Genetic Analysis Of A Conventional Progeny Testing Scheme In Iran

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Introduction

The most important selection strategy especially in dairy cattle is the four pathways selection (Rendel and Robertson, 1950). This strategy is consisted of Sire of Sons (SS), Sire of Daughters (SD), Dam of Sons (DS) and Dam of Daughters (DD) pathways. Design of progeny testing scheme affects the rate of genetic improvement and economic profit in different selection pathways (Norman et al., 2003). Powell *et al.* (2003) recommended that each country should analyze its own progeny testing scheme; because success in progeny testing scheme in different countries is not comparable even if their selection goals are similar. There is no comprehensive study on breeding program using four pathways selection in Iranian Holstein. Therefore, the aim of the current study is to evaluate the genetic response in milk production in each selection pathway, considering progeny testing program and selection scheme in the Iranian Holstein.

Material and methods

Current Iranian progeny testing program. There have been 502000 Holstein cows in Iran in 2008. Around 33% of this population is under milk recording program and 30 percent of the recorded population is considered as elite dams. A proportion of the whole cow population (P=20%) is mated to young bulls. This part can be referred to as the test capacity. Average number of daughters for genetic evaluation of sampled young bulls in Iran is 100. Every year 21 and 25 percent of dam and sire population will be replaced by new heifers and new proven bulls, respectively. Heifers are consisted of two parts: P proportion resulted from mating of the young bulls and ($1\text{-}P$) proportion is considered as the progenies from active bulls. Sons from $SS \times DS$ are considered as young bulls and a number of them (72) will go into progeny testing process after pre-selection phase which is independent from breeding goal. After progeny testing process the best part of tested bulls is selected as SS.

Selection pathways. Based on the structure of current breeding program the number of available and needed animals in each pathway, including the extra pathway for Young Bulls

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(YB) were defined. By dividing the number of needed animals over the number of available animals in each pathway, the proportion selected was calculated for the relevant pathway (Table 1). Selection intensities were calculated assuming truncation selection procedure. Selection accuracies were calculated based on the number of daughters per young bull in the sire pathways and based on one single record per individual in the dam pathways (Milk heritability=0.26 (Toghiani, 2007)).

Table 1: Number of needed and number of available animals and proportion selected in each pathway[1]

Path	No. of needed animals	No. of available animals	Proportion Selected
SS	$n_{SS}=\frac{N_{DS}I_n rr_{SS}}{d}=\frac{NteI_n rr_{SS}}{d}$	$N_{SS}=f_{ps}\times n_{YB}$	$p_{SS}=\frac{nI_n err_{SS}}{Pdrr_f f_{ps}}$
SD	$n_{SD}=\frac{[N(1-P)]I_n rr_{SD}}{d}$	$N_{SD}=f_{ps}\times n_{YB}$	$p_{SD}=\frac{nI_n(1-P)rr_{SD}}{t\,Pr\,r_f df_{ps}}$
YB	$n_{YB}=\frac{Nt\,Pr\,r_f}{n}$	$N_{YB}=\frac{n_{YB}}{f_{ps}}=\frac{Nt\,Pr\,r_f}{nf_{ps}}$	$p_{YB}=f_{ps}$
DS	$n_{DS}=\frac{N_{YB}j}{o}=\frac{NtPrr_f j}{nf_{ps}o}$	$N_{DS}=eNt$	$P_{DS}=\frac{Pr\,r_f\,j}{nf_{ps}eo}$
DD	$n_{DD}=\frac{Nrr_f}{w}$	$N_{DD}=N$	$P_{DD}=\frac{rr_f}{w}$

[1] N:Population Size (N=502000), t: percent of cows on milk recording (t=0.33), P: percent of cows inseminated with young bull semen (P=0.2), n: progeny group size (n=100), In: number of insemination per pregnancy (In=2.2), d: dose of semen used by each progeny tested bulls (d=18000), e: fraction of cows suitable for selection as dam of sons (elite dams) (e=0.3), j: number of needed elite pregnancies to obtain a young male (j=6.1), o: fraction of young bulls suitable for progeny testing (o=1), rr_f: cow replacement rate (rr_f=0.2), rr_{SS}: replacement rate of sire of sons (r_{SS}=0.25), rr_{SD}: replacement of sire of daughters (rr_{SD}=0.25), w: live daughters per dam of daughters (w=0.4), f_{ps}: fraction of young bulls pre-selected (f_{ps}=1).

By multiplying selection intensity and selection accuracy in each pathway, genetic superiority in units of genetic standard deviation, was calculated as follow:

$$\Delta G=\Delta G_{SS}+\Delta G_{SD}(1-P)+\Delta G_{YB}P+\Delta G_{DS}+\Delta G_{DD}$$

Test capacity and number of daughters per young bulls were changed to find the optimum value of them for the Iranian situation.

Results and discussion

Genetic gain under the current breeding program. Genetic improvement in each pathway for Iranian Holsteins, considering equations in Table 1, was 5.105 genetic standard deviation per generation. These improvement in SS, SD, YB, DS and DD were 2.23, 1.38, 0, 1.39 and 0.38 genetic standards deviation per generation, respectively. The results indicated that 44 and 27 percent of genetic gain is resulted from SS and DS paths, respectively. There is no selection intensity in YB pathway; because no pre-selection is happening for milk production when sampling YBs.

Considering sex-age distribution in each pathway, generation interval was 6.5, 7.5, 3.37, 4.22 and 4.10 year for SS, SD, YB, DS and DD pathways, respectively. Average generation interval according to 20% test capacity was 5.37 years. By genetic standard deviation of 540 kg for milk production (Toghiani, 2007) genetic improvement for milk production would be 128.7 kg /year. Ayoghi et al. (2007) and Shadpoor et al. (2008) reported the expected maximum genetic gain for milk yield in Iranian Holsteins around 71.8 and 77 kg, respectively. The smaller predicted value on their studies could be a consequence of not considering all effective pathways in predicting genetic improvement which has led to underestimation of expected genetic gain.

The genetic trend of milk production trait in Iranian Holstein cows estimated in the current study (44.44 kg per year in dam pathways) was higher than the results of 33 kg per year reported by Razmkabir et al. (2006) from 1988 to 2002. This result could indicate that the 4-pathway selection is not performed in Iran and this is, in turn, a consequence of considering traits other than milk yield in selection. Also the result could be somewhat due to lower accuracy and intensity of selection than is expected from the model. The other reason is that in the current model, it has assumed that semen from the best proven bulls is used by dairymen. While in most situations, dairymen do not respect the rules and buy their favorite sire's semen which sometimes lead to more inbreeding or even overestimation of genetic gain, leading to less efficient selection. There is a high variation in number of daughters per young bulls in Iran. This variation could be the other reason for lower genetic improvement in practice compared to the expected values.

Change in number of daughters per YB and test capacity. Maximum genetic improvement, holding test capacity unchanged, occurred when the number of daughters per young bulls (*n*) increased to 46 daughters in genetic evaluation of YBs ($\Delta G=5.25\ \sigma^{2}_{A}$/generation). Increase in the number of daughters resulted to the higher selection accuracy in sire pathways. But it also decreases the number of sampled young bulls, which leads to lower proportion of selection in the corresponding pathways. Also, the maximum genetic gain was observed when 30% of cow population were mated to YBs ($\Delta G=5.21\ \sigma^{2}_{A}$ /generation). The most important path in defining the maximum genetic improvement by changing the test capacity was SD path. The number of sampled young bulls on 30% test capacity and with 100 daughters per YB was 107. By increasing *P*, the proportion of cow population inseminated by young bulls increase and it leads to increasing the genetic contribution of young sires in the population. However this is a positive factor in term of shortening the generation interval, but, it has unfavorable effect due to reduction of the contribution of proven sires in the next generation. Simultaneous change in young bull's test capacity (*P*) and number of daughters per young bulls resulted in the highest genetic improvement at $P=0.3$ and $n=57$ ($\Delta G=5.28\ \sigma^{2}_{A}$ /generation). Around 188 young bulls have to be sampled under this optimal condition. The trend is shown in Figure 1. Optimization of progeny testing program could be more effective when considering concurrent change of *n* and *P*.

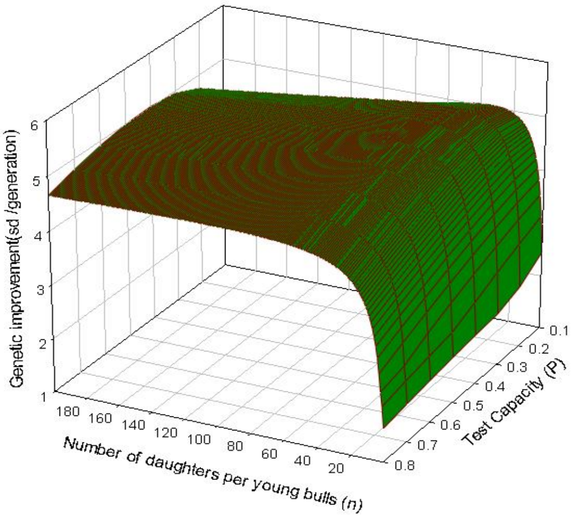

Figure 1: Change in genetic improvement (genetic standard deviation per generation) by simultaneous change in test capacity and number of daughters

Conclusion

Because of moderate value of heritability for milk production, it is expected that by considering multi trait selection index procedure and including traits with low heritability (functional traits) or with negative correlation with milk production (fat yield) number of needed daughters per young bulls will increase somewhat. Importance of improvement of genetic trend inside the country, using a managed progeny testing scheme and considering the relation between different selection pathways are necessary in breeding program in Iran. Although considering new molecular techniques like genomic information in animal breeding, makes investigation of different traits easier than before, it is expensive for developing countries. Therefore importance of conventional progeny testing scheme is yet considerable.

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