



HAL
open science

OPTIMIZING HONEYBEE BREEDING SCHEMES: REDUCING THE GENERATION INTERVAL OF DAMS TO ONE YEAR WITH PARTIAL PHENOTYPING

Tristan Kistler, E.W. Brascamp, Benjamin Basso, Florence Phocas, Piter
Bijma

► **To cite this version:**

Tristan Kistler, E.W. Brascamp, Benjamin Basso, Florence Phocas, Piter Bijma. OPTIMIZING HONEYBEE BREEDING SCHEMES: REDUCING THE GENERATION INTERVAL OF DAMS TO ONE YEAR WITH PARTIAL PHENOTYPING. EurBee 10th Congress of Apidology, Sep 2024, Tallinn, Estonia. hal-04754999

HAL Id: hal-04754999

<https://hal.science/hal-04754999v1>

Submitted on 26 Oct 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

OPTIMIZING HONEYBEE BREEDING SCHEMES: REDUCING THE GENERATION INTERVAL OF DAMS TO ONE YEAR WITH PARTIAL PHENOTYPING

T. Kistler^{1,2,3}, E. W. Brascamp³, B. Basso^{4,2}, F. Phocas^{1,2} and P. Bijma³

¹ Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France; ² UMT PrADE, France; ³ Wageningen University & Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands; ⁴ INRAE, UR 406 Abeilles et Environnement, 84914 Avignon, France

INTRODUCTION

In honeybee breeding schemes, the generation interval is often two years on the dam path. This allows phenotyping of certain traits, such as honey yield, during a full beekeeping season to measure early to late-season harvests. Other traits, however, such as hygienic behavior (HYG), can be phenotyped early, within the first year of birth of queens. Using simulation, we investigated the impact of reducing the dam's generation interval from two to one year on the genetic gain and inbreeding build-up, after 20 years of selection.

METHODS

We simulated populations under selection, with individual queens, worker groups, and drones, using an polygenic model adapted to bee specificities.

We simulated two breeding schemes. In the 'base' scheme, the dam and sire generation interval were both two years, allowing the phenotyping of honey yield in addition to HYG on both potential dams (breeding queens, BQs) and potential sires (drone-producing queens, DPQs). In contrast, in the alternative scheme, the dam generation interval was reduced to one year, allowing for the phenotyping of only HYG on BQs, while the sire generation interval remained two years with complete phenotyping of DPQs. A yearly winter mortality randomly eliminated 25% of all BQs and all DPQs.

The genetic correlation between honey yield and HYG was either 0, -0.6, or +0.6. The breeding goal was the sum of breeding values of honey yield and HYG with the same weights.

RESULTS

In all scenarios, the alternative scheme outperformed the base scheme, yielding 40 to 45% greater genetic gain. However, this additional genetic gain was accompanied by an increase in inbreeding of 20% to 35%.

CONCLUSION

Reducing the generation interval proved to be a powerful way of increasing genetic gain even though it meant that honey yield could not be phenotyped on potential BQs. However, it also brought more inbreeding.