

STUDY OF GENETIC CONNECTEDNESS IN GENETIC EVALUATION BY COMPUTER SIMULATION

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Abstract

Connectedness is a statistical approach that could help breeder, under specific animal breeding situations in better deciding for animal selection from different environment. The accuracy of the comparison between EBVs from different herds depends upon the degree of connectedness between them. 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) and identification of (CR) between herd(s), birth weight (BW), weaning weight (WW) and staple length (SL) traits 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. It is very high if the 100% of the offspring in both herds are from common sires. Connectedness ratings were higher for highly heritable traits and lower for traits with low heritability.

Key words: Genetic connectedness, Genetic evaluation, Computer Simulation

INTRODUCTION

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 can not be compared accurately to the EBVs estimated in other herds. [1]

The concept of connectedness in experimental design was first defined by statisticians (BOSE, 1947). To prevent lack of connectedness, FOULLEY and CLERGET DARPOUX (1978) and FOULLEY et al (1983) developed the use of reference sire progeny testing schemes.[2], [3] Geneticists also developed methods to check for disconnection (PETERSON, 1978) or to measure the degree of connectedness in a design. (FOULLEY et al, 1984, 1990, 1992). [3], [4]

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.

MATERIAL AND METHOD:

First, a base population defined with parameters (additive genetic SD, environment SD), that before had reported in the research papers then divided to 10 herds (genetic groups) with equal number animals (500 ID). [5], [6] 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 (Meyer, 1997).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: [4]

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

Where $A =$ additive genetic value of parent and $ASD =$ additive genetic standard deviation in base population. If phenotypic observations (P) are required, an environmental term (E) simulated as

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

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

$A_o = 1/2 A_p + 1/2 A_m + MS$

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

Inbred population,

$\text{Var}(MS) = 1/2 \sigma_A^2$

So the MS term can be simulated as

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

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

$Y_{ijk} = \mu + 1/2 A_{si} + 1/2 A_{dj} + MS_{ijk} + e_{ijk}$

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

$Y_{ijkmn} = (HY)_i + X_j + D_k + M_m + e_{ijkmn}$

Where

Y_{ijkmn} = an observation from an offspring;

$(HY)_i$ = 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_{ijkmn} = 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 (HY) _{i} , X and X_j are coefficients matrix;

d = the vector of direct genetic effects of animal, Z_1 is coefficients matrix;

m = the vector of maternal genetic effects, Z_2 is 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

$Y_{ijkmn} = (HY)_i + X_j + D_k + M_m + P_m + e_{ijkmn}$

Where

Y_{ijkmn} = an observation from an offspring;

$(HY)_i$ = 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_{ijkmn} = 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 (HY) _{i} , X and X_j are coefficients matrix;

d = the vector of direct genetic effects of animal, Z_1 is coefficients matrix;

m = the vector of maternal genetic effects, Z_2 is coefficients matrix;

p = the vector of permanent environmental of animals' dam, Z_3 is 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. [6], [7]

RESULTS AND DISCUSSIONS

Statistics analysis, from simulation data for estimating of variance components and genetic parameters by use of animal model (single trait and repeatability record) for BW, WW and SL traits in three case of connectedness are shown in tables.

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

Common sires		Son of sire		relatives			
Single trait	Repeated record	Single trait	Repeated record	Single trait	Repeated record		
--	0.39	--	0.45	--	0.35	R ¹	
0.385(0.12)	0.305(0.12)	0.41(0.14)	0.39(0.14)	0.32(0.14)	0.29(0.14)	h ² (SE) ²	BW ⁷
1.96	3.65	2.03	2.97	2.41	3	σ _p ^{2 3}	
1.205	2.23	1.2	1.63	1.64	1.95	σ _e ^{2 4}	
--	0.31	--	0.18	--	0.18	σ _{pe} ^{2 5}	
0.755	1.113	0.83	1.16	0.77	0.87	σ _a ^{2 6}	
--	0.39	--	0.32	--	0.35	R	
0.3(0.14)	0.19(0.13)	0.29(0.13)	0.25(0.13)	0.32(0.13)	0.30(0.13)	h ² (SE)	WW ⁸
13.13	20.64	15.0	13.75	11.70	17.63	σ _p ²	
9.19	12.59	10.65	9.35	7.96	11.46	σ _e ²	
--	4.13	--	.96	--	.88	σ _{pe} ²	
3.94	3.92	4.35	3.44	3.74	5.29	σ _a ²	
--	0.66	--	0.63	--	0.60	R	
0.6(0.14)	0.45(0.13)	0.48(0.12)	0.53(0.12)	0.35(0.12)	0.4(0.12)	h ² (SE)	SL ⁹
1.61	4.56	1.20	3.96	2.03	3.66	σ _p ²	
0.64	1.55	0.61	1.47	1.32	1.46	σ _e ²	
--	0.96	--	0.40	--	0.74	σ _{pe} ²	
0.97	2.05	0.59	2.09	0.71	1.46	σ _a ²	

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 (and PBV)

Lack of (GC)		PBV			
Single trait	Repeated record	Single trait	Repeated record		
--	0.3	--	0.35	R	
0.27(0.12)	0.24(0.12)	0.32(0.14)	0.3(0.14)	h ² (SE)	BW
1.96	3.65	1.85	3.61	σ _p ²	
1.43	2.56	1.26	2.35	σ _e ²	
--	0.21	--	0.18	σ _{pe} ²	
0.53	.87	0.59	1.08	σ _a ²	
--	0.25	--	0.30	R	
0.2(0.14)	0.15(0.13)	0.31(0.12)	0.20(0.12)	h ² (SE)	WW
13.13	20.64	13.13	24.36	σ _p ²	
10.5	15.48	9.06	17.05	σ _e ²	
--	2.06	--	2.44	σ _{pe} ²	
2.63	3.09	4.07	4.87	σ _a ²	
--	0.50	--	0.65	R	
0.49(0.14)	0.38(0.13)	0.50(0.14)	0.45(0.14)	h ² (SE)	SL
1.61	4.56	1.61	2.98	σ _p ²	
0.82	2.28	0.81	1.05	σ _e ²	
--	0.55	--	0.20	σ _{pe} ²	
0.79	1.73	0.80	1.73	σ _a ²	

CONCLUSIONS

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 less than %25 of offspring in another herds, the maximum level of connectedness rating possible is about %15 even if more than %50 of the offspring in the original herd are produced from the common sires. However, if the sires have more than %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.

REFERENCES

- [1] Banos G., Smith C., Selecting bulls across countries to maximize genetic improvement dairy cattle, *J. Anim. Breed. Genet.* (1991)108: 174-181.
- [2] Hanocq E., Boichard D., Foulley JL., A simulation study of the effect of connectedness on genetic trend, *J. Genet.Sel. Evol.* (1996)28: 67-82.
- [3] Kennedy B.W., Turs D., Consideration on genetic connectedness between management units under an animal model, *J. Animal Sci.* (1993) 71:2341-2352
- [4] Kennedy B.W., Quantitative genetics theory in animal breeding, Center for genetic improvement of livestock animal and poultry science, University of Guelph, 1995.
- [5] Mathur P.K, Sullivan B., Chesnais J., A new method for assessing connectedness between herds, (1998). [URL://
http://www.mark.asci.ncsu.edu/nsif/98proc/mathur.htm](http://www.mark.asci.ncsu.edu/nsif/98proc/mathur.htm)
- [6] Radjabalizadeh K., Genetic connectedness between herds by computer simulation, (2007). *proc the England Sci Congress.*
- [7] Radjabalizadeh K., Application of inverse problem and computer simulation in genetics, (2004).*proc the Turkey Sci Congress.*