OP-240 [Beekeeping Technology and Quality]
Genetic parameters for honey production in a small size and recently created bee breeding nucleus in France

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BACKGROUND/PURPOSE
They are still limited reports of selective breeding programs for honey production operated by professional beekeepers controlling the male pathway in optimized BLUP based breeding designs of small size. We report estimations of genetic parameters and breeding values (EBVs) for honey production in such small-sized breeding program recently established by professional beekeepers (L'Abeille Ligérienne, Lagord, France).

METHODOLOGY
Virgin queens were mated naturally, in island mating station or inseminated with drone-producing colonies with queens from selected dams. 1 234 queens were phenotyped from 2017 to 2024 in 29 apiaries by 12 beekeepers. Genetic parameters were estimated with BLUP methodology and software previously adapted to bee biology. The pedigree relationship matrix was calculated using an R program (Brascamp and Bijma, 2019). Genetic parameters and EBVs were estimated using AIREMLF90 of BLUPf90 software package, applying a linear mixed model with a single direct genetic effect considered, either the queen effect (Queen Model: QM) or workers' one (Workers Model: WM).

RESULTS
Significant year, apiary, beekeeper effects and pedigree structure indicated the opportunity to limit these effects, increase genetic ties between apiaries and improve contributions of parents across apiaries. Heritability (standard error) for Workers (WM) and Queen (QM) Models were 0.53 (0.11) and 0.37 (0.10). The colony ranking did not change according to the model used (Pearson correlations 0.94 to 0.96). The colony rankings between EBVs and colony performances corrected for year and apiary were consistent (correlations of 0.80 with WM and 0.88 with QM). Selection the 10% best queens on pedigree-BLUP EBVs by the two models led to increases in selection response of 6% and 22.5% when compared to mass selection on phenotypes corrected for environmental effects (with QM and WM respectively).

CONCLUSIONS
The breeding design, even for a small size breeding nucleus, was able to capture additive genetic variance. Heritability were in the higher range reported by previous authors. An improvement of the genetic evaluation is expected with the next 2025 year-classes for which apiaries will be genetically better connected. Selection pressure applied in managing inbreeding is expected to increase EBVs.

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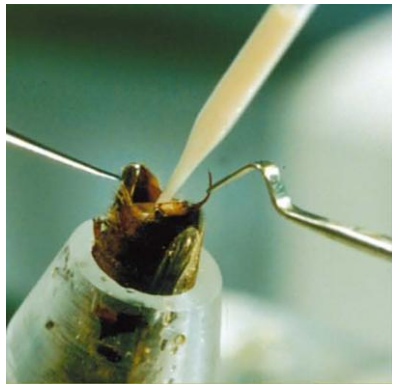

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Context

- Main future challenges in bee genetic selection: improvement of robustness, disease resistance, adaptation to climate change, production yield, management of inbreeding
  ⇒ **Multi-traits BLUP genetic selection (family selection)**

- Large scale and/or pioneering applications of family-based selective breeding programs in bee (e.g. in Germany, Austria, Swisserland, New Zealand, Quebec…)

DEUTSCHER IMKERBUND E.V.

A. m. carnica

apisuisse

A. mellifera (MEL), *A. m. carnica* (SAR)

ACA AUSTRIAN CARNICA ASSOCIATION

ZAC!

A. m. carnica

erbel

A. m. iberiensis

crea Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria

A. m. ligustica, *A. m. siciliana*

GRF GELÉE ROYALE FRANÇAISE®

A. mellifera

Goal of the project : Make a proof of concepts to apply family-based selection (BLUP selection) in small or medium size breeding nucleus more adapted to the French organization

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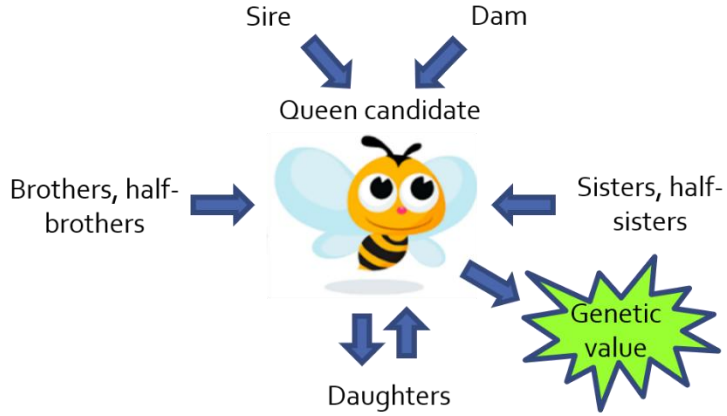
What is BLUP genetic selection applied to bee breeding?

- The **more robust and modern selection** method applied worldwide (mammals, poultry, fish, shellfish, shrimps and some plants)

- Allow to predict the **breeding value** of a queen candidate in :
  - in considering **performances** from related individuals (sisters, brothers, uncles, grand-parents…) weighted according to their **relationships**
  - in taking into account **fixed** (apiary, beekeeper…) and **random** (year…) **effects**
  - in managing **inbreeding**



- Needs :
  - Large and well organized data set with family tracking
  - Family tracking = Maternal and paternal pedigree + performances + effects…
  - Use of genetic software adapted to bee genetics (Bienefeld et al., 2007 ; Brascamp and Bijma, 2014)

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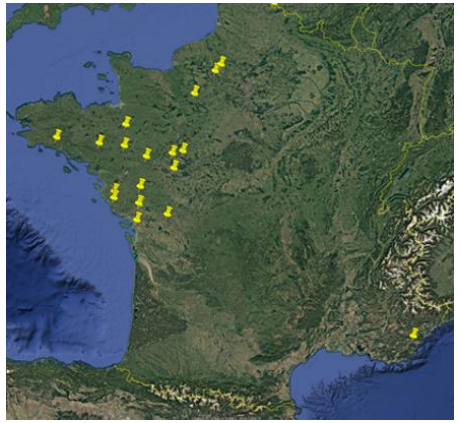
A 1st pilot case study by Abeille Ligérienne

https://www.abeille-ligerienne.com/



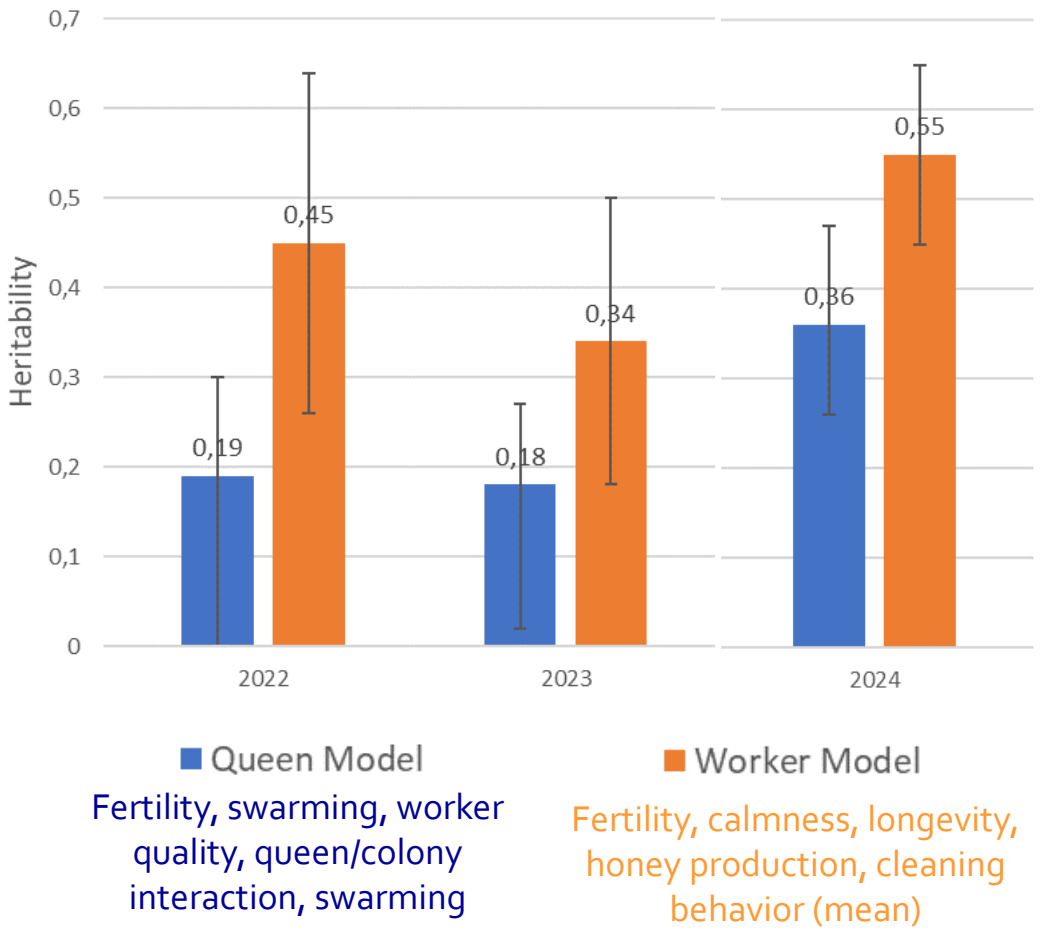
- Non-profit association of professional beekeepers created in 2014
  - 20 beekeepers (29 apiaries)
  - Objectives : to be autonomous in genetically selected material
  - 6 mating stations and artificial insemination

- Annual genetic meeting with all beekeepers for assistance to the creation of the families, their allocation within apiaries, homogenization of the phenotypes collected between beekeepers
- Number of founders of the line: 61 sires x 140 dams
- 1249 colonies with full pedigree and performance in 2024

Year of performance collection	2017	2018	2019	2020	2021	**2022**	**2023**	**2024**	Total
Number of colonies	14	30	66	174	119	**302**	**205**	**339**	**1249**

Estimation of heritability for honey production in the 1st generation

Genetic gain / generation = $h^2 * S$



- Heritability higher than null value
- Progressive increase of heritabilities and decrease of the errors in adding 2023 and 2024 year classes
- 2024
  - Year class produced from first proposed optimizations of the design in 2022
  - Introduction of new genetic resources

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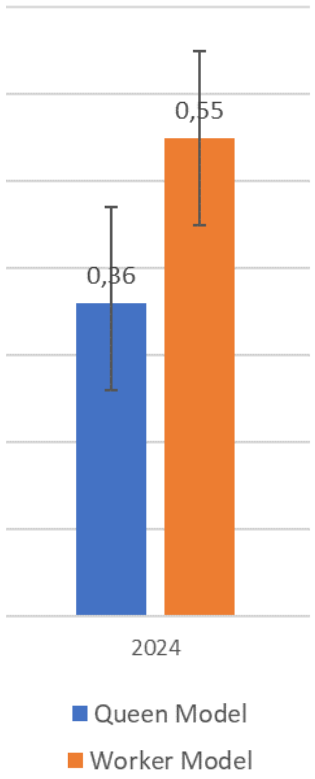
Comparison to the literature (updated from Basso et al., 2023)



Reference	*A. mellifera* sub species	Population size	Model	h^2	HONEY
Guichard et al. (2020)	*mellifera*	1066	QM	h_q^2	0.10 ± 0.06
		1066	WM	h_w^2	0.06 ± 0.09
Guichard et al. (2020)	*carnica*	1007	QM	h_q^2	0.11 ± 0.06
		1007	WM	h_w^2	0.27 ± 0.13
Andonov et al. (2019)	*ligustica*	3931	CM	h_m^2	0.12 ± 0.01
		3931	CM	h_d^2	0.33 ± 0.03
		3931	QM	h_q^2	0.26 ± 0.04
Brascamp et al. (2018)	*carnica*	14,948	CM	h_m^2	0.70 ± 0.14
		14,948	CM	h_d^{2a}	1.34 ± 0.16
Tahmasbi et al. (2015)	*meda*	10,000	QM	h_q^2	0.22 ± 0.02
Zakour et al. (2012)	*syriaca*	1088	QM	h_q^2	0.27 ± 0.32
Hoppe et al. (2020)	*carnica*	224,081	QM	h_m^2	0.23 ± 0.03
		224,081	WM	h_w^2	0.42 ± 0.05
		224,081	CM	h^2	0.34 ± 0.03
Maucourt et al. (2020)	*mellifera*	604		h^2	0,20 ± 0.13

- In the highest estimations but with high standard errors
- Why such differences?
  - Rearing practices?
  - Environments?
  - Genetic data structure ?
  - Multi-subspecies genetic resource?
  - New genetic resources?

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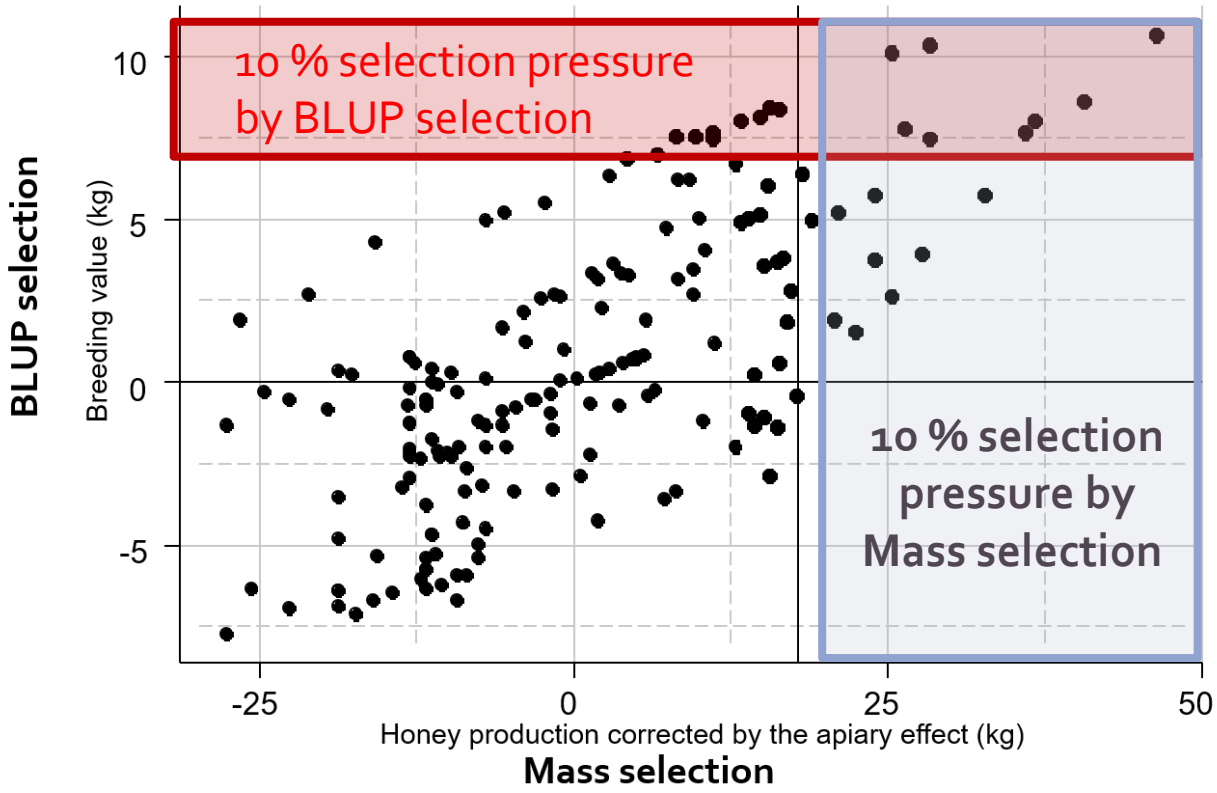
Do the candidates selected by mass ou BLUP selection are the same?



- Queens selected with BLUP differ than with mass selection
- BLUP selection allows to select queens in adding informations from sibs (more precise)

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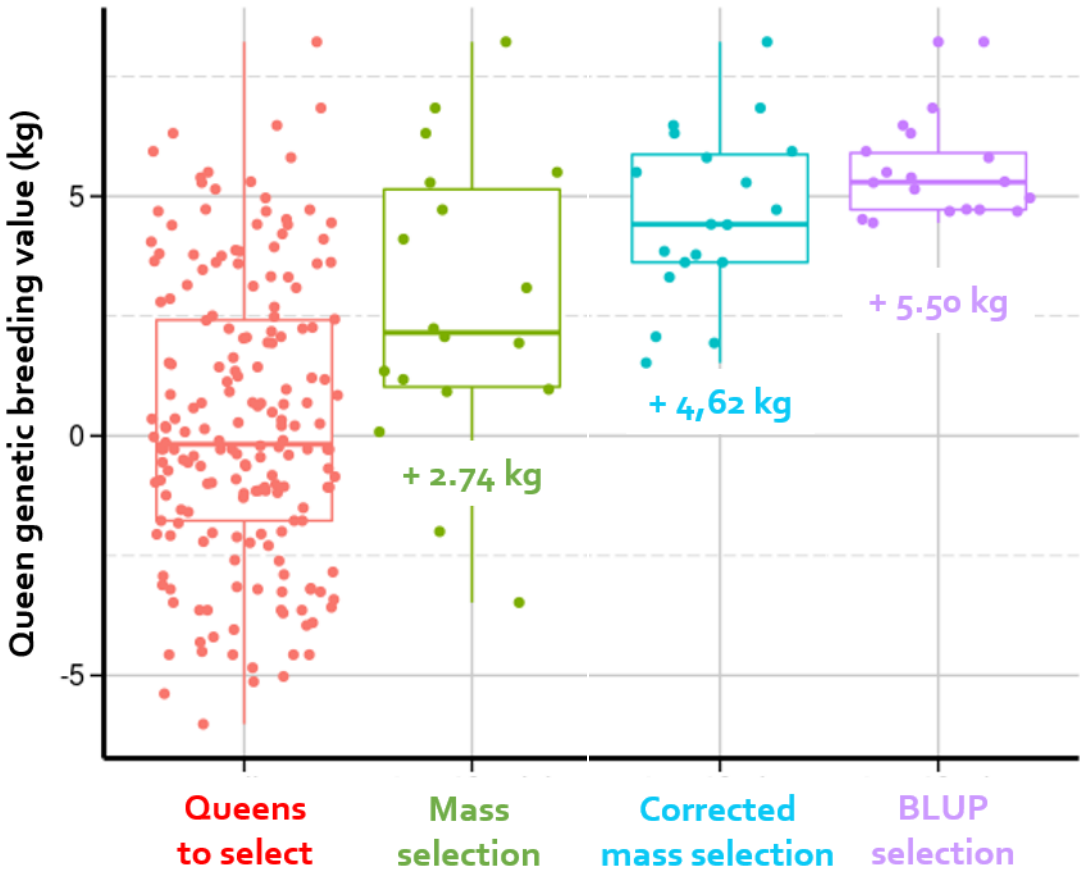
What means more precise (with 10 % selection pressure)?



- Over estimation of the genetic gain as no management of inbreeding
- BLUP selection should out perform « Mass selection » (+ 68 %) and « Corrected mass selection » (+ 20 %)
- Added value of BLUP selection
  - Higher gain
  - Management of inbreeding
- 1st generation → Potential bias as still non equilibrated genetic structure

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Take-home message

- The proof of concept of « limited size » family-based selective breeding program of honey bee is in progress
- Investment in the design, the equilibration of the families between apiaries and an adequate data collection system provided improvement from the next generation
- Already ≈ 20 % selection pressure performed in 2024
- "Genotype x Environment" interaction at the scale of the study is limited as suggested by intermediate heritability
- The breeding nucleus is planned to increase in the coming years targeting 500-1000 colonies / year
- Multi traits indexation will be estimated in 2025

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We thank you for your attention

Question?

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