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# Estimation of Genetic Parameters, Inbreeding Trend and its Effects on Production and Reproduction Traits of Native Fowls in Fars Province

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Abstract: In this study, the data and pedigree records of the native fowls collected by Fars Native Fowls Breeding Center during 1990-2004 were analyzed. A pedigree file collected on 30855 hens and roosters was used to calculate the inbreeding coefficients and its trend and its effect on production and reproduction traits. The average of inbreeding coefficient for all birds was 0.002% ranging from 0 to 14.8%. In this population, 14% of the birds were inbred with an average inbreeding coefficient of 0.019%. The Inbreeding coefficient was considered as covariate to estimate its effect on economic traits including body weight in 12 weeks (BW<sub>12</sub>), egg number during 12 weeks (EN), mean egg weight between 28 to 32 weeks (MEW) and Age of Sexual Maturity (ASM). Results showed that inbreeding does not have a significant effect on the traits under study (p>0.05). Moreover, heritability, genetic and phenotypic correlations between traits was estimated through a multiple traits animal model procedure by restricted maximum likelihood using ASREML software. The estimated heritabilities were 0.53, 0.47, 0.57 and 0.22 for body weight in 12 weeks (BW<sub>12</sub>), Age of Sexual Maturity (ASM), mean Egg Weight (EW) and Egg Number (EN), respectively. Because of relatively high heritabilities of productive and reproductive traits, it is possible to achieve more genetic gains in these traits using appropriate genetic selection.

Key words: Inbreeding coefficient, heritability, correlation, animal model, Fars native fowls

## INTRODUCTION

Generally, indigenous breeds are considered as the national capital and strategic reservoir in each country where their conservation and reproduction is of great importance. They have continued to exist and reproduce after thousands of years natural and artificial selection, overcoming all environmental limitations and calamities. Iranian native chickens are the basic genetic material for breeding programs in their habitat. Therefore, a detailed understanding of these genetic resources can serve as a more accurate basis for breeding programs in the future and at the same time, can result in a reduced period for these programs and optimal use of available resources in order to increase production (Kamali, 1995). In this manner, conservation of these breeds along with an accurate plan to increase their productivity and profitability are very important. In fact, improving native chicken breeds leads to higher economic benefits and attracting more people in this section with an ultimate result of increased production, employment and even reducing migration from rural to urban areas (Flock et al., 1991).

In many developing countries, the genetic composition of native breeds still forms the basis for poultry breeding. The genetic resources of indigenous breeds of poultry can serve as the starting point for suitable breeds with appropriate production which is adapted to rural conditions (Hoffmann, 2005).

The breeding programs for Iranian native fowls began in 1981 and breeding centers are active in West Azerbaijan, Fars, Mazandaran and Isfahan provinces. Birds are evaluated and selected based on traits including body weight at weeks 8 and 12, the number of egg laying during 12 weeks, egg weight and age of sexual maturity (Kamali, 1995). These traits were selected with the aim of improving growth rates and increasing egg production so that meat and egg requirement in rural areas can be provided. A survey of genetic trends and performance of native fowls in different regions of the country shows a modest improvement in growth rate and egg production traits (Kamali, 1995).

The purpose of this study was estimating the genetic parameters, inbreeding trend and its effects on some production and reproduction traits of native fowls in Fars.

#### MATERIALS AND METHODS

Fars Native Chicken Breeding Center is located in Shams Abad, 70 km north of Shiraz. Selection in base population was based on phenotypic records and mating was random up to 1999. Recording was individual for all considered traits.

Data of 6032 roosters and 24823 hens were used to estimate the inbreeding coefficient and its effect on production and reproduction traits and also estimation of genetic parameters. The traits under study included body weight at week 12 (BW<sub>12</sub>), age of sexual maturity (ASM), number of eggs laid during 12 weeks (EN<sub>12</sub>) and mean egg weight in 28, 30 and 32 weeks (MEW) during 11 generations. Firstly, the accuracy of pedigree and data files was checked and inbreeding coefficients for all birds calculated using CFC program. Inbreeding coefficients were included in the analysis models for all traits as a covariate so that regression coefficient of each trait on inbreeding coefficient was considered as inbreeding depression. Final model for each trait was determined using GLM procedure through SAS software. Also the genetic and environmental Co (var) components were estimated using Derivative Free Restricted Maximum Likelihood (DFREML) algorithm (Meyer). The following multiple traits model was used:

$$y_i = X_i b_i + Z_i u_i + e_i$$

where, y<sub>i</sub> is the vector of observations in ith trait, b<sub>i</sub> is the vector of fixed effects (b<sub>1</sub> for BW included generation, hatch and sex, b<sub>2</sub> for EN<sub>12</sub> included generation, hatch and Days in Production (DIP) as covariate and b<sub>3</sub> and b<sub>4</sub> for AFE and MEW included generation and hatch), u<sub>i</sub> is the vector of random additive genetic effects of animals, e<sub>i</sub> is the vector of random residual effects and finally, X and Z are incidence matrices relating fixed and random effects to the records, respectively.

#### RESULTS AND DISCUSSION

Structure of the data with descriptive statistics is presented in Table 1. The highest phenotypic variation was related to  $EN_{12}$  with a CV% of 32, while the lowest phenotypic variation was related to MEW with a CV% of 7.3.

Average inbreeding coefficients of all birds, roosters, hens and inbred birds were 0.002, 0.016, 0.002 and 0.0019, respectively. The number of inbred birds was 4363 with a ratio of 14.14%. This was mainly due to preventing from mating the related birds. Results showed that productive and reproductive did not affected by level of inbreeding.

Table 1: Descriptive statistics of studied traits in Fars station

					Standard	
Trait	N	Mean	Min.	Max.	deviation	CV%
BW12	28701	840.3	300	1670	185.2	22
ASM	23816	166.6	88	268	18.4	11
EN12	23881	53	1	121	17.2	32.3
MEW	23246	43.8	19.5	65.9	3.2	7.3

 $BW_{12}$ : Body weight at week 12, ASM: Age of sexual maturity,  $EN_{12}$ : Number of eggs laid during 12 weeks, MEW: Mean egg weight

It seems that this caused by low number of inbred birds in this population. The reported average inbreeding coefficients of 0.048, 0.055, 0.047 and 0.676% for all, female, male and inbred birds in this population, respectively (Flock *et al.*, 1991). Also 34.5% of Fars province chickens were inbred with an inbreeding coefficient of 0.028% (Nwagu *et al.*, 2007). The inbreeding effects on productive and reproductive traits in chickens were studied by many researchers (Szwacczkowski *et al.*, 2004; Yerturk *et al.*, 2008; Sewalem *et al.*, 1999; Nwagu *et al.*, 2007) who reported the negative effect of inbreeding on economic traits.

The average of body weight at week 12, age at sexual maturity, egg number and egg weight were 840.3 g, 166.6 days, 53.0 n and 43.8 g, respectively. As it is clear in Table 2, the heritabilities of these traits were 0.53, 0.47, 0.57 and 0.22, respectively where the heritability for the EN<sub>12</sub> was low compared with BW<sub>12</sub>, MEW and ASM with high values. The heritabilities reported for body weight at 12 weeks, age at sexual maturity, egg number and egg weight at weeks 30 and 32 using a half sib model using three generations for this station were 0.70, 0.55, 0.29 and 0.52, respectively (Kamali, 1995).

Also the estimated heritabilities for BW<sub>12</sub>, EN<sub>12</sub>, MEW and ASM were 0.68, 0.40, 0.64 and 0.49, respectively (Flock et al., 1991). The heritabilities reported using multiple traits animal model for BW12, WSM (weight at sexual maturity), ASM, EN, EW<sub>28</sub>, EW<sub>30</sub> and EW<sub>32</sub> were 037, 0.34, 0.35, 0.19, 0.31, 0.40 and 0.39, respectively (Ibe et al., 1983). On the other hand the heritabilities of 0.24, 0.14, 0.36 and 0.15 for BW<sub>8</sub>, EP, EW and ASM for Mazandaran station was reported (Ibe et al., 1983). The estimated heritabilities reported in Rhode Island Red breed was 0.29, 0.75, 0.79 and 0.73 for egg number, egg weight, roosters and hen's body weight, respectively (Hagger, 1994). On the other hand, in the present study, a high negative genetic correlation was estimated between EP and ASM (-0.80), whereas the genetic correlation between EP with BW<sub>12</sub> and MEW were -0.21 and 0.22, respectively. The genetic correlation between EP with MEW, BW and ASM reported before, were -0.15, -0.07 and -0.44, respectively (Ibe et al., 1983). They also estimated correlations of 0.33 and 0.13 between MEW with BW and ASM, respectively.

Table 2: Estimated heritabilities (Diagonal), Genetic correlations (Upper diagonal) and phenotypic correlations (Lower diagonal)

Trait	BW12	EN12	MEW	ASM
BW12	0.53	0.22	0.17	-0.04
EN12	0.17	0.22	-0.21	-0.80
MEW	0.22	-0.12	0.57	0.22
ASM	-0.12	-0.60	0.19	0.47

 $BW_{12}$ : Body weight at week 12, ASM: Age of sexual maturity,  $EN_{12}$ : No. of eggs laid during 12 weeks, MEW: Mean egg weight

The genetic correlation between  $EN_{12}$  and MEW and  $EN_{12}$  and ASM was negative. This means that selection on each trait decreased the genetic gain in the opposite trait. On the other hand, there was a positive correlation between  $BW_{12}$  and MEW. So selection on body weight can improve the genetic mean in egg weight and vice versa.

Genetic correlations of MEW with BW<sub>12</sub> and MEW were positive (0.17 and 0.22, respectively). Therefore, by selection on each trait it is possible to achieve genetic improvement in another. Finally, there was a negative correlation between ASM and BW<sub>12</sub> (-0.44).

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