

NEW APPROACH FOR ESTIMATING OF HERITABILITY IN HONEYBEE POPULATION

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ABSTRACT: In honeybee colonies most of the economic, behavioral and race traits are influenced by queen significantly. In this study, heritability of honey production was estimated by maternal model which has been suited for farm animals previously. For our estimation, ASReml software and honey recording data from 3 generation pedigree of Iranian honeybee breeding stock were used. In current study, the heritability was reported 0.18 ± 0.05 . Our estimation for honey production is the first step for estimating and improving of other important traits of beekeeping industry in the Mid East.

Key words: heritability, honey production, maternal model, ASReml software.

INTRODUCTION

Heritability (h^2) is the proportion of phenotypic variation in a population that is due to genetic variation between individuals. Phenotypic variation among individuals may be due to genetic and/or environmental factors. Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. It is measured by estimating the relative contributions of genetic and non-genetic differences to the total phenotypic variation in a population. Heritability is an important concept in quantitative genetics, particularly in selective breeding and behavior genetics (for instance the Twin study), but is less widely used in population genetics [1].

Heritability measures the fraction of phenotype variability that can be attributed to genetic variation. This is not the same as saying that this fraction of an individual phenotype is caused by genetics. In addition, heritability can change without any genetic change occurring. For example, if both genes and environment have the potential to influence intelligence, but if a given sample of individuals shows very little genetic variation and a great deal of environmental variation, then the contribution of genetic variability to phenotype variability in that sample will be lower than if the sample showed greater genetic variability. Because of this heritability is specific to a particular population in a particular environment [1].

Individuals with the same genotype can exhibit different phenotypes through a mechanism called phenotypic plasticity, which makes heritability difficult to measure in some cases. Recent insights in molecular biology have identified changes in transcriptional activity of individual genes associated with environmental changes. However, there are a large number of genes whose transcription is not affected by the environment [1].

It is important to estimate heritability of a desirable characteristic before beginning a program of selective breeding. The estimate of h^2 is a pragmatic measurement that predicts breeding success.

If a characteristic can be rapidly changed with selective breeding heritability will probably fall. As a general rule, it is reasonable to attempt selective breeding if $h^2 > 0.25$ [2].

There are essentially two schools of thought regarding estimation of heritability:

One school of thought was developed by Sewall Wright at The University of Chicago, and further popularized by C. C. Li (University of Chicago) and J. L. Lush (Iowa State University). It is based on the analysis of correlations and, by extension, regression. Path Analysis was developed by Sewall Wright as a way of estimating heritability. Methods such as selection experiments, comparison of close relatives, large complex pedigrees are located in this category [1].

The second was originally developed by R. A. Fisher and expanded at The University of Edinburgh, Iowa State University, and North Carolina State University, as well as other schools. It is based on the analysis of variance of breeding studies, using the intraclass correlation of relatives. Various methods of estimating components of variance (and, hence, heritability) from ANOVA are used in these analyses [1].

For several decades Robinson (1980) concerned the existence and importance of maternal effects in beef cattle, dairy cattle and swine. It is clear that maternal effects are important in all these three species. Unless management programs and selection methods take maternal effects into consideration, selection efficiency will be reduced [3].

Furthermore, Moretto et al (2004) reported that all breeder queens of Africanized honeybee (*Apis mellifera*) with high rate of acceptance rate will also generate daughter queens with high acceptance rate [4]. Bienefeld and Pirchner (1990), moreover, reported that honeybee queen genotype influences the gentleness of workers noticeably [5]. Velthuis (1997) stated that honeybee queen pheromones affect behavior of colony [6].

Since in our breeding stock we did not have any strategy for distinguishing drone producing colonies and there had not been recorded any performance data for drone producing colonies we used maternal model to estimate heritability of honey production and compare its quantity with reported range by other scholars.

MATERIALS AND METHODS

Original breeding stock

This study was conducted on the existed breeding stock in animal science research institute, Karaj, Iran. In breeding stock, every generation those quality queens which showed gentle behavior, less swarming behavior and high honey production selected and propagated for production of daughter queens.

Honey production

Honey production was measured by weighing the boxes of honey as they were removed by the staff and subtracting the tare weight of the boxes from the total weight [7].

Adult bee population. Adult worker bee population was visually determined by estimation of combs number covered by bees in each colony. The frames that covered thoroughly in 2 sides by adult bees considered as 1 frame whilst the less populous frames accounted fraction of 1 frame [7] (Figure 1).



Figure 1. Measuring of adult bee population.

Brood population. The brood population was measured as following: one prototype frame which divided to 5*5 cm² compartments was used. By lodging this frame on the brood frames of each colony the compartments of the brood population was accounted for trial colonies [8] (Figure 2).

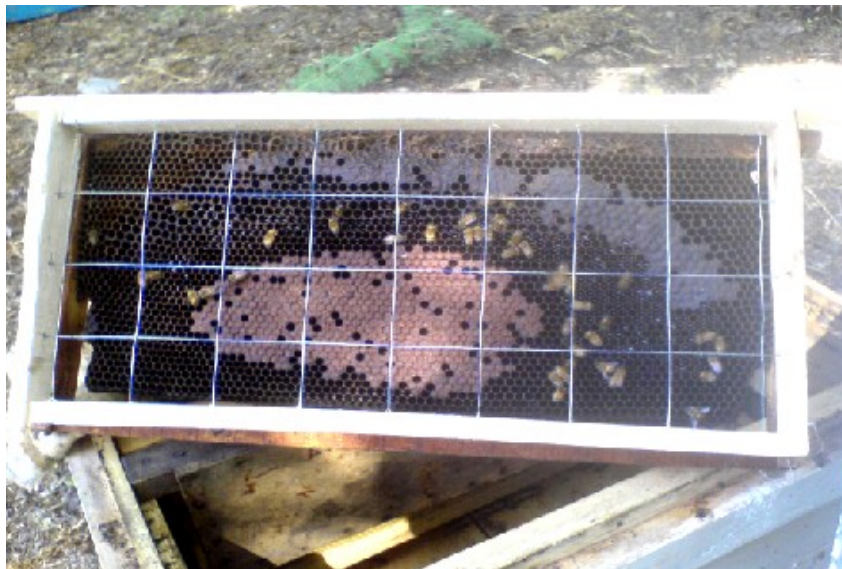


Figure 2. Measurement of brood population.

Data Analysis

Briefly model can be explained in following equation

$$y_{ijklm} = \mu + S_j + b_k (\text{Brood}_k - \overline{\text{Brood}}) + b_l (\text{Adult}_l - \overline{\text{Adult}}) + d_m + e_{ijklm}$$

In this model y_{ijklm} is the performance of i_{th} colony in 3 consecutive year ($j= 1, 2,3$) with especial brood population(k) , adult population(l) and special maternal effect. Furthermore, brood population (Brood_k) and adult population (Adult_l) was considered as a covariate. In addition to, d_m , an additive genetic of breeder m , was considered as a random effect. Moreover, e_{ijklm} was considered as a residual effect.

BULP animal model with maternal effect used in analysis can be explained by formula as follows:

$$y = Xb + Zm + e$$

y = performance vector

b = vector of fixed effects

d = vector of random effects (additive genetic of queen)

e = vector of error effect (residual effect)

x = matrix which contributes observations to fixed effects

z = matrix which contributes observations to random effects

Matrix of variance covariance between maternal and residual effects, also, is shown below:

$$V \begin{bmatrix} m \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_m^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix}$$

In this equation, A is the matrix of relationship between all queens in the pedigree. In addition to, σ_m^2 and σ_e^2 shows the genetic variance of maternal effects and residual effects accordingly. Prediction of genetic variance and variant was obtained from maternal model analysis using ASREML software with NRM inclusion [9]. Convergence was assumed achieving when two iterations resulted loglikelihood value of less than 0.0002.

Estimation of maternal effect heritability was based on

a quotient: $h^2 = \sigma_m^2 / \sigma_p^2$. In this equation σ_p^2 is total phenotypic variance.

For significance test of heritability, confidence interval of 95% was used.

RESULTS AND DISCUSSION

Interestingly, heritability of honey production has been reported in a massive range, from 0.07 to 1 in different breeds. Our range for heritability is similar to reported range of Pirchner and Ruttner (1962) and Ruttner (1962). Pirchner and Ruttner (1962) reported 0.23 for heritability of honey production [11]. Bienefeld and Pirchner (1990), moreover, based on performance of workers and queens declared 0.26 and 0.15 for heritability of honey production respectively [10]. Nevertheless, other scholars have reported different quantities for heritability of honey production. For instance, Malkov and Sedykh (1980) for honey production announced massive range from 0.7 to 0.27 [12]. Oldroyd et al. (1987), furthermore, based on diallel crosses reported heritability of honey production around 0.42 ± 0.24 [13]. In addition to, Soller (1967) asserted that there was around 0.57, 0.6 and 0.58 for heritability of honey production during spring months, summer months and throughout the year accordingly [14]. Banby (1967) based on clover and linen reported heritability of honey production around 1 and 0.75 respectively [15]. Collins et al. (1984) inseminated inbred *Apis mellifera Italica* daughter queens with a single drone from *Apis mellifera mellifera* or Africanized honeybee colonies and thereafter evaluated workers performance. They reported heritability of honey production from 0.2 to 0.92 for different environmental conditions [14].

Low heritability of honey production in our study ($h^2 = 0.18 \pm 0.05$) shows that in our breeding stock honey production is more affected by non-additive genetic variance and environmental agents. Therefore, it is thought that applying two way selections for generating inbred lines and thereafter crossing them is effective way for rising honey production in Iranian honeybee.

On the other hand our method for estimating of heritability is compatible for other important traits in honeybee population such as race morphological traits, general behavior, colony development, productivity and resistance to diseases and pests. Massive pedigree information and controlled drone congregation area, moreover, will estimate genetic component accurately and accelerate improving of breeding stock.

CONCLUSION

Since many of important and economic traits in honeybee colonies are affected with queen directly or indirectly, we inspired to estimate heritability of honey production based on maternal model which is more compatible in farm animals such as cattle and sheep. We hope, also, to estimate heritability of other important traits based on this model.

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