Population and Functional Genomics of Black Soldier Fly Mass Rearing

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EAAP
European Federation of Animal Science

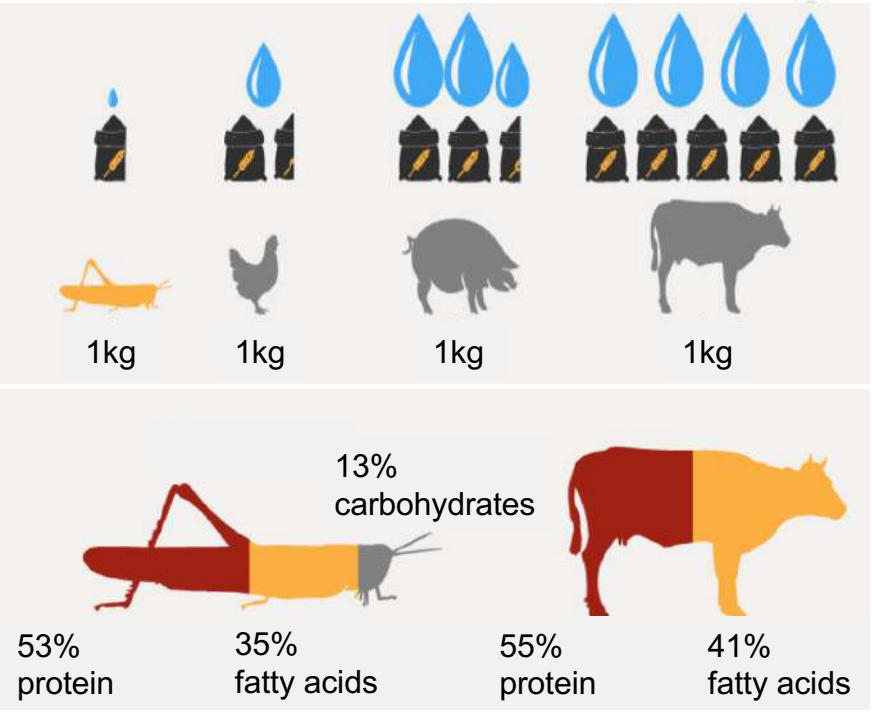
Stellenbosch UNIVERSITY IYUNIVESITHI UNIVERSITEIT

INSECT GENETICS IMPrOVEMENT IMPlementation act

The Promise of Insect Farming…

…Reduce, Resilience, Reliable…

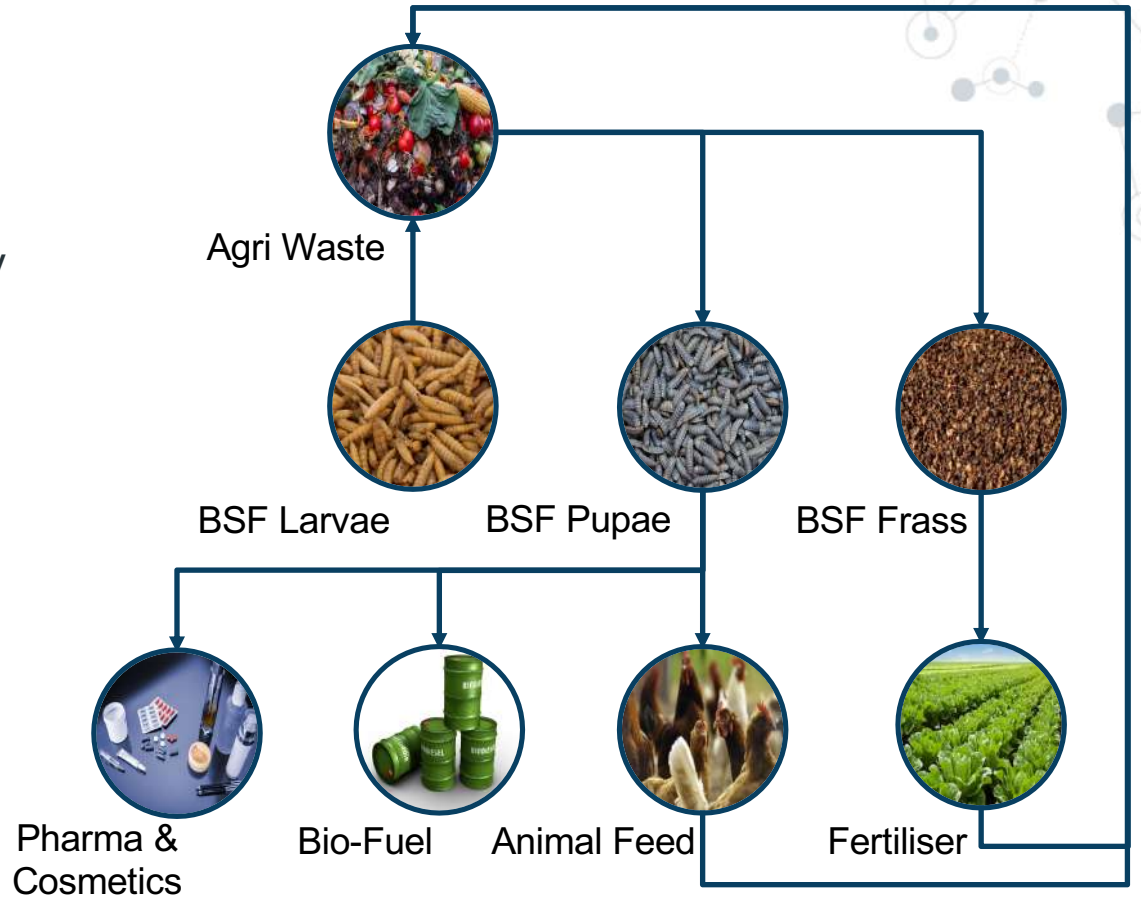
- Growing human population
- Diminishing natural recourses
- Threat of global climate change
- Food and nutritional insecurity



The Black Soldier Fly (BSF)…

…An emerging hero for insect farming?

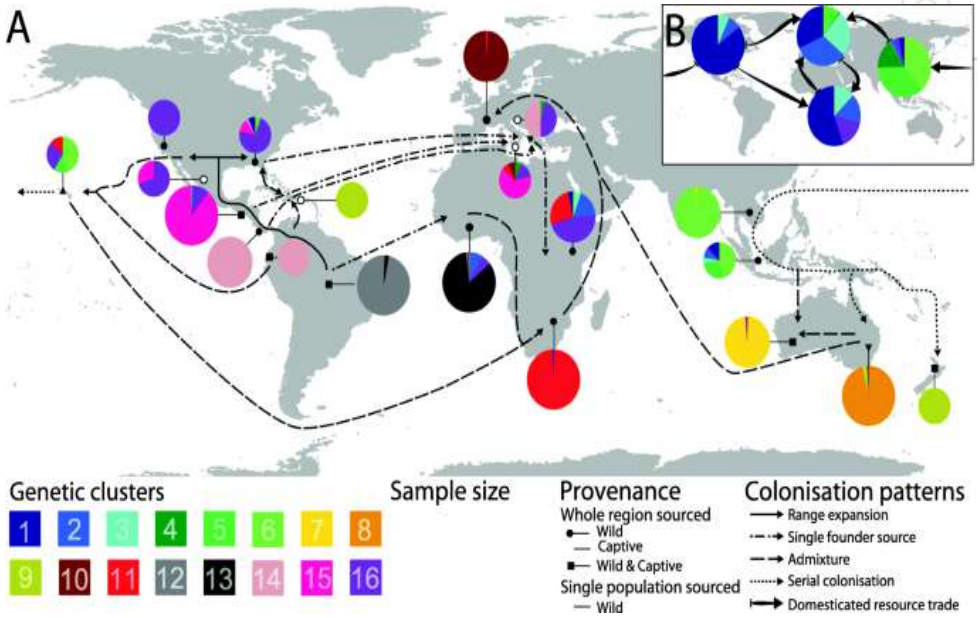
- Advantages of insect farming
- Added bioremediation capacity
- Circular Agricultural Economy
- Sustainability



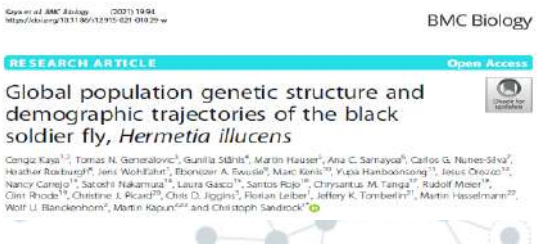
“What” is the Black Soldier Fly (BSF)?

…Is it a bird? Is it a wasp? No, it’s SuperFly!

- Cosmopolitan species of the Stratiomyidae family
- South American origin
- Human mediated global distribution
- Benign ‘invader’
- Commercial production globally
- Genetic and phenotypic variation



Kaya et al., 2021



BMC Biology

RESEARCH ARTICLE Open Access

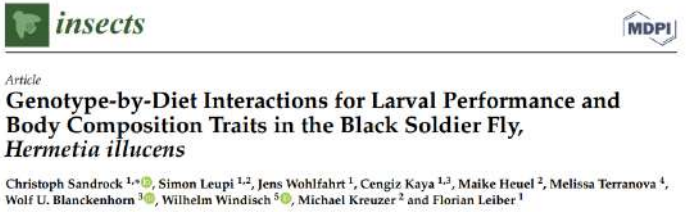
Global population genetic structure and demographic trajectories of the black soldier fly, *Hermetia illucens*

Black Soldier Fly (BSF) Diversity

A rich germplasm resource for genetic improvement

- Advantages
  - High genetic diversity – high evolutionary potential
    - Scope for artificial selection
  - Opportunities for cross breeding strategies – hybrid vigour

- Caution
  - GxE might alter phenotypic performance
  - Outbreeding depression


insects

MDPI

Article

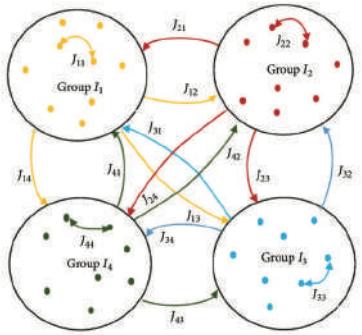
Genotype-by-Diet Interactions for Larval Performance and Body Composition Traits in the Black Soldier Fly, *Hermetia illucens*

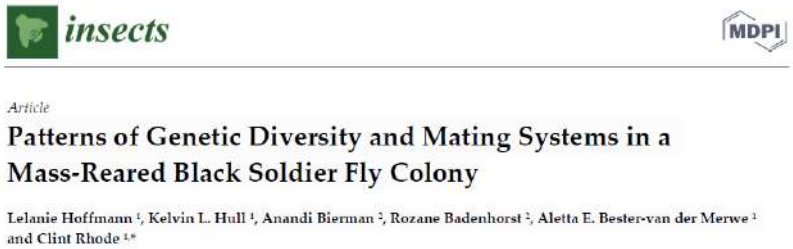
Christoph Sandrock [1,*], Simon Leupi [1,2], Jens Wohlfahrt [1], Cengiz Kaya [1,3], Maike Heuel [2], Melissa Terranova [4], Wolf U. Blanckenhorn [3], Wilhelm Windisch [5], Michael Kreuzer [2] and Florian Leiber [1]

Black Soldier Fly (BSF) Diversity

Factors that impact the genetic diversity of populations

- Insect populations are demographically dynamic
  - Frequent extinction and recolonisation events, metapopulations
- Insects have r-selected life history characteristics
  - Short life cycle
  - High fecundity
  - Skewed reproductive success
- A variety of mating systems
  - Positive assortative mating and genetic polyandry in BSF
- Selection pressures with functional intersections
  - Phenotypic plasticity?




insects

MDPI

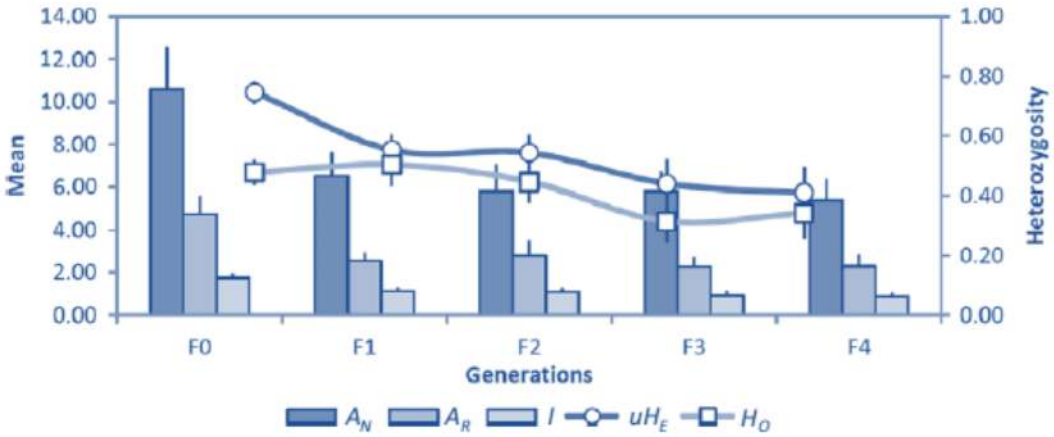
Article

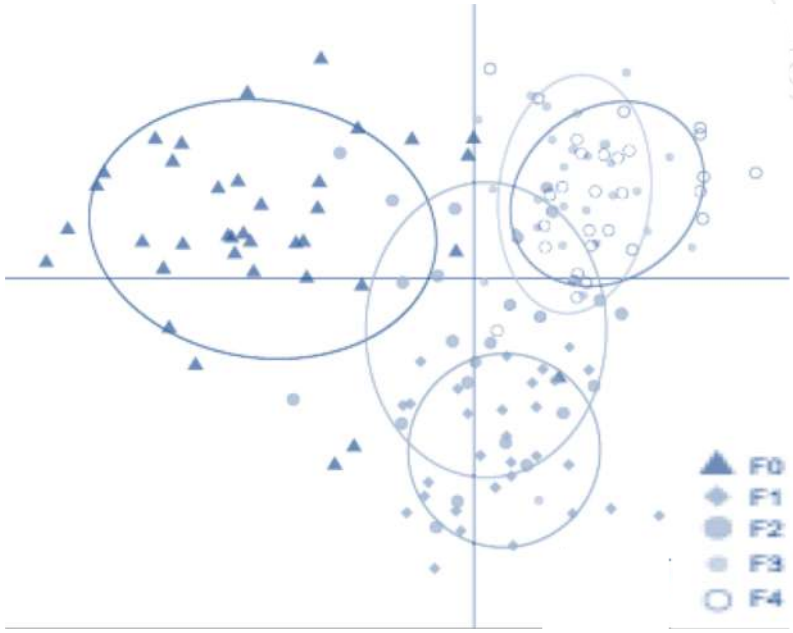
Patterns of Genetic Diversity and Mating Systems in a Mass-Reared Black Soldier Fly Colony

Lelanie Hoffmann [1], Kelvin L. Hull [1], Anandi Bierman [2], Rozane Badenhorst [2], Aletta E. Bester-van der Merwe [1] and Clint Rhode [1,*]

Black Soldier Fly Populations

…What happens during a colonisation event?





ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics
doi: 10.1111/age.12961

Genetic and phenotypic consequences of early domestication in black soldier flies (*Hermetia illucens*)

C. Rhode*, R. Badenhorst*,†, K. L. Hull*, M. P. Greenwood*, A. E. Bester-van der Merwe*, A. A. Andere‡, C. J. Picard‡ and C. Richards†

*Department of Genetics, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa. †AgriProtein Holdings Ltd, 1 Farnham Road, Guildford, SurreyGU2 4RG, UK. ‡Department of Biology, Purdue School of Science, Indiana University – University of Purdue Indianapolis, SL 306, 723 W Michigan Street, Indianapolis, IN 46202, USA.

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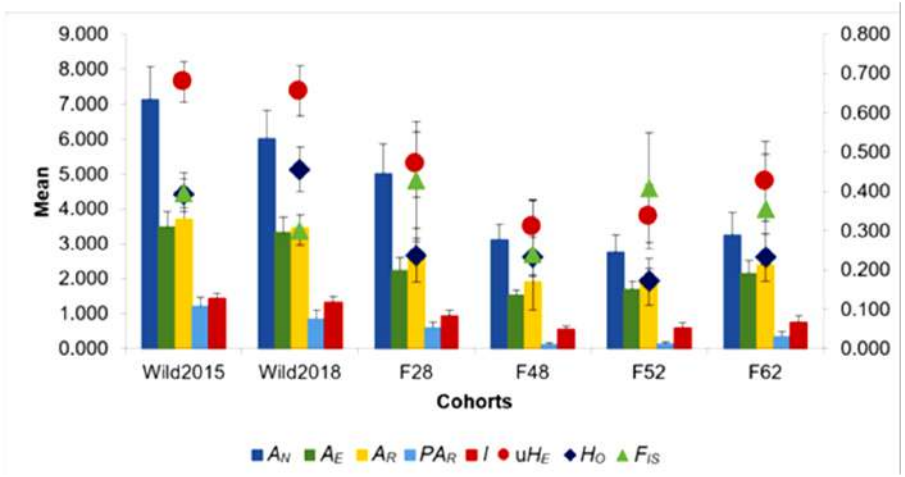

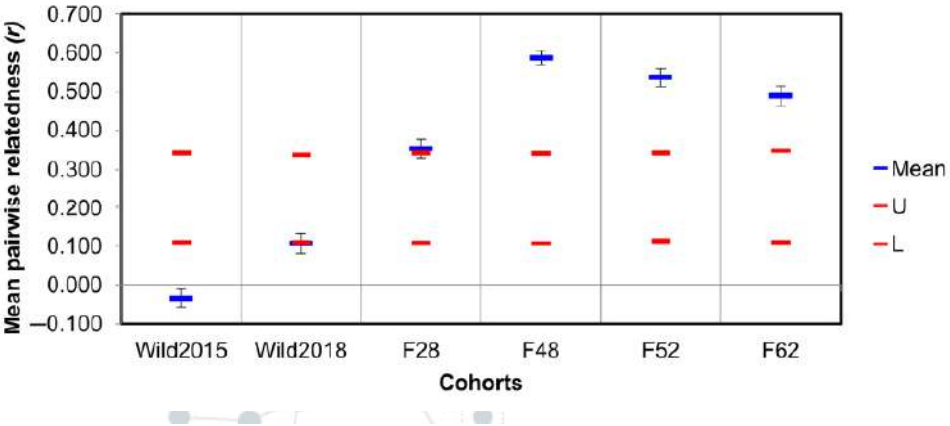

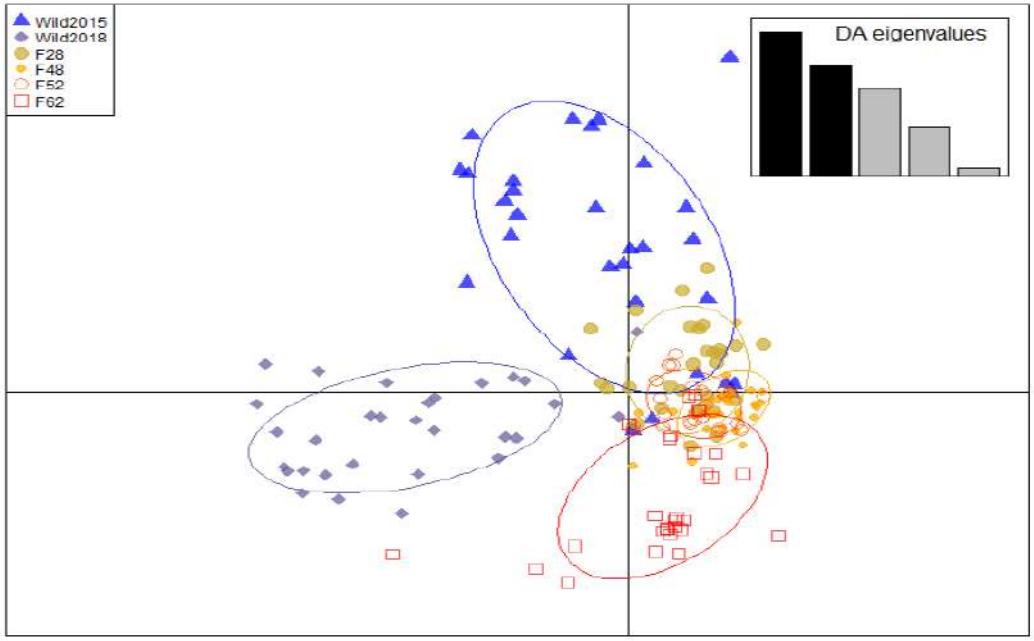

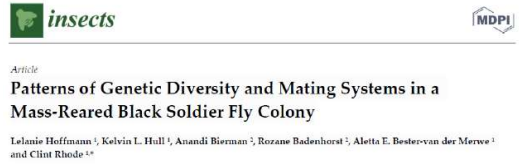

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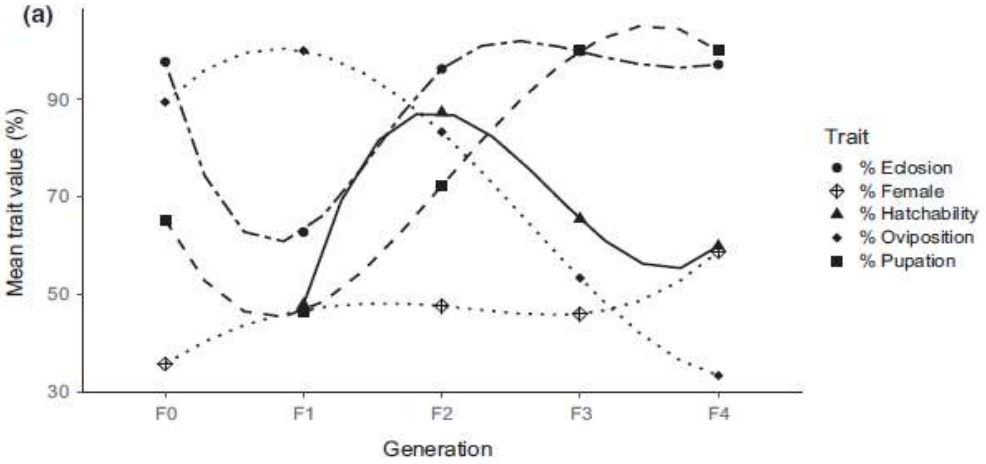

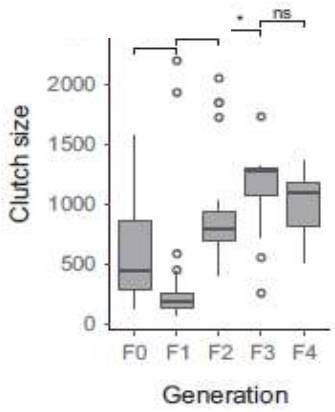

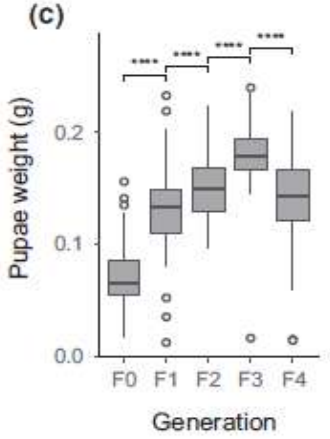

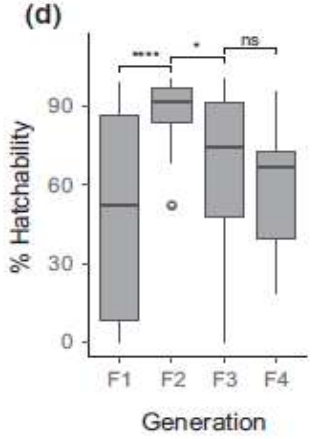

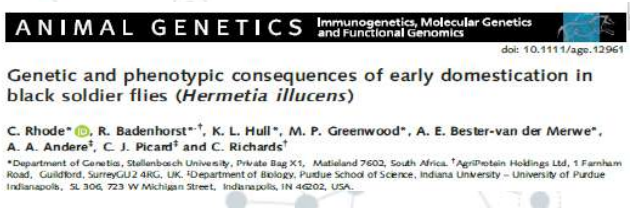

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Research Question & Objectives

What are the evolutionary drivers of genetic and phenotypic variation in BSF?

- Objective 1: Comparative genomic assessment of BSF strains
- Objective 2: Population genomics of a colonisation event
- Objective 3: Transcriptomic analysis of differential gene expression
- Objective 4: Microbiome of BSF strains on different feeds

Objective 1
Comparative genomics of BSF strains

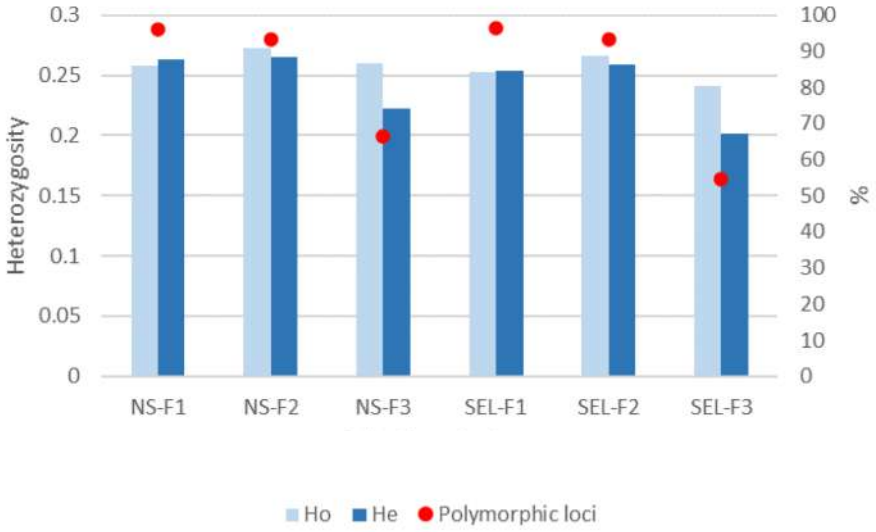
Hull et al. in prep.

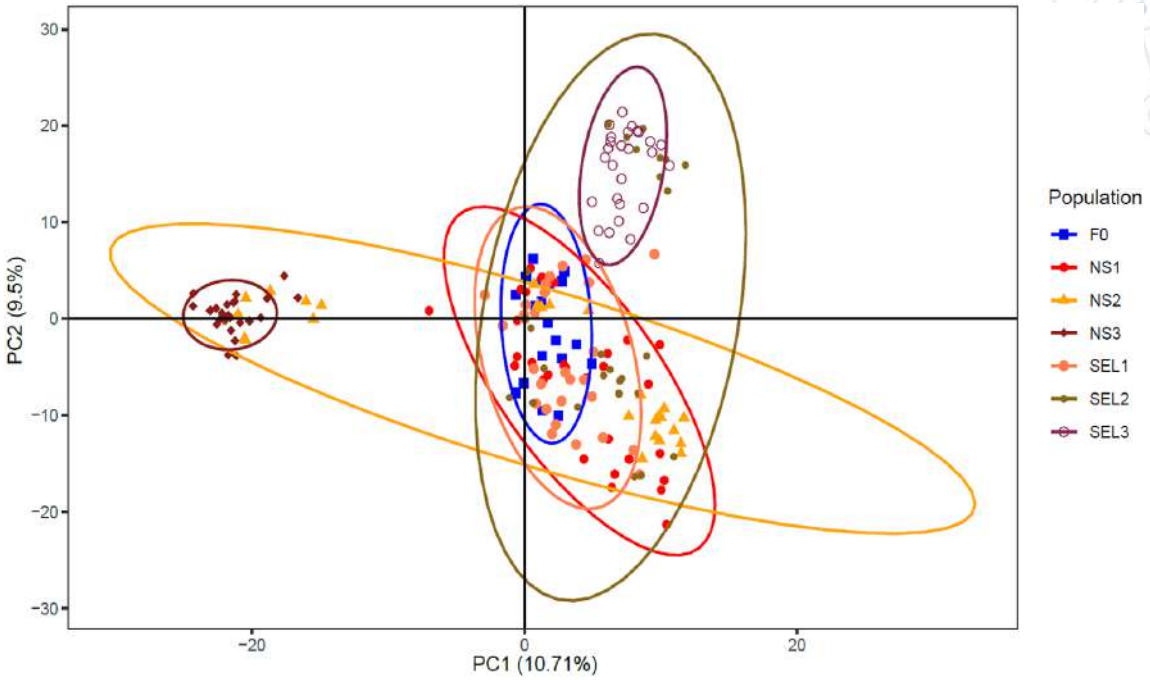
Generalovic et al. 2021

Zhan et al. 2020

Objective 2

Population genomics of BSF colonisation event

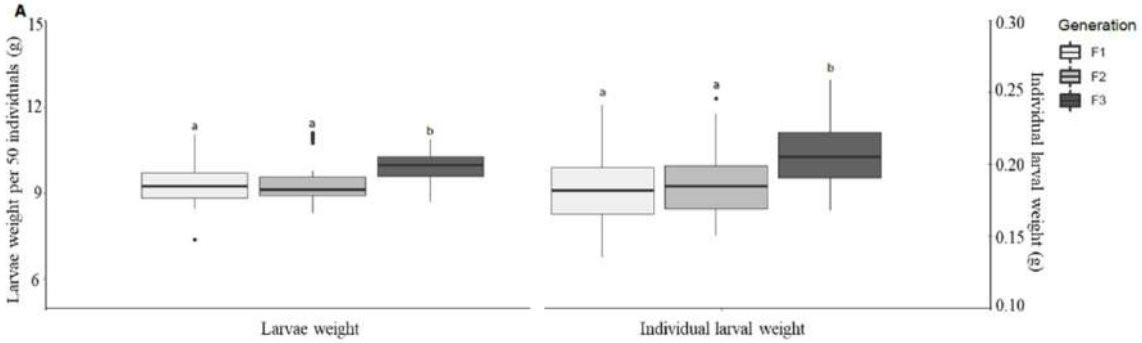


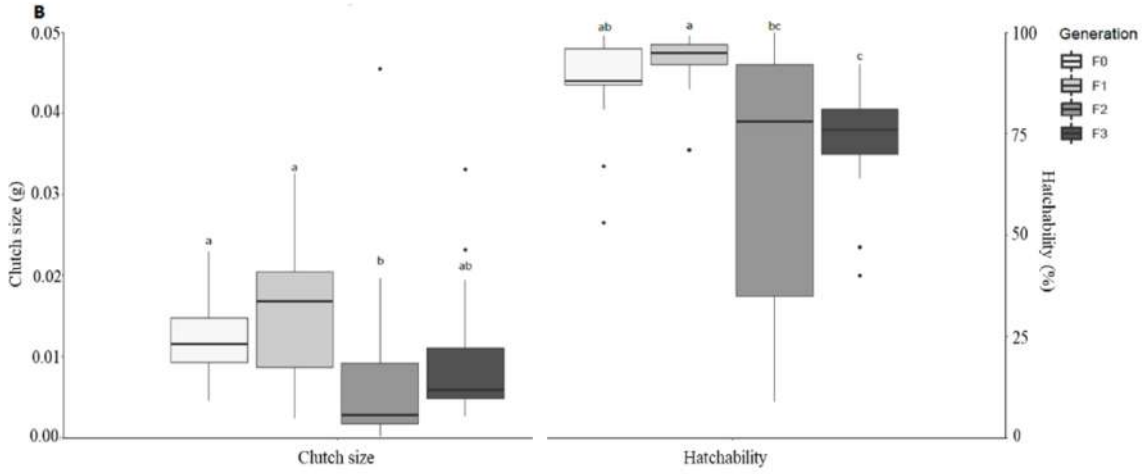


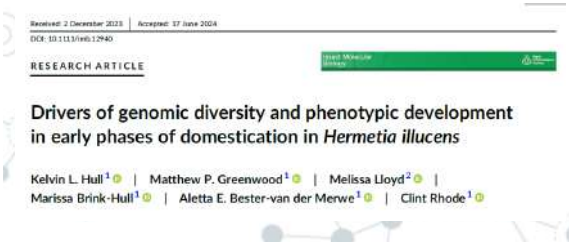
- Reduced polymorphism
  - Population bottlenecks limited N_E
    - Random drift
  - Selective sweeps
    - Purge genotypes
    - Favoured genotypes

Objective 2

Population genomics of BSF colonisation event







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RESEARCH ARTICLE

Drivers of genomic diversity and phenotypic development in early phases of domestication in *Hermetia illucens*

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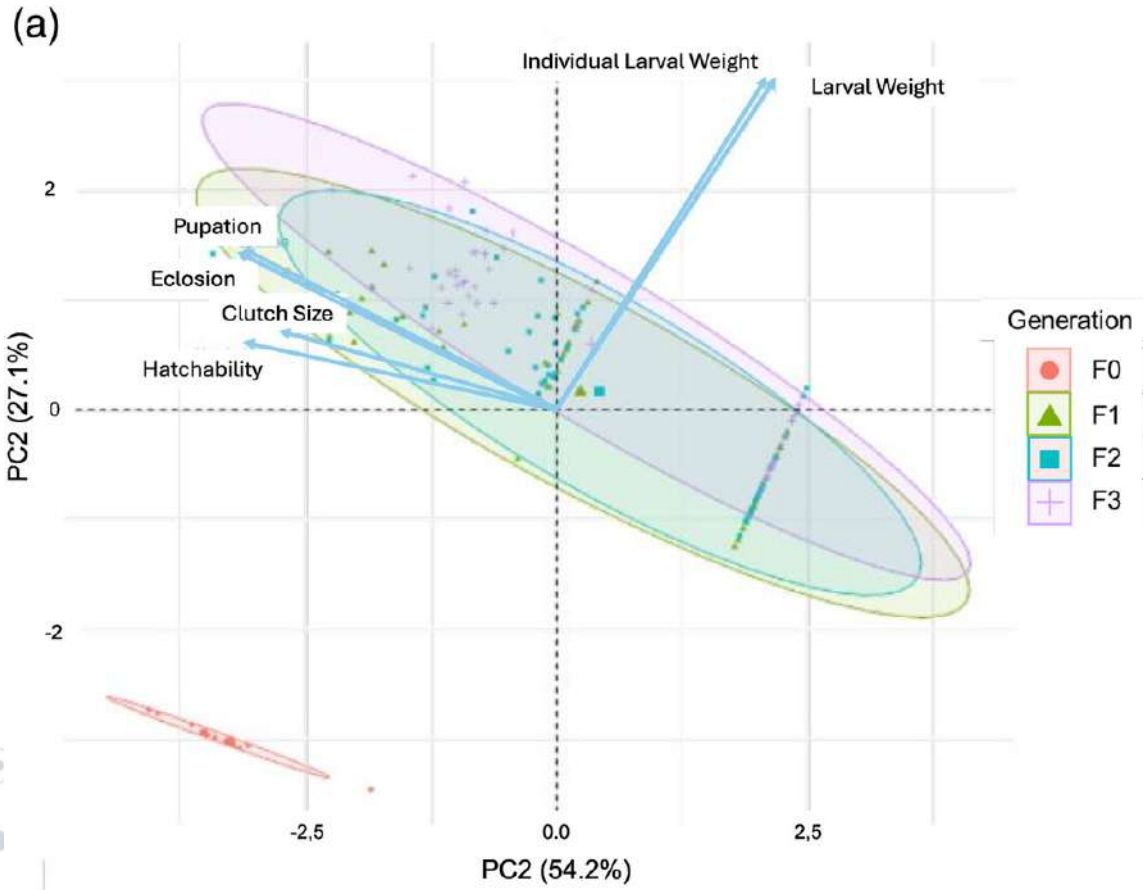

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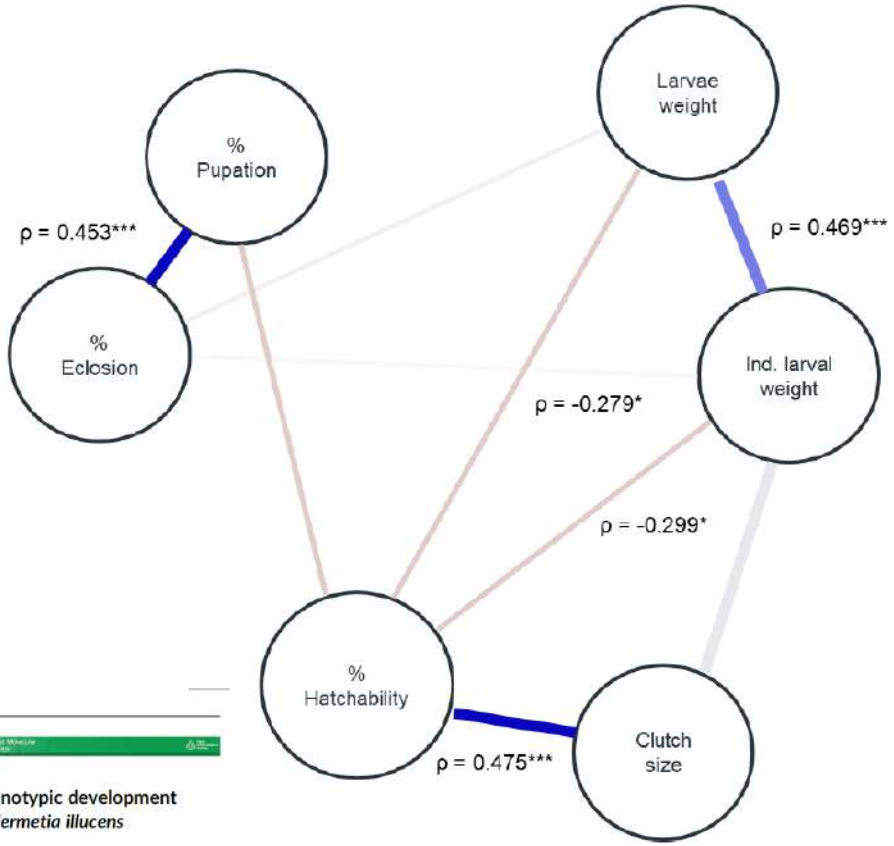

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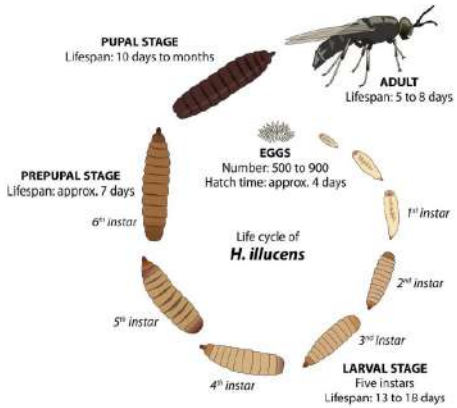
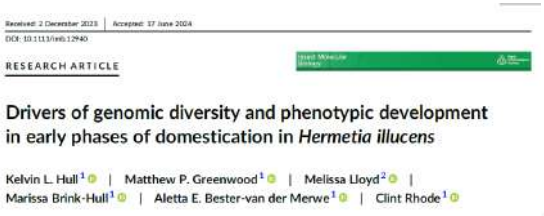
Trait	h^2_{SNP}
Larval Mass	~0.18
% Eclosion	n.s.
% Pupation	n.s.
% Hatchability	~0.16
Clutch Size	~0.06

Objective 2

Population genomics of BSF colonisation event



De Smet *et al*. 2018



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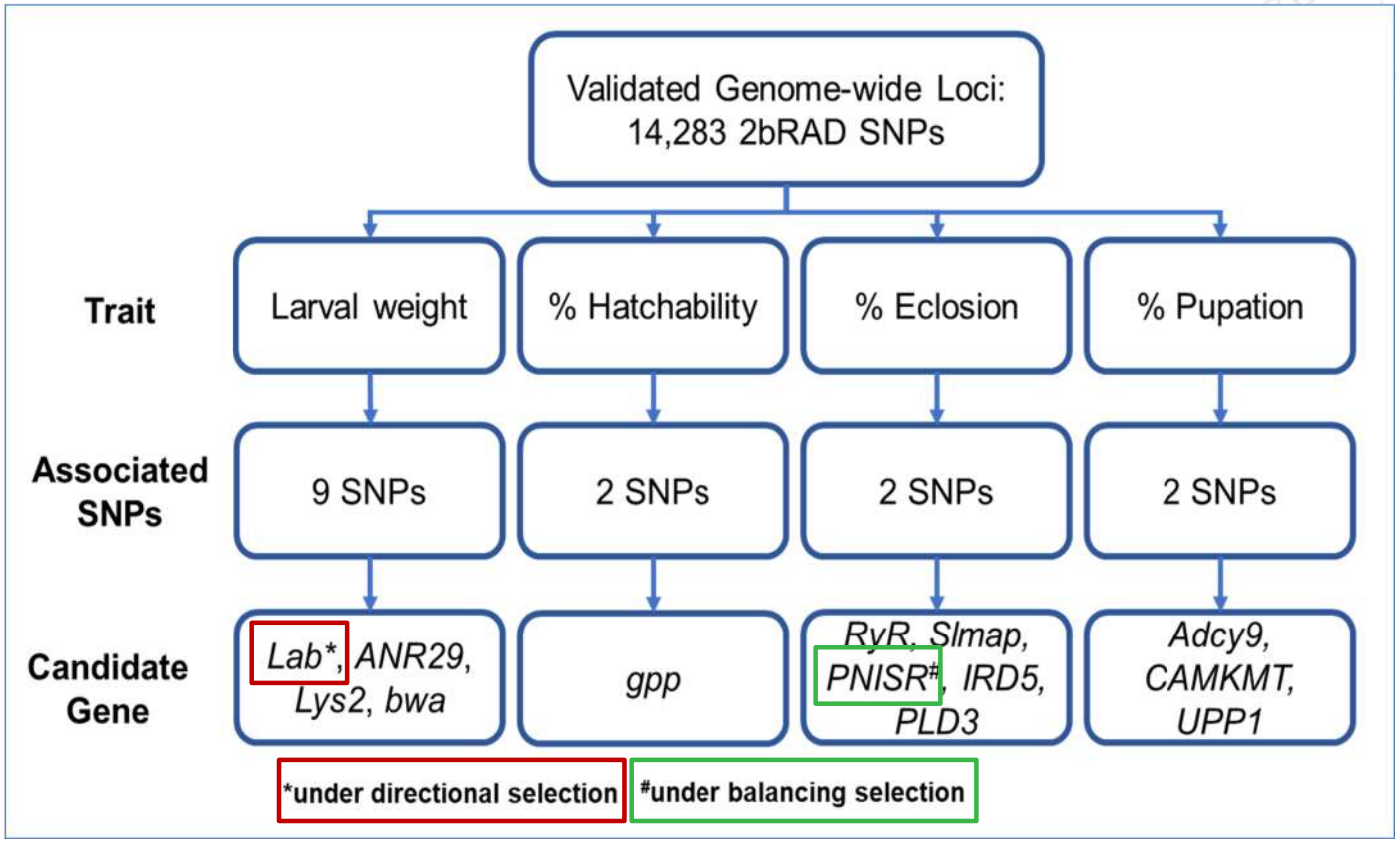
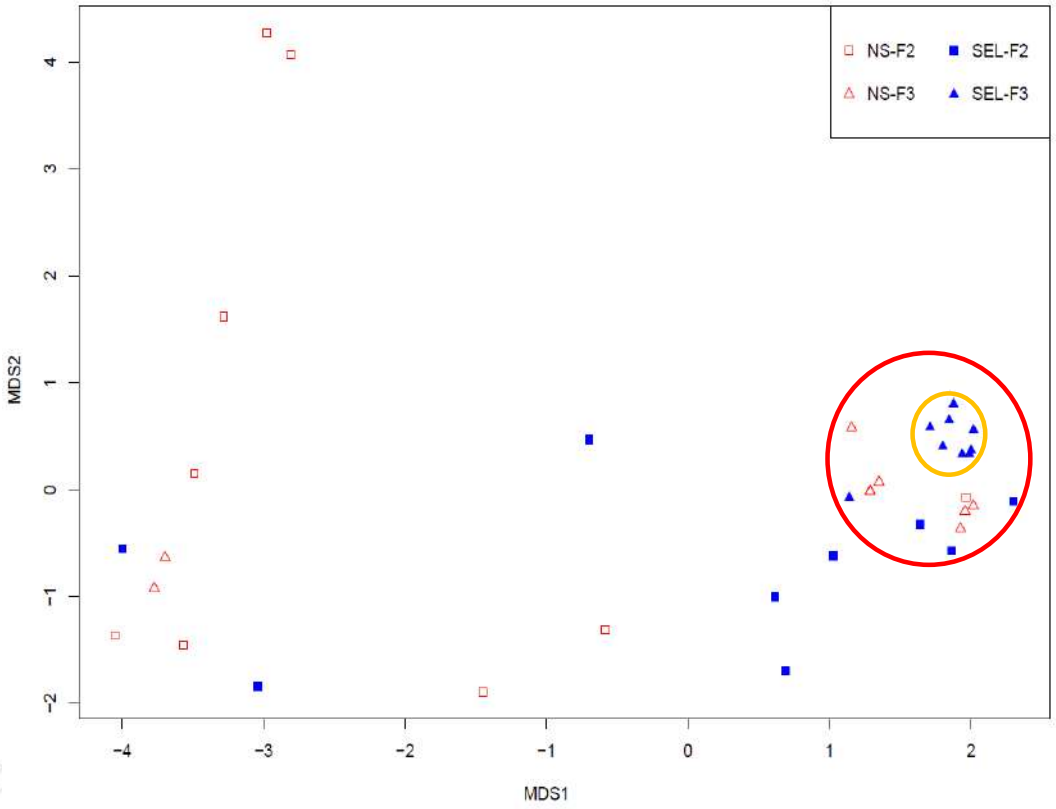
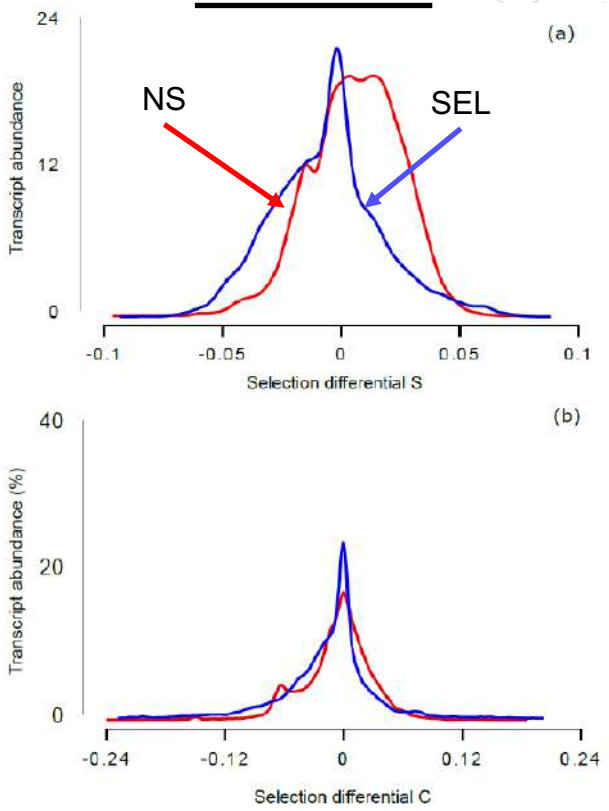


Objective 3

Population Transcriptomics of BSF colonisation event



Generation



Objective 3

Population Transcriptomics of BSF colonisation event

Experimental grouping → **Differentially Expressed Genes**

Generational cohorts: F2 *vs* F3

898 Genes
GO Enrichment
- Immune Response
- Metabolism
- Catalytic Activity
- Developmental processes

Negative correlation with larval weight

Selection Regime cohorts: Non-selected *vs* Selected for growth

231 Genes
GO Enrichment
- Metabolism
- Catalytic Activity


Insect Molecular Biology

Royal Entomological Society

Original Article | Open Access

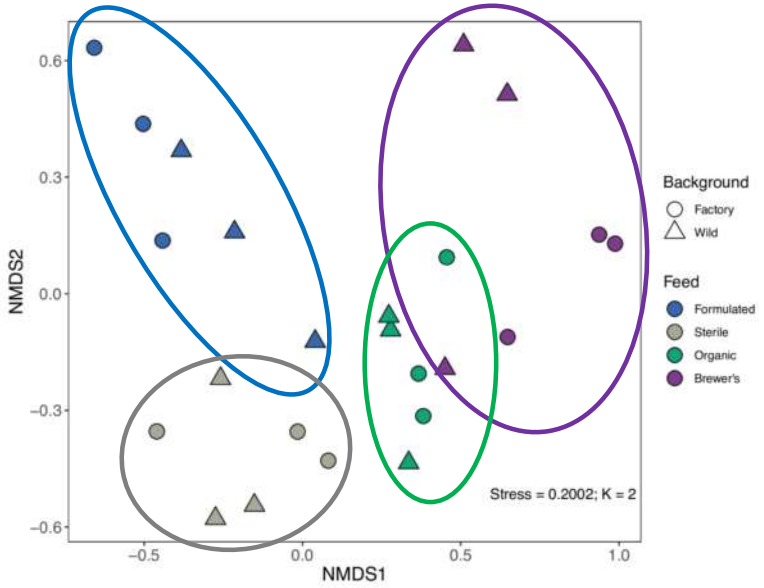
Gene expression differentials driven by mass rearing and artificial selection in black soldier fly colonies

Kelvin L. Hull, Matthew P. Greenwood, Melissa Lloyd, Aletta E. Bester-van der Merwe, Clint Rhode

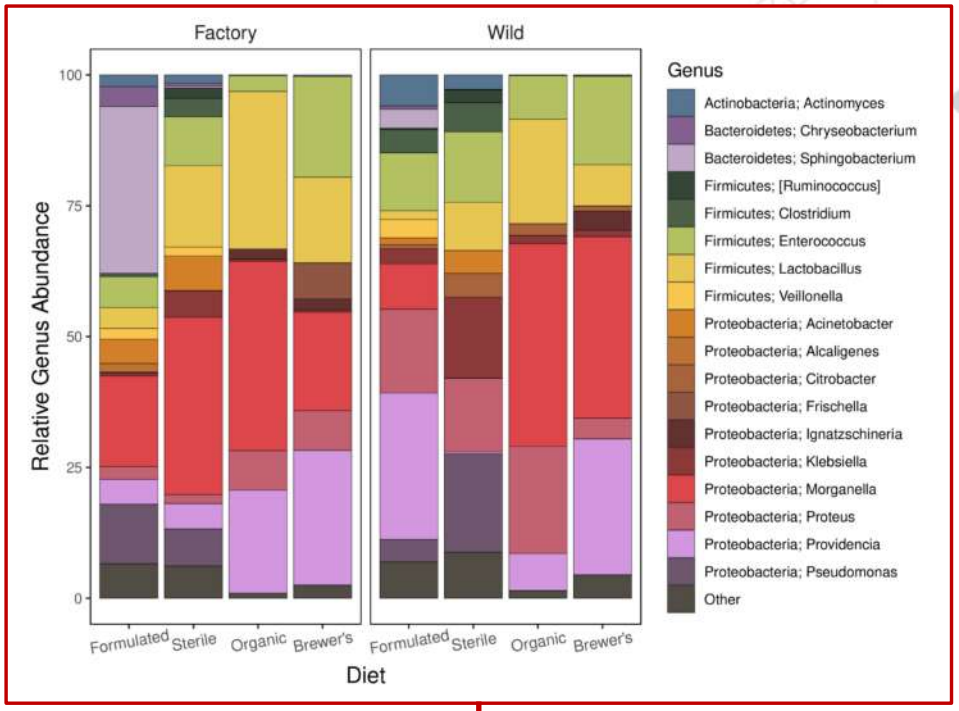
First published: 02 November 2022 | https://doi.org/10.1111/imb.12816

Objective 4

Microbiome of BSF strains on different feeds



Data Partition	Df	SS	R^2	Pseudo-*F*	*p*
Background (G)	1	0.357	0.078	3.053	0.009
Feed (E)	3	1.714	0.374	4.885	<0.001
Background × Feed (G × E)	3	0.637	0.139	1.815	0.031
Residual	16	1.872	0.409		
Total	23	4.580	1.000		



Association with Protein : Fat ratios of larvae

insects MDPI

Article

Feed and Host Genetics Drive Microbiome Diversity with Resultant Consequences for Production Traits in Mass-Reared Black Soldier Fly (*Hermetia illucens*) Larvae

Matthew P. Greenwood [1], Kelvin L. Hull [1], Marissa Brink-Hull [3], Melissa Lloyd [2] and Clint Rhode [1,*]

Conclusions

- Unique accessory genes amongst global BFS strains
- Random genetic drift was the major evolutionary driver of genomic diversity (Drift-barrier hypothesis)
- Functional trade-offs between growth metabolism and immune function; Production traits and Fitness traits
- Microbiomes act as classical quantitative genetic trait with correlations with other traits

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Matthew Greenwood, M.Sc.

Lelanie Hoffmann, M.Sc.

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