

Genetic and Phenotypic variability in the Black Soldier Fly, *Hermetia illucens*

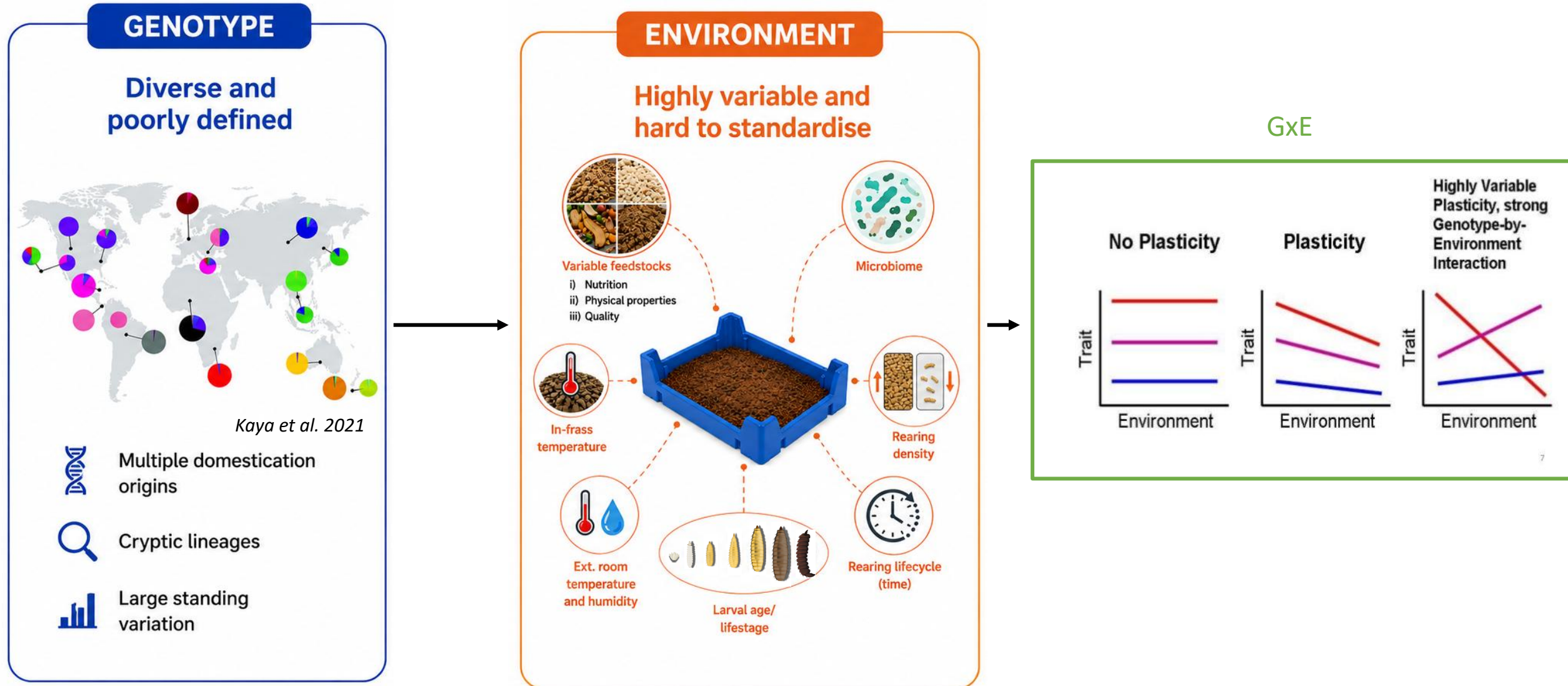


Tomas N. Generalovic

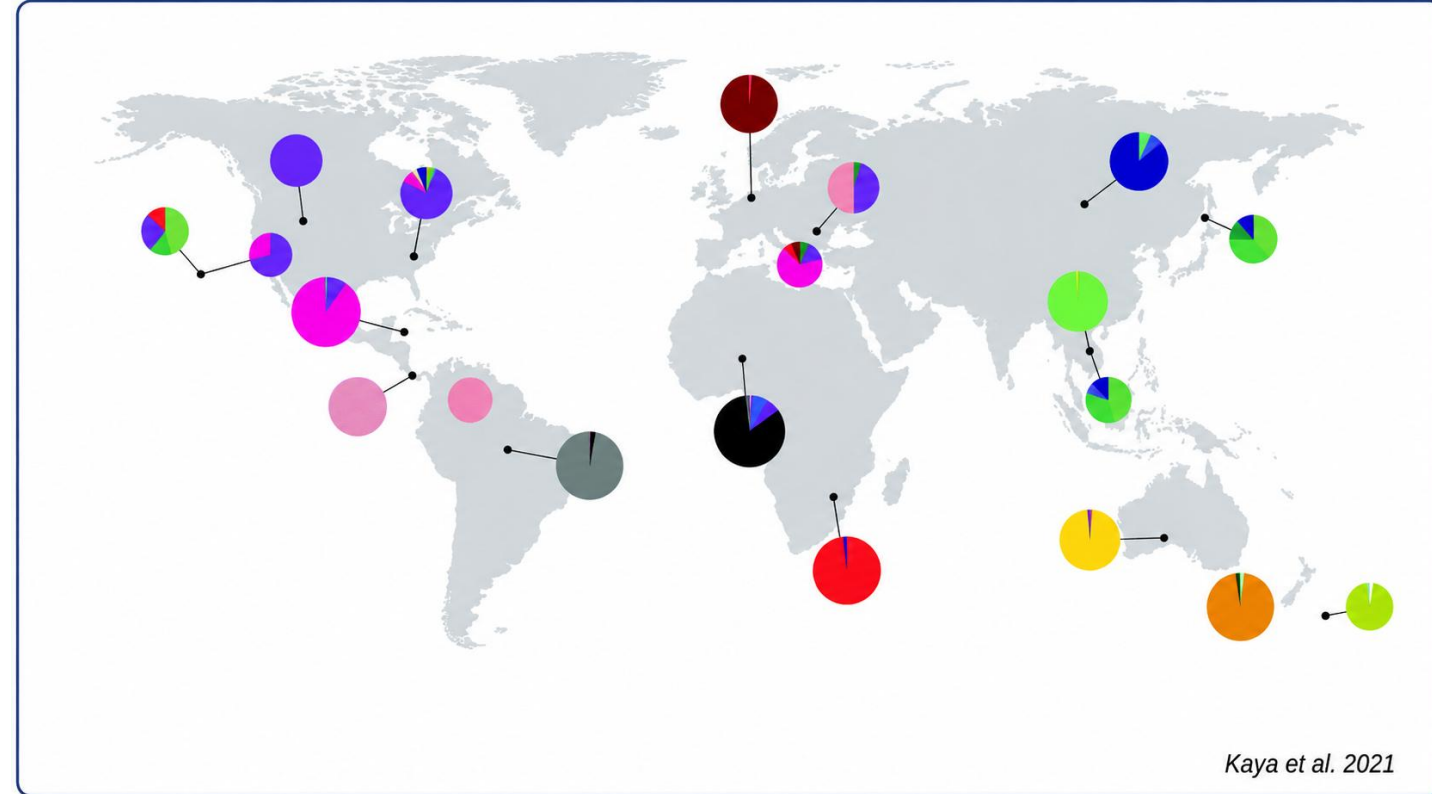
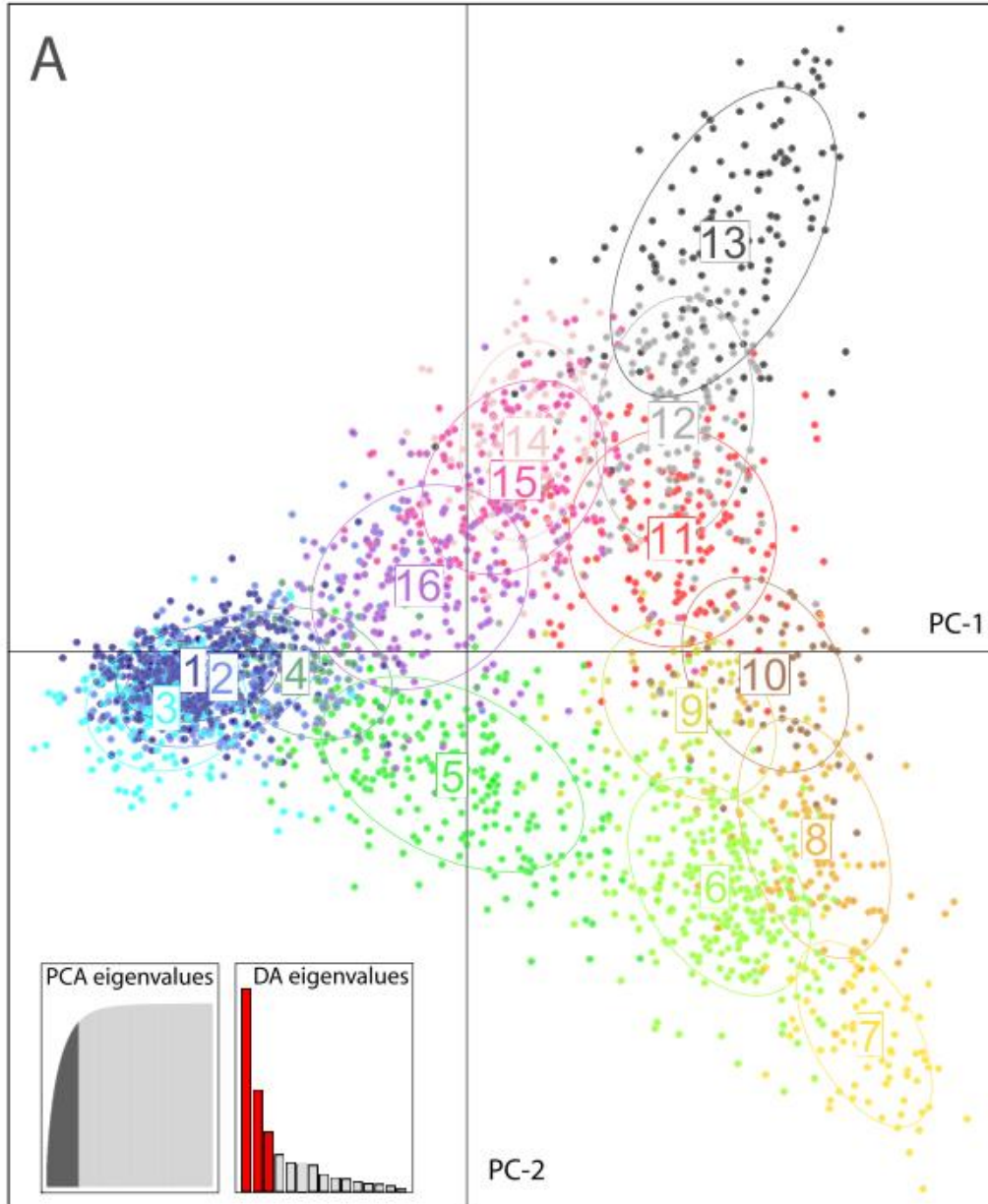
tng23@cam.ac.uk | tgeneralovic@gmail.com

Genetic and phenotypic variation is prominent in the insect industry

Industrial insect systems operate under highly **heterogeneous** environmental conditions while relying on **genetically diverse** and uncharacterised populations in an industry **lacking in standardisation**.



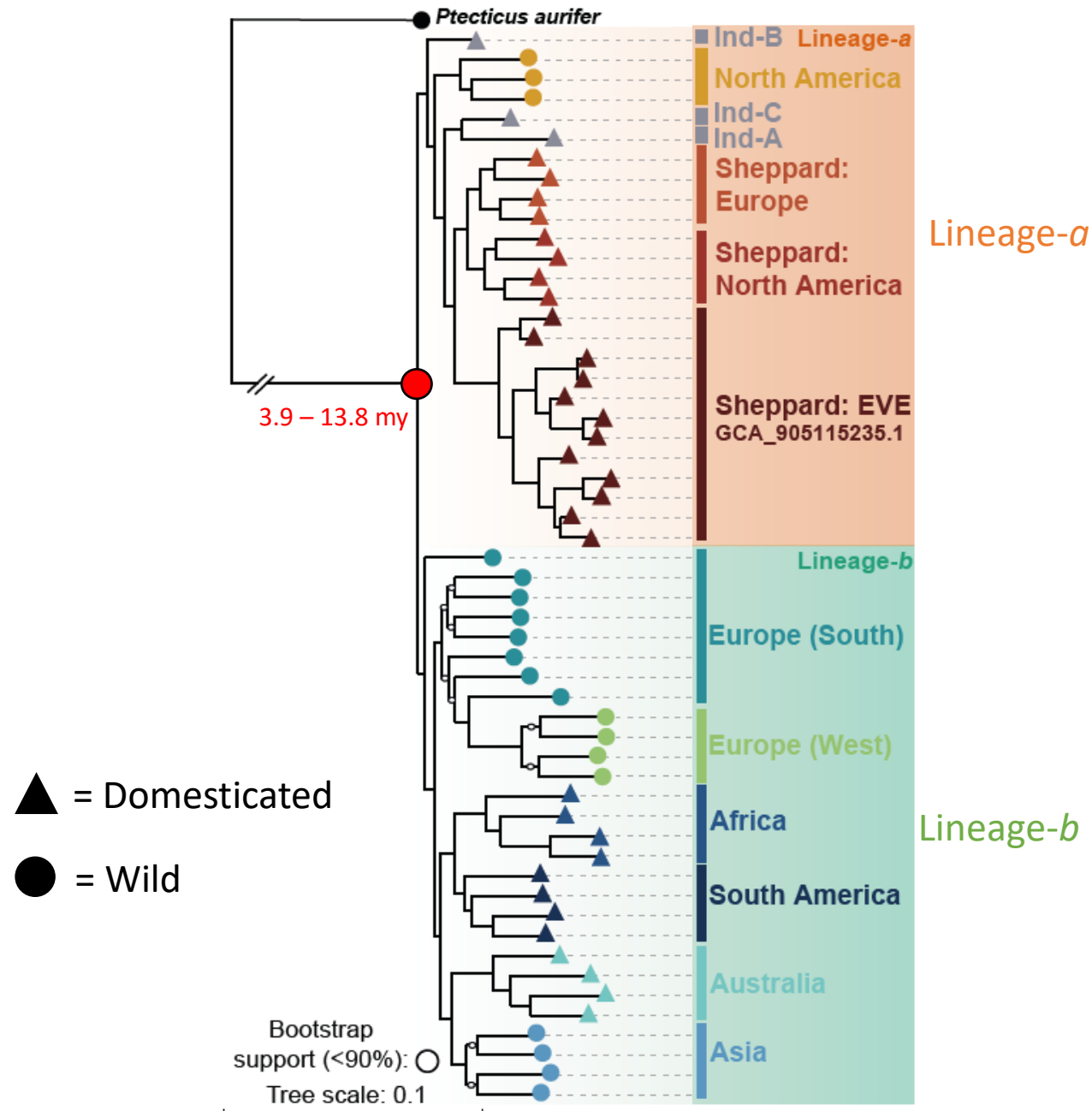
The BSF species is highly genetically diverse and globally distributed



- Microsatellite marker genetic analysis on a **global scale**:
 - 2,862 individuals
 - 150 populations
 - 57 countries
- Included both **captive** and **wild** populations.
- Identified **16 major genetic clusters & vast diversity**.

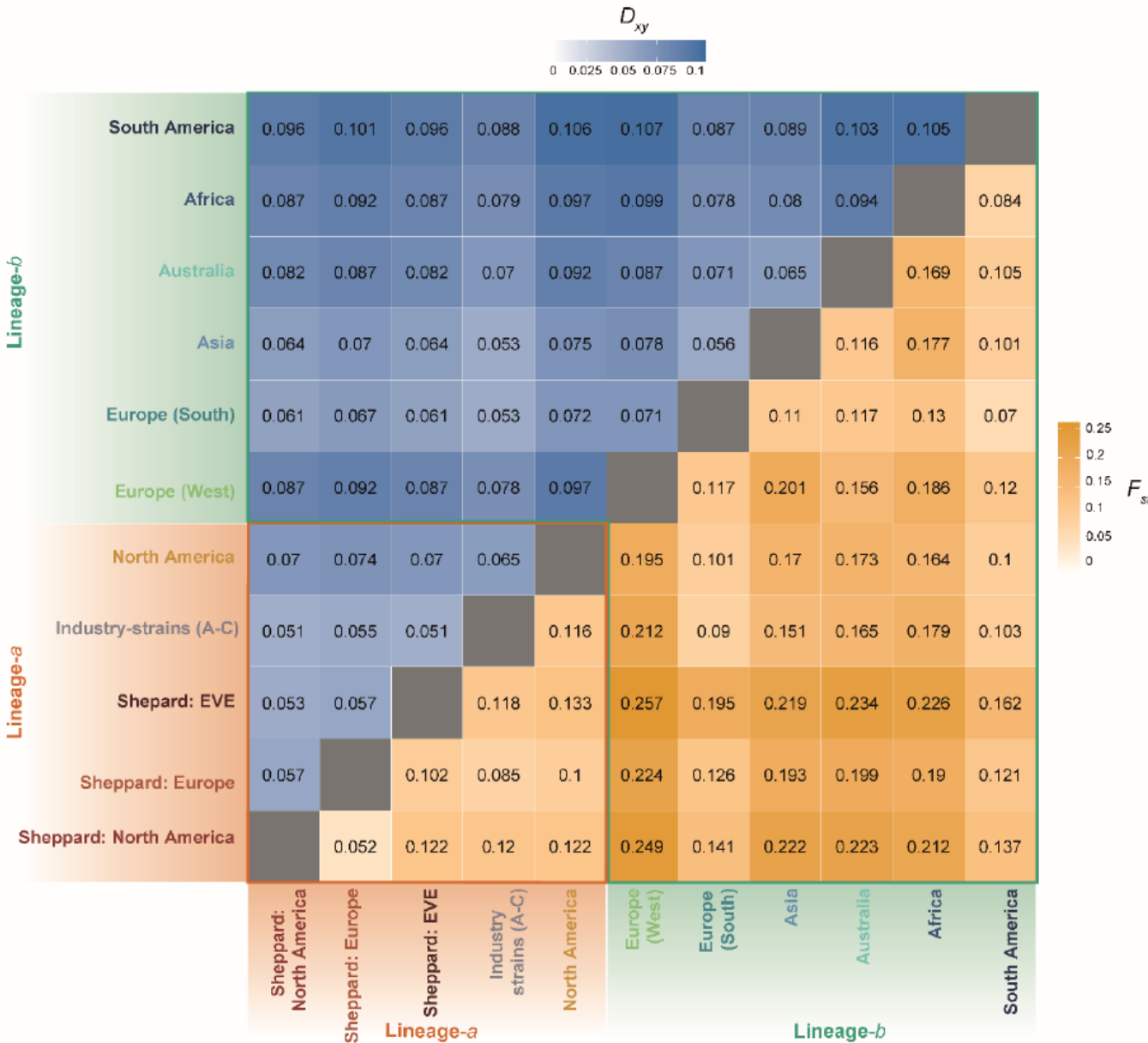


Whole-genome insights reveals a deep cryptic population structure

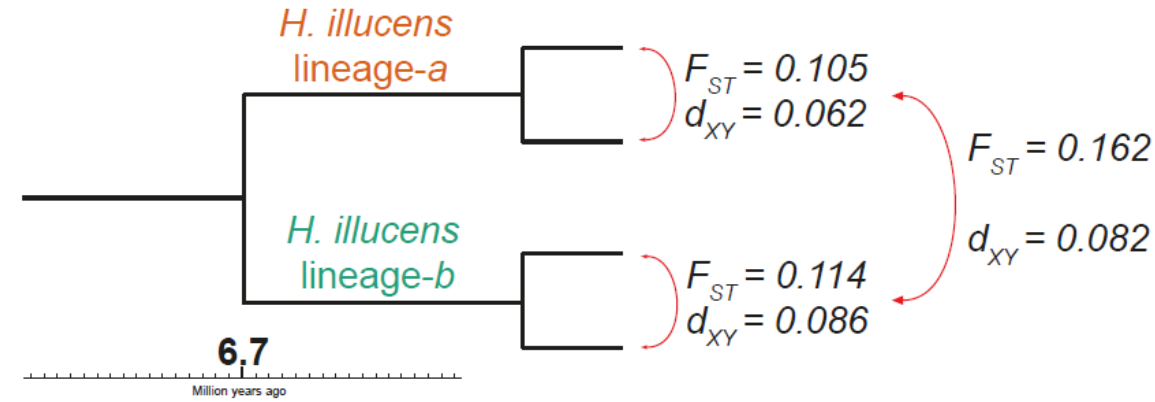


- We **whole-genome** sequenced and reconstructed phylogenetic structure.
- Striking divergence between **two major lineages** split by **millions of years**.
Primitively named a & b until further collections can refine.
- Domesticated populations found across both lineages suggesting **independent domestication events**
 - Particularly found in **Asia, South America & North America**.
- Identified “**intermediate**” samples suggesting potential mode of genome “mixing” in some regions.

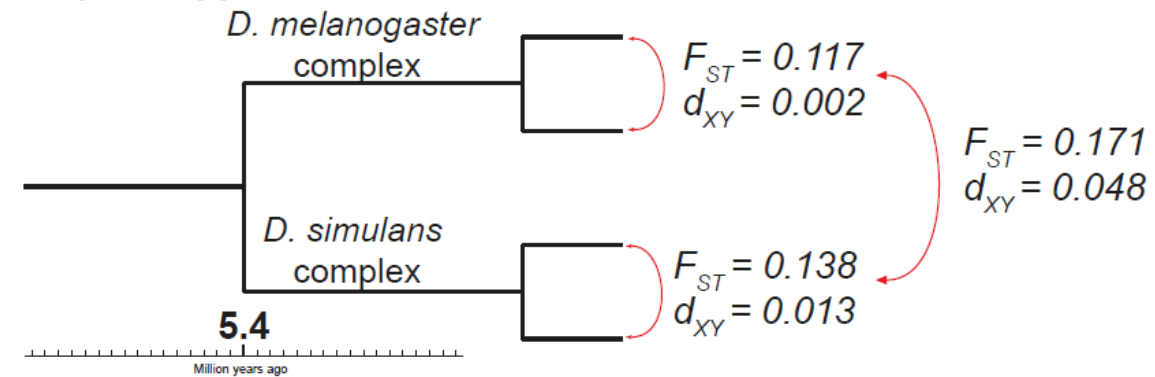
Extreme genetic differences between BSF lineages



Hermetia illucens spp.



Drosophila spp.



BSF offers significant opportunity when compared to other commercial insects

Fig. 1: Phenotypic diversity in silkworms.

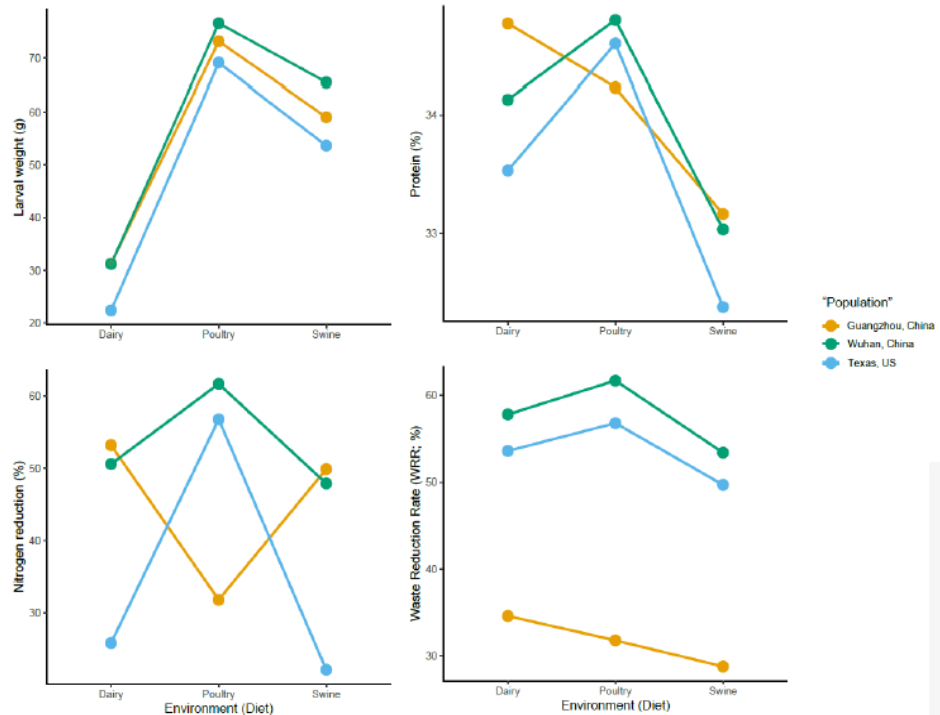


[Tong et al. 2022](#)

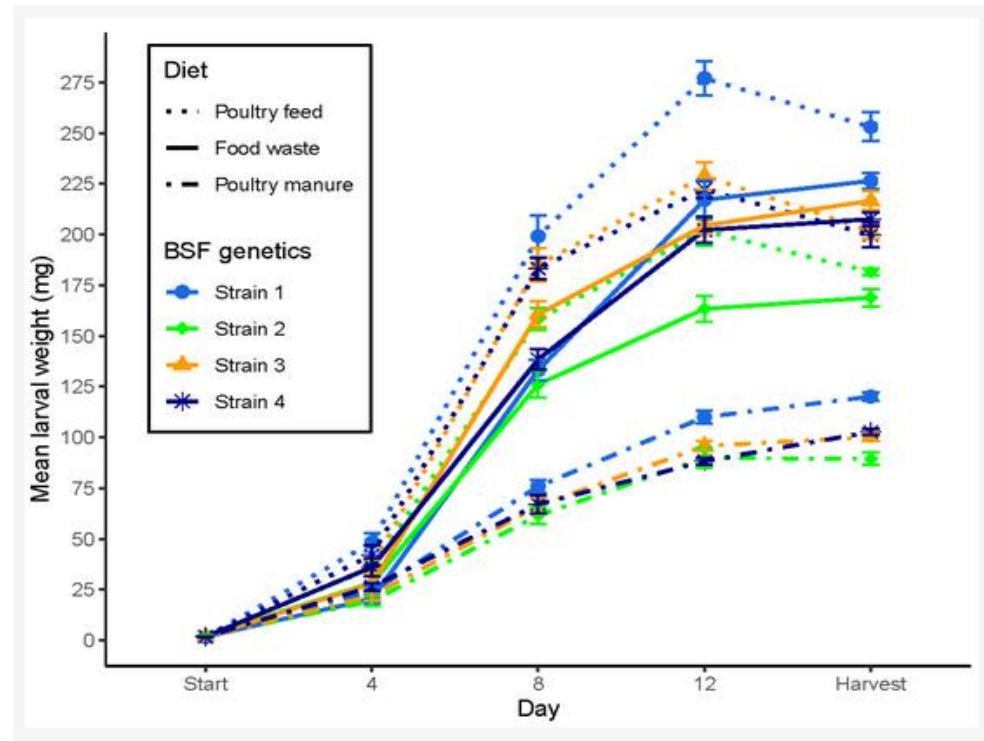
- The **silkworm**:
 - **Vast range** of phenotypic diversity.
 - **Limited number** of commercial strains.
 - Domesticated **~5000 years ago**.
- Whereas **BSF**;
 - **Vast range** of phenotypic diversity.
 - Available **wild & domesticated** strains.
 - **Ongoing** domestication.
 - **Millions of years** divergence between lineages.
 - Divergent lineages hybridise (Meyermans & Broeckx et al. 2025)

= Lots of opportunity for selective breeding

Lots of evidence for phenotypic variance in nutrition, performance, morphology...



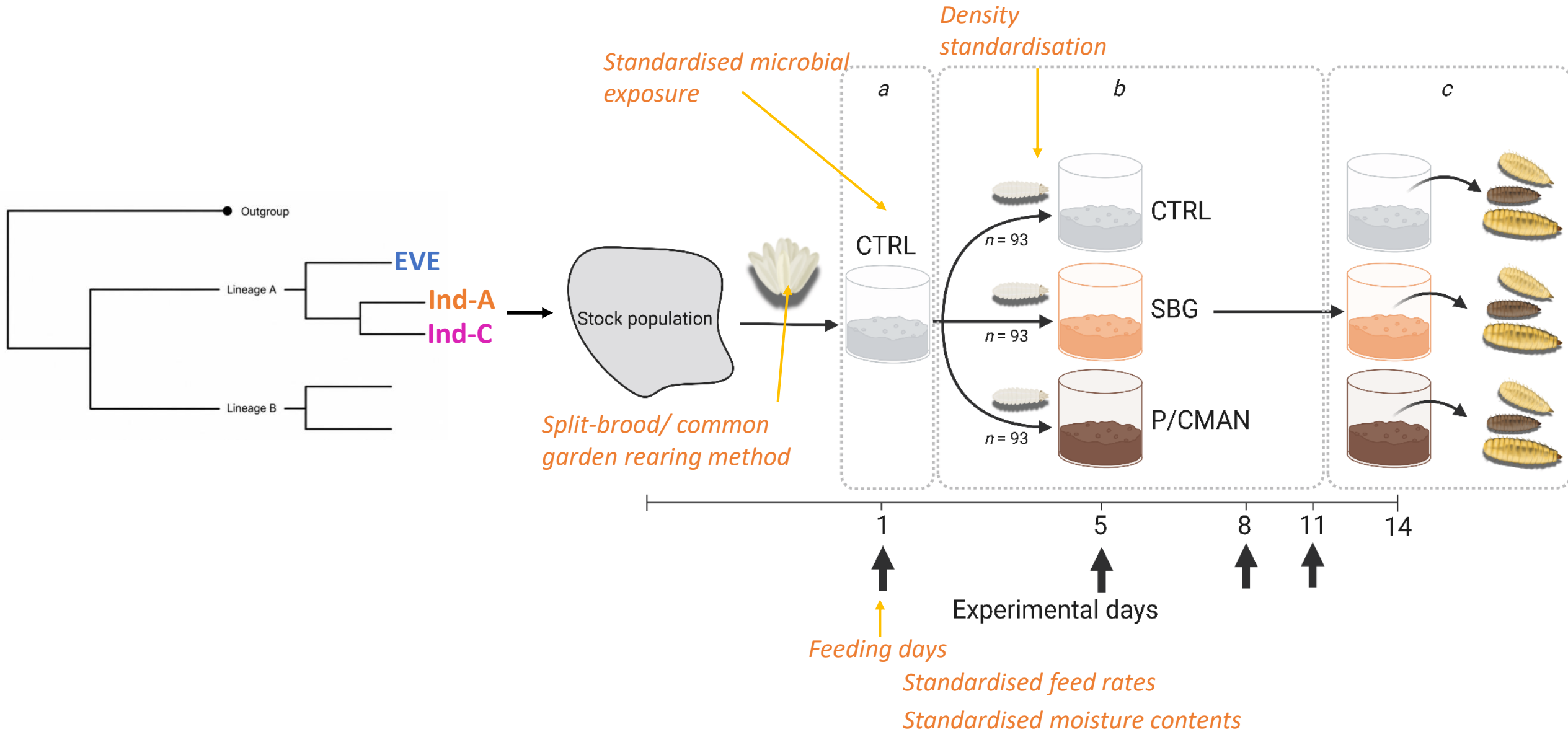
Adapted from Zhou *et al* 2013



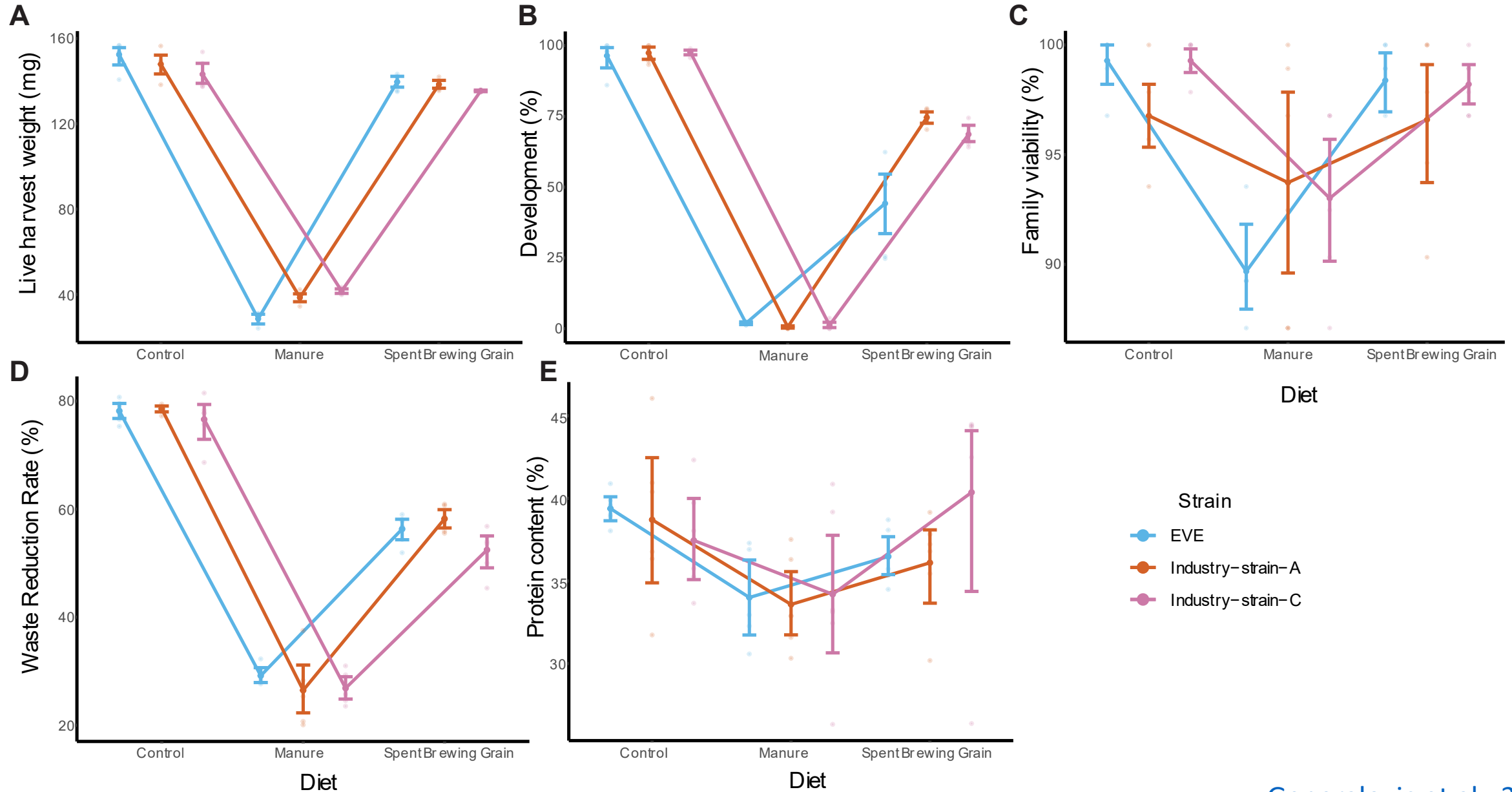
Sandrock *et al* 2022

And many Lit Reviews...

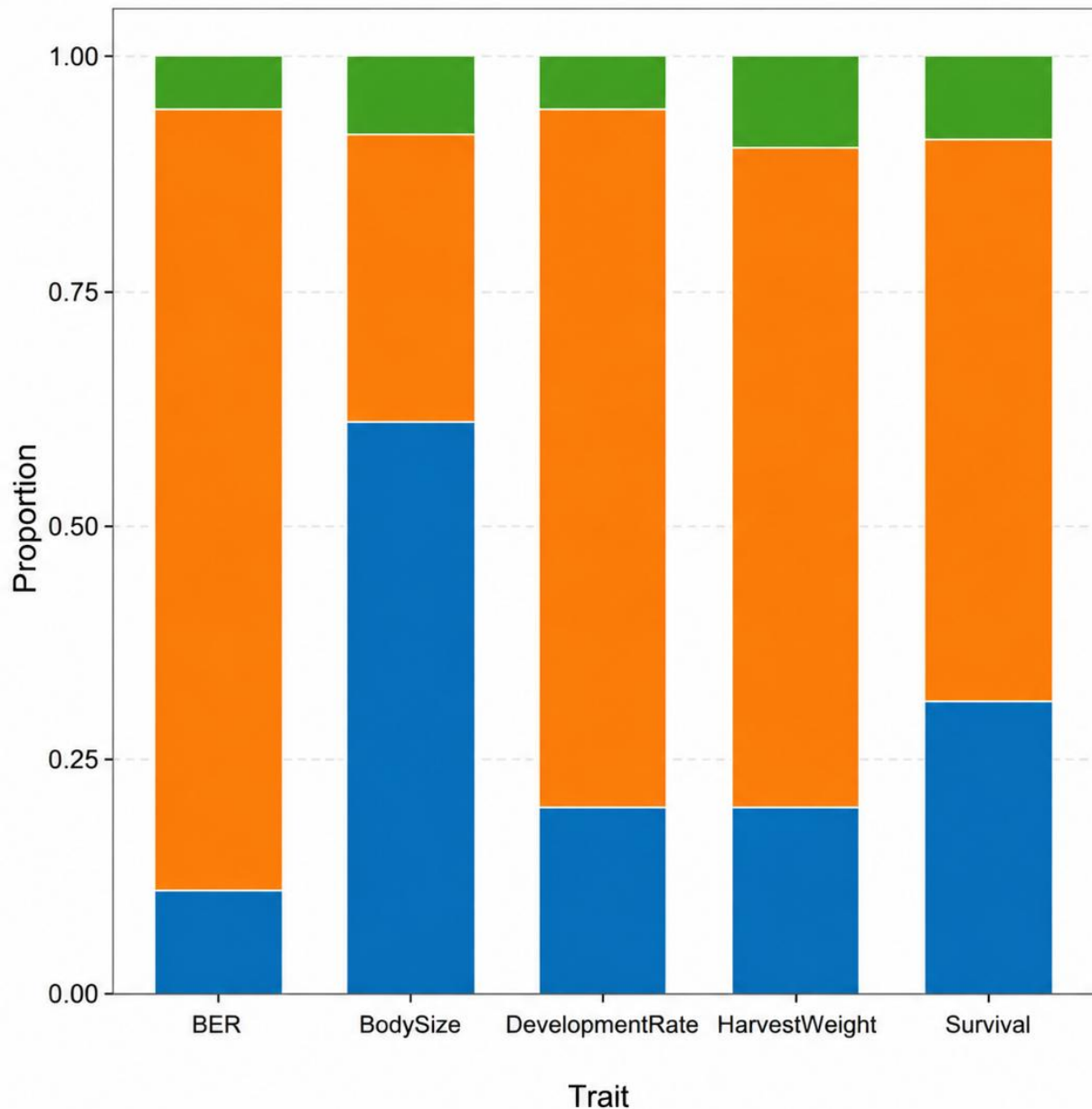
What happens when different strains experience different environments?



Within-lineage phenotypic variation



Environment is the major driver in explaining variation in traits of interest

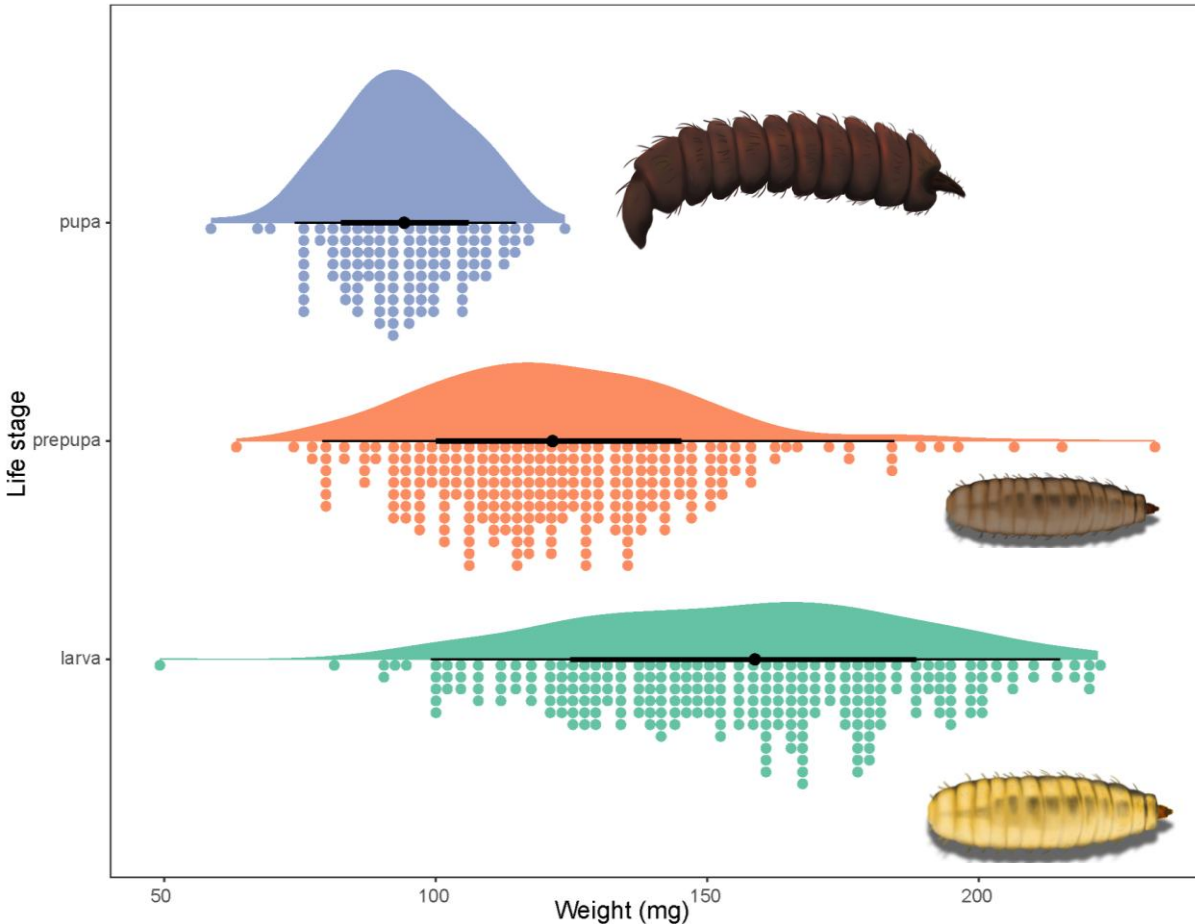


- Crude variance estimates modelled from the study suggest:

- Environment: ~60% variance
- Genetics: ~30% variance
- GxE: ~10% variance

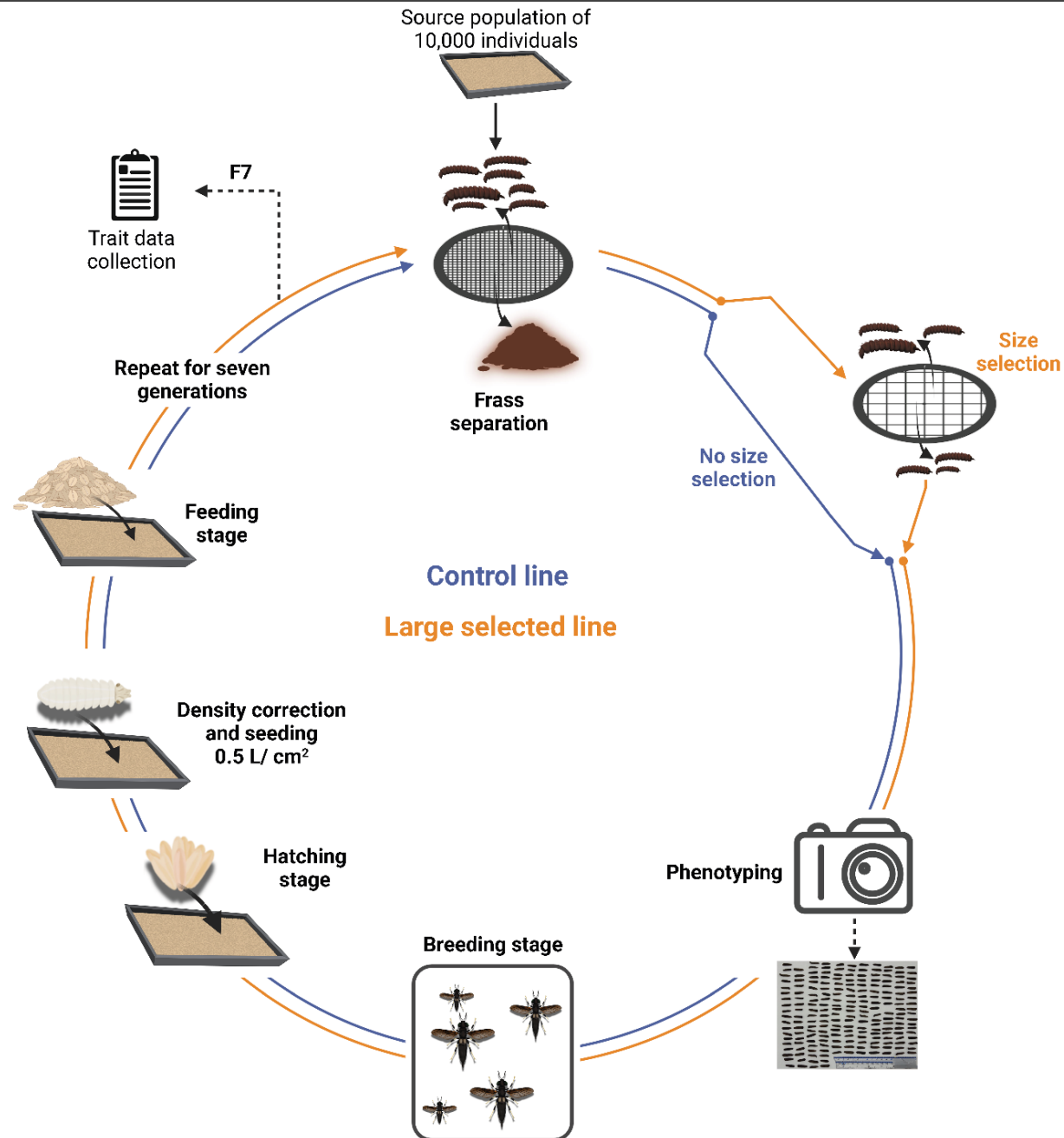
- Optimise the lowest hanging fruits first!

Variation, a problem or opportunity?

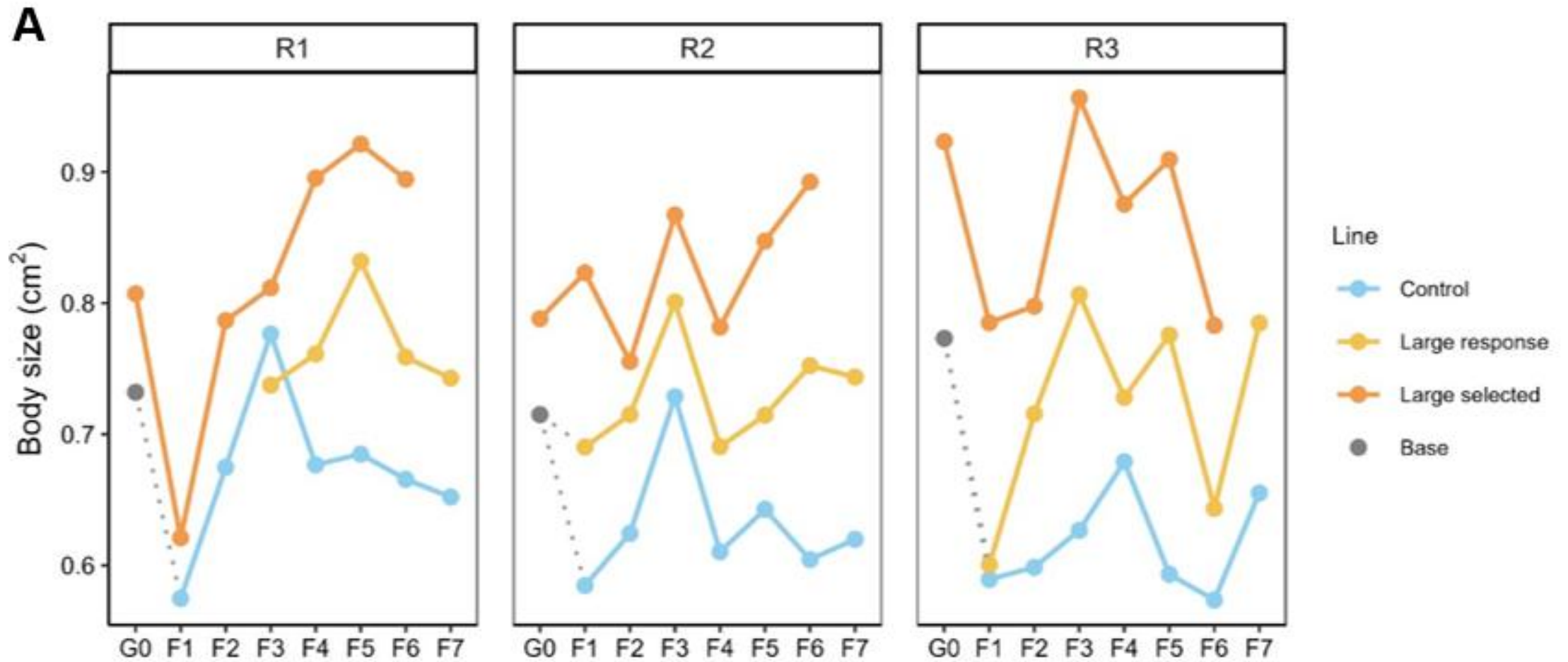


- **Standing genetic variation** is required to make genetic gains.
- **Body size** is a direct commercial KPI for yield = €.
- Pupal body size is ideal trait for selection as
 - Non-moving (easy to handle)
 - Doesn't feed (minimal change to size)
- Experimental Evolution setup:
 - **3 independent** experiments
 - Internal **Environmental control**
 - Measured phenotypes for **>110,000 individuals**
 - Maintained **7 generations**

Setting up a low-cost method for artificially selecting BSF populations



Repeatable phenotypic response to body size selection



F7 results:

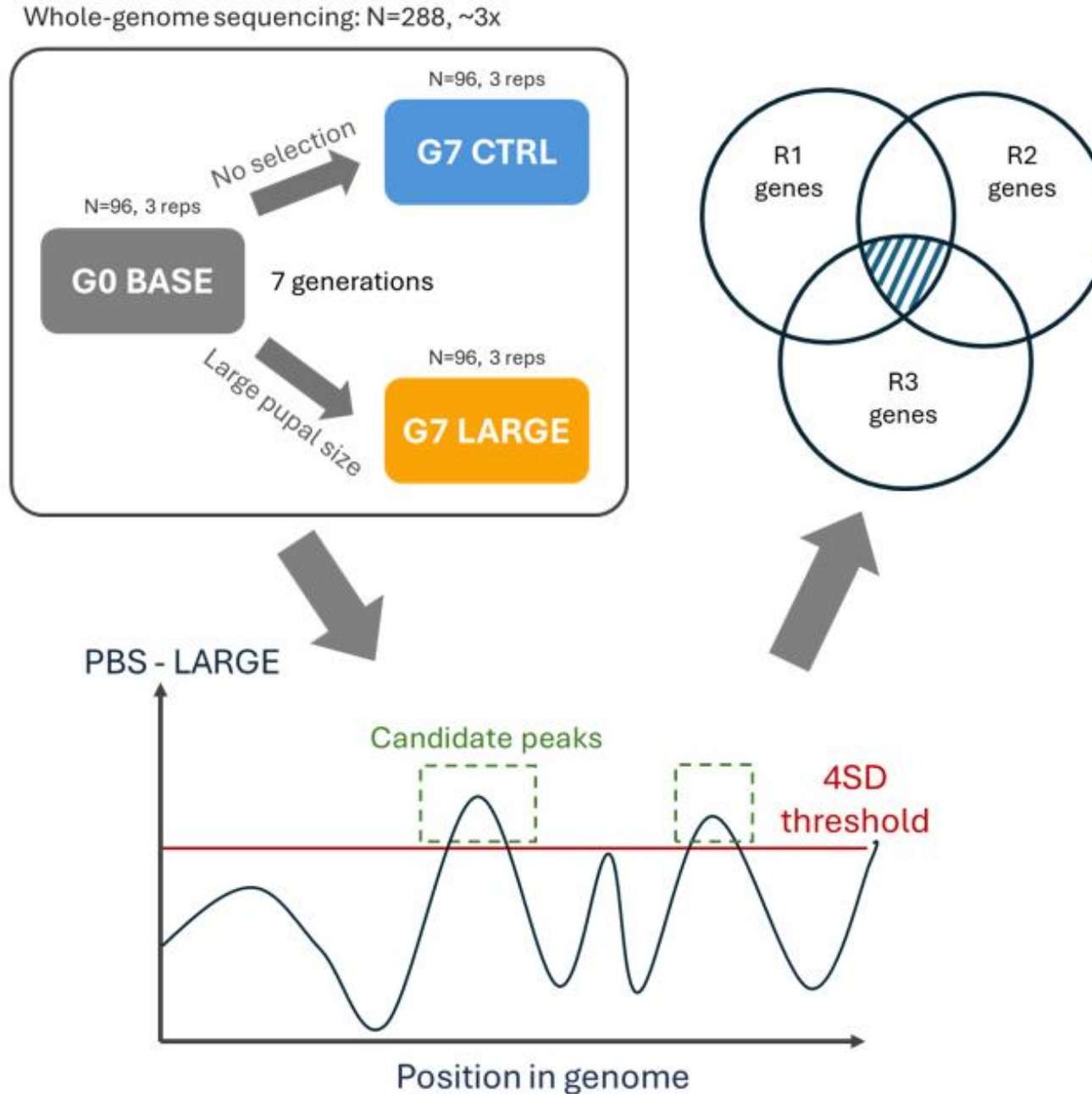
R1: 12% ↑

R2: 17% ↑

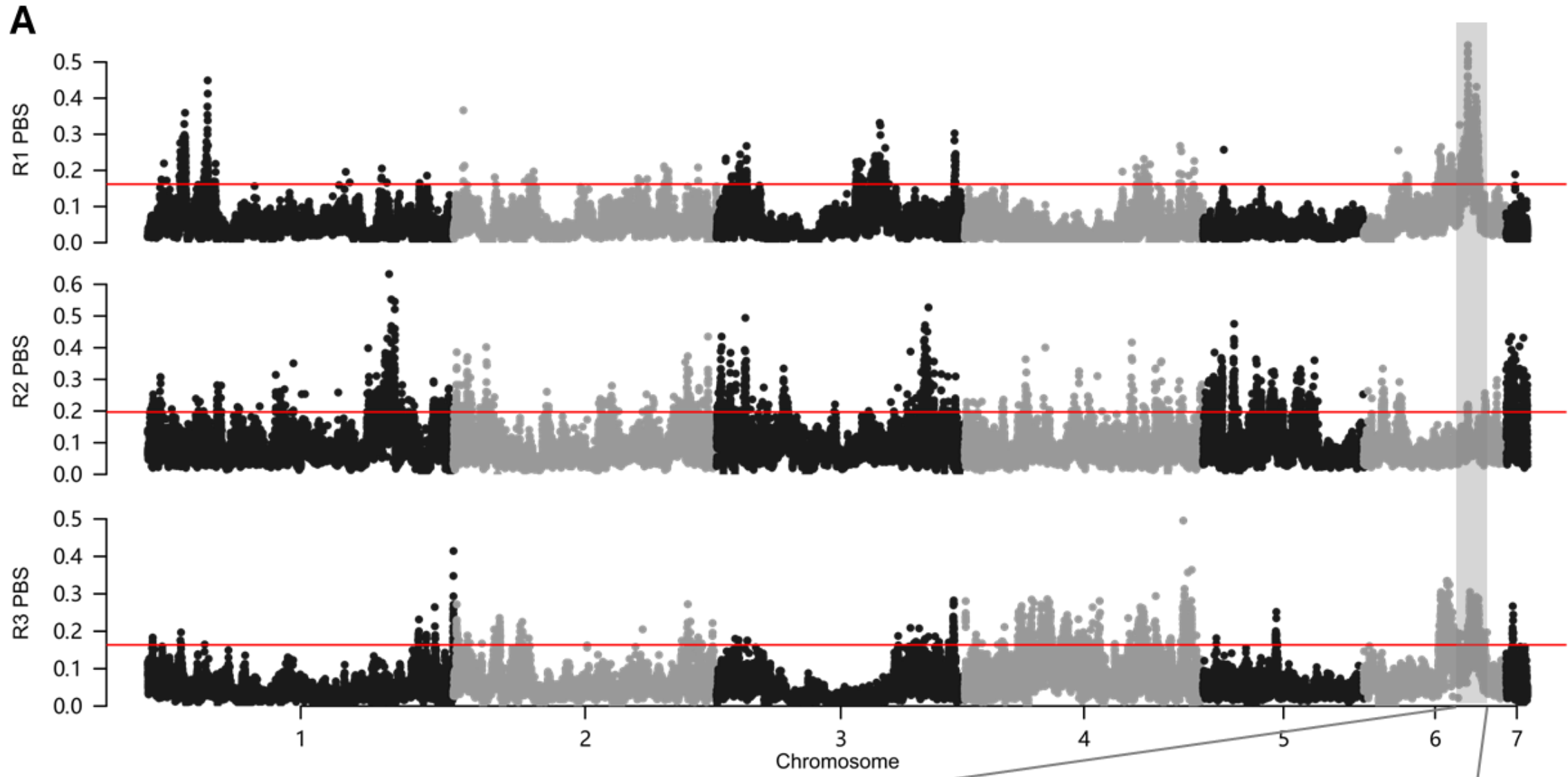
R3: 17% ↑

Heritability also established $h^2 = 0.26-0.47$ 95% CI for body size trait.

Identifying many loci involved in the genetic response to selection



Genetic response to body size selection is highly polygenic (many genes)

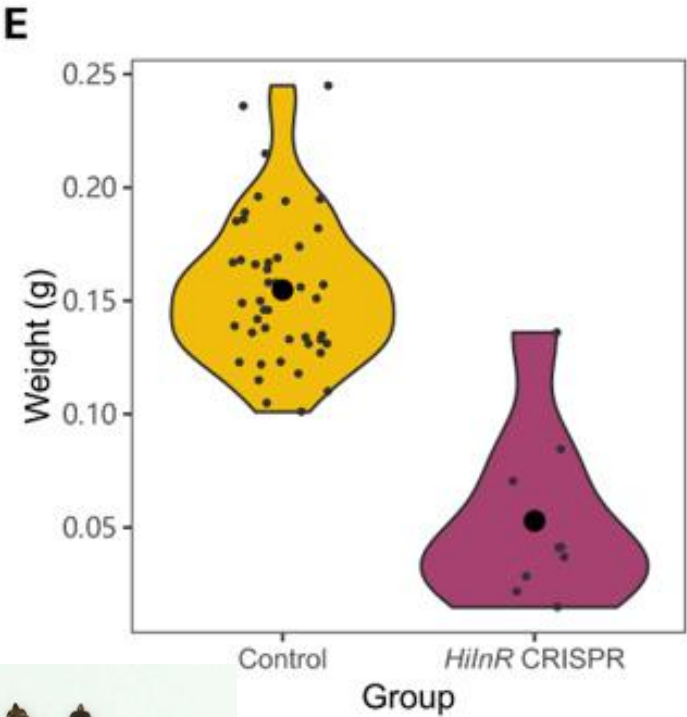
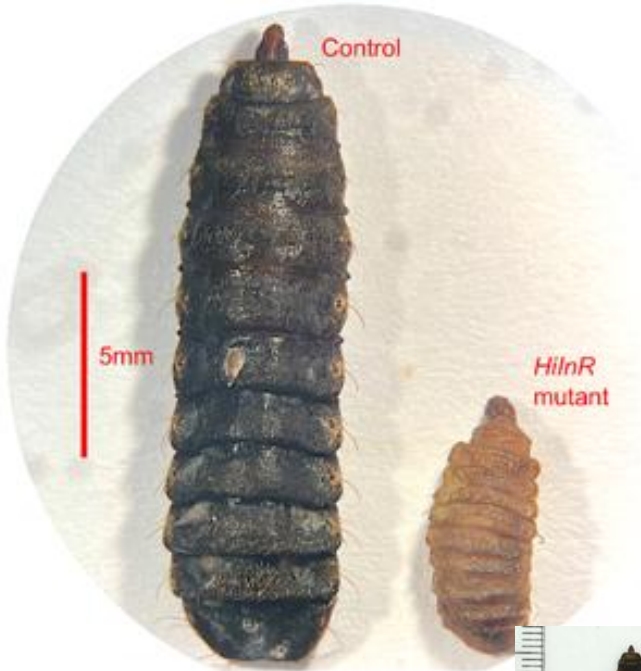
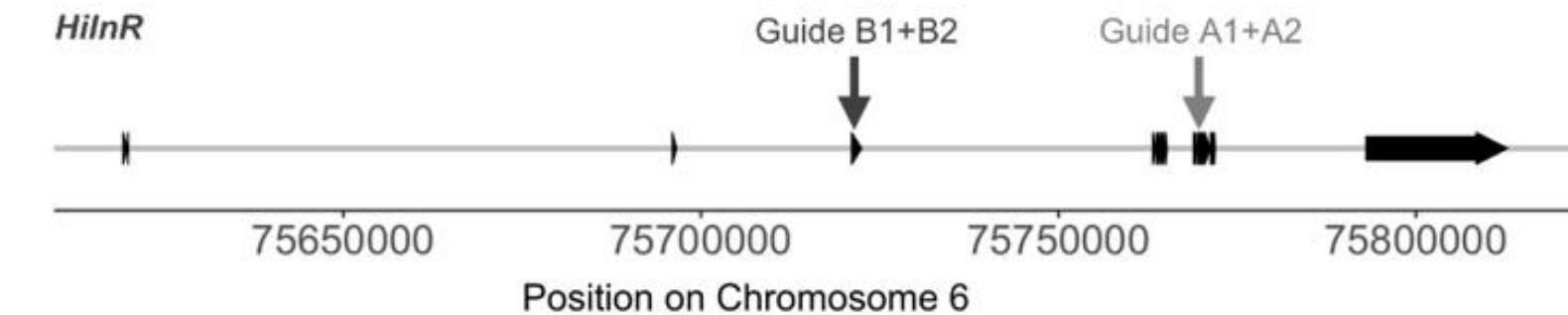
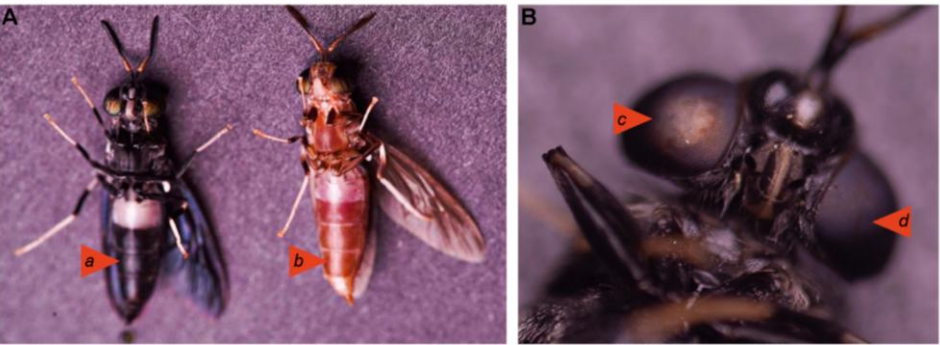


Genetic response varied across all three replicates with **only one loci** overlapping across all: *HilnR*

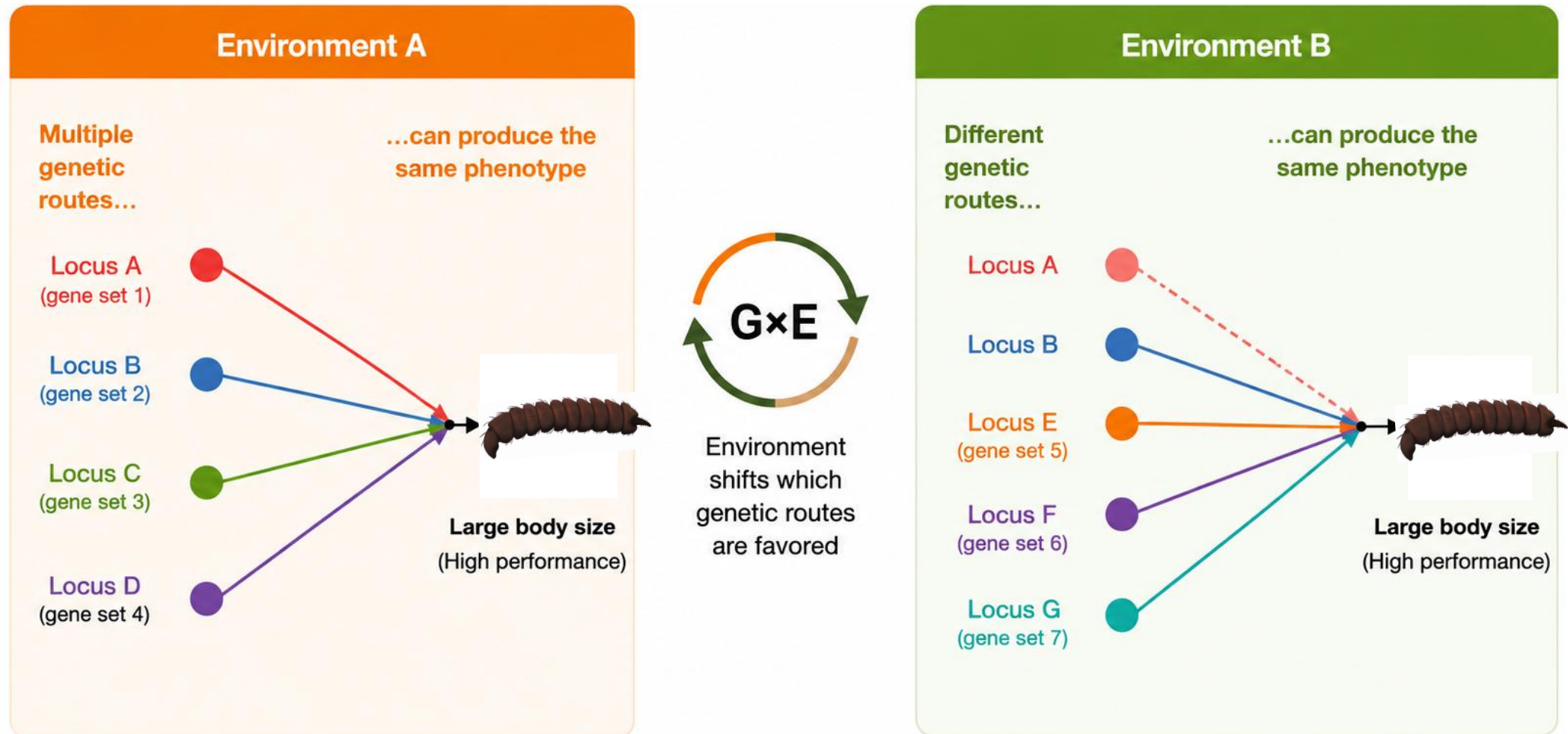
Identifying loci involved in the genetic response to body size selection



Establishing CRISPR PoC and functional candidate gene validation



Convergent phenotype but divergent genetic basis highlights importance of genetic redundancy



Genetic redundancy, where multiple genetic solutions can generate the same phenotype/ function.

Conclusions

- 1) BSF contains **extensive genetic** and **phenotypic diversity**.
 - *Strain characterisation and reporting is improving but still absent from literature base.*
- 2) Performance outputs of BSF are **strongly influenced by the GxE** component alongside G&E effects.
 - *A core standardised methodology for both academic & industry scale trials remains absent.*
- 3) Selection responses may be **repeatable phenotypically but genetically redundant**.
 - *Understanding your strains base performance and its life-history paired with tight environmental control (incl. diet) is essential to predict the output of your breeding programs and minimise unexpected trade-offs.*

Acknowledgments



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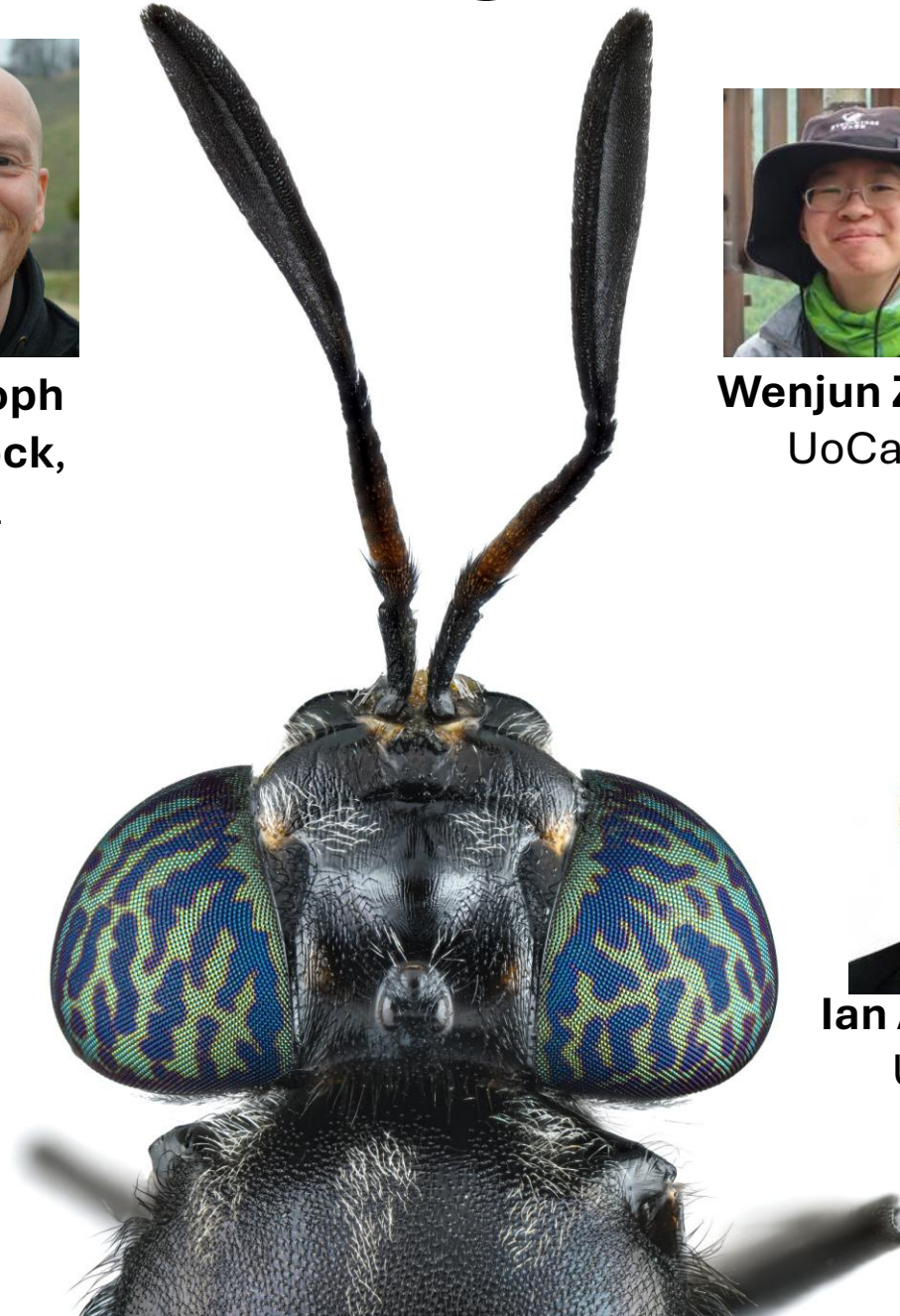
Erika de Castro,
UoCam



Miha Pipan, BO

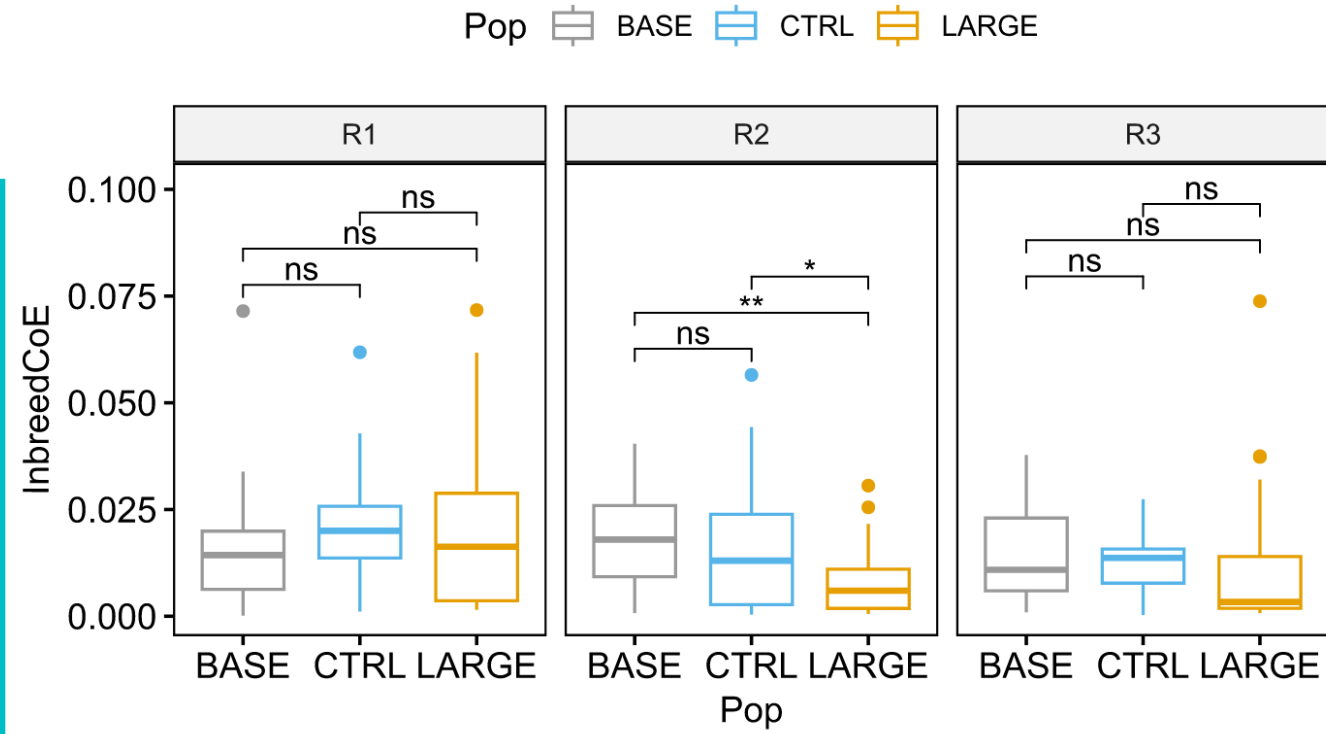


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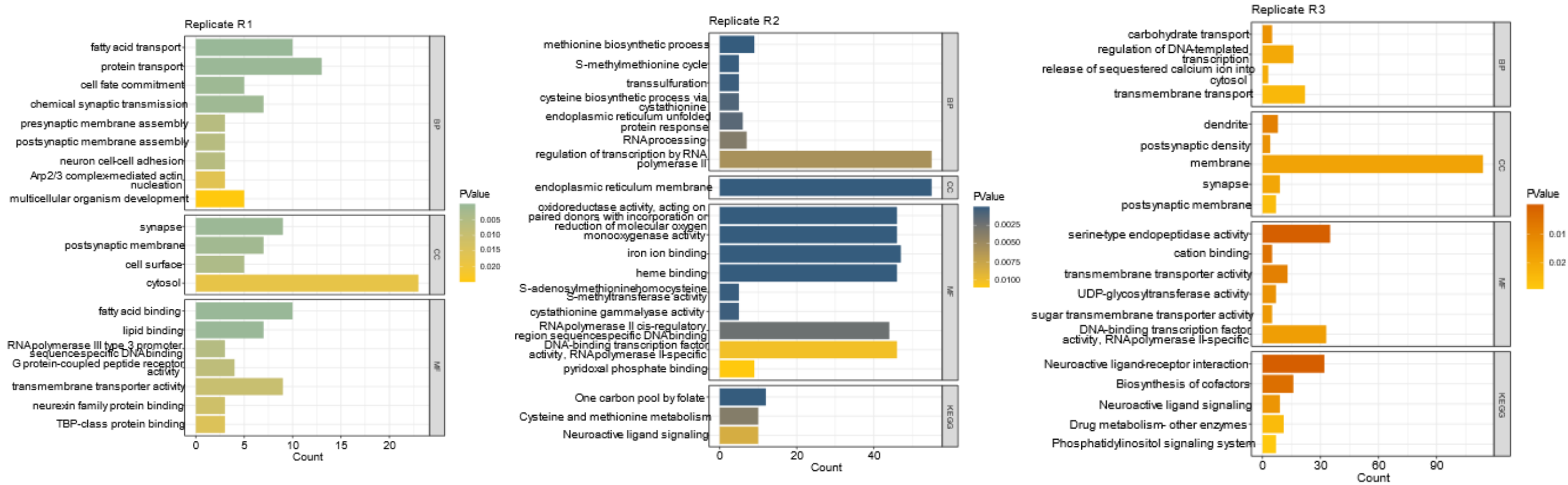


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APPENDIX 1



APPENDIX 2



APPENDIX 3

