

## A Study of the Effect of Connectedness on Genetic Trend

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**Abstract:** The main objective of animal breeding is to improve genetic merit of the animals to produce more efficiently in the later generations. Production traits (milk, fat and protein yields) are the most important traits which affect the economic efficiency of dairy cows. 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 EBV's from different herds depends upon the degree of connectedness between them. 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. Data of Holstein cattle of Ardabil from 1990 to 2010 were obtained from the National Animal Breeding Center of Iran. Data included first lactation records of milk, fat and protein yields. Records were adjusted for milking times (2x) and 305 days in milk. Genetic trend was estimated as the linear regression of average estimated breeding values of animals on the birth year. The objective of this study was to estimate the genetic trends for production traits in two cases lack and unlack Genetic Connectedness (GC) between herd (s) of Holstein cattle by using a multitrait animal model and Matvec program.

**Key words:** Genetic trend, genetic evaluation, animal model, production trait, genetic connectedness

### INTRODUCTION

The main objective of animal breeding is to improve genetic merit of the animals to produce more efficiently in the later generations. Production traits (milk, fat and protein yields) are the most important traits which affect the economic efficiency of dairy cows (Abdallah and McDaniel, 2000). Genetic trend was estimated as the linear regression of average estimated breeding values of animals on the birth year (Rokouei *et al.*, 2010). Phenotypic expression of a trait is a function of both the genotype of the animal and the environment that influences it (Roman *et al.*, 1999). 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 (Radjabalizadeh and Khani, 2011). 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 (Foulley and

Darpoux, 1978; Foulley *et al.*, 1983). This study was in order to consider the effect of genetic connectedness on the genetic trend in two case lack and unlack (GC) in herds during 1990 to 2010.

### MATERIALS AND METHODS

Data of Holstein cattle from 1990 to 2010 were obtained from the National Animal Breeding Center of Iran. Data included first lactation records of milk, fat and protein yields. Records were adjusted for milking times (2x) and 305 days in milk. The statistical description of milk, fat and protein yields is shown in Table 1.

The population was divided into M subpopulations of the same size and structure. Each subpopulation corresponded to an independent company operating in its own region and included N males and N<sub>x</sub>n females per generation. The generations were separate and there were no female exchanges between subpopulations. Selection was applied on a single trait. The females were not selected. After a progeny test M<sub>x</sub>N<sub>x</sub>π sires of males were selected for each generation to sire 1/π sons each (Hanocq *et al.*, 1996; Radjabalizadeh, 2007) (Table 2).

Table 1: Number of records, average, standard deviation, Min. and Max. of milk, fat and protein yields in the Holstein dairy cows of Iran

Traits	N	Average	SD	Min.	Max.
Milk yield	98034	6231.00	1426.00	1106	13192
Fat yield	86163	195.10	48.96	34	551
Protein yield	7573	210.20	39.87	47	409

The connections among subpopulations were initially nonexistent and were gradually generated through two different mechanisms. First, planned connections were established using a proportion of link sires in several subpopulations. Secondly, unplanned links were generated through the policy of male replacement which allowed some exchange among subpopulations (Hanocq *et al.*, 1996).

Data were analyzed using a multitrait animal model and Matvec program. The following mathematical model was fitted for all traits:

$$y_{ij} = \mu + HYS_i + \beta X_{ij} + a_j + e_{ij}$$

Where:

- $y_{ij}$  = The observation of the  $j$ th animal in the  $i$ th HYS
- $\mu$  = The overall mean
- $HYS_i$  = The fixed effect of the  $i$ th Herd-Year-Season

Table 2: Parameters used in the connectedness scheme

Parameters	Notation	Value
Number of subpopulation	M	4
Number of males per subpopulation and generation	N	48
Number of daughter per male	n	50
Selection rate of sires	$\pi$	1/3

$\beta$  = The linear regression coefficient of  $y_{ij}$  on the age at calving ( $X_{ij}$ )

$a_j$  = The additive genetic effect of  $j$ th animal

$e_{ij}$  = The random residual effect

Genetic trend was estimated as the linear regression of average estimated breeding values of animals on the birth year. Finally the environmental trend was estimated by subtracting the genetic trend from phenotypic trend.

## RESULTS AND DISCUSSION

The annual genetic, environmental and phenotypic trends with their standard errors (within parenthesis) in two case lack and unlack Genetic Connectedness (GC) are shown in Table 3 and 4 for all traits.

In the present study the estimated genetic trend values for milk, fat and protein yields in the lack of genetic connectedness were  $33.84 \pm 2.81$ ,  $0.64 \pm 0.05$  and  $1.00 \pm 0.08 \text{ kg year}^{-1}$ , respectively in the un-lack of genetic connectedness case were  $39.74 \pm 1.9$ ,  $0.73 \pm 0.05$  and  $1.63 \pm 0.85 \text{ kg year}^{-1}$ , respectively (Fig. 1a-b).

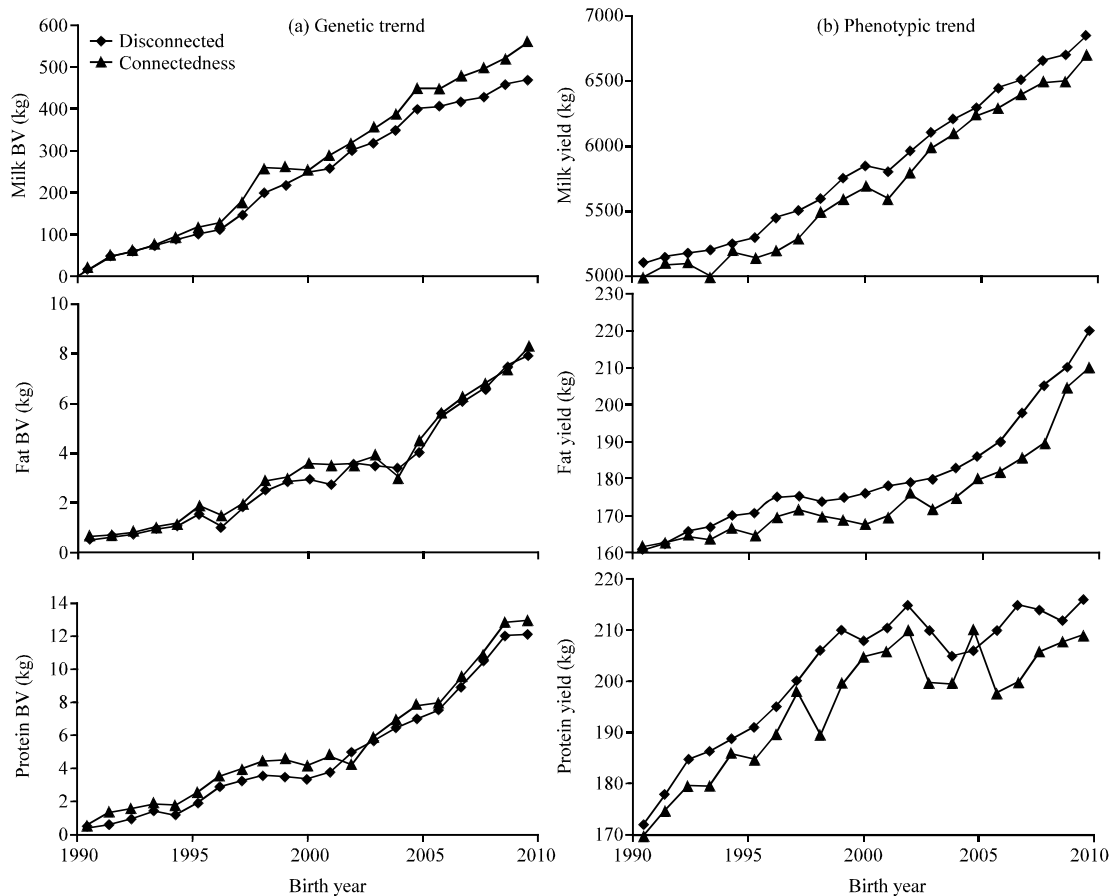


Fig. 1: a-b) Estimated genetic and phenotypic trends for milk, fat and protein yields in two case lack and unlack (GC)

Table 3: Annual genetic, environmental and phenotypic trends for production traits in the lack of Genetic Connectedness (GC)

Items	Genetic	Environmental	Phenotypic
Milk yield	33.84 (2.10)**	88.44	122.28 (3.18)**
Fat yield	0.64 (0.05)**	3.78	4.42 (0.33)**
Protein yield	1.00 (0.08)**	2.06	3.06 (0.78)*

Table 4: Annual genetic, environmental and phenotypic trends for production traits in the un-lack of Genetic Connectedness (GC)

Items	Genetic	Environmental	Phenotypic
Milk yield	39.74 (1.90)**	79.44	119.18 (2.97)**
Fat yield	0.73 (0.05)**	4.63	5.36 (0.26)**
Protein yield	1.63 (0.85)**	1.87	3.50 (0.48)*

\*, \*\*Estimates are significant at  $p < 0.05$  and  $p < 0.01$ , respectively

### CONCLUSION

In general results of this investigation showed that genetic improvement for production traits was at an acceptable level in Holstein cattle of Ardabil. There is significant difference between average EBV's in lack and un-lack genetic connectedness between herds. The present study shows that connections were more beneficial for subpopulations with a lower initial genetic level and a smaller size. However, showed that the subpopulation with the highest initial level can also obtain a genetic trend equal to or greater than that without connections. Another more classical interpretation of the advantage of using connections to increase genetic trend is the increase in genetic variance, due to the additional between subpopulations variability which is not available with traditional selection using closed subpopulations.

The lack of connectedness induces a large bias in the estimation of the genetic level of the subpopulations because the differences among subpopulations are not estimable and are assumed to be zero. It could be concluded that genetic levels when connectedness is large enough to make these differences estimable and when the selection and replacement policy allows one to take advantage of the best genes by appropriate gene flows.

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