



Effects of inaccurate genetic identification for single-trait and multi-trait genetic markers in honeybees

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DESCRIPTION

Numerous quantitative variables in different honeybee populations have had their heritabilities and genetic and residual variances calculated. These estimations include both prospective new selection qualities, frequently linked to parasite or disease resistance, and well-established breeding features, such as honey yield or gentleness. To evaluate the likelihood of a genetic response in recently established breeding populations, heritability estimates for traditional variables are used. They also keep track of genetic alterations brought on by selection and genetic drift in populations that have undergone repeated breeding over a long period of time (Bienefeld, 2016). Heritability estimations are a crucial consideration when looking for new breeding traits since they indicate whether a trait will be included in a breeding programme and how responsive it will be to selection.

The genetic and residual variances and covariances of features must also be presupposed when using sophisticated genetic evaluation approaches like Best Linear Unbiased Prediction (BLUP). In various honeybee populations, these methods have been successfully applied after being modified for the honeybee. Many honeybee breeding programmes still rely on phenotypic selection rather than more complex types of genetic evaluation, however, as BLUP breeding value estimations need significant theoretical understanding and computational infrastructure (Bashaw, 2007). Furthermore, given the very high standard errors that are frequently linked to heritability estimates for the honeybee, it is currently unknown if the superiority of BLUP selection over phenotypical selection endures. The majorities of characteristics in honeybees is assessed at the colony level and are frequently impacted by the queen and her worker class. As a result, the genetic influence is divided into a maternal queen effect and a direct worker group effect, just like the maternal and

direct impacts are divided in other agricultural species. The precise estimate of trait parameters for honeybees is significantly hampered by the division of genetic variance into two effects. The honeybee queen's behaviour of mating with many drones from different colonies in mid-air further complicates accurate parameter calculations by providing imperfect paternal pedigree information. When data scarcity requires developing breeding programmes to use genetic parameters that were estimated in other populations, this produces a high probability of inaccurate genetic parameters as input data for the BLUP technique. The topic of how inaccurately assessed genetic factors affect BLUP-based breeding success in terms of genetic response and inbreeding development thus emerges (Hazel, 1943).

Other agricultural animals likewise exhibit biased estimates of genetic characteristics. It has been challenging to evaluate genetic links between maternal and direct impacts in particular. Evidence suggests that incorrect assumptions about the direction or strength of these connections, however, have only a little impact on the outcome of genetic analyses. It has been demonstrated that upwardly biased heritability estimates for BLUP evaluations significantly lower inbreeding rates with few concessions on genetic gain. However, a study on the consequences of incorrect parameter assumptions for breeding value predictions is lacking (Meyer, 1991). Additionally, we are not aware of any direct comparisons between phenotypic selection in animal breeding and BLUP selection with incorrect parameters.

For a large number of agricultural species, parallel selection for various traits is frequently used. However, it is little represented in the theoretical literature on animal breeding, which also includes simulation research. Due to potential genetic and residual connections across characteristics, which increase the number of estimated parameters, the simultaneous estimation of genetic

parameters for more than one trait is further difficult. If additional qualities' associations with the original features are not properly taken into consideration, their inclusion in a selection index hinders genetic advancement. The significance of accurate estimates of genetic correlations between coequal breeding variables in BLUP evaluations, however, has not been studied to our knowledge. This study examines the effects of selection and inbreeding rates in honeybee breeding programmes for a variety of attributes using several genetic evaluation methods (Laurenson, 1994). These include BLUP-based across-family selection with either accurate genetic parameters or incorrect genetic parameters, as well as phenotypic selection. We discuss both single-trait and multi-trait selection in this section.

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