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# Genetic Analysis of Economic Traits in One of the Iranian Native Fowls Using Beysian Method

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**Abstract:** The genetic parameters including heritabilities and genetic, phenotypic and environmental correlations between most important economic traits in Mazandaran native chicken were estimated using baysian method with gibbs sampling. Data of Mazandaran breeding and conservation center collected during 15 generation was body weight at 8 weeks ($BW_8$), age at sexual maturity (ASM), mean egg weight (MEW) and egg production (EP). All traits were analyzed using Baeysian method and a multiple traits animal model including the direct additive genetic effect. The used software for estimation the (co) variances and parameters was BLUPF90 with a number of rounds of Gibbs sampling that had to be discarded as burn-in ranged between 4000 and 10000 for single and multiple traits analysis, respectively. The estimated heritabilities for $BW_8$, ASM, MEW and EP were 0.2764, 0.3513, 0.4730 and 0.1667 respectively. Most genetic correlations were negative except between MEW with BW8 and ASM. The highest positive and negative genetic correlation was between $BW_8$ and MEW (0.4241) and ASM with EP (-0.2084), while the lowest values was related to ASM with MEW (0.1800) and $BW_8$ and EP (-0.0474).

**Key words:** Heritability · Baysian method · Gibbs sampling · Economic traits · Native chickens

## INTRODUCTION

There is a variable climate condition in Iran caused by its extent and geographical location. The high genetic diversity between native chicken breeds resulting from their adaptation to diverse local environmental condition. Mazandaran Native fowl is one of the most important endemic breeds in region of northeastern Iran near the Caspian Sea under a national breeding and conservation project. This breed is a double purpose for meat and egg production often maintained in small populations in rural areas. According to the evidence there is a usable variation in this breed for growth and egg production characteristics.

An efficient selection program relies on estimated genetic and environmental parameters of the traits involved. So understanding of estimates for genetic and environmental parameters is helpful in determining the selection method to predict direct and correlated genetic progress.

Fig. 1: The map of Iran in which the Mazandaran Province near the Caspian Sea is highlited

The origin of term Bayesian is from the Reverend Bayes, who suggested Bayes' rule, which is the computational basis of Bayesian methods. Using the Bayesian methods in animal breeding was introduced in the context of threshold traits [1, 2]. However, although Bayesian techniques were theoretically effective and powerful, but they commonly led to formulas in which we

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have to solve multiple integrals in order to calculation the marginal posterior distributions used for Bayesian inference.

On the other hand because these integrals could not be solved, using the approximate methods, Bayesian inference was based on the mode of posterior distributions, often have similar results to the REML. Bayesian inference, especially Gibbs sampling would be an alternative for estimation the (co)variance components, genetic parameters and breeding values for economic traits. Recently, Bayesian analysis methods have been developed to linear models for estimation of breeding values in farm animal populations. The Gibbs Sampling algorithm can estimate random samples of parameter estimates on the basis of a given data set, by generating posterior distributions of parameter values. These values are proportional to the product of the observation probabilities and parameter probabilities. This method has only recently been applied to problems of animal breeding [3-11]. The aim of this study was to estimate the genetic parameters values for most economic traits in Iranian native chickens.

## MATERIALS AND METHODS

**Description of Data:** Data on 49536 pedigree, breeding and performance records of a native chickens maintained at the Conservation and Multiplying Station, Mazandaran (Iran) during 15 generations were utilized for the present study. The following traits were measured:

- Body weight at 8 weeks ($BW_8$): This trait was obtained by weighing the surviving hen at 8 weeks
- Age at sexual maturity (ASM): This was obtained by recording the age at first egg for hens
- Mean egg weight (MEW): This was obtained by taking the average weight of eggs at 28, 30 and 32 weeks and
- Egg production (EP): Eggs laid from first egg during 12 first weeks of production.

The number of records, varied between traits summarized in Table 1.

**The Analysis Model:** Editing consisted of pedigree and data file was carried out using Visual FoxPro program. The final model was select according the analysis of data using GLM procedure and SAS software.

All traits were analyzed using the following multiple traits animal model.

Table 1: Summary of data including observed mean, standard deviation and coefficient of variation

| | Trait | | | |
|---|---|---|---|---|
| | BW8 | ASM | MEW | EP |
| No of records | 49150 | 35461 | 35663 | 35965 |
| Average | 526.48 | 160.54 | 47.27 | 38.54 |
| Standard deviation | 125.98 | 17.96 | 4.46 | 16.89 |
| Coefficient Variation (%) | 23.92 | 11.19 | 9.44 | 43.82 |

$$y=Xb+Zu+e$$

Where:

y was the phenotypic vector of traits, b was the vector of fixed effects (sex, generation and hatch for $BW_8$, sex and generation for MEW and ASM and sex, generation and days in production as covariate for EP), u was the vector of random additive genetic value and e was the vector of random residual effect. X and Z were the incidence matrices relating the fixed and random effects to observations relatively.

BLUPF90 was applied for the genetic and environmental (co)variances and parameters estimation. The number of rounds of Gibbs sampling that had to be discarded as burn-in ranged between 4000 to 10000 for single and multiple traits analysis, respectively.

The 'boa' package in R was applied for means, modes, medians and standard deviations for all (co)variance components, as well as 95% high posterior density intervals (HPD) intervals based on the algorithm of Chen and Shao [13].

## RESULTS AND DISCUSSIONS

Table 2 displays the marginal posterior summaries for the heritabilities, genetic and environmental correlations of the fitted model.

The results showed that there are a very good genetic variation in this center especially for egg production and body weight so that the coefficient of variation of these traits are 24% and 44% respectively.

Estimates of heritabilities with their ranges presented in Table 2 were 0.2764(0.2532- 0.2994), 0.3513(0.3160-0.3869), 0.4730(0.4416-0.5042)and0.1667(0.1447-0.1847) for traits of $BW_8$, ASM, MEW and EP, respectively.

The genetic and environmental correlation of traits is in Table 2. As is clear heritabilities for $BW_8$, ASM, MEW and EP are 0.2764, 0.3513, 0.4730 and 0.1667 respectively. In the other hand the ratio of additive genetic to phenotypic variance for MEW is higher than other traits.

Table 2: Estimates, Minimum and Maximum of heritabilities, genetic and environmental correlations between body weight at 8 weeks (BW8), Age at Sexual Maturity (ASM), Mean Egg Weight (MEW) and Egg Production (EP)

| | BW8 | | | ASM | | | MEW | | | EP | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Trait | Estimate | Min | Max | Estimate | Min | Max | Estimate | Min | Max | Estimate | Min | Max |
| BW8 | 0.2764 | 0.2532 | 0.2994 | -0.12040 | -0.18650 | -0.02170 | 0.4241 | 0.3532 | 0.5093 | -0.0474 | -0.1476 | 0.0389 |
| ASM | -0.1793 | -0.2180 | -0.1484 | 0.35130 | 0.31600 | 0.38690 | 0.1800 | 0.1042 | 0.2879 | -0.3954 | -0.5080 | -0.3043 |
| MEW | 0.0496 | 0.0156 | 0.0796 | 0.07751 | 0.03589 | 0.12167 | 0.4730 | 0.4416 | 0.5042 | -0.2084 | -0.3071 | -0.1102 |
| EP | 0.0255 | -0.0008 | 0.0565 | -0.17520 | -0.20780 | -0.14020 | 0.0102 | -0.0193 | 0.0462 | 0.1667 | 0.1447 | 0.1847 |

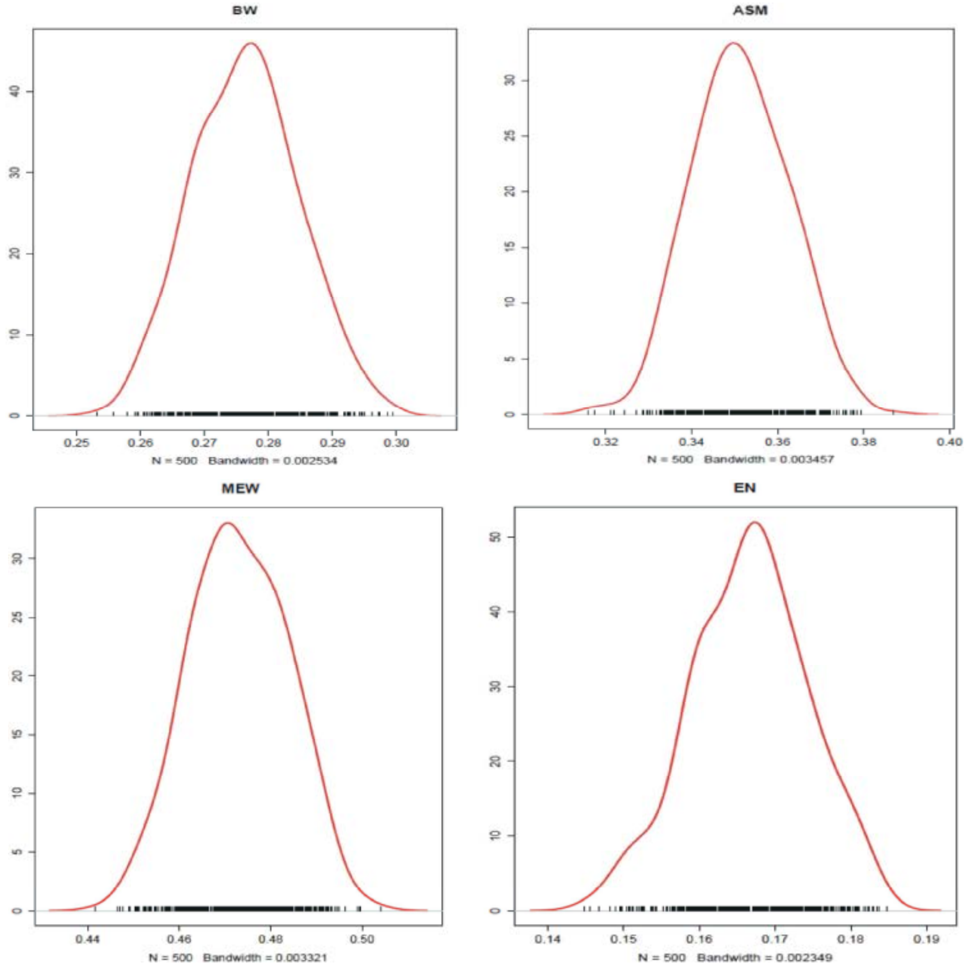

Fig. 2: Posterior densities of heritabilitie of body weight at 8 weeks, Age at Sexual Maturity, Mean Egg Weight and Egg Production

These results are very close to values reported by some Iranian researcher using Baysian method [14] but with a smaller ranges (0.21- 0.33 for BW, 0.30- 0.40 for ASM, 048- 0.53 for MEW and 0.13-0.19 for EP, respectively). Also these parameters were close to estimated values with small differences [15]. The differences between estimated heritabilities can caused by different fitted models, differences between structure of used population and data analysis method. Also differences can cause by genetic response from selection during last generations.

On the other hand the direct genetic correlation between traits presented in Table 2. The correlation of $BW_8$ with ASM, MEW and EP was -0.1204, 0.4241 and -0.0474, respectively.

The correlation of ASM with MEW and EP was 0.1800 and -0.3954, respectively and between MEW and EP was -0.2084.

Most genetic correlations were negative except between MEW with $BW_8$ and ASM. The highest positive and negative genetic correlation was between $BW_8$ and

MEW (0.4241) and ASM with EP (-0.3954), while the lowest values was related to ASM with MEW (0.1800) and $BW_8$ and EP (-0.0474).

Results showed that there are medium and negative genetic correlation between ASM and EP. This means that by selecting hens with less age at sexual maturity egg production will be increased. The positive genetic correlation between ASM and MEW show that we delaying in sexual maturity can cause heavier eggs and reversely. Generally there is a good genetic variation in native fowls for economic traits can be applied in breeding strategies in the future.

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