

EFFECT OF THE GENETIC CONNECTEDNESS ON ANIMAL RANKING AND SELECTION RESPONSE

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ABSTRACT

Lack of genetic connectedness across flocks is typical for smallholder farming system where animal mating usually takes place within flock. The genetic connectedness across flocks can be established through sire referencing scheme using both artificial insemination (AI) or natural mating. In smallholder farming system where flock of each farmer is located near by, the genetic connectedness can be established through ram rotation scheme. Genetic evaluation of across flocks animals will increase the selection intensity which in turn it will increase the selection response. To study the effect of genetic connectedness on the animal ranking and the selection response, a stochastic computer simulation study was conducted. A set of data applying simple animal model with one fixed effect of general mean and random polygenic additive effect of animal was simulated. Three animal owners representing different flocks were assumed. A series of scenario combining two schemes: (1) genetically connected (ram rotation) or disconnected (ram static) and (2) three level of heritabilities (0.1, 0.3, 0.5 and 0.7) were simulated. Five generations of random mating were run and the selected animals based on the BLUP EBV were then mated regardless of the animals' owner. The results showed that within the same heritability, the rank correlation of the TBV and BLUP EBV of the genetically connected population was higher than the genetically disconnected population. Whether the population was genetically connected or disconnected, the rank correlation increased when the heritability increased. The selection response was higher on the genetically connected population. The selection response increased when heritability increased.

Keywords: Genetic connectedness, BLUP EBV, rank correlation, selection response

INTRODUCTION

Genetic connectedness is important in animal breeding aspect when selection is across flocks. BLUP methodology has become the choice of method in animal breeding for genetic evaluation since the introduction of the method (Henderson, 1984) and its application is amplified by the computing capability for dealing with large data set. One of the BLUP property is that the EBV of the population level can be compared fairly across fixed effects for instance flocks or regions if the genetic connectedness is established across flocks or regions. When selection is across flock and genetic connectedness does not exist, the BLUP EBV becomes non-estimable and cannot be compared (Kennedy and Trus, 1993).

The problem of precision of BLUP genetic evaluation due to genetic disconnectedness has been addressed in the literatures for instance by Foullet et al. (1992), Kennedy and Trus (1993) and Laloë (1993), Zhang et al. (2004).

Smallholder farming system which usually allows within flocks animal mating causes the genetic disconnectedness among flocks. The BLUP genetic evaluation on this type of management system will result in less accurate genetic evaluation. The objective of the study was to assess the effect of the genetic connectedness on animal ranking and the selection response. The effect of the heritability on those aspects was also studied.

MATERIALS AND METHODS

A stochastic computer simulation was done applying simple animal model for generating the data including general mean as fixed effect and polygenic additive (A) and residual (E) as random effects where A and E were sampled from standard normal distribution ($A \sim N(0, \sigma_a^2)$) and ($E \sim N(0, \sigma_e^2)$). The computer programs were written in a standard ANSI FORTRAN 90 language and were compiled using the free GNU FORTRAN compiler (GFortran, 2011). Pseudo random number generators of ran0 and gasdev (Press et al. 1998) were used in the simulation. In the base population, three sires and 30 dams were generated and were assigned into three owners. The base animals were randomly mated for five generations and the mating was either within or across owners. The EBV of the selection candidates were evaluated using BLUP method applying the same model as for generating the data. The BLUP analysis was done with DMU package of Madsen and Jensen (2008). The best sires and dams were selected based on BLUP EBV and were mated regardless of animals' owner. The mean polygenic additive of animals (TBV) of the progeny was then calculated to compare the effect of genetic connectedness on the selection response.

Two main scenarios were simulated: (1) genetically connected (ram rotation) or disconnected (ram static) and (2) three levels of heritability (0.1, 0.3, 0.5 and 0.7). When scenarios were with ram rotation, rams were moved to another owner before mating was done. The combination of the two main scenarios was run for the study. The ranking of animals based on BLUP EBV was compared using Spearman rank correlation of R package (R Development Core Team, 2009). Overall, the simulation was done in a PC powered with 1.5 GB of Random Access Memory (RAM) with Dual Core 1.46 MHz processors installed with Ubuntu (Linux) Operating System.

RESULTS AND DISCUSSION

The polygenic additive effects (True Breeding Value) generated in the simulation can be used to validate the FORTRAN codes written and the random

number generators used in the simulation. With random mating, the TBV was expected to distribute following the mean and to vary within its variance ($A \sim N(0, \sigma_a^2)$). The deviation of the observed mean TBV was due to random sampling. Even though the mean TBV showed variation of its expected mean, the pattern clearly showed the effect of random mating resulting no change of the mean TBV (Figure 1).

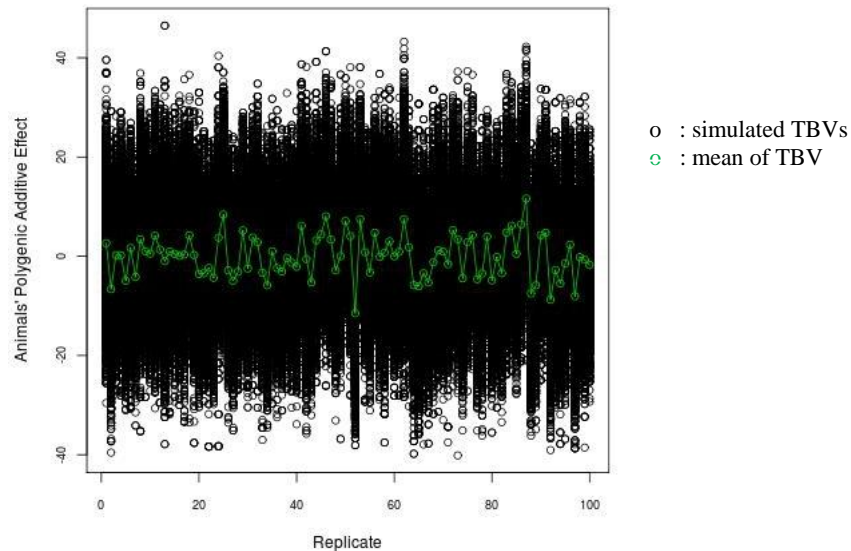


Figure 1. Distribution of the simulated TBV

The effect of genetically disconnected population (ram static scheme) on inbreeding was significant on the inbreeding level of the population on each generation. Table 1 shows the trend of inbreeding level of both genetically connected and disconnected population of the two schemes. Ram rotation scheme increased the effective population size which resulted in the inbreeding level of the population maintained around 0.05-0.08. In another hand, the ram static scheme maintained the effective population size low even though the population was developed from the same number of sires and dams in the population. As a consequence, the inbreeding level of the population increased as the generation expanded (Table 1).

Table 1. Inbreeding trend of both genetically connected and disconnected schemes

Generation	Genetically Connected		Genetically Disconnected	
	Number of Individuals	Inbreeding Level	Number of Individuals	Inbreeding Level
1	33	0.00	33	0.00
2	300	0.00	300	0.00
3	588	0.05	556	0.25
4	540	0.08	528	0.38
5	262	0.07	264	0.44
6	54	0.06	58	0.47

Genetic connectedness increased the rank correlation between the BLUP EBV and the TBV. In the genetically connected population, BLUP analysis estimated the EBV with minimum error (BLUP EBV was accurately estimated). This increase of accuracy was due to the genetic relationship of animals of the different owners. In other words, the mean standard error of prediction (MSEP) of the EBV decreased when the population in different contemporary groups (owners) was genetically connected (Kennedy and Trus, 1993). This effect of genetic connectedness on the rank correlation of TBV and BLUP EBV was observed similarly on rank correlation within males, females or regardless of animals sex. The heritability increased the magnitude of the rank correlation of TBV and BLUP TBV. This is clearly understood since the portion of additive genetic effect was increasing with the increasing value of heritability. Selection response for both male and female animals was also affected by the genetic connectedness. Though this was the indirect effect due to the false ranking of BLUP EBV when selecting the best animals. Table 2 presents rank correlation and selection response when the same number of base sires and dams were selected of the genetically connected scheme. The same variables of the genetically disconnected population were presented in Table 3.

In a smallholder farming system, the genetic connectedness will gradually be established across flocks (owners) following the period of introducing the selected sires across flocks. Where AI is applied to the population, the establishment of the genetic connectedness across flock will be achieved quicker as the spread of semen for AI is faster than the use of rams with natural mating (Kuehn et al, 2008).

Table 2. Rank correlation of TBV and BLUP EBV and the selection response of genetically connected population and the standard error

Variable	h ² = 0.1		h ² = 0.3		h ² = 0.5		h ² = 0.7	
	mean	SE	mean	SE	mean	SE	mean	SE
r _{TBV,EBV} ¹	0.371	0.006	0.598	0.006	0.733	0.005	0.831	0.003
r _{TBV,EBV} ²	0.383	0.006	0.612	0.006	0.743	0.005	0.836	0.003
r _{TBV,EBV} ³	0.377	0.006	0.605	0.006	0.738	0.005	0.834	0.003
R _{male}	13.883	0.690	20.667	0.643	24.220	0.626	26.760	0.576
R _{female}	14.432	0.650	20.548	0.671	24.000	0.650	26.750	0.583

¹ Spearman rank correlation for male individuals

² Spearman rank correlation for female individuals

³ Spearman rank correlation regardless of animals' sex

Table 3. Rank correlation of TBV and BLUP EBV and the selection response of genetically disconnected population

Variable	h ² = 0.1		h ² = 0.3		h ² = 0.5		h ² = 0.7	
	mean	SE	mean	SE	mean	SE	mean	SE
r _{TBV,EBV} ¹	0.198	0.005	0.349	0.006	0.458	0.007	0.553	0.008
r _{TBV,EBV} ²	0.221	0.005	0.377	0.006	0.483	0.008	0.570	0.008
r _{TBV,EBV} ³	0.210	0.005	0.363	0.006	0.471	0.007	0.562	0.008
R _{male}	10.799	0.711	16.126	0.719	19.503	0.713	22.401	0.756
R _{female}	11.130	0.646	16.751	0.625	19.754	0.661	22.636	0.713

¹ Spearman rank correlation for male individuals

² Spearman rank correlation for female individuals

³ Spearman rank correlation regardless of animals' sex

CONCLUSION

The study concluded that the genetic connectedness increased the accuracy of BLUP genetic evaluation and ranked animals' BLUP EBV more correctly. The selection response increased when the population was genetically connected. The effect of genetic connectedness was more obvious on the traits with low heritability on both the animals' BLUP EBV rank correlation and the selection response.

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