

Consideration on Genetic Connectedness under an Animal Model by Computer Simulation

¹K. Radjabalizadeh and ²H. Khani

¹Ardabil Branch, Islamic Azad University, Ardabil, Iran

²Department of Animal Breeding, Tehran University, Tehran, Iran

Abstract: Phenotypic expression of a trait is a function of both the genotype of the animal and the environment that influences it. Connectedness among management units is of concern in genetic evaluation. In this study, for considering effect of genetic connectedness effect on the genetic evaluation, comparisons of estimated evaluations and genetic parameters in two cases lack and un-lack (GC) have been written in the C++ language program by simulation method in sheep herds with consideration of natural conditions (fertility percent, mortality percent). It is argued that connectedness increases as the proportion of offspring from common sires. A high level of connections improved the accuracy of the genetic evaluation. Connectedness ratings were higher for highly heritable traits and lower for traits with low heritability.

Key words: Animal model, prediction of genetic evaluation, computer simulation, genetic connectedness, C++ language, Iran

INTRODUCTION

Phenotypic expression of a trait is a function of both the genotype of the animal and the environment that influences it. Connectedness can be defined as a measure of the relationships between herds or contemporary groups as they affect the accuracy of comparing the genetic values of animals from one herd or group to the other. The higher the connectedness, the more accurate the comparisons of EBVs across groups or herds. A simple approach to increase connectedness between paired herds is to use common sire by Artificial Insemination (AI). The magnitude of this increase depends upon the magnitude of their use in both herds. If there are few or no genetic connectedness between a herd and the remainder of the tested population, the EBVs of animals in that herd cannot be compared accurately to the EBVs estimated in other herds (Banos and Smith, 1991).

The concept of connectedness in experimental design was first defined by statisticians (Bose, 1947). To prevent lack of connectedness developed the use of reference sire progeny testing schemes (Hanocq *et al.*, 1996; Kennedy and Turs, 1993).

Geneticists also developed methods to check for disconnection or to measure the degree of connectedness in a design (Peterson, 1978; Foulley *et al.*, 1990, 1992). In this study for considering effect of genetic connectedness on the genetic evaluation, comparisons estimated evaluations and genetic parameters in two case

lack and un-lack (GC) in herds with consideration of natural conditions have been written in C++ language by Stochastic simulation method.

MATERIALS AND METHODS

First, a base population defined with parameters (additive genetic SD, environment SD) that before had reported in the research studies then divided to 10 herds (genetic groups) with equal number animals (500 ID) (Mathur *et al.*, 1998; Radjabalizadeh, 2007).

The genetic groups defined in the situation of connectedness (common sire, son of sire, relative). The simulation program has been written in the C++ language.

The Components of (Co) variance and genetic parameters for BW, WW and SL were estimated by DFREML software. With infinite loci additive genotypic values are normally distributed in large randomly mated populations in Hardy-Weinberg equilibrium. We assume that parents are unrelated and are sampled from an infinite base population in equilibrium. Additive genetic values can be simulated from a normal (0, 1) random number generator as follows (Kennedy, 1995):

$$A = \text{Normal}(\text{iseed}) * \text{ASD}$$

Where:

A = Additive genetic value of parent

ASD = Additive genetic standard deviation in base population

If Phenotypic observations (P) are required, an Environmental term (E) simulated as:

$$E = \text{Normal}(\text{iseed}) * \text{ESD}$$

Where, ESD = Environmental Standard Deviation, can be added to G. Offspring additive genetic values (A_o) can be simulated from parental additive genetic values plus a term for Mendelian Sampling (MS) as:

$$A_o = \frac{1}{2} A_p + \frac{1}{2} A_m + \text{MS}$$

Where, A_p and A_m are the additive genetic values of the sire and dam, respectively. In a non-inbred population:

$$\text{Var}(\text{MS}) = \frac{1}{2} A^2_A$$

So, the MS term can be simulated as:

$$\text{MS} = \text{Normal}(\text{iseed}) * \text{ASD} * \sqrt{0.5}$$

This process can be repeated over any number of generations. In general for each trait in next generation can be simulated as:

$$Y_{ijk} = \mu + \frac{1}{2} A_{si} + \frac{1}{2} A_{dj} + \text{MS}_{ijk} + e_{ijk}$$

Where:

- Y_{ijk} = An observation on an offspring of the i th sire and j th dam
- μ = Population mean for trait
- A_{si} = Genetic value i th sire
- A_{dj} = Genetic value j th dam
- MS_{ijk} = Effect of Mendelian sampling of k th offspring of i th sire and j th dam
- e_{ijk} = Environmental effect

The genetic evaluation can be estimated for each animal by Animal model in single trait as:

$$Y_{ijklmn} = (\text{HY})_i + X_j + D_k + M_m + e_{ijklmn}$$

Where:

- Y_{ijklmn} = An observation from an offspring
- $(\text{HY})_i$ = Herd-year effect (fixed effect)
- X_j = The fixed effect of gender (sire or dam)
- D_k = The random effect of additive genetic (direct effect)
- M_m = The random effect of maternal genetic related to offspring's dam
- e_{ijklmn} = The random effect of residuals

In matrix notation, the model is:

$$Y = Xb + Z_1d + Z_2m + e$$

Where:

- Y = The vector of animal trait
- b = The vector of fixed effects $(\text{HY})_i$
- X and X_j = Coefficients matrix
- d = The vector of direct genetic effects of animal
- Z_1 = Coefficients matrix
- m = The vector of maternal genetic effects
- Z_2 = Coefficients matrix
- e = The random effects of residuals

The genetic evaluation can be estimated for each animal by Animal model in record repeated model as:

$$Y_{ijklmn} = (\text{HY})_i + X_j + D_k + M_m + P_m + e_{ijklmn}$$

Where:

- Y_{ijklmn} = An observation from an offspring
- $(\text{HY})_i$ = Herd-year effect (fixed effect)
- X_j = The fixed effect of gender (sire or dam)
- D_k = The random effect of additive genetic (direct effect)
- M_m = The random effect of maternal genetic related to offspring's dam
- P_m = The random effect of permanent environmental of animals dam
- e_{ijklmn} = The random effect of residuals

In matrix notation, the model is:

$$Y = Xb + Z_1d + Z_2m + Z_3p + e$$

Where:

- Y = The vector of animal trait
- b = The vector of fixed effects $(\text{HY})_i$
- X and X_j = Coefficients matrix
- d = The vector of direct genetic effects of animal
- Z_1 = Coefficients matrix
- m = The vector of maternal genetic effects
- Z_2 = Coefficients matrix
- p = The vector of permanent environmental of animals dam
- Z_3 = Coefficients matrix
- e = The random effects of residuals

The high performance individuals in each generation base upon the selection method (phenotype or genotype) evaluated then selected for creation of next generation. The selected parents have been crossed in random case (Radjabalizadeh, 2004, 2007).

RESULTS AND DISCUSSION

Statistics analysis: From simulation data for estimating of variance components and genetic parameters by use of

Table 1: Comparison of variance components and genetic parameters estimated for three case of GC

Parameters	R ¹	Common sires		Son of sire		Relatives	
		Single trait	Repeated record (0.39)	Single trait	Repeated record (0.45)	Single trait	Repeated record (0.35)
BW ⁷	h ² (SE) ²	0.385 (0.12)	0.305 (0.12)	0.41 (0.14)	0.39 (0.14)	0.32 (0.14)	0.29 (0.14)
	σ_p^2 ³	1.96	3.65	2.03	2.97	2.41	3
	σ_e^2 ⁴	1.205	2.23	1.2	1.63	1.64	1.95
	σ_{pe}^2 ⁵	-	0.31	-	0.18	-	0.18
	σ_a^2 ⁶	0.755	1.113	0.83	1.16	0.77	0.87
	R	-	0.39	-	0.32	-	0.35
WW ⁸	h ² (SE)	0.3 (0.14)	0.19 (0.13)	0.29 (0.13)	0.25 (0.13)	0.32 (0.13)	0.30 (0.13)
	σ_p^2	13.13	20.64	15.0	13.75	11.70	17.63
	σ_e^2	9.19	12.59	10.65	9.35	7.96	11.46
	σ_{pe}^2	-	4.13	-	0.96	-	0.88
	σ_a^2	3.94	3.92	4.35	3.44	3.74	5.29
	R	-	0.66	-	0.63	-	0.60
SL ⁹	h ² (SE)	0.6 (0.14)	0.45 (0.13)	0.48 (0.12)	0.53 (0.12)	0.35 (0.12)	0.4 (0.12)
	σ_p^2	1.61	4.56	1.20	3.96	2.03	3.66
	σ_e^2	0.64	1.55	0.61	1.47	1.32	1.46
	σ_{pe}^2	-	0.96	-	0.40	-	0.74
	σ_a^2	0.97	2.05	0.59	2.09	0.71	1.46
	R	-	0.66	-	0.63	-	0.60

1: Repeatability; 2: Heritability; 3: Phenotypic variance; 4: Error variance; 5: Permanent environmental variance; 6: Additive genetic variance; 7: Birth weight; 8: Weaning weight; 9: Staple length

Table 2: Comparison of variance components and genetic parameters estimated for the lack of GC and PBV

Parameters	R	Lack of GC		PBV	
		Single trait	Repeated record (0.3)	Single trait	Repeated record (0.35)
BW	h ² (SE)	0.27 (0.12)	0.24 (0.12)	0.32 (0.14)	0.3 (0.14)
	σ_p^2	1.96	3.65	1.85	3.61
	σ_e^2	1.43	2.56	1.26	2.35
	σ_{pe}^2	-	0.21	-	0.18
	σ_a^2	0.53	0.87	0.59	1.08
	R	-	0.25	-	0.30
WW	h ² (SE)	0.2 (0.14)	0.15 (0.13)	0.31 (0.12)	0.20 (0.12)
	σ_p^2	13.13	20.64	13.13	24.36
	σ_e^2	10.5	15.48	9.06	17.05
	σ_{pe}^2	-	2.06	-	2.44
	σ_a^2	2.63	3.09	4.07	4.87
	R	-	0.50	-	0.65
SL	h ² (SE)	0.49 (0.14)	0.38 (0.13)	0.50 (0.14)	0.45 (0.14)
	σ_p^2	1.61	4.56	1.61	2.98
	σ_e^2	0.82	2.28	0.81	1.05
	σ_{pe}^2	-	0.55	-	0.20
	σ_a^2	0.79	1.73	0.80	1.73
	R	-	0.50	-	0.65

animal model (single trait and repeatability record) for BW, WW and SL traits in three case of connectedness are shown in Table 1 and 2.

CONCLUSION

There is significant difference between average EBVs in lack and un-lack genetic connectedness between herds. The study shows that connectedness increases as the proportion of offspring from the common sire increases. It is very high if 100% of the offspring in both herds is from common sires.

If the proportion of offspring from the common sires is low in one of the herds, the other herd has to have a large proportion of offspring to reach a higher level of connectedness. If the sires have <25% of offspring in

another herds, the maximum level of connectedness rating possible is about 15% even if >50% of the offspring in the original herd are produced from the common sires. However, if the sires have >75% of the offspring in the other herd, the connectedness rating increases with the percentage of offspring in the original herd. Connectedness ratings were higher for highly heritable traits and lower for traits with low heritability.

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