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Genetic parameters for weight, morphometry and oviposition of Africanized honeybee queens using simulated data

[*Parâmetros genéticos para peso, morfometria e oviposição de abelhas rainhas africanizadas sob simulação*]

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ABSTRACT

This study aimed to estimate genetic parameters for simulated data of body weight (BW), abdominal width (AW), abdominal length (AL), and oviposition. Simulation was performed based on real data collected at apiaries in the region of Campo das Vertentes, Minas Gerais, Brazil. Genetic evaluations were performed using single- and two-trait models and (co)variance components were estimated by the restricted maximum likelihood method. The heritability for BW, AW, AL and oviposition were 0.54, 0.47, 0.31 and 0.66, respectively. Positive genetic correlations of high magnitude were obtained between BW and AW (0.80), BW and oviposition (0.69), AW and oviposition (0.82), and AL and oviposition (0.96). The genetic correlations between BW and AL (0.11) and between AW and AL (0.26) were considered moderate and low. In contrast, the phenotypic correlations were positive and high between BW and AW (0.97), BW and AL (0.96), and AW and AL (0.98). Phenotypic correlations of low magnitude and close to zero were obtained for oviposition with AL (0.02), AW (-0.02), and BW (-0.03). New studies involving these characteristics should be conducted on populations with biological data in order to evaluate the impact of selection on traits of economic interest.

Keywords: *Apis mellifera*, correlation, heritability, selection

RESUMO

Objetivou-se estimar parâmetros genéticos para dados simulados de peso corporal (PC), largura abdominal (LA), comprimento abdominal (CA) e oviposição (OV). A simulação foi conduzida com base em dados reais, coletados em apiários da região do Campo das Vertentes, Minas Gerais. As estimativas das análises genéticas foram realizadas por modelos uni e bicarácterísticos, sendo os componentes de (co) variância estimados pelo método da máxima verossimilhança restrita. As herdabilidades para PC, LA, CA e OV foram de 0,54, 0,47, 0,31 e 0,66 respectivamente. As correlações genéticas foram positivas e de alta magnitude para PC e LA (0,80), PC e OV (0,69), LA e OV (0,82) e CA e OV (0,96). Para PC e CA (0,11) e LA e CA (0,26), as correlações genéticas foram moderadas e de baixa magnitude. As correlações fenotípicas foram positivas e de alta magnitude para PC e LA (0,97), PC e CA (0,96) e LA e CA (0,98). Para OV e CA (0,02), OV e LA (-0,02) e OV e PC (-0,03), foram encontradas correlações fenotípicas de magnitude baixa e próximas de zero. Novos estudos devem ser realizados em populações com dados biológicos, a fim de se observar o impacto da seleção em características de interesse econômico.

Palavras-chave: Apis mellifera, correlação, herdabilidade, seleção

INTRODUCTION

The queen bee is the only female with a fully developed reproductive system in a hive and can be morphologically differentiated from workers by the amount of royal jelly that she receives as food at the beginning of life (Page and Peng, 2001). The lifespan of a queen in the natural environment is 1 to 3 years and this queen bee is responsible for egg laying in the colony (Lee *et al.*, 2019). However, according to these authors, queens gradually lay fewer eggs over the years and beekeepers thus replace them annually. These individuals become essential for the dissemination of genetic material to their progeny (Zayed, 2009; Delaney *et al.*, 2010) and can be selected to increase the productivity of the hive.

Within this context, effective selection requires knowledge of the behavior of variables that influence the performance of the hive in terms of the desired selection (Tarpy *et al.,* 2012). Morphometric characteristics such as abdomen length and width, associated with body weight and oviposition, are indicators of the reproductive efficiency of the queen (Kahya *et al.*, 2008), which is decisive for maintaining a large hive (Pankiw, 2004). Genetic evaluation of each of these variables and how they are correlated is important to estimate genetic gains when selecting these individuals. It is therefore necessary to know the heritability and genetic correlations between these variables (Merila *et al.*, 2001).

In commercial beekeeping, data collection for research purposes is usually not feasible because of the economic dependence of beekeepers on the activity, in addition to the difficulty in obtaining trained personnel for daily management of the apiary. One alternative to overcome the problems associated with the collection of phenotypic data is the use of simulated data, which have been employed in apiculture research by several authors such as Gupta *et al.* (2013), Brascamp and Bijma (2014), and Plate *et al.* (2019). This method allows to create a numerous population from a reduced number of individuals for simulated genetic-statistical analyses. The results can be extrapolated to the real population (Cunha, 2006), which permits the application of actions to interfere in breeding programs.

In view of these considerations, this study aimed to estimate genetic parameters for body weight, abdomen width and length and oviposition in a simulated population obtained from the biological data of Africanized honeybees collected in the region of Campo das Vertentes, Minas Gerais, Brazil.

MATERIAL AND METHODS

The biological data used for simulation were collected at commercial apiaries in the towns of São João del-Rei, Coronel Xavier Chaves, Lagoa Dourada and Resende Costa, municipalities belonging to the region of Campos da Vertentes, Minasgerais, Brazil, between April 2016 and May 2017. During the experimental period, the beekeepers continued the habitual management of their apiaries, including wax exchange, division of the hive and queen replacement only when necessary. No artificial feed was offered to the hives during the period of data collection.

For data collection, the queens were localized manually amidst the workers, regardless of the size of the hives. The following variables were measured: body weight (BW), abdominal width (AW), abdominal length (AL), and oviposition. The BW of each queen was measured in gram (g) with a digital scale to the nearest 0.01g. The morphological measurements (AW and AL) were obtained with a digital caliper in millimeter (mm). Oviposition was evaluated using a method adapted from Al-Tikrity (1971). In this method, the frames containing the queen's eggs, which comprised an area of 840cm² with 4.4 alveoli/cm², were placed in clear plastic bags and the areas of oviposition occupied with larval eggs and pupae of workers and drones on each side of the combs were delimited with a permanent water-resistant pen. This size of this area was calculated using a 1 x 1cmgrid paper. At the end of data collection, complete data were obtained for 24 individuals and these parameters were used as *a priori* information for simulation of the data.

The data were simulated using the QMSim software (Sargolzaei and Schenkel, 2009). The historical population initially consisted of 1,000 individuals per generation. This number was maintained up to generation 1,000, followed by a gradual reduction in the size of the population up to generation 2,000, which was composed of 100 individuals. In addition, this population was

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generated considering random matings; thus, the progeny was produced by the random union of gametes. In the next step of simulation, the animals of the last generation of the random population were considered the founders (5 males and 5 females) of the expanded population, which comprised five generations considering 30 progeny per female per generation, with exponential growth of the number of females, random union of gametes, and absence of selection. For each trait, the simulations were repeated 10 times and the results are reported as the means and standard deviations of the repetitions for each scenario.

The descriptive statistics of the biological and simulated data were obtained using the PROC MEANS procedure of the Statistical Analysis System® package (Statistical…, 2011). The source of non-genetic variation (generations) in the variables of the simulated population was evaluated using the generalized linear models procedure (PROCgLM) of the Statistical Analysis System® package (Statistical…, 2011), and was included in the model for all traits studied assuming a level of significant of 5% (P<0.05).

Single- and two-trait models were used for genetic analysis and the (co)variance components were estimated by the restricted maximum likelihood method (REML) using the AIREMLF90 software developed by Misztal *et al.* (2002). The complete model used for two-trait analysis can be written in matrix form as:

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix} \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix}$$

where Y_1 is the vector of records of trait 1; Y_2 is the vector of records of trait 2; β_1 is the vector of fixed effects for trait 1; β_2 is the vector of fixed effects for trait 2; μ_1 is the vector of random additive genetic effects for trait 1; μ_2 is the vector of random additive genetic effects for trait 2; $X_1(X_2)$ is the incidence matrix associating elements of $\beta_1(\beta_2)$ with $Y_1(Y_2)$; $Z_1(Z_2)$ is the incidence matrix associating elements of $\mu_1(\mu_2)$ with $Y_1(Y_2)$; ε_1 is the vector of random residual effects for trait 1, and ε_2 is the vector of random residual effects for trait 2. The direct heritability (h_a^2) was estimated using the following formula (Falconer, 1987):

$$h_a^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

where σ_a^2 is the component of direct additive genetic variance, and σ_p^2 is the component of total phenotypic variance. The genetic correlation coefficient (r_g) was calculated using the following formula (Falconer, 1987):

$$r_g = \frac{cov_{g12}}{\sqrt{\sigma_{g1}^2 \times \sigma_{g2}^2}}$$

where cov_{g12} is the component of genetic covariance between trait 1 and trait 2; σ_{g1}^2 is the component of direct additive genetic variance of trait 1; σ_{g2}^2 is the component of direct additive genetic variance of trait 2. The phenotypic correlation coefficient (r_p) was estimated as follows (Falconer, 1987):

$$r_p = \frac{cov_{p12}}{\sqrt{\sigma_{p1}^2 \times \sigma_{p2}^2}}$$

where cov_{p12} is the component of phenotypic covariance between trait 1 and trait 2; σ_{p1}^2 is the component of phenotypic variance of trait 1; σ_{p2}^2 is the component of phenotypic variance of trait 2.

RESULTS

Tables 1 and 2 show the descriptive statistics of the biological and simulated data, respectively. Differences were observed in the coefficients of variation obtained for the traits studied, indicating that phenotypic variability exists to a greater or lesser extent in the Africanized honeybee population.

The heritability estimates for BW, AW, AL and oviposition exhibited variation, although all of them were of moderate to high magnitude (Table 3), ranging from 0.31 to 0.66. These estimates suggest the existence of additive genetic variability in these variables within the population evaluated.

Table 1. Descriptive statistics for biological data of weight, morphometry and oviposition of Africanized honeybee (*Apis mellifera*) queens

Variable	N	Mean (SD)	CV (%)	Minimum	Maximum
BW (g)	36	0.26 (0.03)	10.36	0.19	0.32
AW (mm)	36	5.29 (0.56)	10.61	4.04	5.92
AL (mm)	36	14.12 (1.39)	9.82	10.86	16.60
Oviposition (eggs/frame)	24	3,874.80 (1,458.79)	37.64	1,296.54	5,686.25

BW = body weight; AW = abdominal width; AL = abdominal length; N = number of observations; SD = standard deviation; CV = coefficient of variation.

Table 2. Descriptive statistics for simulated data of weight, morphometry and oviposition of Africanized honeybee (*Apis mellifera*) queens

Variable	N	Mean (SD)	CV (%)	Minimum	Maximum
BW (g)	680	0.16 (0.03)	18.20	0.06	0.25
AW (mm)	680	4.84 (0.80)	16.56	2.03	7.24
AL (mm)	680	10.49 (1.94)	18.50	3.98	16.50
Oviposition (eggs/frame)	680	2,890.53 (412.98)	14.29	1,671.24	4,255.86

BW = body weight; AW = abdominal width; AL = abdominal length; N = number of observations; SD = standard deviation; CV = coefficient of variation.

Table 3. Estimates of heritability (diagonal), genetic correlation (above the diagonal) and phenotypic correlation (below the diagonal) for simulated data of Africanized honeybee (*Apis mellifera*) queens

Variable	BW	AW	AL	Oviposition
BW (g)	0.54	0.80	0.11	0.69
AW (mm)	0.97	0.47	0.26	0.82
AL (mm)	0.96	0.98	0.31	0.96
Oviposition (eggs/frame)	-0.03	-0.02	-0.02	0.66

BW = body weight; AW = abdominal width; AL = abdominal length.

Positive genetic correlations of high magnitude were observed between BW and AW (0.80), BW and oviposition (0.69), AW and oviposition (0.82), and AL and oviposition (0.96). In contrast, the results indicated a low genetic association between BW and AL (0.11) and between AW and AL (0.26) (Table 3). The phenotypic correlations between BW and AW (0.97), BW and AL (0.96) and AW and AL (0.98) suggest that a high phenotypic association exists between the traits studied. However, the phenotypic correlations of oviposition with BW (-0.03), AW (-0.02) and AL (-0.02) were close to zero, indicating a weak phenotypic association between these traits.

DISCUSSION

The heritability estimates obtained in this study indicate that selection for the morphological and reproductive traits evaluated in this population can promote genetic gain over generations given that variability exists in the traits studied (Gianola and Rosa, 2015). The results demonstrated additive genetic effects; however, part of the variability in the traits studied was due to environmental factors and non-additive genetic action, which should be controlled whenever possible.

In a study on honeybees, Bienefeld *et al*. (2007) reported that the egg-laying capacity of the queen is influenced by genetic and environmental factors, in agreement with the present study in which oviposition exhibited 66% variation due to additive genetic action and 34% due to non-additive genetic and environmental effects. Lee *et al*. (2019) suggested that the poor brood quality of queens is related to the inadequate quantity and quality of sperm stored during the queen's mating flight with drones. These results highlight the importance and the need for controlling and monitoring the genetic and environmental conditions during the production process since these conditions are directly related to the productive capacity of bees.

The genetic association observed between the traits was favorable for the population studied and might be related to pleiotropy and/or genetic linkage (Falconer, 1987). Regardless of their

intensity, all genetic correlations were positive, indicating the same direction of these associations, i.e., an increase of one trait would consequently result in an increase of the other (Table 3).

The traits BW, AW and oviposition showed high genetic correlations, suggesting that they are directly related. In a study on *Melipona quadrifasciata anthidioides* bees, Faquinello *et al.* (2013) reported positive correlations between queen weight and the number of brood disks, which might be directly related to the egg-laying capacity of bees. Akyol *et al.* (2008) found positive correlations of queen weight with brood area and diameter of the spermatheca in *Apis mellifera anatoliaca*. Kahya *et al.* (2008) also reported favorable correlations between queen weight and size of the spermatheca in *Apis mellifera caucasica*. These associations might be explained by the fact that the reproductive system occupies space and/or interferes with the weight of individuals.

Thus, it is believed that, because of the location of the spermatheca in the abdominal region of bees, their size may influence AW and consequently permit the storage of a greater amount of semen, a fact that would increase the queen's egg-laying capacity and therefore explain the results observed. Although positive, the genetic correlations of AL with BW and AW were of low magnitude, suggesting a less intense association but not less important for breeding programs. According to Kumar and Mall (2018), the physical development of the queen and her genetic constitution are fundamental characteristics that determine her egg-laying capacity.

Genetic parameter estimates for morphometric and reproductive traits of bees are scarce in the literature but are of great importance for breeding programs since they can be used as selection criteria. It would be expected from the present results that the population studied responds to indirect selection, that is, selection for one trait would result in genetic changes in other variables. The intensity and direction of these changes will depend mainly on the existing genetic correlations between traits, but also on their heritability and variances (Merila *et al.*, 2001).

According to Akyol *et al.* (2008), queen weight would be the most important characteristic to be evaluated for selection since it is positively correlated with reproductive characteristics such as brood area, diameter of the spermatheca and number of spermatozoa. However, we recommend the use of oviposition as a selection criterion in the biological population studied because of its high capacity of transmission to progeny and high genetic correlations with the other traits studied. In addition, it is the most easily measurable characteristic and does not require to identify the queen in the colony amidst workers.

CONCLUSION

The variables body weight, abdominal width, abdominal length and oviposition can be used as selection criteria in this Africanized bee population. However, the genetic and phenotypic correlation between these characteristics is used in order to determine which will be used as a selection criterion due to the feasibility of its collection. Further studies involving these traits should be performed in populations with biological data in order to observe the impact of selection on traits of economic interest.

ACKNOWLEDGEMENTS

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