ,  $0.084 \pm 0.01$ ,  $0.088 \pm 0.02$ ,  $0.035 \pm 0.01$ ,  $0.032 \pm 0.01$ ,  $0.196 \pm 0.01$ ,  $0.195 \pm 0.02$ , respectively. The results showed that the model with genetic correlation between direct and maternal effects seems to be reliable, and also demonstrated the possibility of application of the threshold model for routine genetic evaluation of reproductive traits in Ghezel sheep.

**Key words:** heritability; non-linear models; genetic parameter; reproductive traits; animal model

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### INTRODUCTION

One of the Iranian native fat-tailed and medium-sized sheep breed which is distributed in mountainous areas of Iran North-West, especially in Western and Eastern Azerbaijan provinces, is Ghezel sheep. Valuable products of this sheep are meat, milk, wool and skin (meat and milk are mostly focused). Growth rate of this sheep is high ( $200 \text{ g.day}^{-1}$ ) (Izadifard and Zamiri, 2007). This sheep's color usually varies from light brown to dark brown (legs wool is usually darker). A sidewise looking at the tail of this sheep represent 'S' shape in which the sheep popularity decreases when the tail is less S-shaped. Both rams and ewes are without horns and most of them have knot in front of their neck.

The Lighvan cheese, a traditional and delicious kind of Iranian cheese, is basically made from Ghezel sheep milk in the area of Sahand mountainside, located in the North-West of Iran. It is the most popular traditional and expensive cheese made from raw sheep's milk in Eastern-Azerbaijan province. The Lighvan cheese is characterized by unique hardness (semi-hard), saltiness and spiciness (Rasouli Pirouzian *et al.*, 2012).

The most important part of the sheep farming income is derived from lamb production. The efficiency of lamb production is influenced by reproduction, mothering ability, milk production of ewe, growth rate and lamb survival (Rao and Notter, 2000). Reproductive traits are the most important factors affecting the profitability of sheep farming (Matos *et al.*, 1997).

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Increase in the number or total weight of lambs weaned per ewe can be achieved by increasing the number and the weight of lambs produced per ewe within a year (Duguma *et al.*, 2002). Within-breed selection of animals from native breeds is an appropriate methodology for genetic improvement of traditional low-input production systems of small ruminants in the tropics (Kosgey *et al.*, 2006).

In the last decade, to analyze discrete traits non-linear methods, resulting in more accurate estimation, are proposed in animal breeding. Generally, linear models consider only the direct genetic variance as an important factor, but others (maternal, environmental) as unimportant ones. Threshold model methods are based on the assumption of an underlying unobservable continuous response variable that follows the assumptions of a mixed linear model (Gianola and Foulley, 1983). Heritability of number of born lambs and number of weaned lambs in Turkish Sakiz sheep were 0.03 and 0.18 (Ceylan *et al.*, 2009) and in Moghani sheep were 0.11 and 0.02 (Rashidi *et al.*, 2011), respectively. Estimates of heritability of genetic effects for reproductive traits were low due to the typical strong influence of environmental factors on reproductive traits. Although estimated heritability values by linear and threshold models are low and response to selection is slow, using threshold model will speed up the response to selection (Mohammadi *et al.*, 2012a). Thus, selection of the most appropriate and accurate model and method for improving this native sheep in case of these traits can speed up the response to selection. Consequently, products like milk, meat, wool, skin and Lighvan cheese will improve the efficacy of this farming branch.

Therefore, this study was carried out to estimate genetic parameters of reproductive traits for native Ghezel sheep using the better and the best method and model, based on the accuracy and Information Criterion (AIC and DIC) that are necessary to develop efficient selection programs to improve reproduction.

## MATERIAL AND METHODS

### Data and management

The data set used in this study included reproductive traits of Ghezel ewes, collected during 1992-2010 in the breeding centre of Ghezel sheep (Miandoab) located in Western-Azerbaijan province of Iran. The aim of this centre is to establish a nucleus source for genetic improvement of other herds in the region. Management system of the flock was semi-migratory. Mating season commences in the late of August to October. First mating of animals was at 18-24 months of age. Artificial insemination (AI) was

done during the breeding season. The ewes used in this research were from one to seven parities. In the mating strategy controlled AI was done, where mating between very close animals was avoided. In every breeding year maximum number of allocated ewes per each AI ram was not more than 25 animals. Animals that could not conceive by AI were subjected to natural servicing, where the ewes were assigned to ram breeding groups with an average mating rate of 10-15 ewes per ram. Lambing season starts on January and continues until April. At the birth, all lambs were identified and birth weight, birth type, sex and pedigree information were recorded. The food of lambs was their mother's milk, and since 15<sup>th</sup> day of age it was also dry alfalfa hay. Weaning of lambs usually occurs at three months of age (90 days). The flock (ewes and weaned lambs) usually grazes in pasture during the day and penned at nights and winter with supplemental feeding consisting alfalfa, wheat straw and barley grain.

### Studied traits

Studied traits can be classified into two main categories: basic and composite traits. The basic traits were conception rate (CR with measure of one or zero, meaning whether ewe was exposed to ram or not), total number of lambs born (NLB, with measures of zero, one, or two, which was the number of lambs born per ewe lambing), number of live born lambs (NLBA, with measures of one or two, which was number of lambs alive at 24 hours of age), number of live born lambs at weaning (NLAW, with measures of one or two, which was number of lambs weaned alive). Conception rate is a binary random variable based on continuous variation on the underlying liability scale expressed when a certain threshold is obtained and all other basic traits have discrete numerical observation.

Composite traits with discrete numerical observation were number of lambs born per ewe exposed (NLBEE = CR × NLB) and number of lambs weaned per ewe exposed (NLWEE = CR × NLAW). The composite traits with continuous expression were total litter weight at birth (TLBW), total litter weight at weaning per ewe lambing (TLWW). Table 1 represents the number of records per each trait.

### Statistical analysis

Significant effects which should be stated in a final model were preliminarily determined by Logistic and GLM procedure of SAS software (SAS Institute, 2002) for discrete and continuous traits, respectively. The fixed effects of the final statistical model were: lambing year with 18 classes (1992-2010), herd of ewe with six classes, age of ewe with seven classes, and random parts were: additive genetics of animal, maternal genetics and permanent environmental

**Table 1: Descriptive statistics of data sets**

Traits*	No. of records	No. of ewes	No. of sires	Mean	S.D	C.V. (%)	range
CR	4173	2420	175	0.89	0.30	33.72	0-1
NLB	3673	1906	163	1.116	0.31	28.49	0-2
NLBA	3669	1906	163	1.112	0.31	28.41	1-2
NLAW	3405	1761	163	1.10	0.31	28.36	1-2
NLBEE	4173	2420	175	0.99	0.44	44.44	0-2
NLWEE	4173	2420	175	0.99	0.43	43.43	0-2
TLBW	3669	1906	163	4.60	1.43	31.08	1.9-7.1
TLWW	3405	1906	163	24.12	2.79	11.56	14.71-29.8

\*CR: conception rate; NLB: number of lambs born per ewe lambing; NLBA: number of lambs born alive per ewe lambing; NLAW: number of lambs alive at weaning; NLBEE: number of lambs born per ewe exposed; NLWEE: number of lambs weaned per ewe exposed; TLBW: total litter weight at birth; TLWW: total litter weight at weaning; S.D.: standard deviation and C.V.: coefficient of variation

of ewe. The variance components for studied traits were estimated with six different univariate animal models,

- 1)  $y = Xb + Z_1a + e$
- 2)  $y = Xb + Z_1a + Wpe + e$
- 3)  $y = Xb + Z_1a + Z_2m + e$        $Cov(a, m) = 0$
- 4)  $y = Xb + Z_1a + Z_2m + e$        $Cov(a, m) \neq 0$
- 5)  $y = Xb + Z_1a + Z_2m + Wpe + e$        $Cov(a, m) = 0$
- 6)  $y = Xb + Z_1a + Z_2m + Wpe + e$        $Cov(a, m) \neq 0$

where  $y$  is vector of records of reproductive traits;  $a$ ,  $b$ ,  $m$ ,  $pe$  and  $e$  are direct additive genetic, fixed effects, maternal effects, permanent environmental and residual effects, respectively.

$X$ ,  $Z_1$ ,  $Z_2$  and  $W$  are the design matrices associating the corresponding effects with elements of  $y$ .

The (co)variance structure for random effects was:

$$var \begin{bmatrix} a \\ m \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_d\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

where:

- $a$  = direct additive genetic effect;
- $pe$  = permanent environmental effect related to repeated records of ewes;
- $m$  = maternal genetic effects;
- $e$  = residual effects;
- $\sigma_a^2$  = direct additive genetic variance;
- $\sigma_{pe}^2$  = permanent environmental variance for repeated records of ewes;
- $\sigma_m^2$  = maternal genetic variance;
- $\sigma_e^2$  = residual variance;

$A$  = additive numerator relationship matrix;  
 $I_d, I_n$  = identity matrices with order equal to the number of ewes ( $d$ ) and records ( $n$ ), respectively.

Based on Akaike's Information Criteria (AIC) (Akaike, 1974) and Deviance Information Criterion (DIC), the most appropriate linear and threshold model for each trait was determined, respectively.

$$AIC_i = -2 \log L_i + 2p_i$$

where  $\log L_i$  is the maximized Log-likelihood of model  $i$  at convergence and  $p_i$  is the number of parameters obtained from each model.

$$DIC = \bar{D}(\theta) + p_D = 2\bar{D}(\theta) - D(\bar{\theta})$$

where  $\bar{D}(\theta)$  is the posterior expectation of the Bayesian deviance represented a measure of the fit of the model, and  $\theta$  is the vector of parameters of the model;  $p_D$  is the effective number of parameters representing penalty for increasing model complexity;  $D(\bar{\theta})$  is the Bayesian deviance evaluated at the posterior mean of the parameters. Smaller values of AIC and DIC indicate better model fit.

The (co)variance components were estimated using AIREMLF90 for linear model and THRGIBBS1F90 software with Gibbs sampling methodology of Bayesian inference for threshold model (Misztal, 2002). Number of samples, length of burn-in and sampling interval in Gibbs sampling methodology of Bayesian inference were 200000, 10000 and 100, respectively.

## RESULTS AND DISCUSSION

### Fixed effects

Herd, year of lambing and age of ewe were fixed significant effects ( $P < 0.01$ ) for all traits. Data set recorded in years 1992, 1993 and 1996 for basic traits; NLBEE and NLWEE had the lowest performance and were mostly records for two year old ewes. But usually by increasing age of the ewe it was improved up to seven years of age and then decreased again. For both TLBW and TLWW, records of 1998-2001 had the lowest performance and were improved by increasing the age of ewe. Coefficient of variation of a trait is a criterion for determining the trait variation. This statistics for the studied traits ranged from 11.56 % for TLWW to 44.44 for NLBEE. Since some part of the recorded data sets of the station was from flocks of people in the region, significant effect of herd can be arisen due to different management system in herds. Climatic changes and its influence on pasture of cultivated plants, different management system and nutrition over the years can cause significant effect of year of lambing (Vatankhah *et al.*, 2008; Bromley *et al.*, 2001; Ekiz *et al.*, 2005). Significant effects of year of lambing on reproductive traits in different sheep breeds have been reported by several authors as well (Mohammadi *et al.*, 2012a; 2012b; Ceylan *et al.*, 2009). Significant effects of ewe age may be due to nursing and maternal behavior of ewe at different ages, as well as maternal effect differences (Ekiz *et al.*, 2005; Rosati *et al.*, 2002; Afolayan *et al.*, 2008). Other authors (Rashidi *et al.*, 2011; Ceylan *et al.*, 2009; Poortahmasb *et al.*, 2007) have reported the significant effect of ewe age on reproductive traits, while other researchers (Mokhtari *et al.*, 2010) reported an insignificant influence of ewe age on NLB and NLAW of Kermani sheep. The reported coefficients of variations in Sabi sheep for CR, NLB, NLW, NLBEE, NLWEE and TLWW were 35.9, 30.5, 48.9, 47.8, 62.9 and 28.00, respectively (Matika *et al.*, 2003).

### (Co)variance components and genetic parameters

All traits were analyzed using six different univariate linear and threshold animal models and basing on their AIC and DIC estimates, the fourth model was the most appropriate (including direct additive genetics of animal and maternal genetics with non-zero covariance between them). Estimates of (co)variance components (direct additive, maternal, residual and phenotype), heritabilities (direct additive and maternal) and correlations (additive genetics and maternal genetics) are listed in Table 2.

The direct heritability estimates with linear model for CR, NLB, NLBA, NLAW, NLBEE, NLWEE, TLBW and TLWW were  $0.077 \pm 0.02$ ,  $0.074 \pm 0.01$ ,  $0.081 \pm 0.01$ ,  $0.088 \pm 0.02$ ,  $0.028 \pm 0.01$ ,  $0.026 \pm 0.01$ ,

$0.195 \pm 0.02$ ,  $0.193 \pm 0.01$ , respectively; and the estimates resulting from threshold model were  $0.080 \pm 0.02$ ,  $0.079 \pm 0.01$ ,  $0.084 \pm 0.01$ ,  $0.088 \pm 0.02$ ,  $0.035 \pm 0.01$ ,  $0.032 \pm 0.01$ ,  $0.196 \pm 0.01$ ,  $0.195 \pm 0.02$ , respectively.

The estimates of maternal genetic heritability with linear model for CR, NLB, NLBA, NLAW, NLBEE, NLWEE, TLBW and TLWW were  $0.04 \pm 0.02$ ,  $0.017 \pm 0.01$ ,  $0.020 \pm 0.01$ ,  $0.016 \pm 0.01$ ,  $0.013 \pm 0.01$ ,  $0.012 \pm 0.01$ ,  $0.054 \pm 0.02$ ,  $0.071 \pm 0.01$ , respectively; using threshold model were  $0.047 \pm 0.02$ ,  $0.032 \pm 0.01$ ,  $0.034 \pm 0.01$ ,  $0.032 \pm 0.01$ ,  $0.025 \pm 0.01$ ,  $0.023 \pm 0.01$ ,  $0.060 \pm 0.01$ ,  $0.074 \pm 0.02$ , respectively.

The estimates for direct heritability of CR, reported by other authors (Mohammadi *et al.*, 2012a, b; Rosati *et al.* 2002; Safari *et al.* 2005), were consistent with the results of this study. The low value of heritability estimate of CR may be due to random environmental effects on variability and categorical expression of trait (Falconer, 1989). Although CR is economically important, genetic improvement of this trait by selection is difficult (Rosati *et al.*, 2002). Observed negative correlations between direct and maternal genetics in Table 2 can be due to differences between direct and maternal genetic effects influencing the trait. Negative covariance between direct and maternal genetic effects indicate that antagonistic pleiotropy (between additive and maternal genetic effects) may maintain genetic variance and limit responses to selection (Wilson and Réale, 2006). Although there is high correlation between direct and maternal genetics, it cannot be considered important due to the low estimates of genetic variance for both of them (Rosati *et al.*, 2002).

Differences between NLBA and NLB may probably be due to influences of environmental effects, e.g. neo-natal diseases, on lamb mortality at the first 24 hours of life and of dead-born lambs (Rosati *et al.*, 2002). Heritability estimate for NLB was reported as  $0.11 \pm 0.01$  for Makooei sheep (Mohammadi *et al.*, 2012b); 0.053 and 0.059 for Turkish Merino and Dormer sheep (Ekiz *et al.*, 2005; van Wyk *et al.*, 2003), respectively. The obtained results for maternal heritability estimates represent little evidence of maternal genetic effects on NLB and NLBA that is due to low estimates of maternal heritability (Rosati *et al.*, 2002).

Lower maternal heritability estimate of NLAW in comparison with direct heritability estimate can indicate that model could not consider whether lambs were artificially or naturally nursed and because the ewe effect probably diminished from birth to weaning (Rosati *et al.*, 2002). Reported heritability estimates in different studies for Makooei and Zandi sheep were  $0.06 \pm 0.01$  (Mohammadi *et al.*, 2012a) and  $0.16 \pm 0.01$  (Mohammadi *et al.*, 2012b), respectively; and other heritability estimate was reported (van Wyk *et al.*, 2003)

**Table 2: Estimates of variance components and genetic parameters from univariate analysis of reproductive traits**

Traits	$\sigma_a^2$	$\sigma_m^2$	$\sigma_e^2$	$\sigma_p^2$	$h_d^2 \pm \text{S.E.}$	$h_m^2 \pm \text{S.E.}$	ram
Linear							
CR	0.007	0.003	0.075	0.085	0.077 $\pm$ 0.02	0.034 $\pm$ 0.02	-0.78
NLB	0.007	0.002	0.091	0.101	0.074 $\pm$ 0.01	0.017 $\pm$ 0.01	0.87
NLBA	0.008	0.002	0.090	0.100	0.081 $\pm$ 0.01	0.020 $\pm$ 0.01	0.89
NLAW	0.009	0.002	0.086	0.097	0.088 $\pm$ 0.02	0.016 $\pm$ 0.01	0.85
NLBEE	0.005	0.002	0.170	0.178	0.028 $\pm$ 0.01	0.013 $\pm$ 0.01	0.82
NLWEE	0.005	0.002	0.167	0.174	0.026 $\pm$ 0.01	0.012 $\pm$ 0.01	0.82
TLBW	0.398	0.112	1.526	2.040	0.195 $\pm$ 0.02	0.054 $\pm$ 0.02	-0.78
TLWW	1.619	0.595	6.168	8.381	0.193 $\pm$ 0.01	0.071 $\pm$ 0.01	0.72
Threshold							
CR	0.007	0.004	0.075	0.086	0.080 $\pm$ 0.02	0.047 $\pm$ 0.02	-0.81
NLB	0.008	0.003	0.091	0.102	0.079 $\pm$ 0.01	0.032 $\pm$ 0.01	0.90
NLBA	0.008	0.003	0.089	0.100	0.084 $\pm$ 0.01	0.034 $\pm$ 0.01	0.91
NLAW	0.009	0.003	0.086	0.098	0.088 $\pm$ 0.02	0.032 $\pm$ 0.01	0.87
NLBEE	0.006	0.005	0.169	0.180	0.035 $\pm$ 0.01	0.025 $\pm$ 0.01	0.88
NLWEE	0.006	0.004	0.166	0.177	0.032 $\pm$ 0.01	0.023 $\pm$ 0.01	0.85
TLBW	0.404	0.123	1.528	2.060	0.196 $\pm$ 0.01	0.060 $\pm$ 0.01	-0.80
TLWW	1.646	0.631	6.177	8.450	0.195 $\pm$ 0.02	0.074 $\pm$ 0.02	0.75

$\sigma_a^2$ : direct genetic variance;  $\sigma_m^2$ : maternal genetic variance;  $\sigma_e^2$ : residual variance;  $\sigma_p^2$ : phenotypic variance;  $h_d^2$ : direct heritability;  $h_m^2$ : maternal heritability;  $r_{am}$ : correlation of direct and maternal genetics; S.E.: standard error

for NLAW in Dormer (0.026), what is in consistence with this study. Poortahmasb *et al.* (2007) reported the heritability estimate for NLW as  $0.06 \pm 0.02$  by linear model and 0.23 by threshold model. Estimated values in this study were comparable with the reported values.

Lower heritability estimates of NLWEE attributed to NLBEE may be probably due to loss of lambs during suckling period which is more related to lamb genotype than to ewe genotype (Mohammadi *et al.*, 2012a; 2012b; Rosati *et al.*, 2002). Previous studies reported direct heritability of NLBEE in Makoei and Zandi sheep of  $0.08 \pm 0.02$  (Mohammadi *et al.*, 2012b) and  $0.12 \pm 0.01$  (Mohammadi *et al.*, 2012a), respectively, and heritability of NLWEE of  $0.04 \pm 0.02$  and  $0.11 \pm 0.01$ , respectively. Estimated values for NLBEE and NLWEE in this study were lower than CR, NLBA and NLAW, respectively and in consistence with weighted mean values reported previously (Safari *et al.*, 2005; Fogarty, 1995).

Total litter weight at birth per ewe lambing indicates the ewe capacity to produce lamb weight at birth without considering the number of lambs born. Observations of this trait are continuous and can be regarded as normally distributed, although skewed

to the right (Mohammadi *et al.*, 2012b). Achieved values in this study are in consistence with the results of Mohammadi *et al.* (2012b) who reported the value  $0.17 \pm 0.03$  for Makoei sheep. Reported estimates are consistent with the estimates measured in this study of Safari *et al.* (2005) and Fogarty (1995). This large estimate shows that it is possible to select for total litter weight at birth per ewe lambing (Mohammadi *et al.*, 2012b). If out-of-season breeding was successful, selection intensity would be larger. Actually, it might cause reduction of generation interval for TLBW observations obtained at birth. Thus, genetic trends would be available more, when generation intervals are larger reduced (Mohammadi *et al.*, 2012b; Rosati *et al.*, 2002). There are evidences that reported estimates (Mohammadi *et al.*, 2012b; Rosati *et al.*, 2002) are in consistence with estimates of this study.

Due to permanent environmental effects, phenotypic variances for basic traits were lower than the composite ones. Increasing the heritability estimate of NLAW attributed to NLBA and NLB may be due to increasing of variation between ewes and increasing similarity within ewes. Estimated (co)variance components by linear model were usually

lower than threshold model. This may be due to nature of threshold model in which a normal distribution for discrete trait is considered and sampling is carried out. In some traits like NLAW both linear and threshold models have the same direct heritability estimate. This may be due to nature and number of data sets and pedigree records.

The results obtained in this study showed that the model with genetic correlation between direct and maternal effects seems to be reliable for genetic evaluation of reproductive traits in Ghezel sheep. This means that the most appropriate model in both linear and threshold models are the same. Although heritability estimate of reproductive traits with both linear and threshold models and response to selection are low, applying the threshold model for categorical traits would increase the accuracy and consequently speed up the response to selection. It should be noted that there is a considerable variation for ewe productivity traits, especially reproductive ones. Despite large phenotypic variations for reproductive traits, heritability estimates for these traits were low. This means that genetic changes by direct selection for these traits would be difficult and non-genetic factors improvement in flocks such as nutrition of ewe before mating (flushing) and late pregnancy and controlling rams fertility can lead to the improvement of these traits.

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