









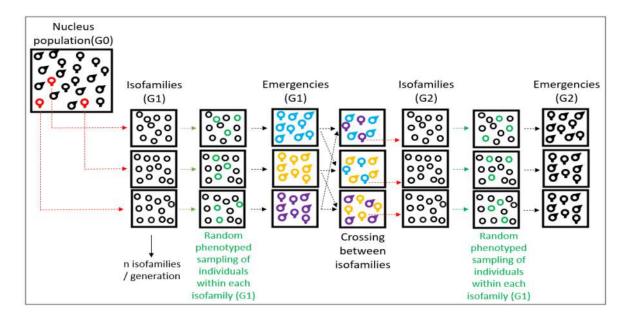
Mating behaviour checking in the black soldier fly (*Hermetia illucens* L.) using SNP data: Parentage assignment for pedigree reconstruction

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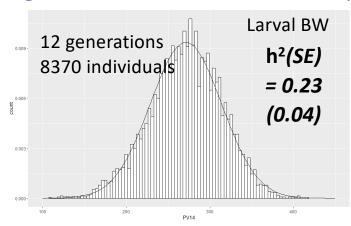
Athens, Greece 29-31/01/2025

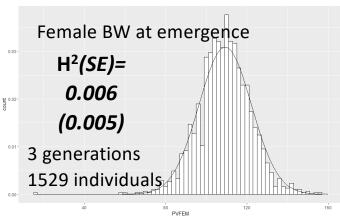
• In 2019, we developed a family pedigree breeding scheme in the black soldier fly (BSF)

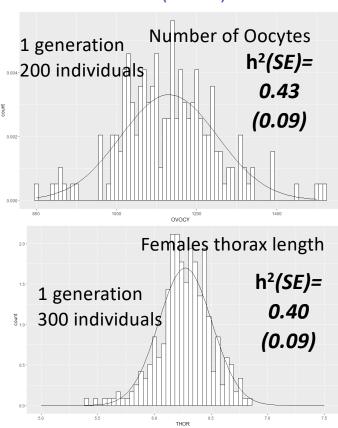


- Clutches are isolated and collected per female, with the assumption that one clutch is mated by a single male and a single female
- Random phenotyped => used to bult pedigree over generation and genetic parameters estimation

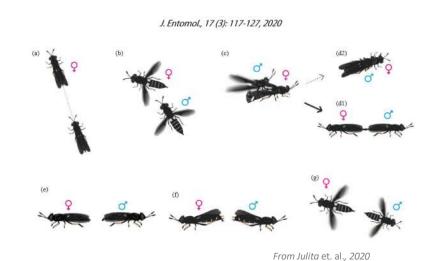
• Using these scheme for *h*² estimation by REstricted Maximum Likelihood (REML)



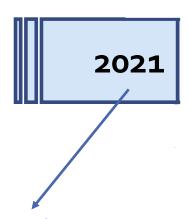




- Beginning of this study in 2019 => no information was available about BSF polygamy
- Up until 2021, no reports in literature of multiple mating in BSF

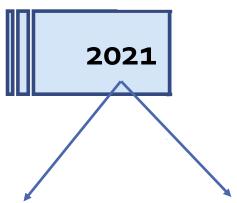


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- But since then:



7-10% of multiple mating in experimental (Jones & Tomberlin, 2021)

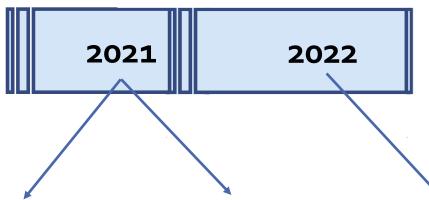
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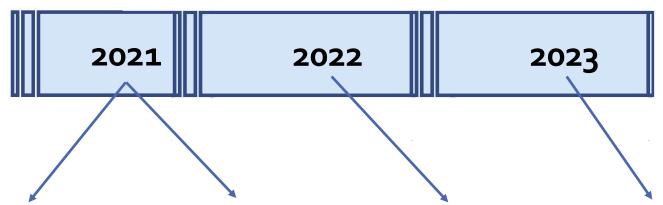


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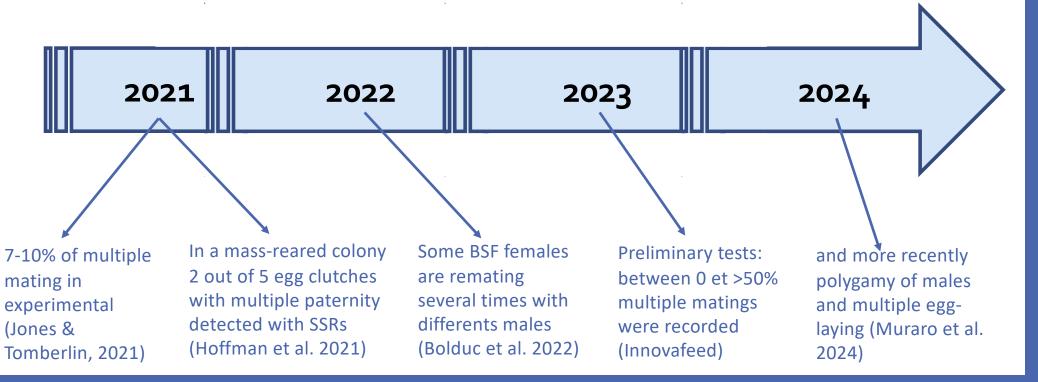


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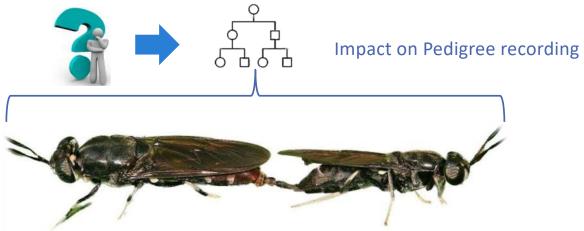
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Preliminary tests: between 0 et >50% multiple matings were recorded (Innovafeed)

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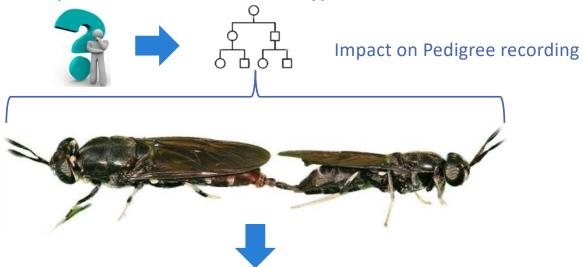


• All these observations raise questions about our initial hypothesis



> Objective

• All these observations raise questions about our initial hypothesis

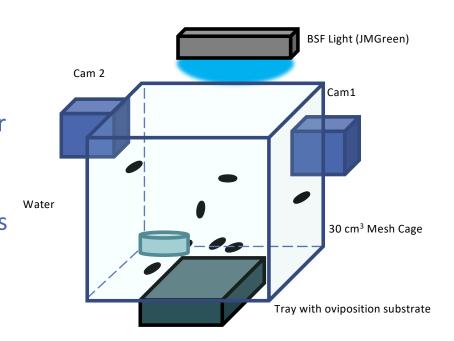


The aim of present study was to test the monogamy hypothesis in our pedigree breeding selection scheme through a parentage assignment design

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

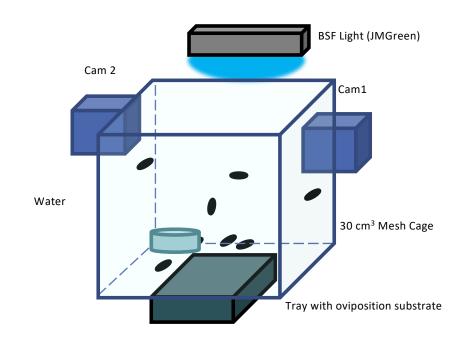
> Experimental setting

- 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



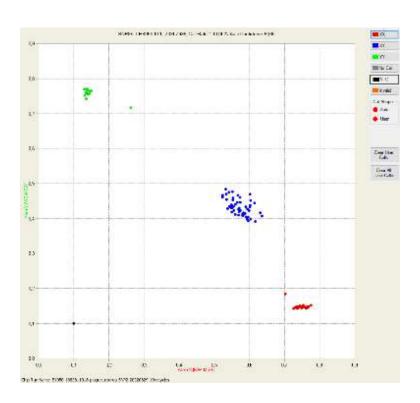


Not recorded: Night-time behaviour, remating behaviour, failed mating attempts

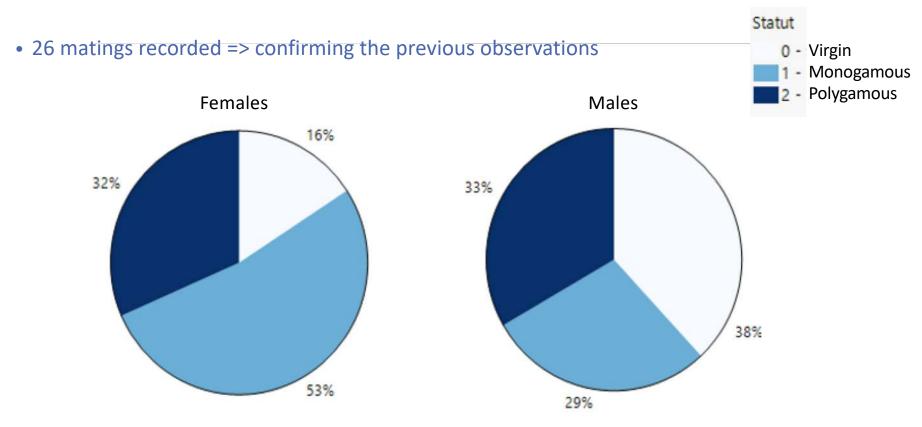
> Experimental setting

- 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



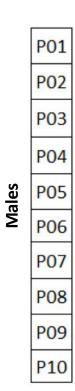
• In order to quantify the paternal contribution to offspring => polygamous females (6) and males (10) and a random sample of around 30 larvae/offspring were genotyped

> Parentage assignment

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



Rate of assignment: 54 %



females	N	% Assignment
Moı	29	34,48
Mo2	30	40
Моз	31	67,74
Мо4	30	76,67
Mo5	30	93,4
Mo6	23	0

 Corresponding to recorded mating patterns

N401	1402	1402	N404	NAOF	1400
M01	IVIUZ	M03	M04	IVIUS	M06

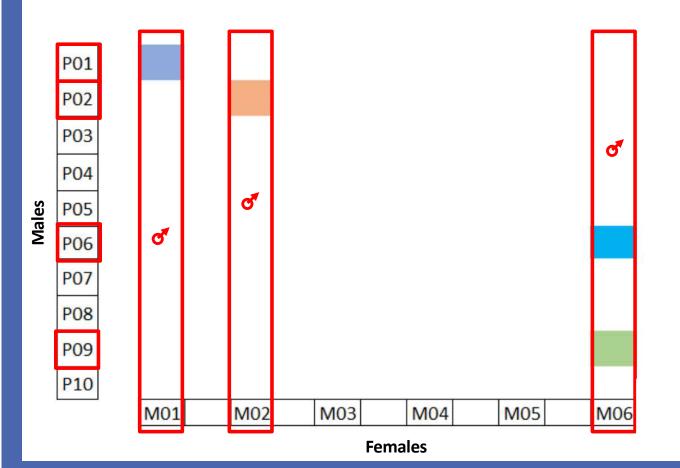
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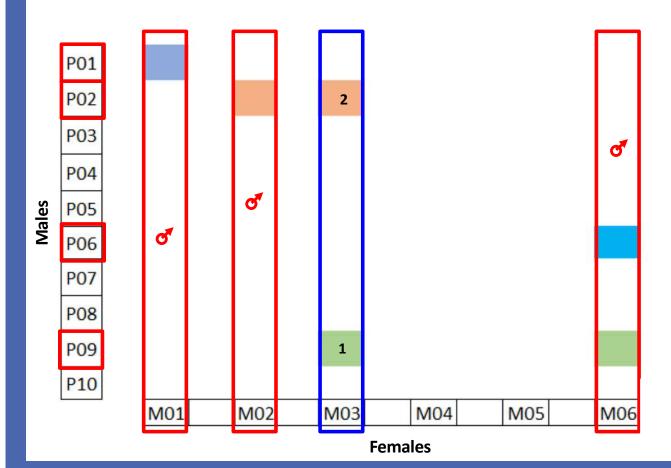


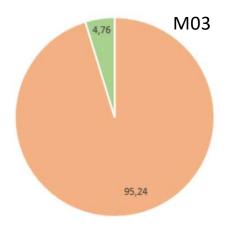
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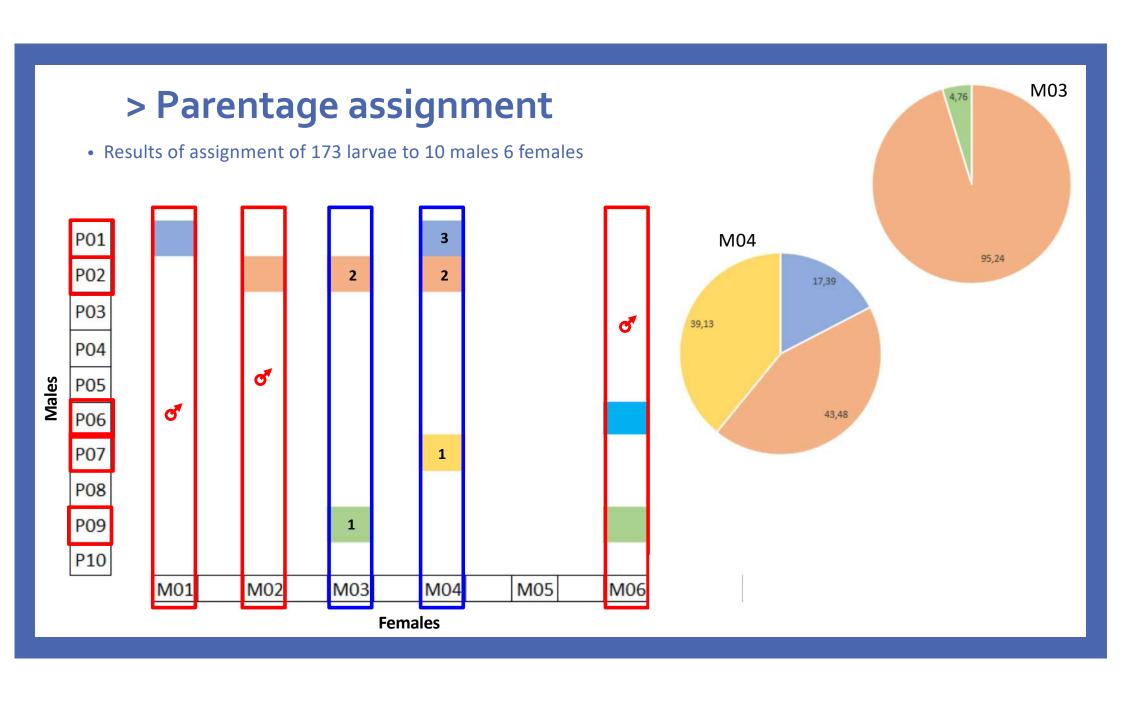
- Corresponding to recorded mating patterns
- 3 families had unsatisfactory
 results (< 50%) because the smale' genotypes were missing

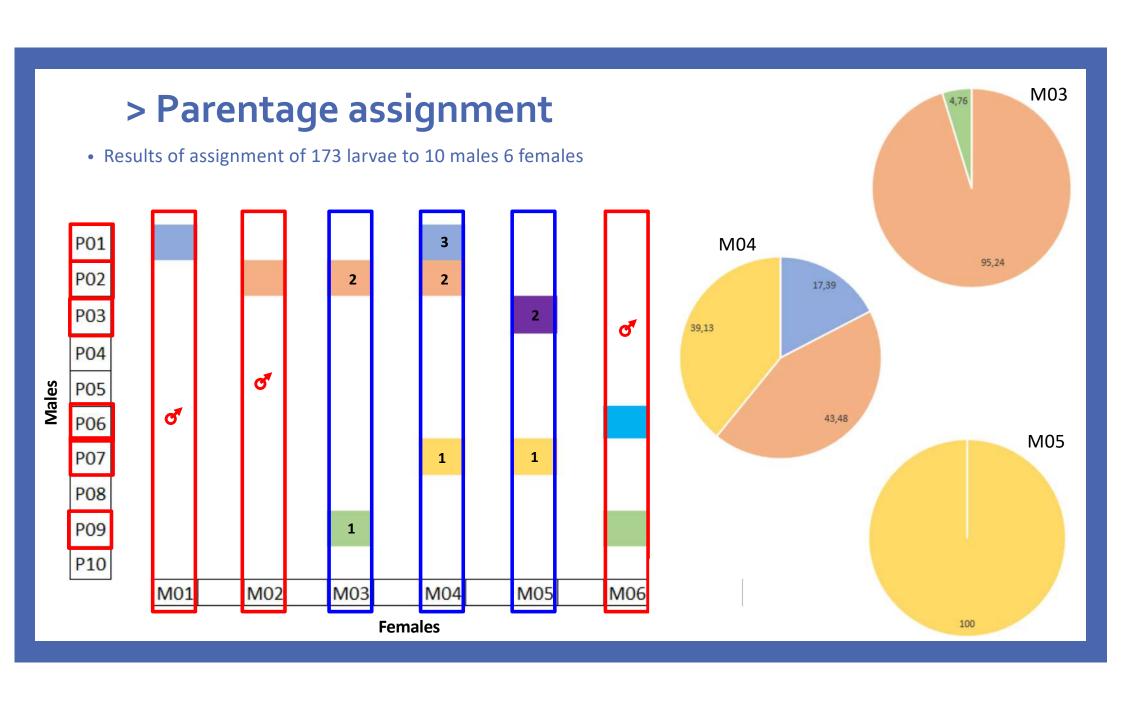
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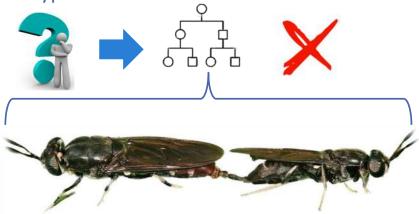






> Conclusion and take-home messages

• No evidence of our initial hypothesis



- \simeq 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:







Alexandra Guigue

Service providers:



Thank you for your attention