Genome domestication of the yellow mealworm using population and quantitative genomics

Lucas Rocha Ferreira

lucas.rochaferreira@cea.fr

François Jacob Institute of Biology, CEA-SEPIA,
Computational Biology team, France

EAAP 1st Insect Genetics Meeting - Athens, Greece
January 29th 2025

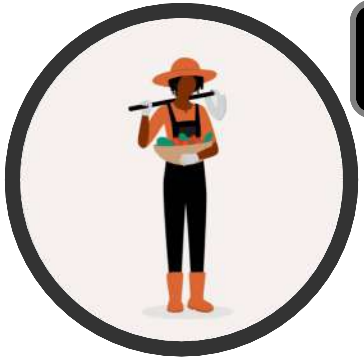
université
PARIS-SACLAY

Doctoral School
Structure and
Dynamics of
Living Systems

Ynsect

What is domestication?

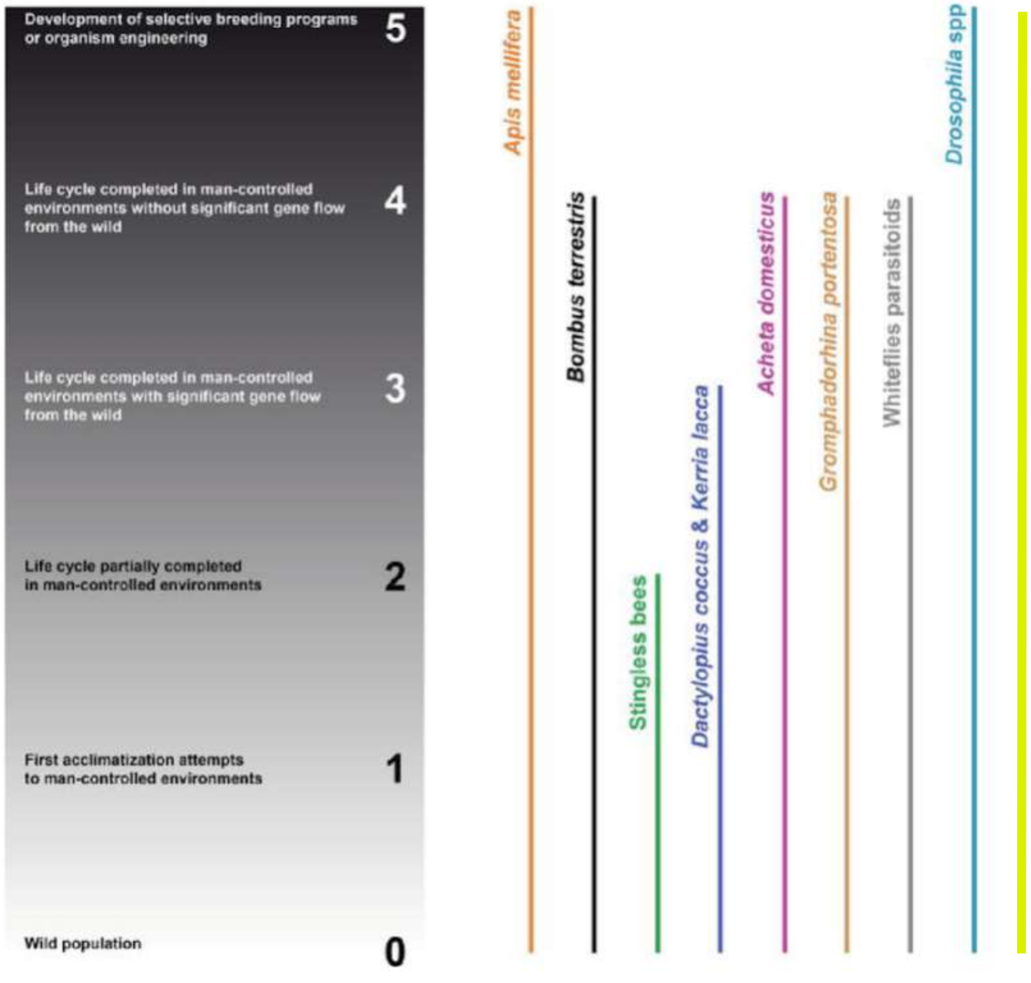
Previous definitions of domestication may (or may not) include:



- Intentionality
- Benefits derived by humans
- Control of the process
- Artificial selection
- Evolutionary change
- Domesticate phenotypes

Purugganan, M.D. (2022). What is domestication? *Trends in Ecology & Evolution*

Insect Domestication



Tenebrio molitor
BSF
…

Domestication as a continuous process starting from a wild population to modern breeding program passing by the control of the life cycle

Lecoq, T. (2018). Insects: The disregarded domestication histories. In *Animal domestication*

Mealworm domestication through academic research

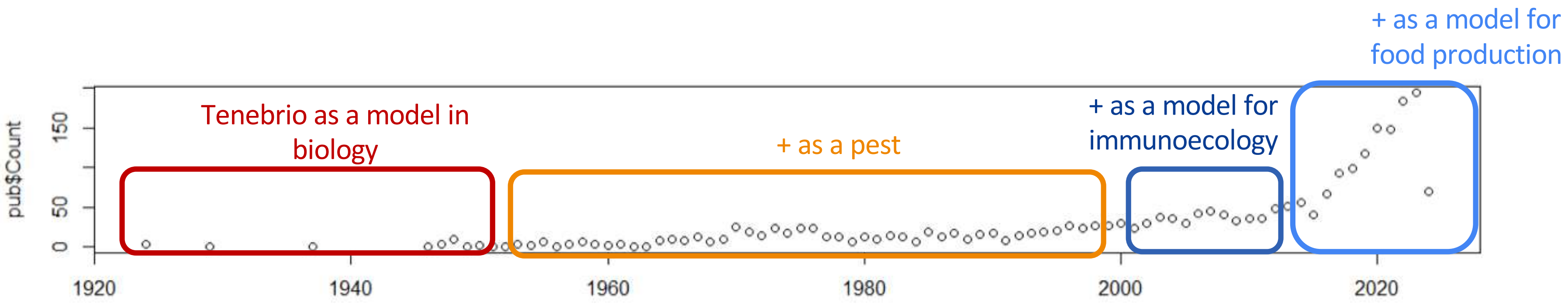
1906
Nettie Stevens
Y chromosome

1915-30's
Arendsen Hein
Quantitative genetics and breeding

1946-60
Jean Leclercq
Mass selection on weight and trade-off with duration of larval development

2000
Juan Morales-Ramos
Mass selection on pupal weigth and correlation with fecundity and feed conversion

Research status promotions



Tenebrio as a model in biology

+ as a pest

+ as a model for immunoecology

+ as a model for food production

Mealworm domestication through farming?

Mealworm as secondary production

Specialized farms

Large vertical farms

Large and synchronized production needs to control reproduction, growth and development
Essentially made through **individuals and eggs sorting.**

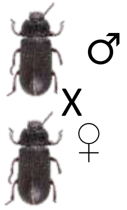
Did the early domestication of yellow mealworms impact their genome and agronomic QTLs?

1. Can we identify genomic loci under selection in domesticated populations?

2. Can we detect QTLs associated with agronomic traits?

3. Do we have overlaps between loci under selection and QTLs?

Updating the genome by constructing chromosomes sequences

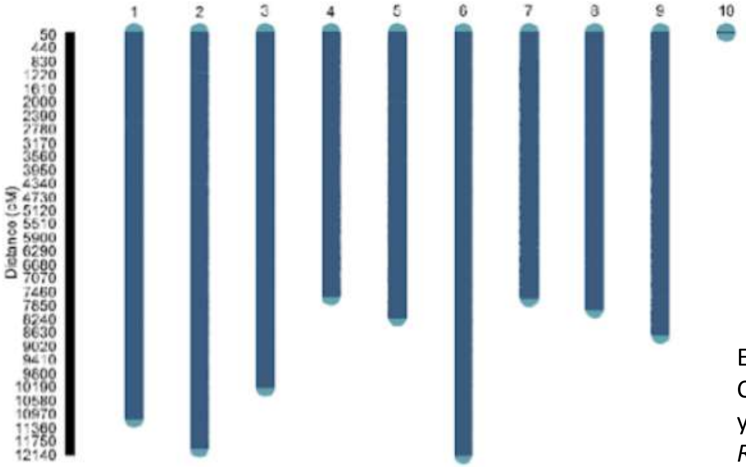


F1
101 individuals

Illumina
genotyping

OneMap

High density genetic map

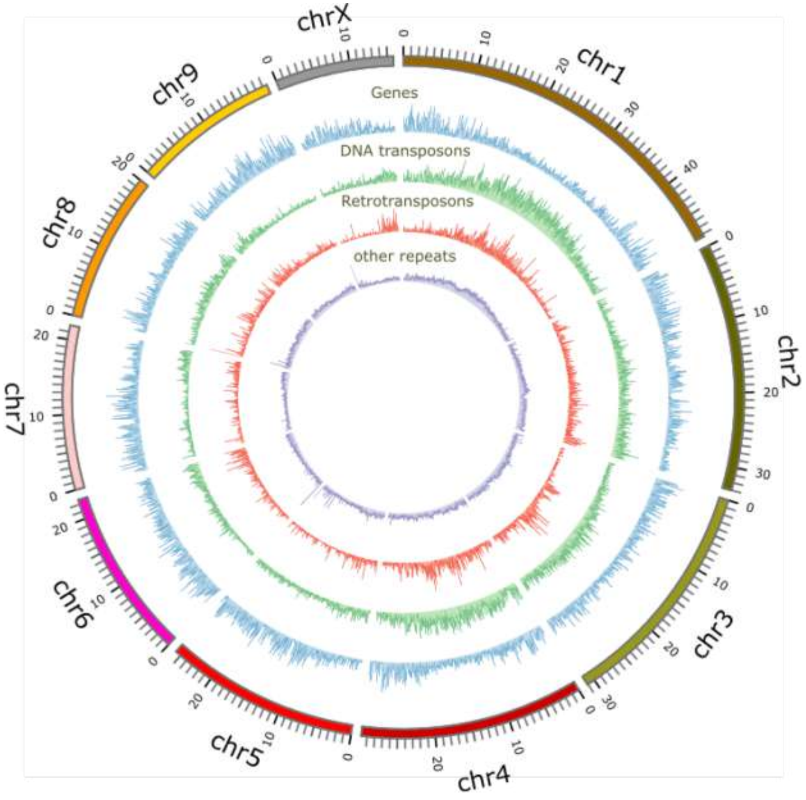


AllMaps

+
Genome assembly
(Nanopore+HiC)

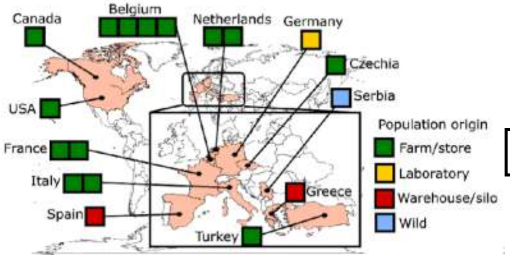
Eleftheriou, E., et al. (2022). Chromosome-scale assembly of the yellow mealworm genome. *Open Res Eur*

T. molitor **chromosomes**



We constructed all 10 chromosomes sequences of *T. molitor* (except for the Y chromosome)

Genomic structure in farmed populations

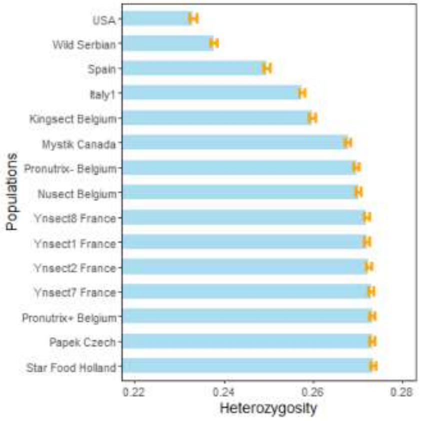


25 pools of 40 individuals

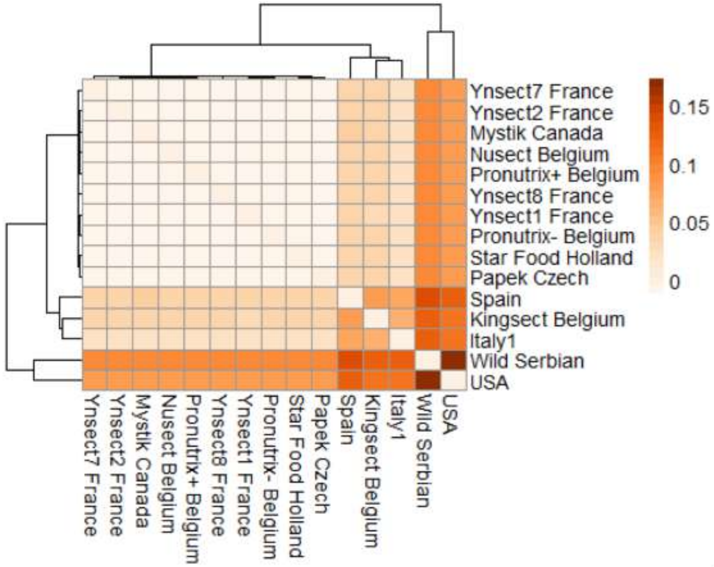
Illumina genotyping
5,285,733 SNPs

poolfstat

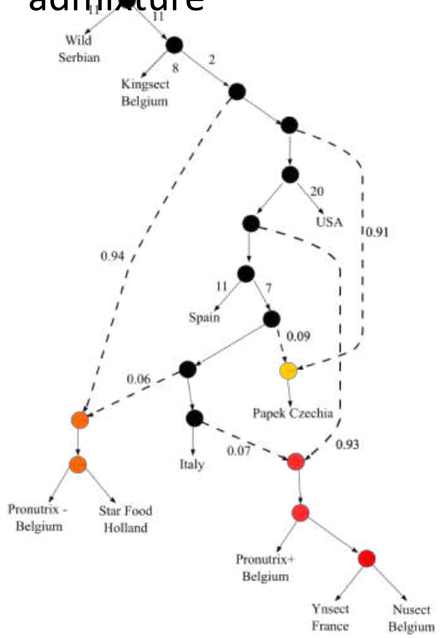
Heterozygosity



Pairwise-F_{ST}



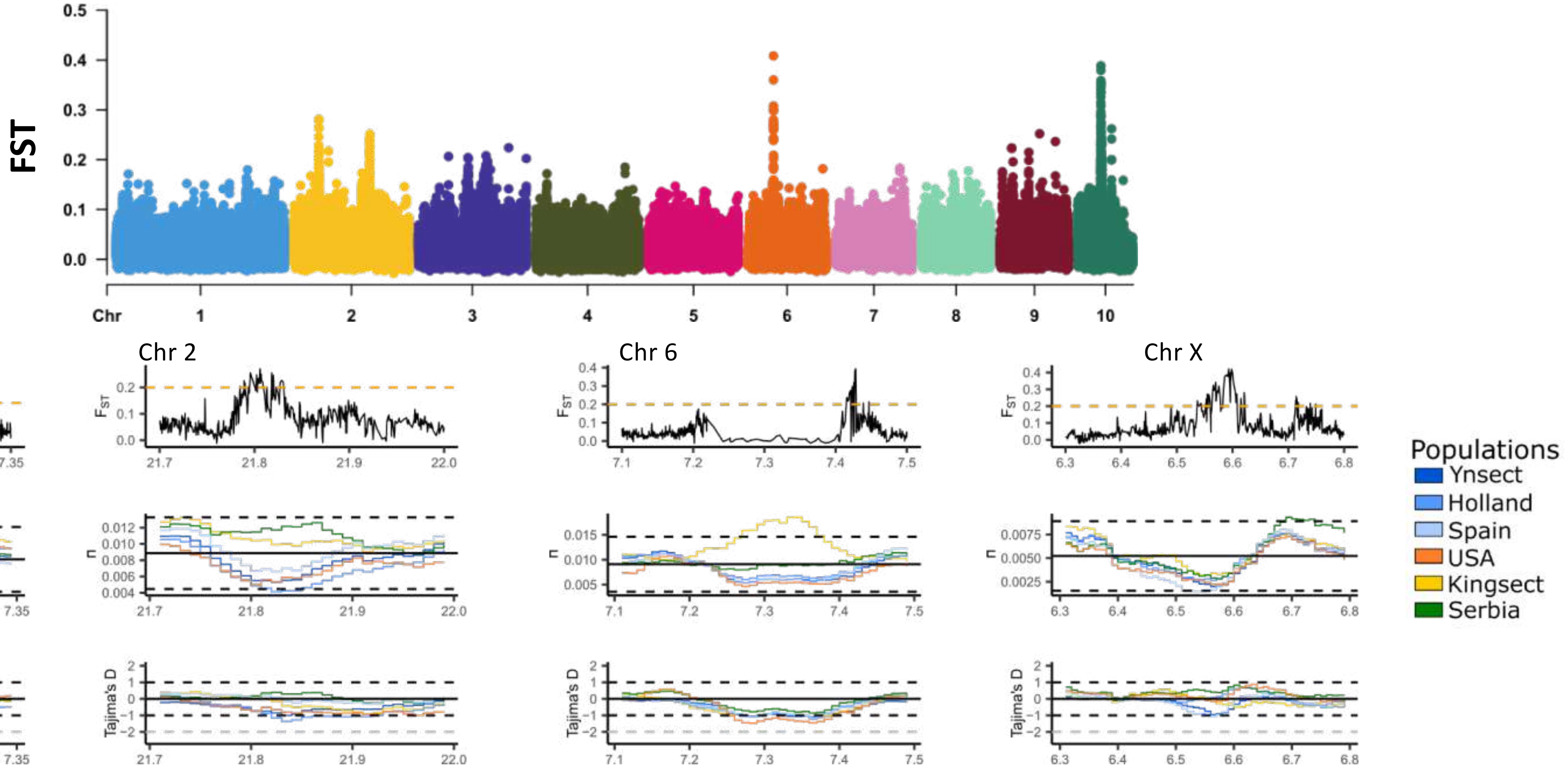
Population admixture



→ Farmed populations share same genetic background and high heterozygosity (large populations)

→ Identification of 3 admixture events, which is expected due to gene flow among farmers

Genomic differentiation in farmed populations



Data for GWAS for Growth

134 individuals

Whole-genome sequencing (Coverage 10X)

~10,000,000 variants

↓

~679,000 variants

↓

AXIOM chip data

↓

~3800 individuals

MAF=0.05; MISS=0.02; HWE=10^{-5}

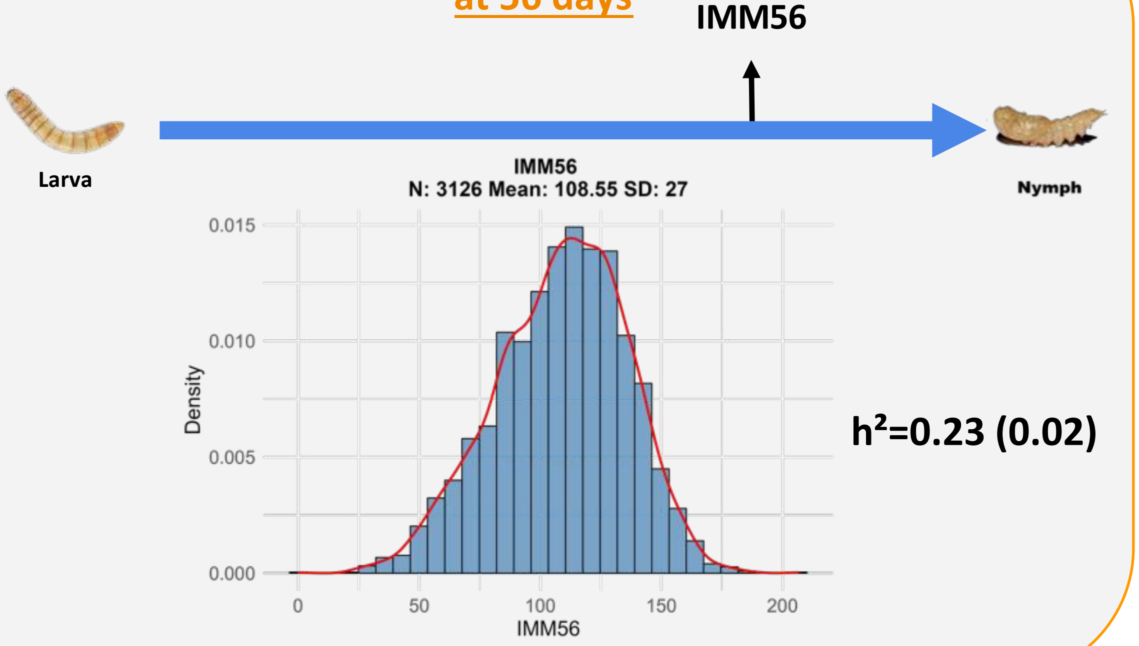
↓ Sample & Variants filtering

284,458 markers for 3,575 samples

Single-locus GWAS
Common LMM
(statgenGWAS R package)

Multi-locus GWAS
Single-step GBLUP
(BLUPF90 programs)

Individual mass of a larva measured in milligrams (mg) at 56 days



h²=0.23 (0.02)

Individual Mass at Day 56

residuals

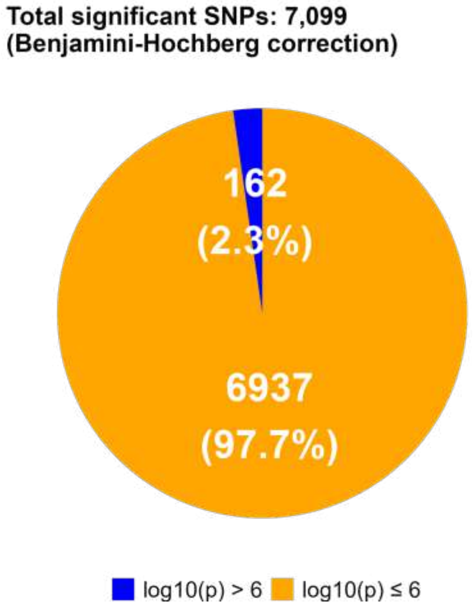
$$y = X\beta + Za + Zc + \varepsilon$$

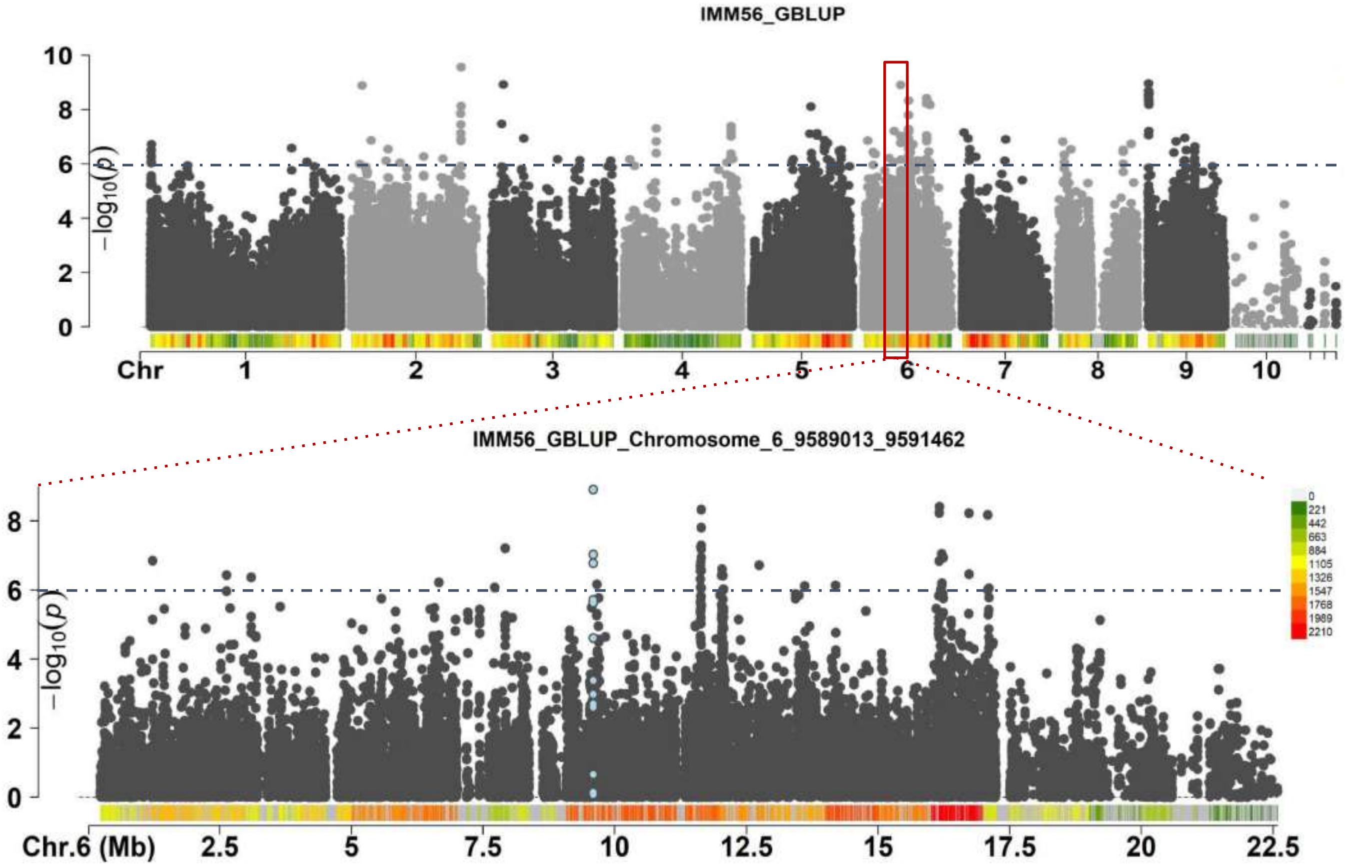
Generation as Fixed effects

Animal as Additive genetic effects

Containers as Common environmental effects

Results: Association mapping with ssGBLUP - IMM56

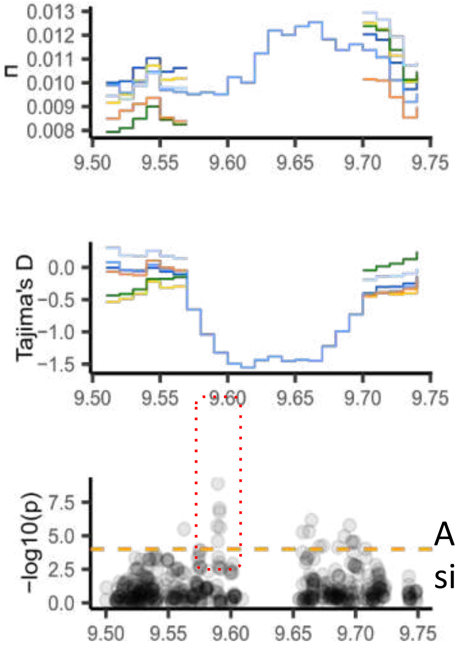




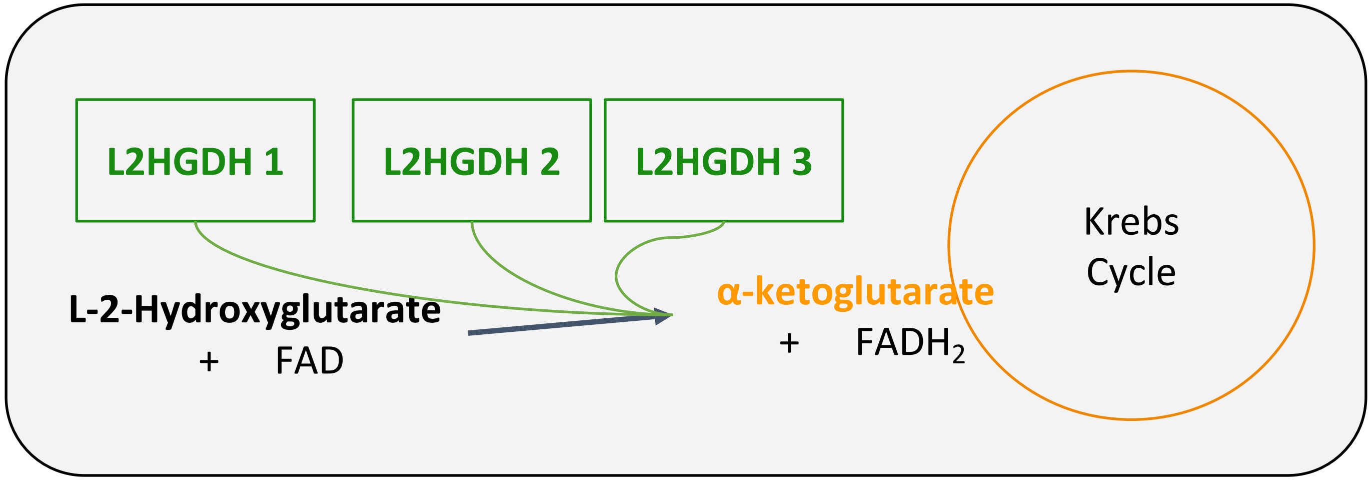
Among 15 candidate QTLs: Chromosome 6 between 9.5 and 9.75 Mb

Multiple proteins coding for an enzyme involved in larval growth in *Drosophila*

QTL of duplicated L-2-Hydroxyglutarate deshydrogenases (L2HGDHs)



A strong GWAS signal for IMM56



L2HGDH 1

L2HGDH 2

L2HGDH 3

L-2-Hydroxyglutarate
\+ FAD

α-ketoglutarate
\+ $FADH_2$

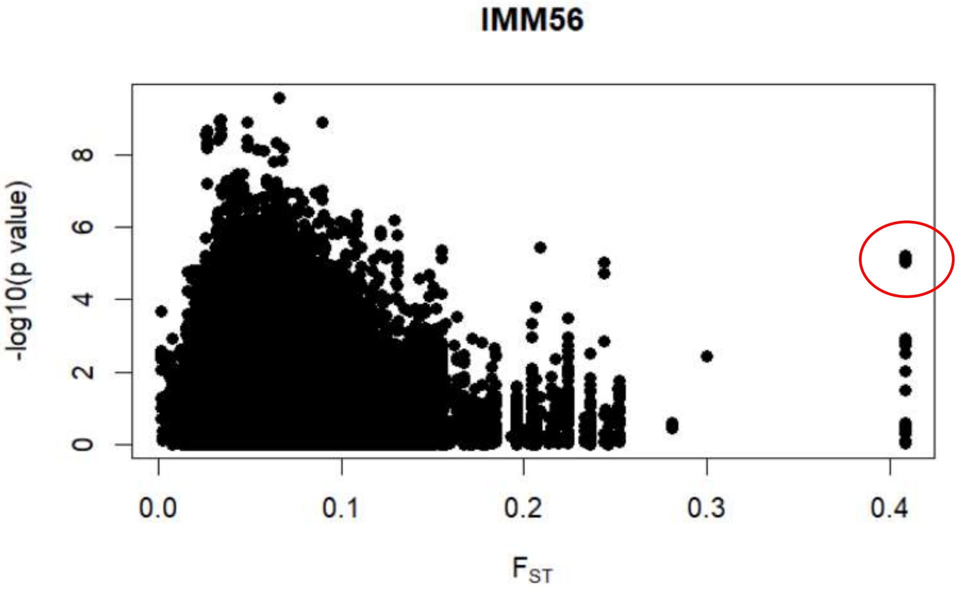
Krebs Cycle

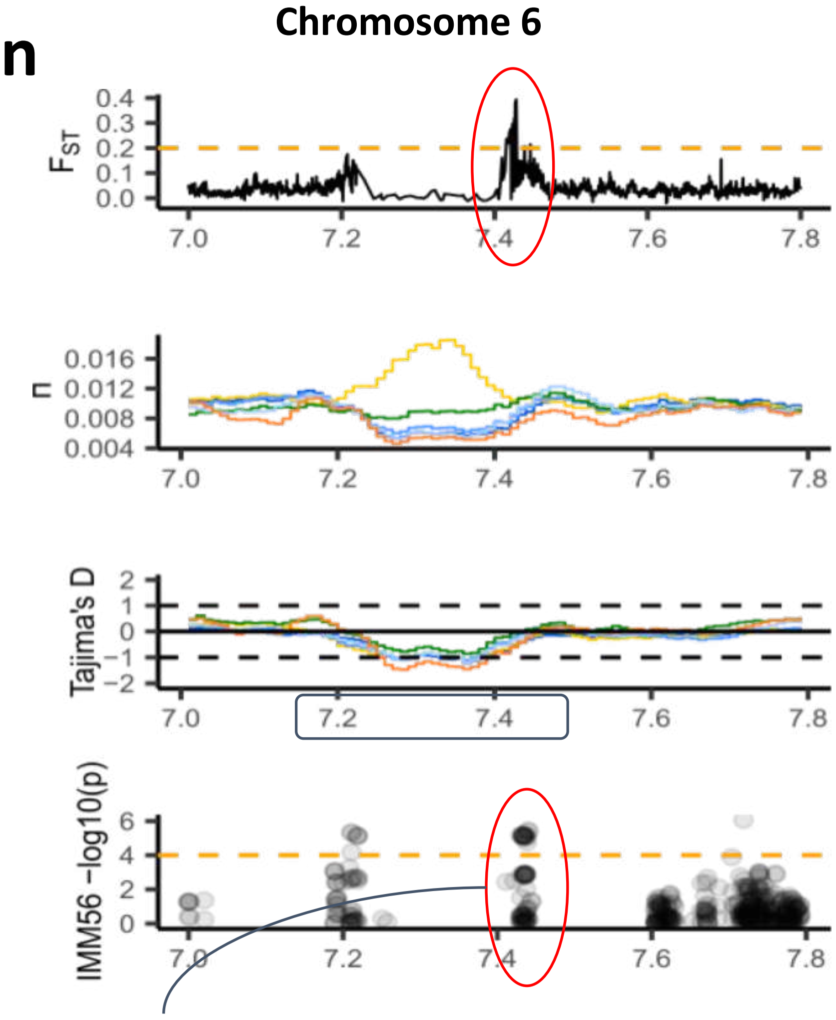
Li et al. 2017 Drosophila larvae synthesize the putative oncometabolite L-2-hydroxyglutarate during normal developmental growth. PNAS

Hypothesis: The observed SNPs in the QTL suggest a potential role in energy production during larval growth through the control of α-ketoglutarate

A genomic signature of positive selection is observed in a farmed population (Star Food, Netherlands)

Genomic signature of domestication





Overlaps with proteins associated with regulator of telomere elongation helicase

Does early domestication of yellow mealworm affected its genome and agronomic QTLs?

1. Can we identify genomic loci under selection in domesticated populations?

Yes

2. Can we detect QTLs associated with agronomic traits?

Yes

3. Do we have overlaps between loci under selection and QTLs?

2 examples identified

Deeper analysis of QTLs is required!

Acknowledgments

Fundings

Horizon 2020
European Union Funding
for Research & Innovation

BBI JU

Bio-based Industries
Consortium

Collaborators

cea

Karine Labadie
Benoit Vacherie
Sana Haddad
Leo Panunzi
Lucas Rocha Ferreira

Ynsect

Thomas Lefebvre
Eliaou Sellem
Qi Li
Katy Paul

UNIVERSITY OF
THESSALY

Christos Rumbos