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► **To cite this version:**

Bastien Gravellier, Florence Phocas. Efficiency of different BLUP indexes accounting for polyandry in bee genetic evaluation. 68. Annual Meeting of the European Association for Animal Production (EAAP), Aug 2017, Tallinn, Estonia. hal-02736780

HAL Id: hal-02736780

<https://hal.inrae.fr/hal-02736780>

Submitted on 2 Jun 2020

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Efficiency of different BLUP indexes accounting for polyandry in bee genetic evaluation

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The best linear unbiased prediction (BLUP) applied to an animal model is the standard method for genetic evaluation of domestic livestock. It requires modelling the relationship matrix between all the animals registered in the pedigree of candidates for selection. For diploid species the derivation of relationship coefficients are well established. But the honey bee (*Apis mellifera*) is a haplodiploid species in which several (10 to 20) haploid drones fertilize a diploid queen. In consequence, the father of a female progeny is in most cases unknown (with the exception of a queen insemination with the semen of a single drone). The bee genetic (male haploidy) and reproductive (polyandry) specificities have therefore to be accounted for in the derivation of the relationship matrix to model relevant paternal gene flows and uncertain paternity of the workers and queen of the colony. The objective of the study was to compare different approaches for deriving the relationship matrix to estimate the bee breeding values by BLUP indexes. The simplest approach is to ignore the paths of paternal gene transmission in a similar way that in diploid species paths of maternal gene transmission have classically been ignored under BLUP – sire model considering a relationship matrix build from triplets “animal – sire – maternal grandsire” in the pedigree file. In a symmetric approach for bee a dam model can be considered with a pedigree file composed of triplets “animal – dam – paternal grand dam”. Such a simplified model was compared to different approaches proposed in the literature to model bee relationship matrix under an animal model. In these last strategies, the group of drone-producing queens is considered as a dummy father, the drones being the male gametes. A stochastic simulation was used to produce a bee population of 5000 queens with known phenotypes and true genetic values for a trait of heritability varying from 0.1 to 0.5. The different BLUP indexes were computed assuming various degree of polyandry. Correlations between true and estimated breeding values were derived in order to evaluate the impacts of the parameters describing the paternal origins. The number of drone producing queens appeared to have the highest impact on the estimates.

Comment citer ce document :

Gravellier, B., Phocas, F. (2017). Efficiency of different BLUP indexes accounting for polyandry in bee genetic evaluation. In: Book of Abstracts of the EEAP annual meeting, Tallinn 2017. Presented at 68. Annual Meeting of the European Association for Animal Production (EAAP), Tallinn. EST (2017-08-28 - 2017-08-31).