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Estimation of genetic parameters for direct and maternal effects of Growth traits in Iranian Adani goats

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ABSTRACT

Five different animal models, which differ in whether or not taking maternal genetic effect into account were used for estimating genetic parameters of growth traits in Iranian Adani goats and were compared via Akaike information Criterion (AIC) and Bayesian Information Criterion (BIC). Random effects in these models included direct and maternal additive genetic effects with direct-maternal genetic covariance, maternal permanent environmental and residual effects. Using five models, both genetic parameters and trends were analyzed with the WOMBAT program. Direct heritability estimates from different multiple traits models differ and ranged from 0.33 to 0.65, 0.20 to 0.63, 0.15 to 0.42, 0.16 to 0.43 and 0.15 to 0.45 for model 1 to 5 respectively. Maternal heritability ranged from 0.02 to 0.19, 0.12 to 0.33, 0.03 to 0.12 and 0.08 to 0.27 for model 2 to 5 respectively. Results indicated that maternal genetic effect has significant influence on growth traits but direct-maternal genetic covariance was not significant. Genetic correlation estimates using appropriate model varied from 0.18 to 0.98. Genetic correlations between adjacent traits were high and decreased as the distance between them increased but always were positive. Phenotypic correlations followed a similar pattern but were lower than the corresponding genetic.

Keywords: Genetic Parameters, Growth traits, Adani goat, maternal effects.

INTRODUCTION

Adani goat is a one of the most important breeds in southern Iran. This breed reared in the coastal areas of the Persian Gulf in Bushehr province. In these areas, the climate is harsh due to high temperatures and humidity and the poor quality pastures. This breed of goat is well adapted to harsh conditions and shortage of forage. Adani goats are maintained as household animal under intensive systems. It has suitable litter size and high pregnancy rate. The average twinning rate is 0.35 and generally it has three pregnancies in two years. Adani goat is a good breed for the export market and is a very quiet in behavior.

Growth is one of the important traits in animal production. Weight gain in animal is determined not only by direct genetic but by other factors as well [24]. Therefore, it would be important to determine the additive genetic, maternal and environmental effects of animals for production. Birth traits are often considered as an early indicator of growth and production because they correlated highly between them [16]. In fact several studies have estimated genetic and phenotypic for growth in Asian goats [6, 22, 24]. Gholizadeh et al. (2010) estimated genetic parameters for Iranian Raeini goats. However, no such a study has been done on Adani goats.

The objective of this study was to estimate the genetic and phenotypic parameters for growth traits of Iranian Adani goats using different multiple traits models.

MATERIALS AND METHODS

Data consisted of growth traits records of Iranian Adani goats born between 2006 and 2013 and were obtained from Adani Goat Breeding Centre of Bushehr province. The farm is located in the coastal area of the Persian Gulf. The region climate is classified as a warm semi-arid climate with annual average temperature of 30°C, relative humidity of 64%, annual rain of 100 mm, and with water deficit during almost all the year. The animals were raised in an intensive breeding system.

The growth traits were birth weight (BW), weaning weigh (WW), 3-months weight (W3), 6-months weight (W6), 9-month weight (W9) and 12-month weight (W12). There are 9840 weight records. Data restricted to only Animals with known dam. Animals with vague or missing pedigree were discarded. After edits, 6021 growth records from birth to 365 days of age, for 1590 goats and progeny of 89 sires and 595 dams were extracted. In pedigree file, the total number of animals evaluated was 2031 and no phantom parent groups were formed for unknown parents in this study. On average, sires had 129 and dams 4 progeny in the data. Summary of the data is given in Table 1, table 2, Figure 1 and 2.

Table 1. Structure of pedigree file

Number of individuals in pedigree	2031	Number of dams	595
Number of individuals with record	1590	Number of dams with records	202
Number of Base Animal	437	Minimum number of progeny per dam	2
Number of sires	89	Maximum number of progeny per sire	15
Minimum number of progeny per sire	1	Average number of progeny per sire	4
Maximum number of progeny per sire	129	Number of Grand sire which progeny records	38
Average number of progeny per sire	17	Number of Grand dam which progeny records	182

Table 2. Structure of data file

Number of animal with records	1590	Number of Records	6102
Number of with 1 record	133	Number of BW records	1590
Number of with 2 records	167	Number of WW records	842
Number of with 3 records	277	Number of W3 records	1250
Number of with 4 records	452	Number of W6 records	1045
Number of with 5 records	370	Number of W9 records	802
Number of with 6 records	191	Number of W12 records	573

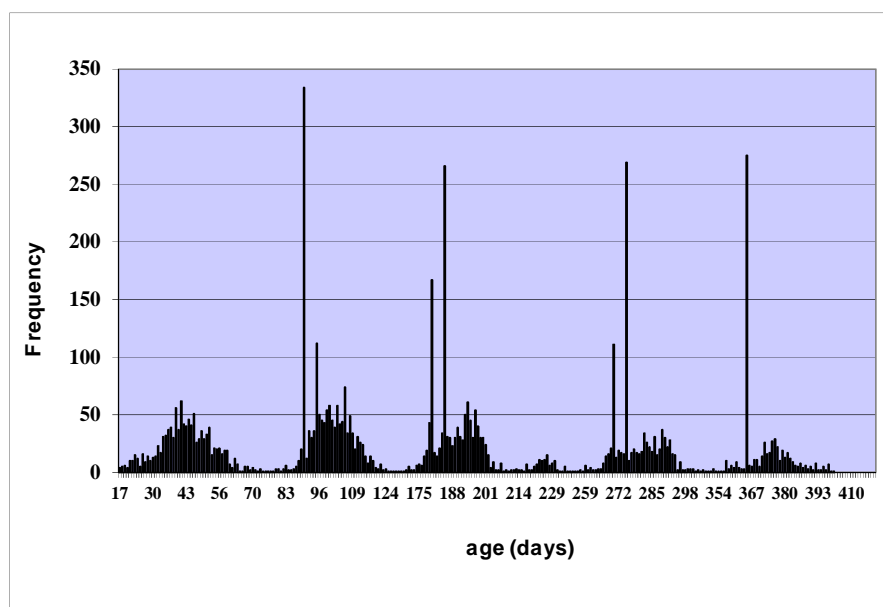


Figure 1. Distribution of weight recordings over the ages in the data set.

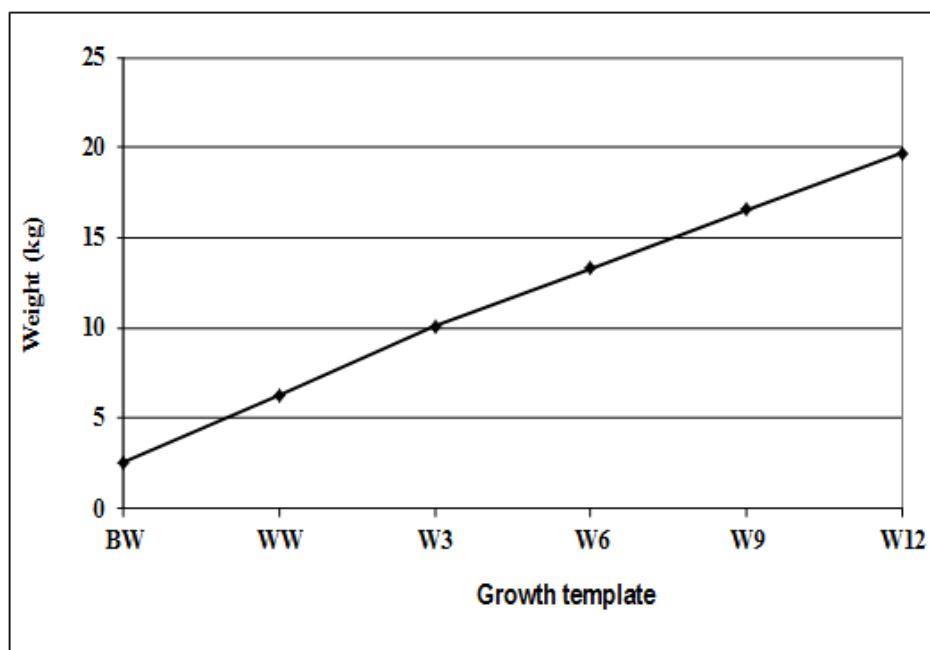


Figure 2. Growth Curve of Adani goats

Variance and covariance components estimated under different multiple traits models. All models included direct additive genetic. Model 1 included only direct additive genetic as random effect. Model 2 included direct additive genetic and maternal additive genetic as a second animal random effect. Model 3 was the same as model 2, but allowed for direct-maternal genetic covariance. Model 4 included direct additive genetic, maternal additive genetic and maternal permanent environment as an additional random effect uncorrelated with all other effects in the model. Finally, Model 5 included direct additive genetic, maternal additive genetic, direct-maternal genetic covariance and maternal permanent environment. The models were as follows:

Model 1: $y = Xb + Z_a a + e$,

Model 2: $y = Xb + Z_a a + Z_m m + e$

With $Cov(a, m) = 0$

Model 3: $y = Xb + Z_a a + Z_m m + e$

With $Cov(a, m) = A\sigma_{am}$

Model 4: $y = Xb + Z_a a + Z_m m + Z_c p + e$

With $Cov(a, m) = 0$

Model 5: $y = Xb + Z_a a + Z_m m + Z_c p + e$

With $Cov(a, m) = A\sigma_{am}$

$$Var \begin{pmatrix} a \\ m \\ p \\ \varepsilon \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_p^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{pmatrix}$$

The following model was used for growth records based on model 4:

$$y_{ijklm} = \mu + CG_i + S_j + T_k + a_l + M_m + Pe_m + \sum_{n=1}^2 b_n DIW_{ijklm} + \sum_{n=1}^2 b_{(n+2)} DA_{ijklm}^n + e_{ijklm}$$

where, y_{ijklm} : Body weights in different ages, μ : mean of population, CG_i : fixed effect of contemporary groups of year and season of kidding. S_j : fixed effect of sex, T_k : fixed effect of birth type, DIW = fixed covariate of age at test (days in recording), DA = fixed covariates of dam age, a_l = animal's random additive genetic effect, M_m = maternal random additive genetic effect, Pe_m : maternal permanent environmental, e_{ijklm} : residual effect

Information criterion of Akaike [1] and Bayesian information criterion [19] tests were also used in the comparison of the models. The information criterion of Akaike can be used to compare models with the same set of fixed effects but with different variance structure. The test considers the best model the one with the lowest information criterion of Akaike value. The Bayesian information criterion test penalizes more models with higher number of parameter in comparison to information criterion of Akaike in such a way the two tests may lead to different results. The values of the Akaike Information Criterion of (AIC) and Bayesian Information Criterion (BIC) are obtained as follows:

$$AIC = -2\log(L_k) + 2p_k$$

$$BIC = -2\log(L_k) + p_k \log(n)$$

Where, L_k : Maximum Log Likelihood for model k, p_k : number parameter for model k, n: number of observation in model k.

Variance components were estimated by the restricted maximum likelihood (REML) method using WOMBAT software [13] with MUV program and AI REML algorithm.

RESULTS AND DISCUSSION

Overall phenotypic means, standard deviation and coefficient of variation for growth traits are presented in Table 3. Recording for body weight started at kidding day for BW and on average continued to 371 days for W12. The coefficient of variation (CV %) of BW was lowest and increased with growth period progressed. Variance was increased as growth period progressed and was highest at W12.

Table 3. Phenotypic mean, standard deviation and coefficient of variation of traits and days in weighting

Traits	BW	WW	W3	W6	W9	W12
DIW						
Mean	1	42.96	99.20	189.35	278.75	371.42
SD	0	8.63	8.01	8.80	8.23	9.12
Growth traits						
Mean	2.55	6.69	10.42	13.86	17.06	20.27
SD	0.48	1.30	2.16	2.66	3.47	4.46
CV%	18.82	19.43	20.73	19.20	20.34	22.00

Table 4: Estimated (co)variance components and genetic parameters for different models

Traits	σ_a^2	σ_m^2	σ_{am}	σ_{pem}^2	σ_e^2	σ_p^2	h^2	m^2	C_m^2
Model 1	BW	0.10	-	-	-	0.08	0.18	0.54	-
	WW	0.42	-	-	-	0.86	1.28	0.33	-
	W3	1.51	-	-	-	2.23	3.74	0.40	-
	W6	2.22	-	-	-	4.21	6.43	0.35	-
	W9	4.58	-	-	-	5.57	10.148	0.45	-
	W12	10.12	-	-	-	5.500	15.618	0.65	-
Model 2	BW	0.05	0.03	-	-	0.10	0.18	0.26	0.19
	WW	0.25	0.15	-	-	0.88	1.28	0.20	0.12
	W3	0.83	0.51	-	-	2.34	3.68	0.22	0.14
	W6	1.48	0.58	-	-	4.33	6.38	0.23	0.09
	W9	3.27	0.87	-	-	5.90	10.03	0.33	0.09
	W12	9.87	0.28	-	-	5.41	15.56	0.63	0.02
Model 3	BW	0.07	0.07	-0.03	-	0.10	0.21	0.31	0.33
	WW	0.26	0.16	-0.004	-	0.91	1.33	0.20	0.12
	W3	0.53	0.43	0.12	-	2.59	3.66	0.15	0.12
	W6	1.66	1.07	-0.42	-	4.41	6.72	0.25	0.16
	W9	3.10	1.19	-0.10	-	6.16	10.36	0.30	0.12
	W12	6.35	2.57	-1.29	-	7.41	15.03	0.42	0.17
Model 4	BW	0.04	0.22	-	0.021	0.10	0.18	0.23	0.12
	WW	0.20	0.04	-	0.148	0.88	1.27	0.16	0.03
	W3	0.69	0.23	-	0.332	2.38	3.63	0.19	0.06
	W6	1.37	0.27	-	0.465	4.268	6.37	0.22	0.04
	W9	2.52	0.48	-	0.811	6.07	9.88	0.26	0.05
	W12	6.33	0.57	-	0.618	7.22	14.74	0.43	0.04
Model 5	BW	0.06	0.05	-0.03	0.017	0.09	0.19	0.32	0.27
	WW	0.23	0.12	-0.012	0.098	0.87	1.30	0.18	0.09
	W3	0.55	0.27	0.15	0.230	2.45	3.65	0.15	0.08
	W6	1.70	0.78	-0.67	0.512	4.08	6.40	0.27	0.12
	W9	2.89	0.98	-0.52	0.746	5.83	9.91	0.29	0.10
	W12	6.75	2.10	-1.60	0.764	6.89	14.90	0.45	0.14

Direct additive genetic, maternal additive genetic, direct-maternal genetic covariance, maternal permanent environmental and residual variance components and direct heritability, maternal heritability and maternal permanent environmental proportion estimates for growth traits based on five models are presented in Table 4.

Results showed that Model 1, which ignored maternal effects, resulted in higher estimates for σ_a^2 and h^2 than the other models. Direct heritability for growth traits differ in used models due to different component and ranged from 0.33 to 0.65 for model 1, 0.20 to 0.63 for model 2, 0.15 to 0.42 for model 3, 0.16 to 0.43 for model 4 and 0.15 to 0.45 for model 5. In all models highest heritability were in 12 months age and except models 3 and 5 lowest heritability were in weaning age. In models 3 and 5 due to positive direct-maternal covariance, lowest heritability observed in 3 months age. The same results were found in previous reports which compared models for various goat and sheep breeds [7, 17, 18, 20]. Meyer (1992) showed that models not accounting for maternal genetic effects could result in substantially higher estimates of additive direct genetic variance and, therefore, higher estimates of heritability. If maternal effects are present but not considered, the estimate of additive genetic variance will include at least a part of the maternal variance. Therefore, estimates of direct heritability will decrease when maternal effects are included. Heritability in this study was higher than other studies [4, 5, 14, 17]. It can be due to use of different models or different components in models.

Weight characteristics were largely influenced by maternal effects [24]. In this study, maternal effects were used in models 2 to 5. Maternal effects included maternal additive genetic, direct-maternal genetic covariance and maternal permanent environment. In models 3 and 5 direct-maternal genetic covariance was used. In this study we found different covariances between direct and maternal genetic effects. Covariances varied -1.29 to 0.12 and -1.60 to 0.15 for models 3 and 5 respectively. Except weight at 3 months age, in other ages, covariances were negative. Several studies were reported negative covariance between direct and maternal additive genetic [5, 7, 8, 20, 21]. Szwaczkowski et al. (2006) showed that the negative covariance between direct and maternal genetic effects indicates different rankings of individuals when the maternal contribution is omitted in the evaluation procedure. However, positive relationships have also been found [15, 23]. Nasholm and Danell (1996) concluded that selection for increased weights will also improve the maternal ability in the case of a positive covariance between direct and maternal genetic effects.

Maternal heritability ranged from 0.02 to 0.19, 0.12 to 0.33, 0.03 to 0.12 and 0.09 to 0.27 for models 2 to 5 respectively. For all models, the largest values were observed at the beginning of the growth period for BW, suggesting a remarkable genetic maternal influence on the total variance at the beginning of the growth period. It showed that, mothers with better additive genetic, transfer these genes to their progeny and therefore their progeny have a higher BW than others. Roy et al. (2008) suggested that maternal additive effects are important only in the early stages of growth. Maternal heritability decreased as progressed growth period (except model 3 and 5 due to positive direct-maternal genetic covariance).

Maternal permanent environment was used in models 4 and 5. In both models, maternal permanent environment variance as a proportion of phenotypic variance was highest for BW. This result is in agreement with some reported results in Iran [4, 5]. In model 4, maternal permanent environment proportion decreased as the growth period progressed and was lowest for w12. This pattern was differed in model 5 due to direct-maternal covariance. These results were in agreement with some reported results [3, 9, 10, 25] but disagreement with Al-Shorepy et al. (2002). In this study, maternal environment at WW lower than BW. Meyer (2001) reported that breed differences in the importance of maternal environmental effects are important and in some breeds lower c_m^2 is due to an earlier decline of the lactation curve than in other breeds.

Table 5. Evaluation criteria for the analyzed models

Model	No of Parameters	Log Likelihood	AIC	BIC
1	42	-3084.95	6253.90	6328.89
2	63	-3062.09	6250.17	6320.66
3	99	-3039.99	6277.97	6938.24
4	84	-3040.76	6249.52	6393.5
5	120	-3031.61	6303.22	7079.31

Log likelihoods, AIC and BIC for the five models are shown in Table 5. According to Table 5, increasing number of parameters for the effects resulted to larger Log L values. Information criterion of Akaike (AIC) and Bayesian information criterion (BIC) values were lowest for model 4 and 2 respectively, which suggested that the model 4 and 2 would be most adequate models in Iranian Adani goats. Model 5 has largest AIC and BIC, which suggests that this model are not adequate model and can be ignored of direct-maternal genetic covariance. These results indicated that

maternal genetic effect has significant influence on growth traits but direct-maternal genetic covariance was not significant. Because model 4 has more parameters, therefore this model was selected as the most appropriate model.

Genetic and phenotypic correlations between growth traits based on model 4 are presented in Table 6. The genetic correlations between growth traits varied from 0.18 to 0.98. Genetic correlations between adjacent traits were high and decreased as the distance between traits increased but always were positive. Phenotypic correlations followed a similar pattern but were lower than the corresponding genetic

Because of high genetic correlation between growth traits, traits in the beginning of the growth period can be considered as an indicator of growth and production.

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations between growth traits.

	BW	WW	W3	W6	W9	W12
BW		0.69	0.48	0.36	0.21	0.18
WW	0.32		0.84	0.69	0.59	0.58
W3	0.24	0.65		0.84	0.70	0.78
W6	0.21	0.48	0.70		0.90	0.93
W9	0.22	0.36	0.49	0.80		0.98
W12	0.19	0.35	0.44	0.68	0.83	

CONCLUSION

Results of this study showed that growth traits are affected by maternal effects include maternal additive genetic and maternal permanent environment but no direct-maternal covariance. Selection on weight in early stage of growth period can improved other weights due to high correlation between them.

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