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Potential of Genomic Breeding Program in Iranian Native Chickens

Research Article

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ABSTRACT

Development of genomic selection can be a new strategy in breeding of native chicken. The main aim of this study was to evaluate application of a genomic selection program in Iranian native chickens from economic and genetic points of view. In this study, two scenarios including conventional scenario with 3360 and 3380 animals and genomic scenario were compared using ZPLAN+ software. The traits in the selection index were egg number, body weight, mean weight of egg and age at sexual maturity. In genomic scenario different reference population size were considered. In this scenario the genomic information from cocks (800 cocks were genotyped) was added to available information in conventional scenario based on selection index method. The generation interval was 14.5 months for all conventional and genomic scenarios. In comparison of scenarios, genetic gain and the economic profit increased by increasing reference population size in genomic scenario (€126.88-€147.45 with 80 cocks) and (€140.20 to €160.77 with 60 cocks) per animal unit. The reliability of selection index was 0.33 for cocks in conventional scenario. The reliabilities of genomic scenarios were 0.61-0.84 for 80 selected cocks and 0.66-0.87 for 60 selected cocks and that were high in comparison to conventional scenario. This study showed that genomic selection can increase the genetic improvement rate of native chickens. However, the costs of genomic scenarios were higher than conventional scenario, but genomic information increased accuracy of selection and genetic gain in breeding goals traits.

KEY WORDS economic profit, genetic gain, genomic selection, simulation.

INTRODUCTION

The village production system comprises more than 80% of world poultry population, and is allocated to 90% of poultry products in some unindustrialized countries (Niknafs *et al.* 2013). Indigenous chickens, despite their low growth rate and egg production, are generally better in disease resistance and could maintain higher level of performance under poor nutrition and high environmental temperatures compared to commercial strains under village systems (Yousefi Zonuzi *et al.* 2013). Over the last 50 years, genetic selection in poultry has proven to be extremely successful (Wolc, 2015). With release of the draft chicken genome sequence (Hillier *et al.* 2004); the first single nucleotide polymorphism (SNP) panel for chicken was developed. With rapid advances in technology, chips density increased from 6000 (2007) to 600000 SNPs (Wolc, 2015). Similarly, the number of available genotypes for analysis has increased from a few hundreds of individuals per line initially to tens of thousands birds now. Routine non-research application of genomic selection was started in 2013, and the first genomic selected birds generated descendants that was entered the market as commercial birds in 2015 (Wolc, 2015). In conventional breeding programs for poultry, selection of birds was based on phenotypic and pedigree information. The development of genomic selection introduces new strategies in animal breeding. Application of genomic selection in breeding programs on the one hand with increasing accuracy of estimated breeding values and decreasing general interval on the other hand, maximize the genetic gain in breeding programs (Van der Werf, 2013). Genomic selection initially was introduced by Nejati *et al.* (1997) who suggested that the accuracy of their total allelic relationship is higher than traditional pedigree relationship, and this method was modified by Meuwissen *et al.* (2001). They showed that the breeding value could be predicted with an accuracy of 0.85 from marker data alone. Genomic selection has a major limitation for implementation since it need genotyping of large numbers of markers for implementation and the costs of genotyping for these markers is high, especially for developing countries (Goddard and Hayes, 2007). To overcome this problem, before applying genomic selection, different scenarios have to be compared using computer simulation. For this purpose, the ZPLAN+ software is was used.

ZPLAN+ software is a very useful tool to optimize conventional and genomic breeding programs (Täubert *et al.* 2010). This software allows modeling of all relevant breeding structures, while taking all relevant biological, technological and economic parameters for complex breeding programs into account (Sitzenstock *et al.* 2013). It accommodates predefined genetic and phenotypic parameters and pre-set breeding objectives and selection criteria by the user along with selection groups (Atiyat, 2014). This software then generates results such as the annual genetic gain for the breeding objective using a pure deterministic approach (Nitter and Graser, 1994).

This program has been based on the discounted gene flow-method (Hill, 1974) and selection index theory (Hazel, 1943). This software calculates genetic gain, discounted return, profit and costs within and over selection paths. The monetary gains are in ZPLAN+ standardized to an animal unit and are given per year.

There are six native chicken breeding centers in Iran. In the last thirty years, these populations were under genetic improvement by traditional methods. However, considering the conditions of this flock, there have been some challenging problems, such as recording of pedigree and yield traits. To overcome this challenge one solution is using genomic selection. Thus, the main aim of this study was to evaluate the value of genomic selection program in Iranian native chickens in Fars breeding province from economic and genetic point of view.

MATERIALS AND METHODS

Fars native fowl center was established in 1986. In 1986, about 4000 cocks and hens were collected from Tropical, mild and cool areas from Fars province. In 1987, about 2500 birds of both sexes remained to produce hatching eggs, and chicks produced from these eggs in 1988. Genetic improvement is done by selecting the best 80 cocks (selection of 80 cocks was on based full-sib and half-sib information) and 880 hens as parents of the next generations. In this center the birds were selected based on egg number at the first 12 weeks of production, body weight in 12 weeks of age, age at sexual maturity and average egg weight at 28, 30 and 32 weeks old of chickens.

In this study for simulation of the native chickens breeding programs, the ZPLAN+ software was used. For this simulation, genetic and phenotypic parameters including economic weights, phenotypic standard deviations, heritability and genetic and phenotypic correlations of traits were used. The selected animals in breeding scenarios which were selected from 7301 proven animals were 3380 hens (in scenario with selection of 80 cocks) and 3360 hens (in scenario with selection of 60 cocks).

A conventional scenario was simulated based on phenotypic information and a genomic scenario was designed based on conventional scenario; in this scenario, the combination of genomic information and phenotypic information were used. In genomic scenario genomic information of 800 cocks, as well as different sizes of reference population were used (500, 1000, 1500 and 2000 animals). Additionally, square of accuracies that were calculated by ZPLAN+ were considered as reliability of breeding values.

Breeding objectives

The traits of breeding objectives in this study were body weight at 12 weeks of age (BW_{12}), egg number (EN) during the first 12 weeks of the laying period due to the average period of Fars native fowl is 12; so that during the selection only 12 weeks of laying period were monitored, average egg weight (AEW) at 28, 30 and 32, weeks old of chickens and age at sexual maturity (ASM). The traits of selection index were the same as breeding objectives traits.

Conventional scenario

A conventional scenario with 3461 and 3441 birds was simulated for a planning period of twenty years for Fars native chickens.

The numbers of animals were the same in each generation. The 880 hens and 80 or 60 cocks were used in each generation. All birds were reared on the floor for 12 weeks. Following that, 2500 female chicks were selected from 4000 reared chicks and 800 male chicks from 4000 cocks in a pre-selection were selected according to their body weights, transferred into the individual cages and their production traits were recorded. The collected data from the individuals included BW_{12}, EN, AEW and ASM.

These selected birds were tested from age 20 to 51 weeks (32 weeks). Then from these 2500 hens, 880 hens were selected. In selection of cocks, for considering different selection intensity two groups 80 and 60 cocks were selected from 800 cocks based on combination of information of 30 half-sibs and 10 full-sibs.

Table 1 provides the economic weights (EW) and phenotypic standard deviations and Table 2 is shown heritability and genetic and phenotypic correlations for studied traits. Economic weights were based on the equations of the study of Kianimanesh *et al.* (2001) and the other parameters were extracted from the study of Deimi and Alijani (2011).

Based on requirements of the ZPLAN+ software, the economic weights were converted to Euro currency. In ZPLAN+ the economic weight is designed per phenotypic standard deviation and they are absolute economic weights. To approximate the value of phenotypic standard deviation, the coefficient value (CV) of traits were assumed 10% and this value product in corresponding means of traits (Alshami, 2014). The variable costs of rearing a cock or a hen were assumed to be €11 per animal (over a period of 20 weeks). During production, daily feeding costs resulted from a feed consumption of 0.11 kg per day at a price of €0.33 per kg. For each cock and hen, additional costs for the animal care (€5) were assumed. Performance testing caused additional costs of €1 per hen. The fixed costs were not considered in conventional scenario, because it was difficult to quantify them in breeding program. However, these costs must reduce from profit.

The interest rate was set to 4% for discounted costs and 5% for discounted returns. For better comparison, obtained values of the conventional scenario were set as 100% and the values of genomic scenario were expressed relative to these reference values.

Genomic breeding program

In ZPLAN+ software a genomic counterpart trait for each conventional trait is defined to be the genomic estimated genomic breeding value (GEBV) for that trait, based on the given reference population size. The background for implementing of genomic information in the selection index on this basis was developed by Dekkers (2007). This approach requires the correlation of the true and the GEBV ($r_{Q\hat{Q}}$) to define for every genomic trait. This is done using the formula presented by Erbe *et al.* (2011):

$$r_{Q\hat{Q}} = w\sqrt{\frac{N\,r_{TI}^2}{N\,r_{TI}^2 + Me}},$$

Where:
N: size of the reference population.
w: calibration factor.
r_{TI}^2 : reliability of the GEBV of the animals used in the reference population.
Me: number of independently segregating chromosome segments, which was derived by Goddard (2009) as:

$$Me = \frac{2NeL}{ln(4NeL)},$$

Where:
Ne: effective population size, which was assumed to be 80 and 60 and L is the length of the genome in Morgan unit which was set to 32, Marker density was 50000 SNP and Markers distribution were three markers per cM based on Groenen *et al.* (2009), leading to Me= 554 (Ne=80) and Me= 429 (Ne=60).

The calibration factor w is the accuracy of GEBV that is hypothetically obtained with a reference population of infinite size using the given SNP density (Sitzenstock *et al.* 2013). For different traits in dairy cattle and for GEBV from a 50 k SNP chip this factor was w~ 0.9 on the basis of study of Erbe *et al.* (2011). Therefore it is assumed that w~ 0.9.

The monetary genetic gain per year was calculated as $\Delta G = \frac{i * r_{TI} * \sigma_T}{\Delta T}$ (Haberland *et al.* 2013):

Where:
i: selection intensity.
r_{TI}: accuracy of the index.
σ_T: standard deviation of the breeding goal.
ΔT: generation interval.

In this scenario, the genomic information of cocks was added to available information in conventional scenario based on selection index method of Dekkers (2007). While all selection decisions were made at the same time as in the conventional scenario.

RESULTS AND DISCUSSION

Conventional scenario

The genetic gain per year for each trait with selection of 80 and 60 cocks from 800 cocks is shown in Table 3. In the ZPLAN+ software the deterministic method is used for simulation, the genetic gain values are used for comparison of scenarios. With increasing of the intensity of selection, genetic gain of traits was improved. Considering these results use of a selection intensity 60 cocks can also reduce cost of the breeding program.

Table 1 Phenotypic standard deviation and economic weights of traits in simulation of breeding programs

Traits	Phenotypic standard deviation	Economic weights (€)
EN (No.)	5.3	0.01
BW_{12} (g)	78.01	0.006
AEW (g)	4.38	0.05
ASM (day)	16.66	-0.03

EN: egg number at the first 12 weeks; BW_{12}: body weight in 12 weeks of age; AEW: average egg weight in 28, 30 and 32 weeks and ASM: mean age at sexual maturity.

Table 2 Used heritability (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) for simulation of studied traits (Deimi and Alijani, 2011)

Traits	EN	BW_{12}	AEW	ASM
EN (No.)	**0.33**	0.03	-0.21	-0.69
BW_{12} (g)	0.10	**0.54**	0.50	-0.11
AEW (g)	-0.10	0.36	**0.64**	0.09
ASM (day)	-0.63	0.16	0.11	**0.51**

EN: egg number at the first 12 weeks; BW_{12}: body weight in 12 weeks of age; AEW: average egg weight in 28, 30 and 32 weeks and ASM: mean age at sexual maturity.

Table 3 Genetic gain per year in the conventional scenario, expressed in genetic standard deviations

Traits	Genetic gain	
	80 cocks	60 cocks
EN (No.)	0.006	0.006
BW_{12} (g)	3.41	3.55
AEW (g)	0.17	0.18
ASM (day)	-0.19	-0.20

EN: egg number at the first 12 weeks; BW_{12}: body weight in 12 weeks of age; AEW: average egg weight in 28, 30 and 32 weeks and ASM: mean age at sexual maturity.

The discounted return per animal unit in the conventional scenario with 80 cocks was €153.64 per year and for 60 cocks were €160.37 per year. The variable costs for conventional scenario with 80 and 60 cocks were €25.73 and €25.88, respectively, per animal unit. This resulted in a profit of €127.91 and €134.48, per animal unit, respectively. By decreasing number of selected cocks from 80 to 60 cocks, the profit of conventional scenario was increased. This could be caused by the increase in selection intensity. The number of animals per animal unit was 2500, resulting in a profit of €0.051 and €0.053 (for 80 and 60 cocks, respectively) per native hen.

Genomic scenario

Since in this scenario, genomic information of cocks was added in the conventional scenario at the time of selection, generation interval was not reduced and it was equal 14.5 months. Also, the costs of the performance testing of the hens were not reduced. The variable costs in genomic scenario were fixed and were equal to €59.07 and €59.41 per animal unit (2500 hens) for scenarios with 80 and 60 selected cocks, respectively.

The discounted returns increased with increasing the number of birds in reference population. The profit in genomic scenario with selection of 80 cocks was higher in all of the reference populations, except for reference population of 500 animals, in comparison to the conventional scenario.

Also, the range of the profit was €126.88 to €147.45 (Figure 1A). Additionally in all of the reference population, the profit of genomic scenario with selection of 60 cocks was higher than conventional scenario and was €140.20 to €160.77 (Figure 1B) per animal unit.

The expected genetic gain changes for studied traits in native hens were compared relative to conventional scenario. These changes are shown in Figure 2 for four reference populations (500, 1000, 1500 and 2000 animals). The gain for all of the traits was higher in comparison to conventional scenario with 80 and 60 cocks. But this increasing in genetic gain was less intense for traits of AEW and ASM.

The gain increased for all of the traits with increasing the number of animals in reference population. The gain for ASM was negative and this is desirable, because by decreasing the age at sex maturity the production of animals will increase.

Reliability of breeding programs

The reliabilities of the selection index in conventional scenario and genomic scenario are shown in Figure 3. The reliability of the selection index in conventional scenario was 0.33 for male path. The reliability in genomic scenario was higher in comparison to conventional scenario (0.61-0.84 for 80 cocks and 0.66-0.87 for 60 cocks). Increasing reliability in genomic scenario is due to adding genomic information to conventional scenario.

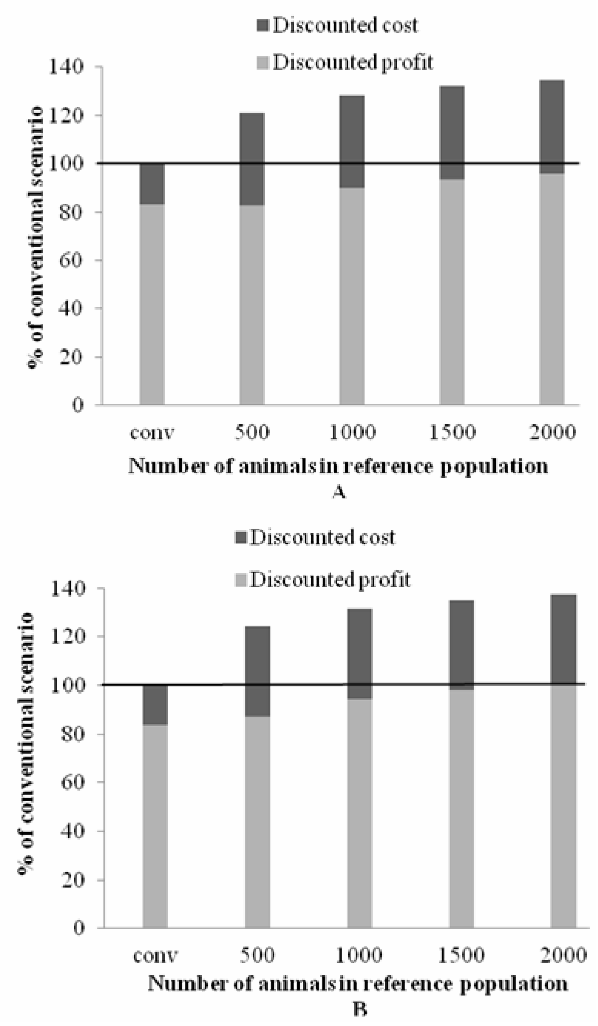

Figure 1 Discounted profit and discounted costs (sum=discounted return) for the genomic scenario with 80 cocks (Figure A) and for the genomic scenario with 60 cocks (Figure B)

The discounted return for conventional scenario is set to 100%

Conv: conventional scenario

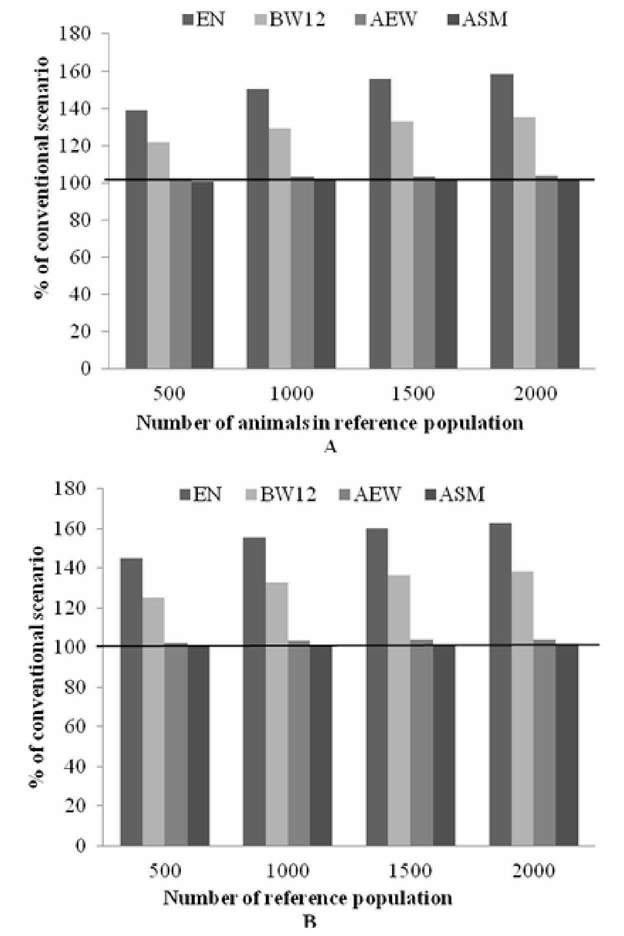

Figure 2 Genetic gain for individual traits in native hens for genomic scenario

EN: egg number at the first 12 weeks; BW_{12}: body weight in 12 weeks of age; AEW: average egg weight at 28, 30 and 32 weeks and ASM: mean age at sexual maturity

Genetic gain relative to the conventional scenario (set to 100%) with 800 genotyped cocks and different sizes of the reference population (Figure A for 80 selected cocks and Figure B for 60 selected cocks)

In this study, a genomic scenario was compared with conventional scenario. In the genomic scenario, the genomic information added as additional information to available information in conventional scenario.

Results show that genomic information have a positive effect on monetary genetic gain in studied genomic scenario in both state of selection and gains were higher in scenarios with 60 cocks in comparison to scenarios with 80 cocks. The reliability of the genomic information and the size of the reference population have a large impact on the benefits from genomic selection. The practical calculations for other farm animals with ZPLAN or ZPLAN+ showed the same trend (König *et al*. 2009; Haberland *et al*. 2010; Sitzenstock *et al*. 2010).

Increasing genetic gain in genomic scenario with 60 cocks was higher than other scenario (conventional scenario and genomic scenario with 80 cocks).

This is due to increasing reliability and selection intensity. In the genomic scenario, increase of genetic gain was associated with a strong increase in costs, mainly for marker genotyping. Higher costs of genotyped animals in reference population led to a considerable investment to be made in order to obtain an expected competitive advantage over a considerable period (20 years), which may or may not materialize and generate an economic profit. The part of these costs could offset by the greater discounted returns.

The genetic gain in individual traits from genomic selection was different between traits. The genetic gains increased with increasing the amount of genomic information and size of the reference population. In the conventional scenario, selection of hens and cocks was carried out after the hens were performance tested, at one year of age. This led to a generation interval of 14.5 months. In the genomic scenario, since genomic information was only added to conventional scenario as additional information, the generation interval was the same as in the conventional scenario.

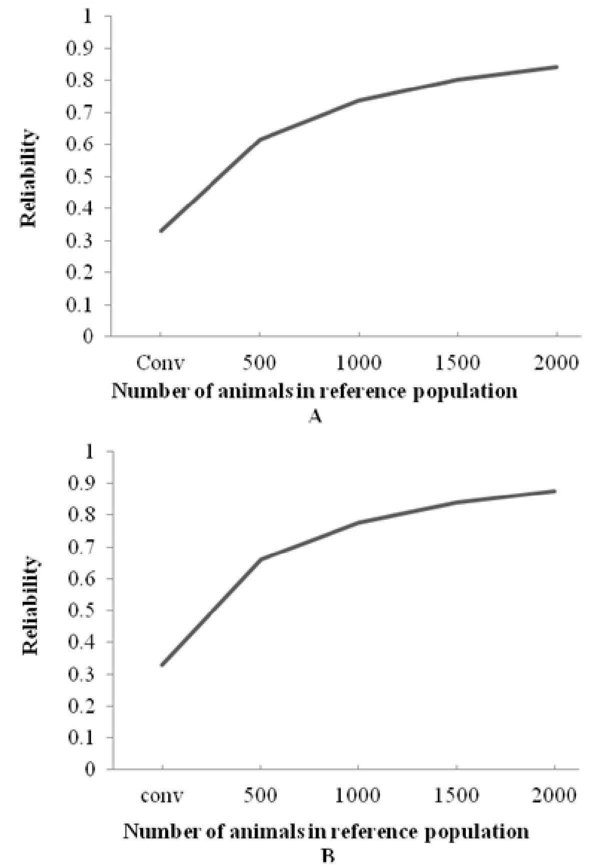

Figure 3 Reliability of breeding programs (Figure A for 80 selected cocks and Figure B for 60 selected cocks)

This study provided basis to optimize native hens breeding programs from an economic point of view. This study showed that with combination of genomic information and available performance information from the present generation in genomic scenario could increase the monetary genetic gain compared to the conventional scenario.

CONCLUSION

This study showed that genomic selection could increase the values of genetic improvement of native chickens. The costs of genomic scenario were higher of conventional scenario, but genomic information increased accuracy of selection and genetic gain of studied traits. To solve the cost problem, use of low-density SNP chips is suggested.

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