

Covariance estimation for yield and behavioral traits in Italian honey bee by linear-threshold model

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An animal two-trait model with fixed effects for performance test year and tester apiary as well as a random effect for their interaction, together with queen direct genetic effect were used for genetic evaluation of honey yield and defensive and swarming behaviors in honey bees in Italy. This study reports the first estimation of heritability and genetic correlations in Italian honey bees. The results may represent a possible direction for the genetic selection of linear and categorical traits of honey bees.

Statistic	Honey yield (kg)	Defensive behavior (1-5)	Swarming behavior (1-5)
σ_a^2	50.57 (6.84)	2.59 (0.57)	4.51 (1.00)
σ_{py-ta}^2	111.24 (16.08)	1.43 (0.44)	1.72 (0.49)
σ_e^2	35.89 (5.24)	3.33 (1.43)	6.35 (1.75)
σ_p^2	198.46	9.33	12.58
h^2	0.25 (0.04)	0.31 (0.07)	0.30 (0.07)

Heritability estimates for all traits were moderate. Similar heritabilities for HY have been reported. For behavior traits (DB and SB) different than our results were reported, from different scoring system and populations. In our study, defensive and swarming behaviors were treated as categorical traits and evaluated with threshold models. Advantages of threshold over linear models have been demonstrated in genetic evaluation of livestock.

Results of performance testing from *A. mellifera ligustica* colonies were obtained from the National Registry for Italian Queen Breeders and Bee Producers for honey yield (HY), defensive behavior (DB), and swarming behavior (SB). The dataset included 4003 records for HY and DB and SB for queens born from 2002 through 2014. After data verification, 3974 colonies with records were used in evaluations. In the Italian honey bee breeding program, mating is not strictly controlled, hence information about the queens' mates was not included. The complete pedigree data included 4160 queen (186 queens were defined as base population, and 1625 were dam queens with an average family size of 2 and 365 grand dam queens with an average family size of 13). Statistical Model contained performance of HY, DB or SB for colony l , a non-genetic effects of test year (py_i , 13 levels) and tester apiary (ta_j , 72 levels) and their interaction and genetic effect of colony ($py-ta_k$, 207 levels), random effect of queen (q_l) and residual (e_{ijkl}). HY was considered to be a continuous trait, DB and SB were considered categorical traits with 5 classes. The program THRGIBBS1F90 was used to estimate variance components and EBVs of all 3 two-trait models with 500,000 Gibbs sampling iterations. A burn-in of 10% of the initial iterations was used. The program POSTGIBBSF90 was used to calculate posterior means.

$$Y_{ijkl} = py_i + ta_j + py-ta_k + q_l + e_{ijkl}$$

A weak genetic correlation (0.15) was found between honey yield and defensive behavior, whereas the genetic correlation between honey yield and swarming behavior was moderate and positive (0.42). Genetic correlation between defensive and swarming behaviors was 0.51. Those estimates are difficult to compare due to methodology and trait definition used in other. Modeling linear and categorical phenotypes in a two-trait model is a feasible option for estimating breeding values in honey bee breeding programs. This model is especially important given the increasing interest in behavior traits. Those traits are usually less recorded than honey production, but can benefit from the considerable genetic correlations.