Mating behaviour checking in the black soldier fly (*Hermetia illucens* L.) using SNP data: Parentage assignment for pedigree reconstruction

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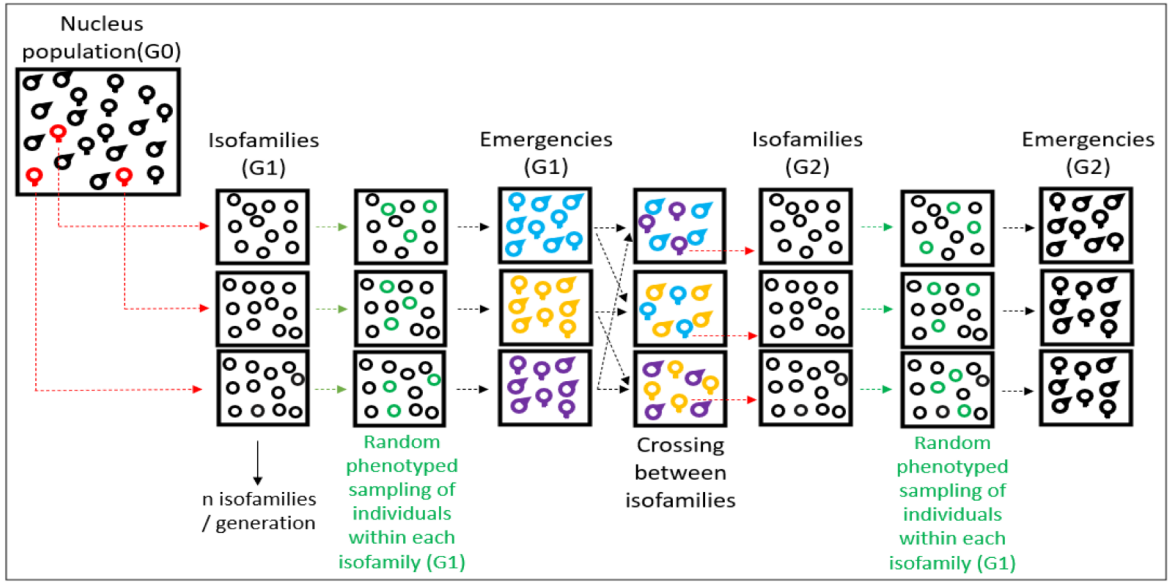
> Background

- In 2019, we developed a family pedigree breeding scheme in the black soldier fly (BSF)

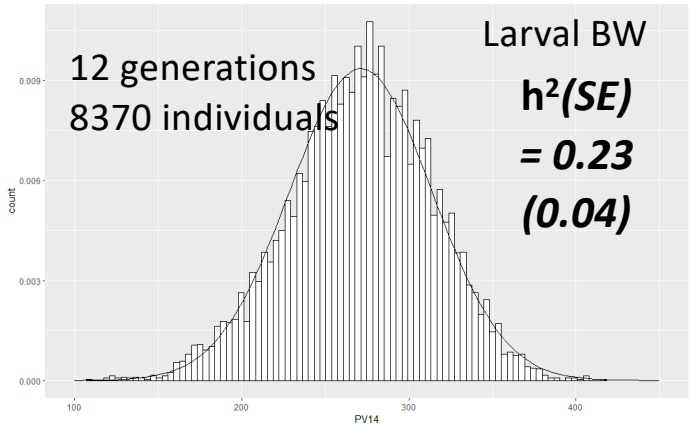


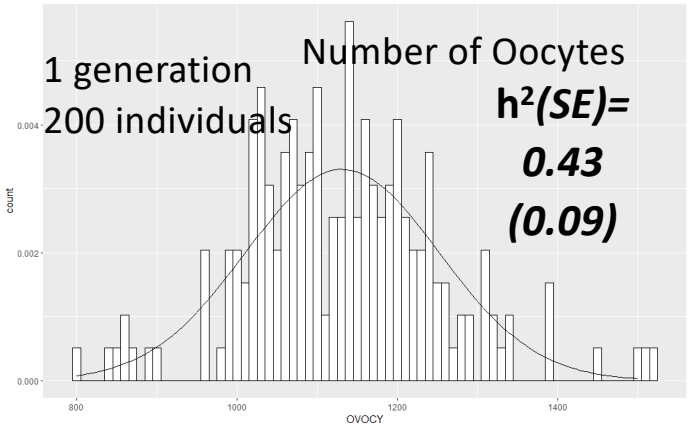
- Clutches are isolated and collected per female, with the assumption that one clutch is mated by a single male and a single female
- Random phenotyped => used to bult pedigree over generation and genetic parameters estimation

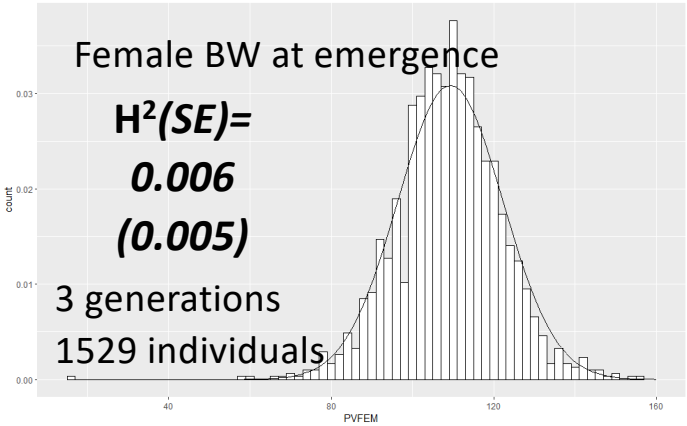
Donkpegan et al. In press

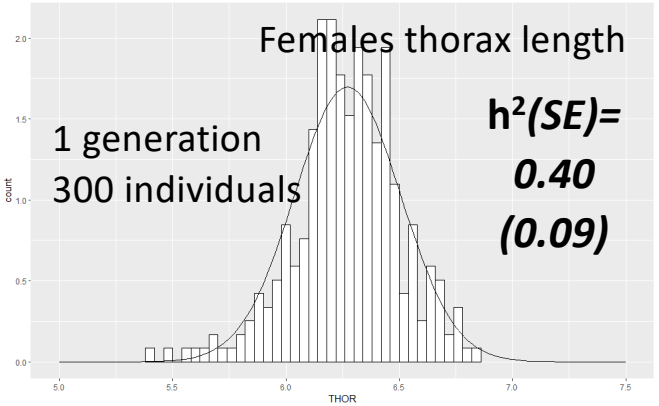
> Background

- Using these scheme for h^2 estimation by REstricted Maximum Likelihood (REML)









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> Background

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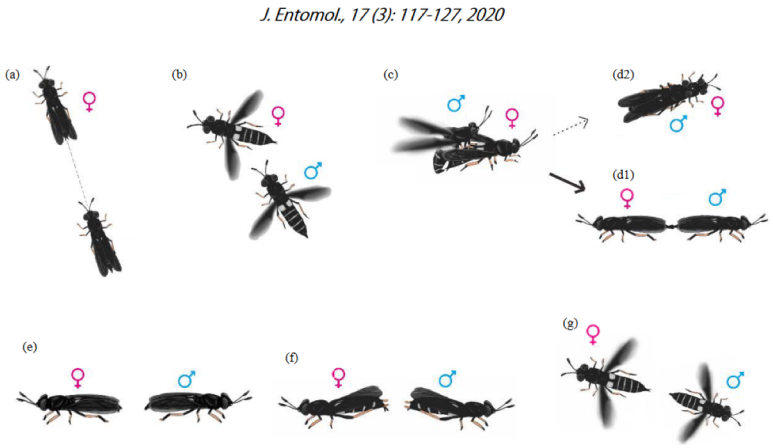
- Up until 2021, no reports in literature of multiple mating in *BSF*



From Julita et. al., *2020*

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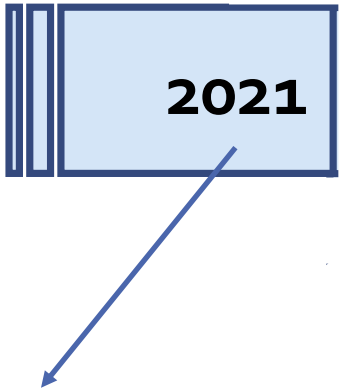

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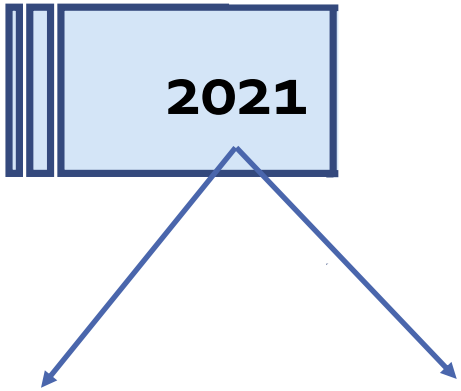

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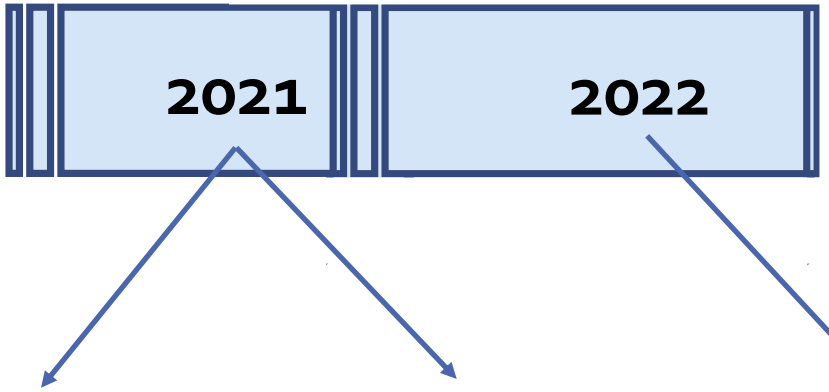

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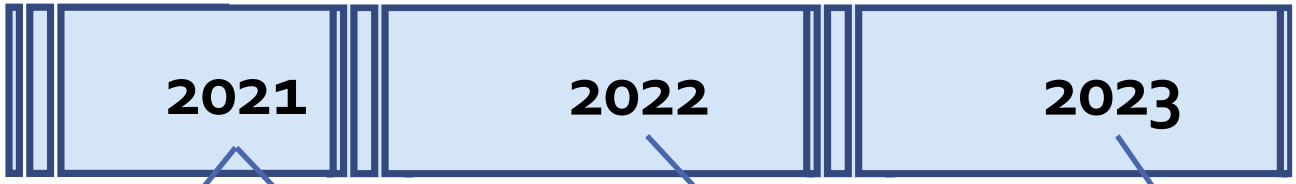

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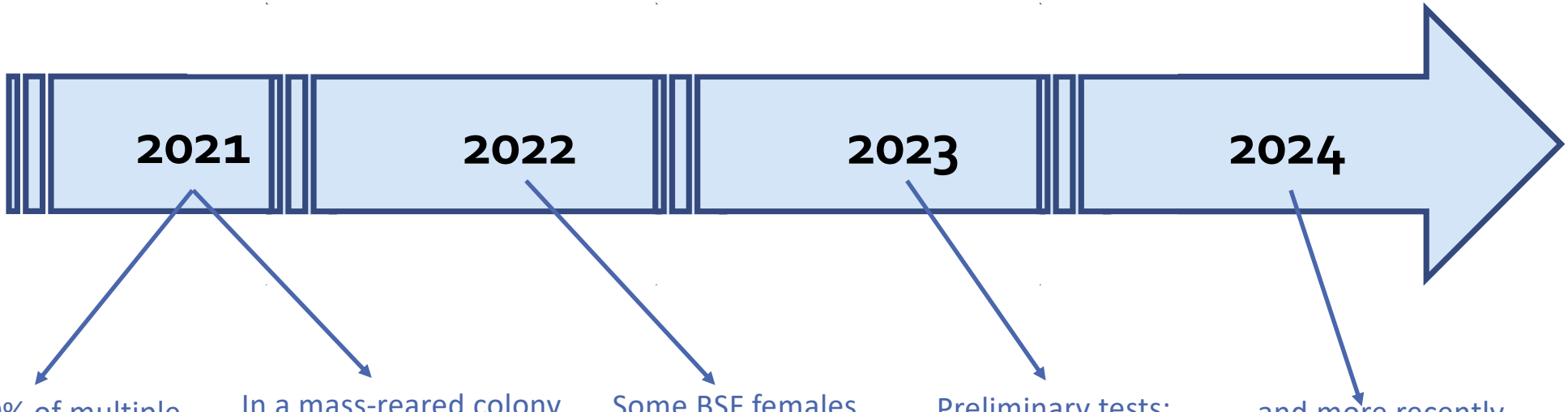

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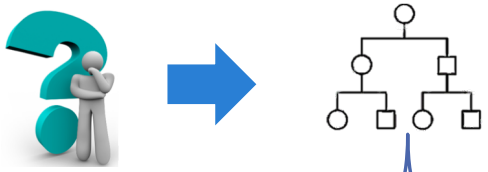
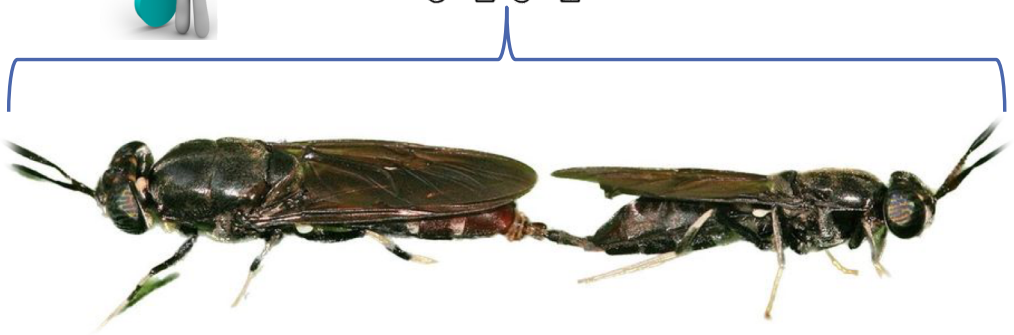
and more recently polygamy of males and multiple egg-laying (Muraro et al. 2024)

> Background

- All these observations raise questions about our initial hypothesis



Impact on Pedigree recording



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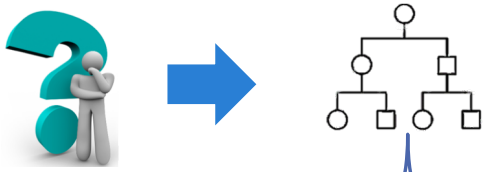

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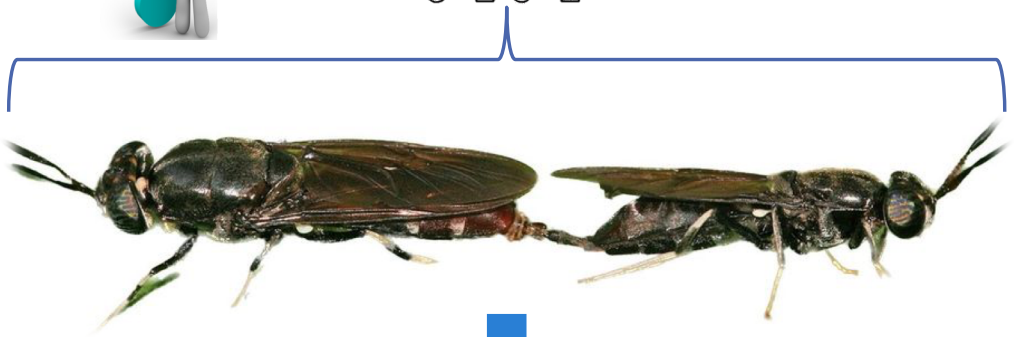
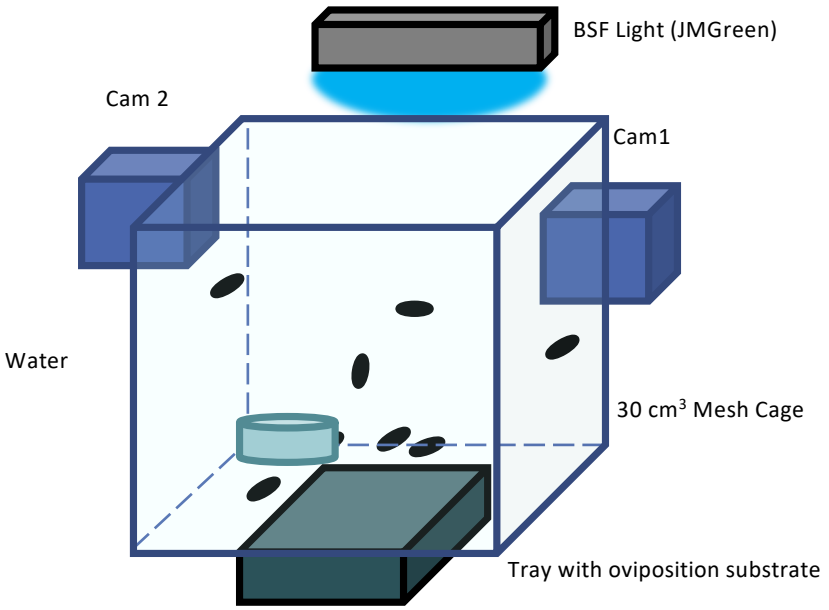


The aim of present study was to test the monogamy hypothesis in our pedigree breeding selection scheme through a parentage assignment design

Specifically, the goal is to quantify paternal contributions to offspring in a multiple mating context.

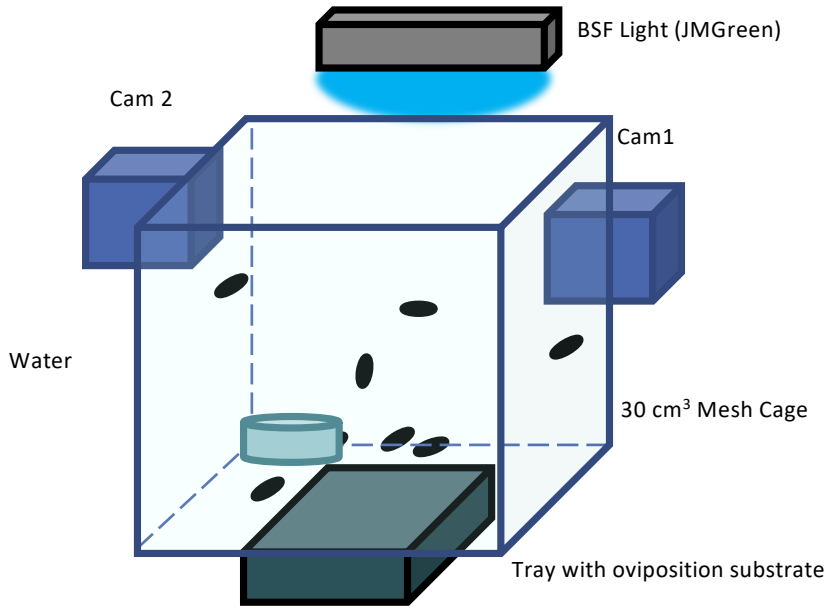
> Experimental setting

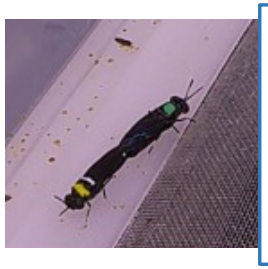
- Rearing of 19 females and 21 males under standard environmental conditions
- Marking of individuals with Posca Markers – marking did not interfere with mating – (derived from Jones & Tomberlin, 2020)
- Water and oviposition substrate are provided
- 2 cameras – 1 pic/30s over 7 days



> Experimental setting

- Number of mating pairs over time and identity of partners
- Timing and duration of mating
- Isolation and collection of clutches/female; with known potential fathers according to mating pairs
- Around 30 larvae selected and genotyped/clutch

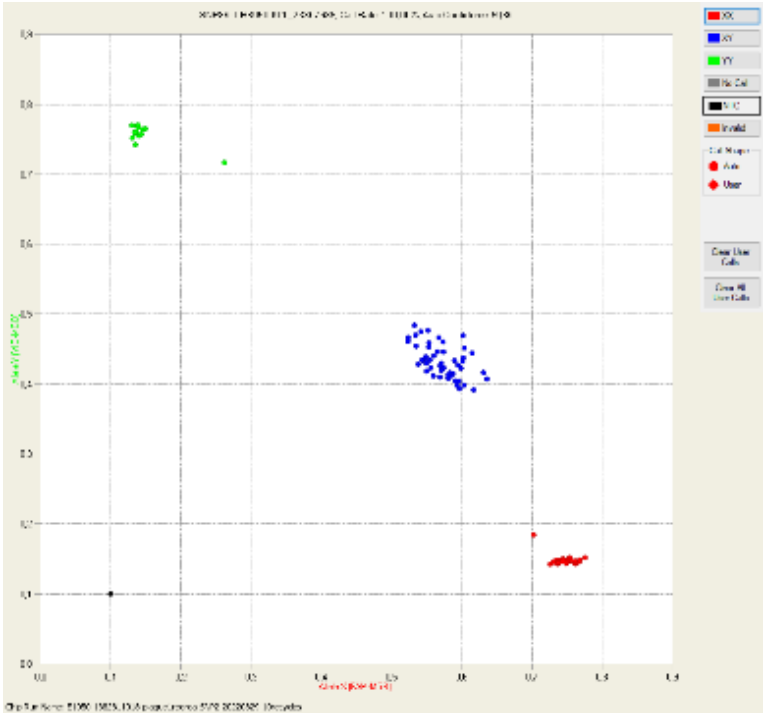




Not recorded: Night-time behaviour, remating behaviour, failed mating attempts

> Experimental setting

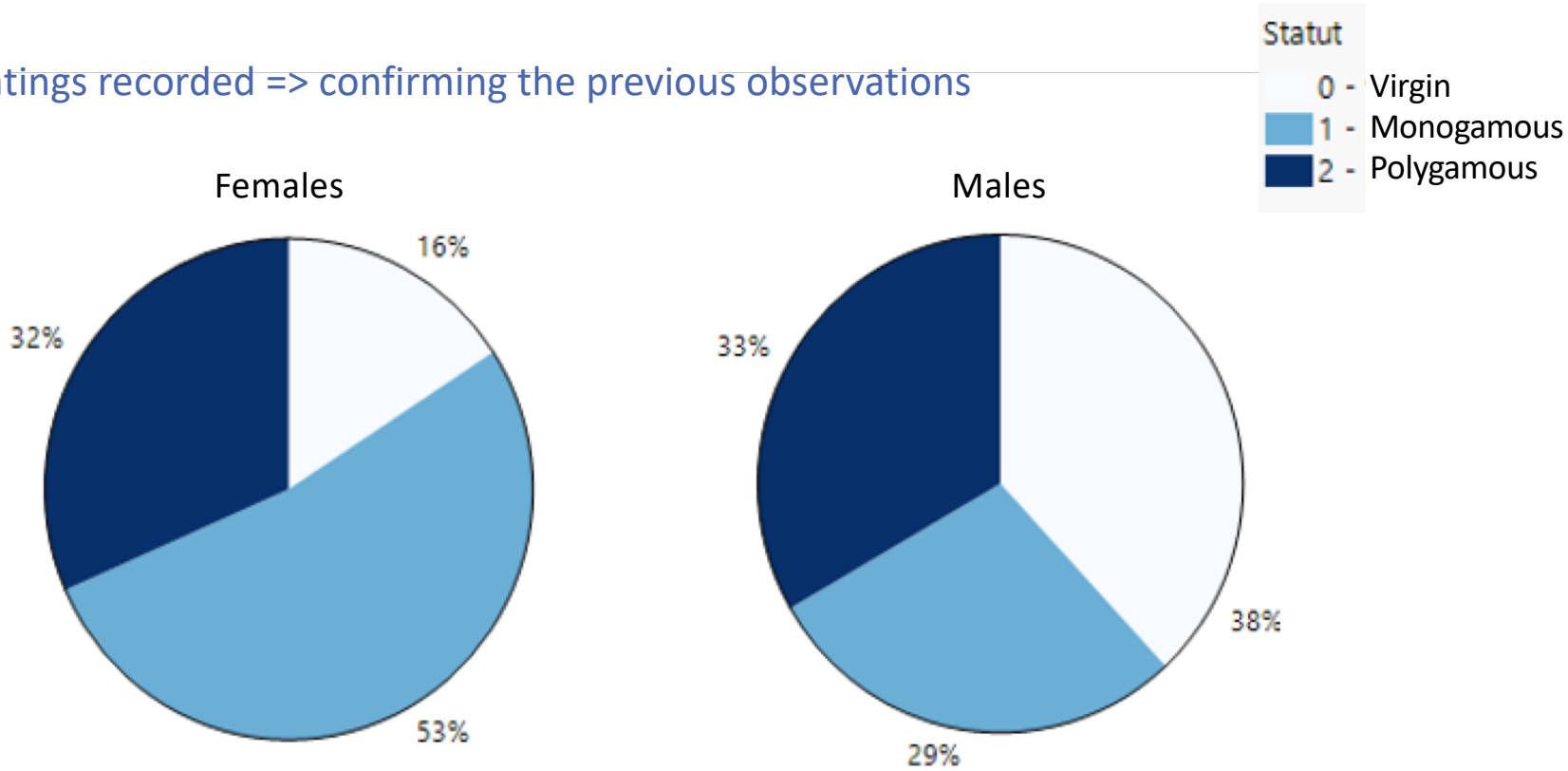
- DNA extraction and genotyping
- 173 offspring from 10 males and 6 females
- using the 96 Kompetitive allele specific PCR (KASP) SNP genotyping chip developed on BSF
- Parentage assignment analysis by probability method (R package APIS)



Griot et al. (2020). APIS: An auto-adaptive parentage inference software that tolerates missing parents. *Molecular ecology resources*, *20*(2), 579-590.

> Mating behaviour

- 26 matings recorded => confirming the previous observations

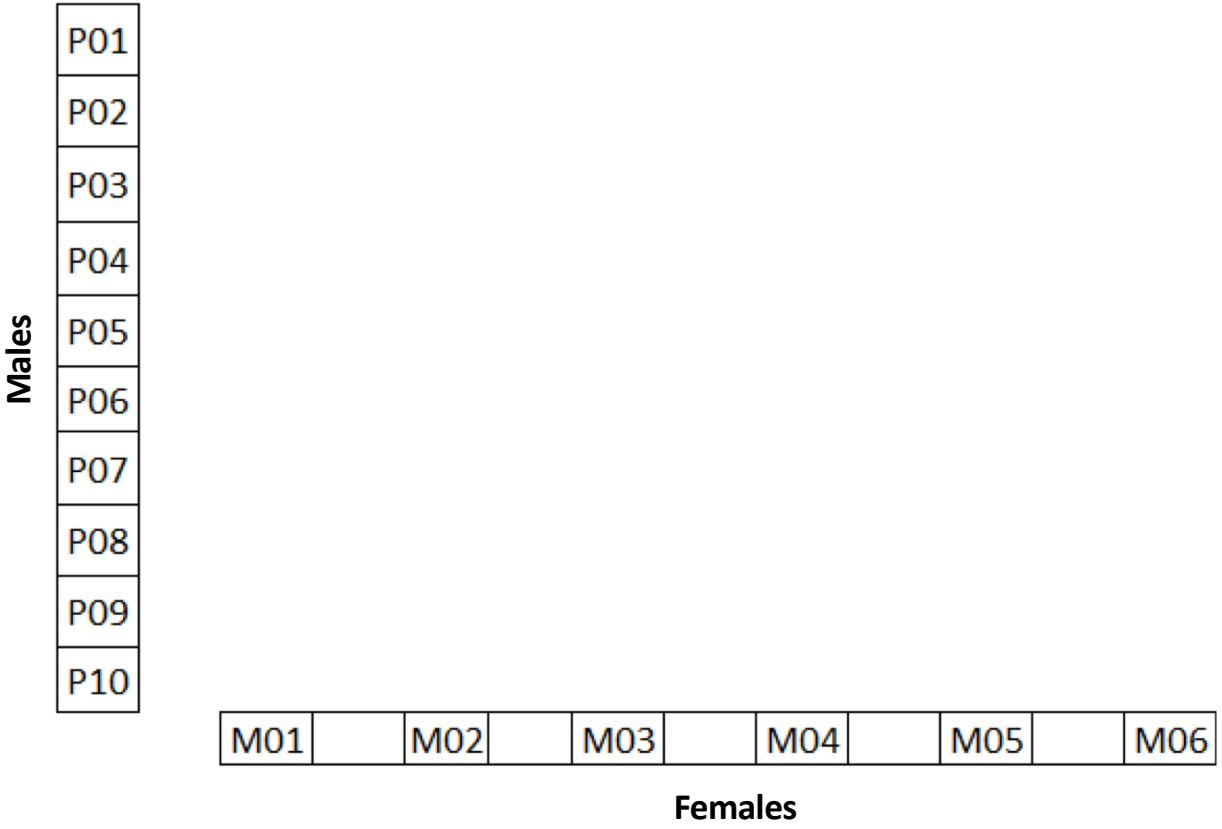


- In order to quantify the paternal contribution to offspring => polygamous females (6) and males (10) and a random sample of around 30 larvae/offspring were genotyped

> Parentage assignment

- Results of assignment of 173 larvae to 10 males 6 females

Rate of assignment: 54 %



females	N	% Assignment
M01	29	34,48
M02	30	40
M03	31	67,74
M04	30	76,67
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M06	23	0

- Corresponding to recorded mating patterns

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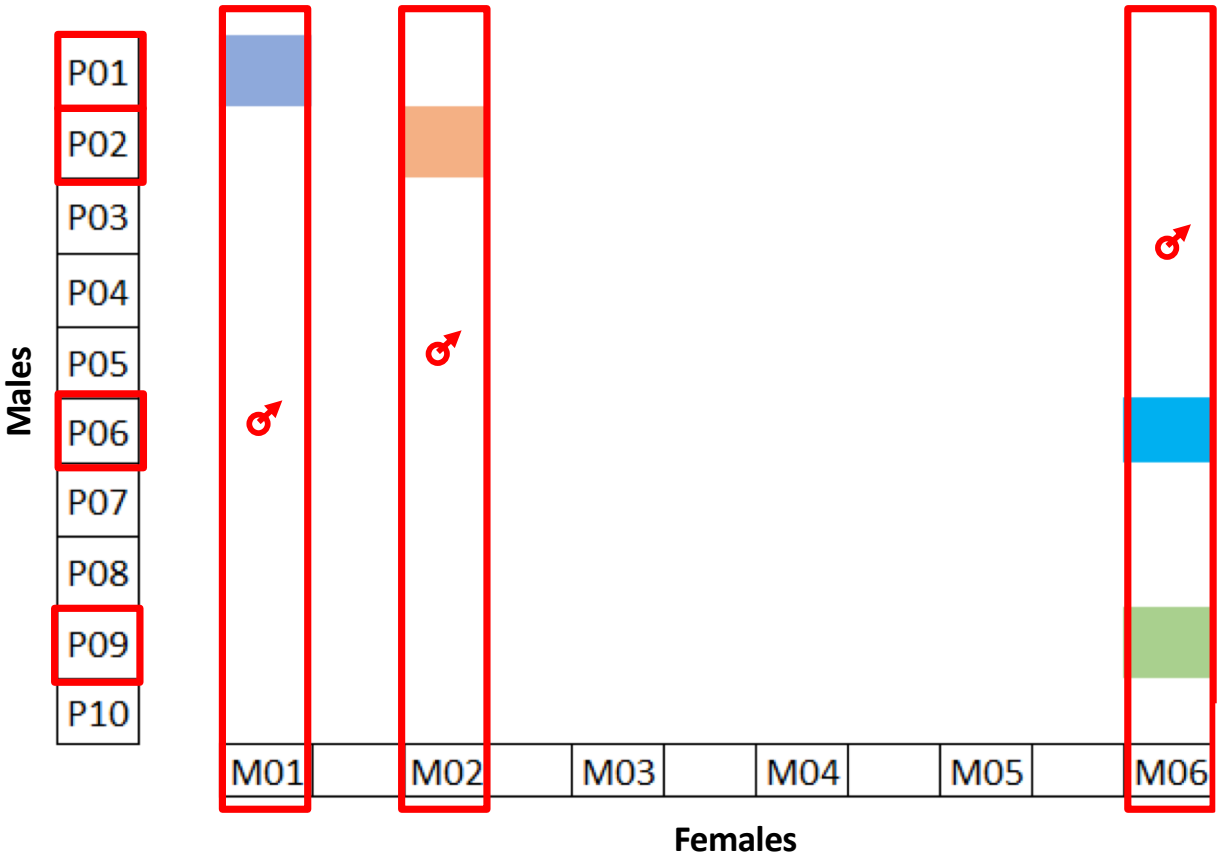

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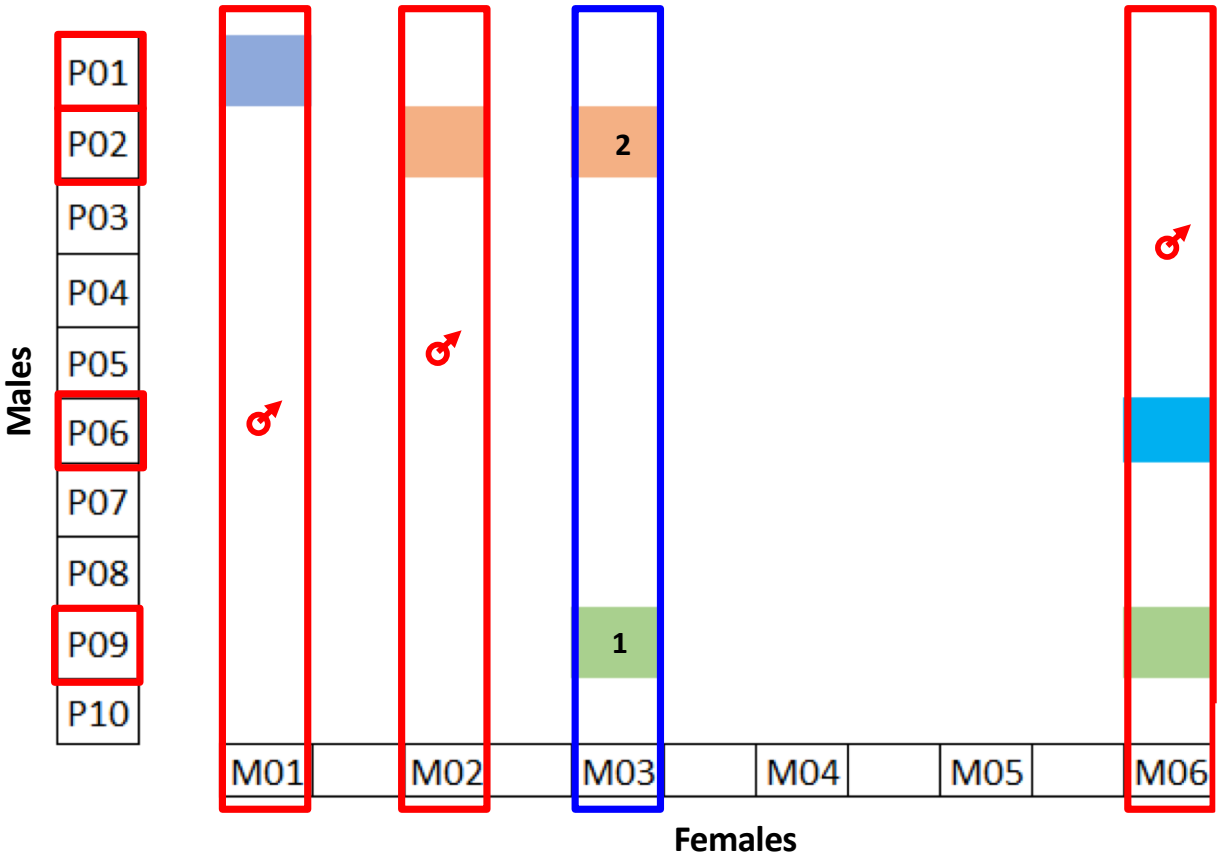

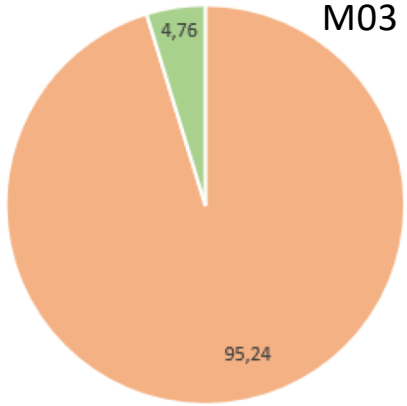

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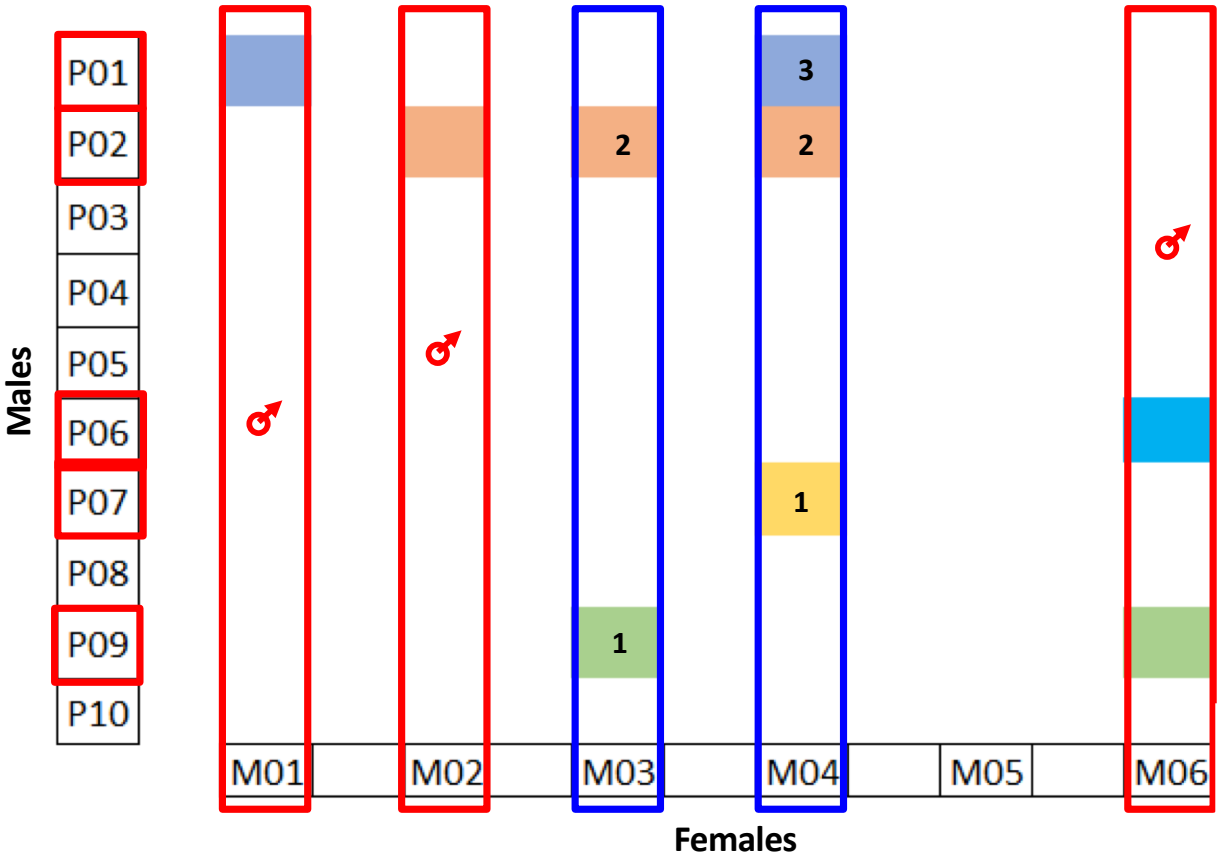

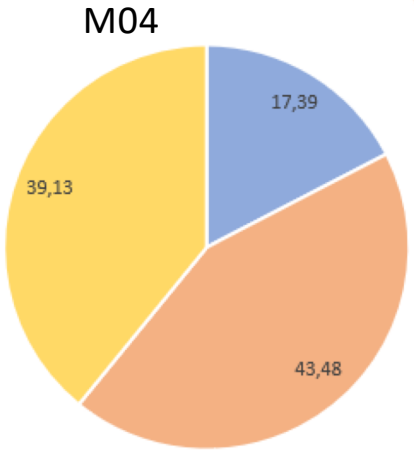

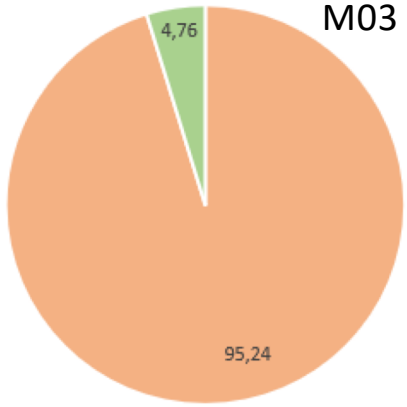

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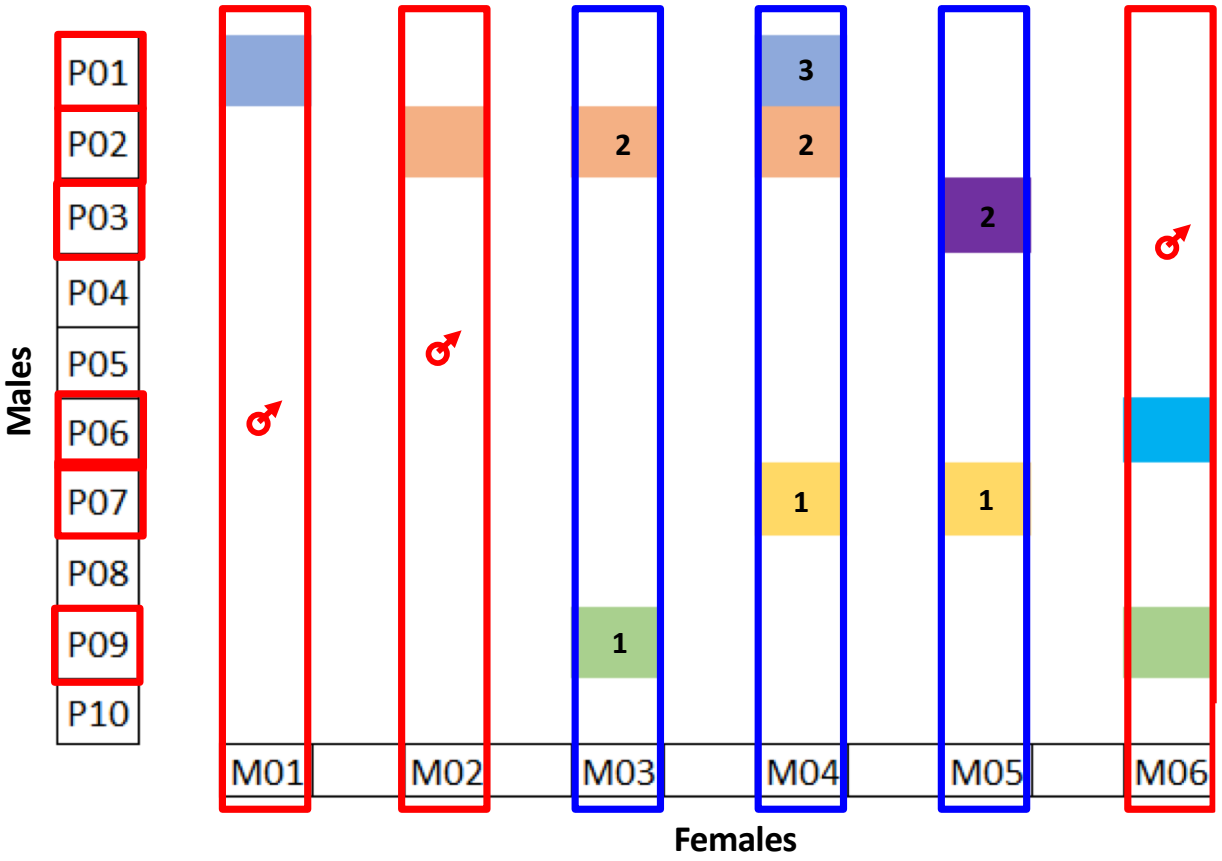
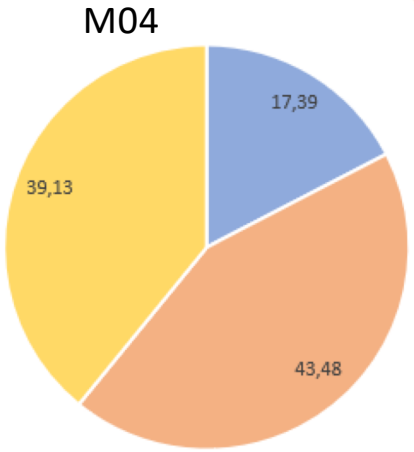
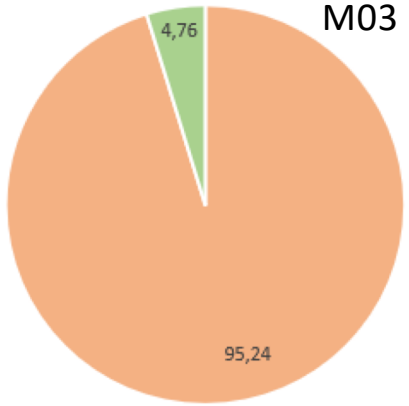
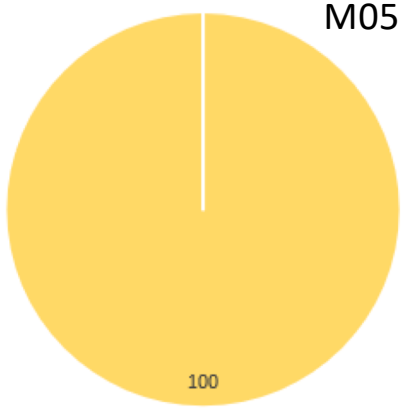


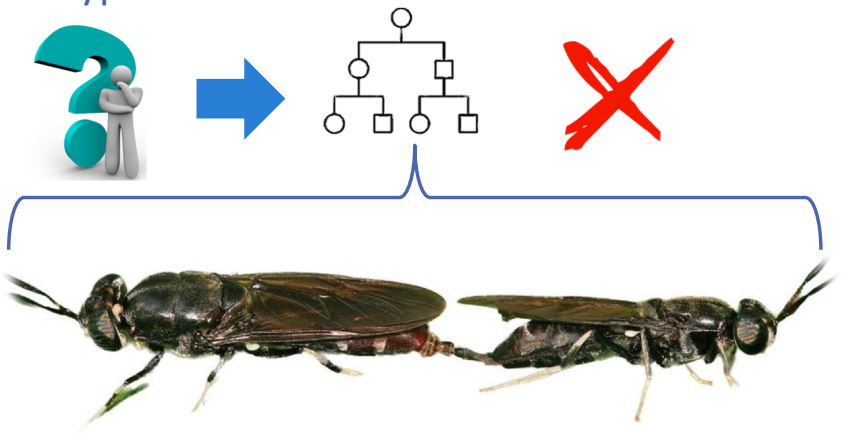






> Conclusion and take-home messages

- No evidence of our initial hypothesis



- ≃ 10 - 20% of pedigree error are probably recorded in our system
- However, do these error proportions have a negative impact on the estimation of genetic parameters and the EBVs prediction ?
- One study on Estimation of Pedigree Errors in the UK Dairy Population and the Impact on Selection, showing that with 8.8 - 13.1% pedigree errors, there is a loss of response to selection of around 2 to 3% (Visscher et al. 2002)
- But we need more data to accurately quantify this error rate in BSF system

> Many thanks

Partners :

SYSAAF

INNOVAFEED

Alexandra Guigue

Service providers :

GENTYANE
PLATE-FORME de
GENOTYPAGE et SÉQUENÇAGE en AUVERGNE

Thank you for your attention