MOLECULAR PHYLOGENETICS

MOLECULAR PHYLOGENETICS

B5791
SSD: BIO/05

MSc in Bioinformatics
academic year 2026 - second semester

6 CFUs - 48 hours total
16 classes of 3 hours each

THE TEACHER

Giobbe Forni

Department of Biological, Geological, and Environmental Sciences

Via Selmi 3 - Natural History museum, second floor on the right

room ???! … just ask at the entrance

giobbe.forni2@unibo.it

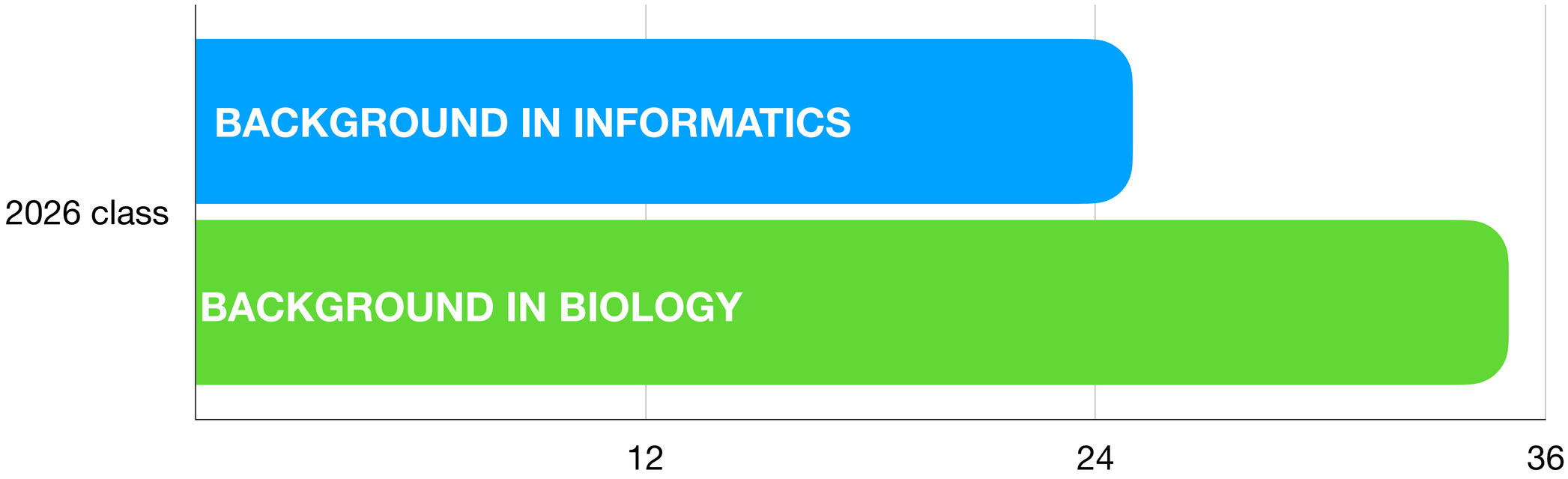
If I do not answer to your email within 48h … please write to me again 😅

*"**The shy cannot learn and the strict cannot teach**"*

In other words, I beg my students:
Please interrupt.
Please ask questions.
Please identify mistakes and let me know that I have erred.
Please do not be afraid of exposing my ignorance and your ignorance - after all, we are all ignorant.
And, please take advantage of office hours."

Dan Graur

YOUR CAREER?


2026 class
BACKGROUND IN INFORMATICS
BACKGROUND IN BIOLOGY
12
24
36

MY PATH

- **BSc** in Biotechnology at University of Bologna

- **MSc** in Biodiversity and Evolution at University of Bologna

- **PhD** in Earth, Life and Environmental Sciences at University of Bologna

- 2 years **PostDoc** at the University of Milan and Naples

- 3 years **Postdoc** at the University of Bologna

MY EXPERTISE

I am an **evolutionary biologist**!

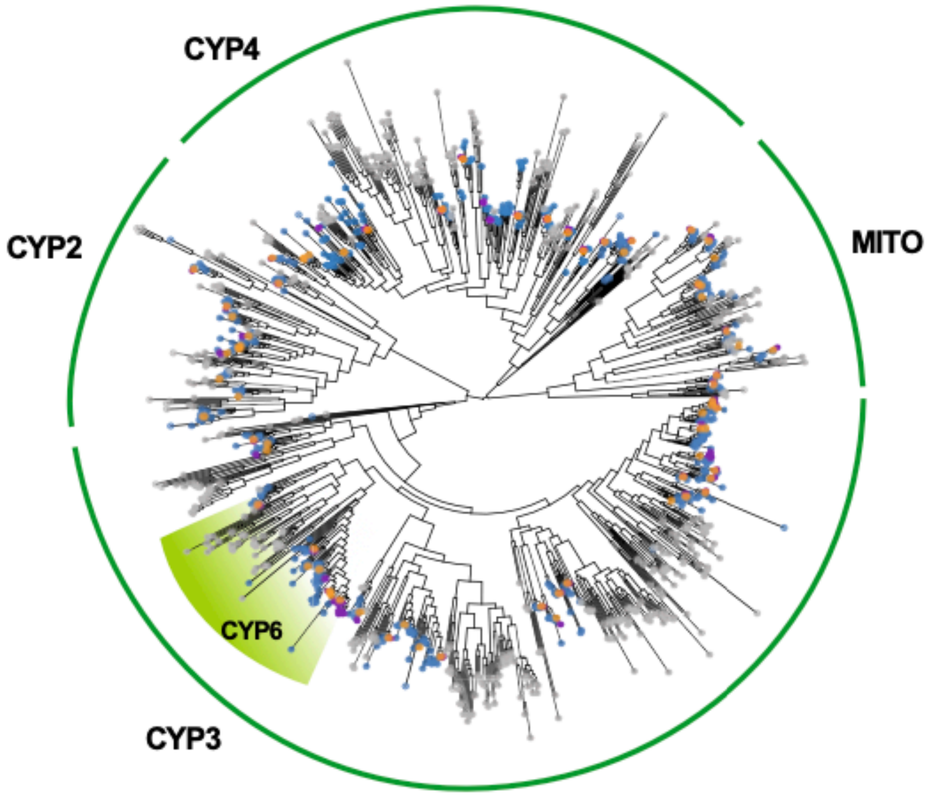
My expertise encompasses:

- phylogenetics comparative methods

- comparative genomics

- comparative transcriptomics

…

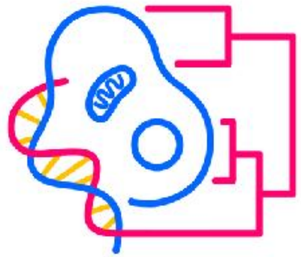


just average knowledge of informatics 🥲

MY NETWORK

SIBE
SOCIETÀ ITALIANA DI BIOLOGIA EVOLUZIONISTICA

SOCIETA ITALIANA DI BIOLOGIA EVOLUZIONISTICA

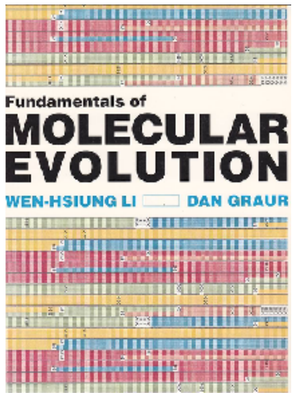


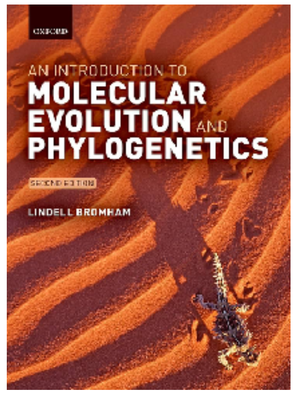
EVOLUTIONARY COMPARATIVE BIOLOGY GROUP @UNIVERSITY OF BOLOGNA

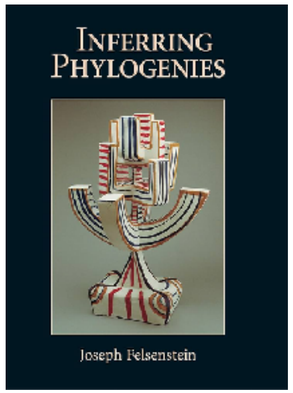
EVOLUTIONARY COMPARATIVE BIOLOGY GROUP

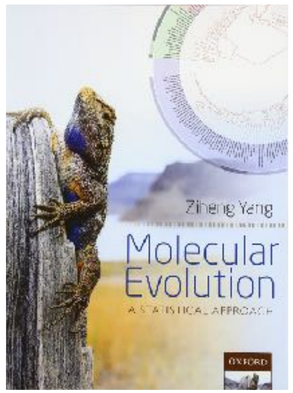
COURSE MATERIAL

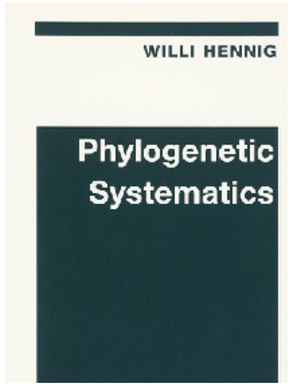
- slides - you are looking at one 😛
- papers (either PDFs or doi)
- books - as additional resources

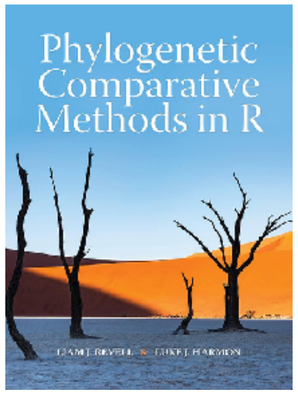












All the course materials will be permanently uploaded to github. Slides and recordings will also be uploaded at the end of each week to a drive folder.

INSTALLATIONS

CONDA is a package manager that will allow us to be flexible with installations.

- mafft
- trimal
- iqtree
- … the list is costantly WIP - see the github for this!

We will also use a handfull of **GUI executables**:

- Aliview
- FigTree
- Tracer
- R & Rstudio

COURSE STRUCTURE

Each lesson will be subdivided in **three parts** (the timing may vary):

- 1h’20 of theoretical explanation of an aspect of phylogenetics

- 20’ of pause - we can relax or chat about the topic of the day

- 1h20’ of practice on the topic of the theoretical session

NB: practical sessions are fundamental for you to consolidate theory. The exam does not include any question on specific commands, **but it will include questions form the practicals.**

course syllabus

lesson 01	03 March (Tu)	10-13	intro to the course + software installation	
lesson 02	04 March (We)	10-13	phylogenetics 101 - part A	**WEEK 1**
lesson 03	05 March (Th)	10-13	phylogenetics 101 - part B	
lesson 04	10 March (Tu)	10-13	orthology infererence and taxon sampling	
lesson 05	11 March (We)	10-13	sequence alignement and filtering	**WEEK 2**
lesson 06	12 March (Th)	10-13	distance-based *versus* charcter-based algorythms	
lesson 07	17 March (Tu)	10-13	MK models of molecular evolution	
lesson 08	18 March (We)	10-13	Maximum Likelihood (ML)	**WEEK 3**
lesson 09	19 March (Th)	10-13	Bayesian Inference (BI)	
lesson 10	23 March (Mo)	10-13	support metrics	**WEEK 4**
lesson 11	08 April (We)	10-13	complex sostitution models	**WEEK 6**
lesson 12	09 April (Th)	10-13	discordance, ILS & the coalescent	
lesson 13	14 April (Tu)	10-13	stochastic and systematic bias	**WEEK 7**
lesson 14	15 April (We)	10-13	divergence times analyses	
lesson 15	21 April (Tu)	10-13	inferring selection	**WEEK 8**
lesson 16	24 April (Fr)	10-13	modelling trait evolution on phylogenies	

THE EXAM

- 22 multiple choiche questions: **1 point each for a total of 22 points**
  only one is correct and there is no penalty for errors

- 2 open ended and general question: **5 points each for a total of 10 points**
  predefined length, you should use your ability to synthetize

The exam is designed to be easy …
if you come consistently to lessons 😓

You can find an exam sample on GitHub.

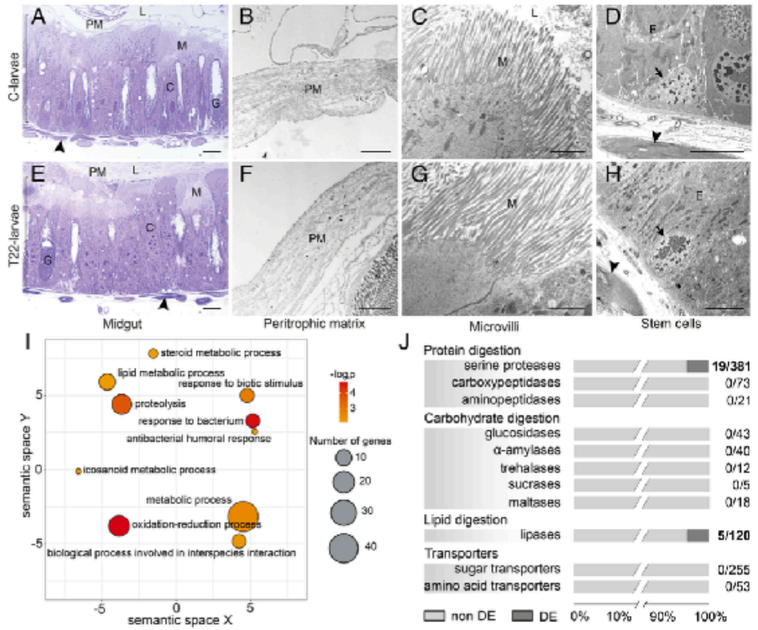
MY RESEARCH

PNAS RESEARCH ARTICLE | APPLIED BIOLOGICAL SCIENCES OPEN ACCESS

A soil fungus confers plant resistance against a phytophagous insect by disrupting the symbiotic role of its gut microbiota

Ilaria Di Lelio[a,1], Globbe Forni[a,1], Giulia Magoga[a], Matteo Brunetti[b], Daniele Bruno[c], Andrea Becchimanzi[a], Maria G. De Luca[a], Martina Sinno[a], Eleonora Barra[a], Marco Bonelli[d], Sarah Frusciante[e], Gianfranco Diretto[e], Maria C. Digilio[a], Sheridan L. Woo[f,g], Gianluca Tettamanti[c,h], Rosa Rao[a], Matteo Lorito[a], Morena Casartelli[c,2], Matteo Montagna[a,2], and Francesco Pennacchio[a,2]

Edited by David Denlinger, The Ohio State University, Columbus, OH; received October 7, 2022; accepted December 16, 2022



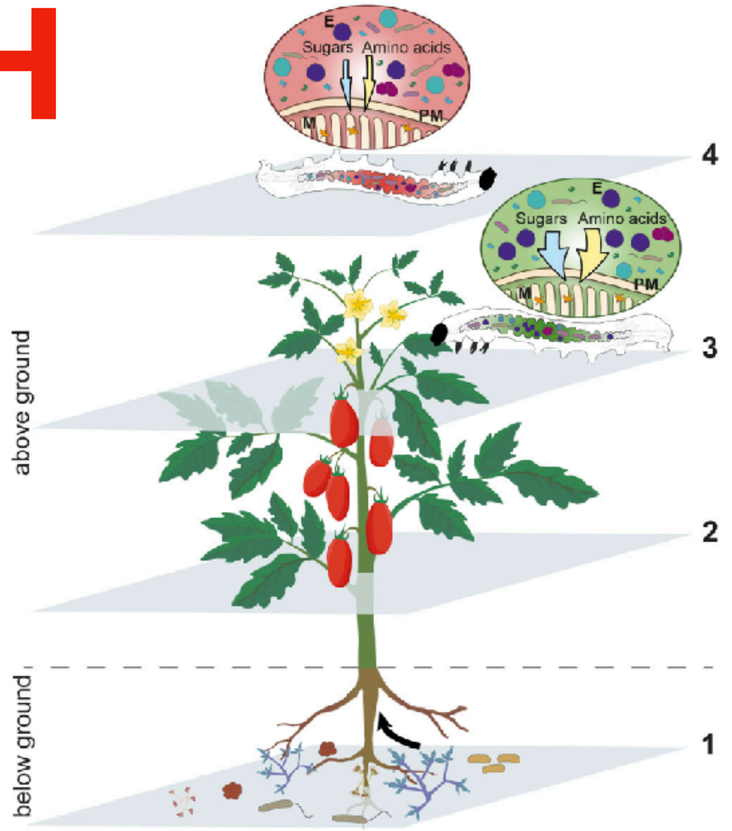
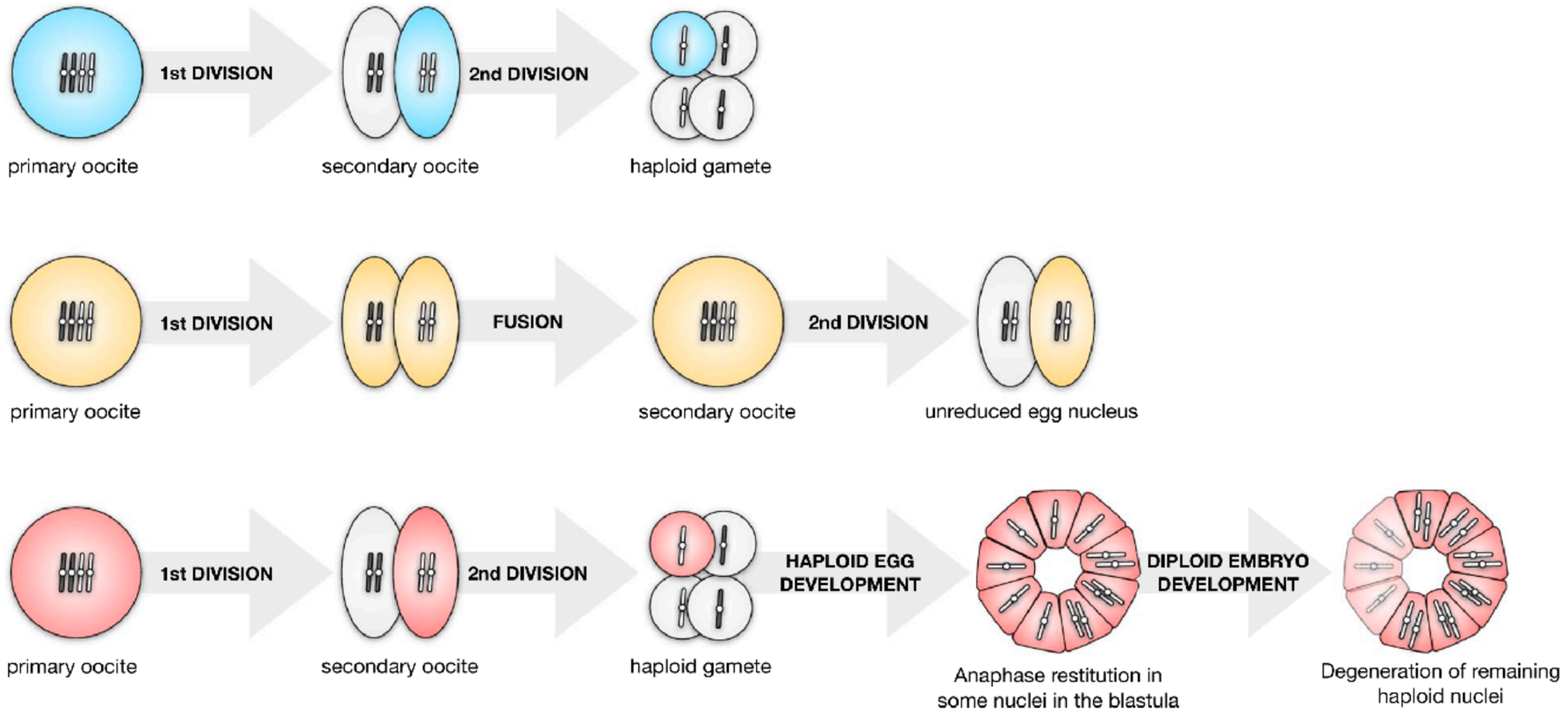


Fig. 6. Schematic representation of the interactions among the plant *S. lycopersicum*, the fungus *T. afroharzianum* strain T22, and the phytophagous insect *S. littoralis* and its gut microbiome. The colonization of *S. lycopersicum* roots by the fungus *T. afroharzianum* strain T22 (1) systemically conditions the plant (2), generating a dysbiosis of the gut microbiome in *S. littoralis* larvae feeding on tomato leaves with neither structural damages to the midgut epithelium and peritrophic matrix nor alterations in the digestive capacity of the insect. This dysbiosis, among others, affects symbiotic bacteria of the genus *Enterococcus* and the functional capability of *E. casseliflavus* to nutritionally support the insect host with sugars and amino acids (3), with a consequent negative impact on *S. littoralis* development and survival (4). E: *E. casseliflavus* bacterial cells; M: microvilli; PM: peritrophic matrix; orange, green, and light blue shapes: insect digestive enzymes.

MY RESEARCH


1st DIVISION
2nd DIVISION
primary oocite
secondary oocite
haploid gamete
1st DIVISION
FUSION
2nd DIVISION
primary oocite
secondary oocite
unreduced egg nucleus
1st DIVISION
2nd DIVISION
HAPLOID EGG DEVELOPMENT
DIPLOID EMBRYO DEVELOPMENT
primary oocite
secondary oocite
haploid gamete
Anaphase restitution in some nuclei in the blastula
Degeneration of remaining haploid nuclei

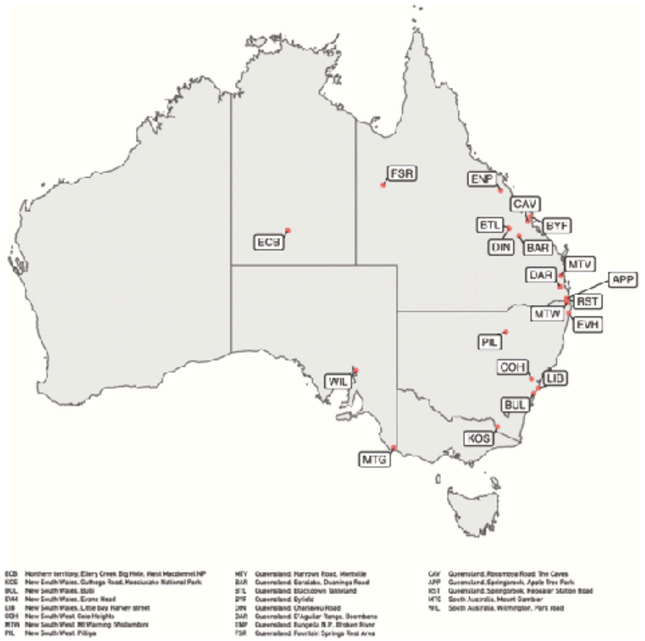
MY RESEARCH

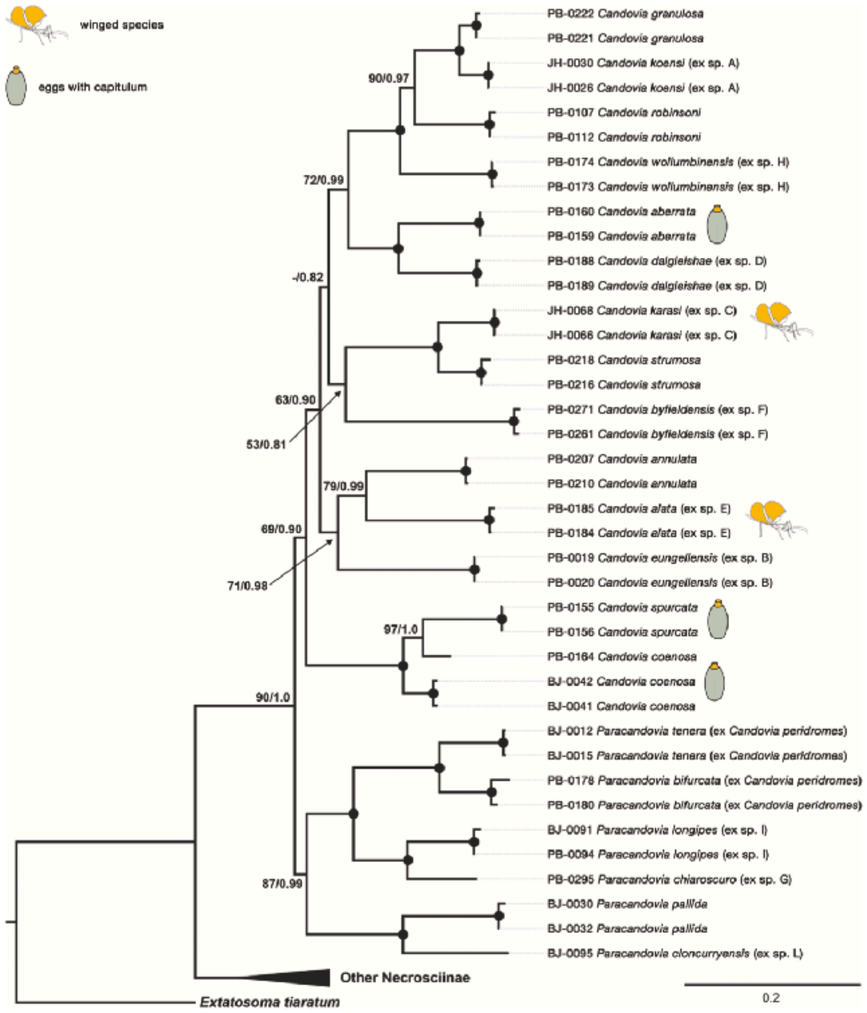
Taxonomic revision of the Australian stick insect genus *Candovia* (Phasmida: Necrosciinae): insight from molecular systematics and species-delimitation approaches

GIOBBE FORNI[1,2,*], ALEX CUSSIGH[1,2], PAUL D. BROCK[3], BRAXTON R. JONES[4], FILIPPO NICOLINI[1], JACOPO MARTELOSSI[1], ANDREA LUCHETTI[1,*] and BARBARA MANTOVANI[1]

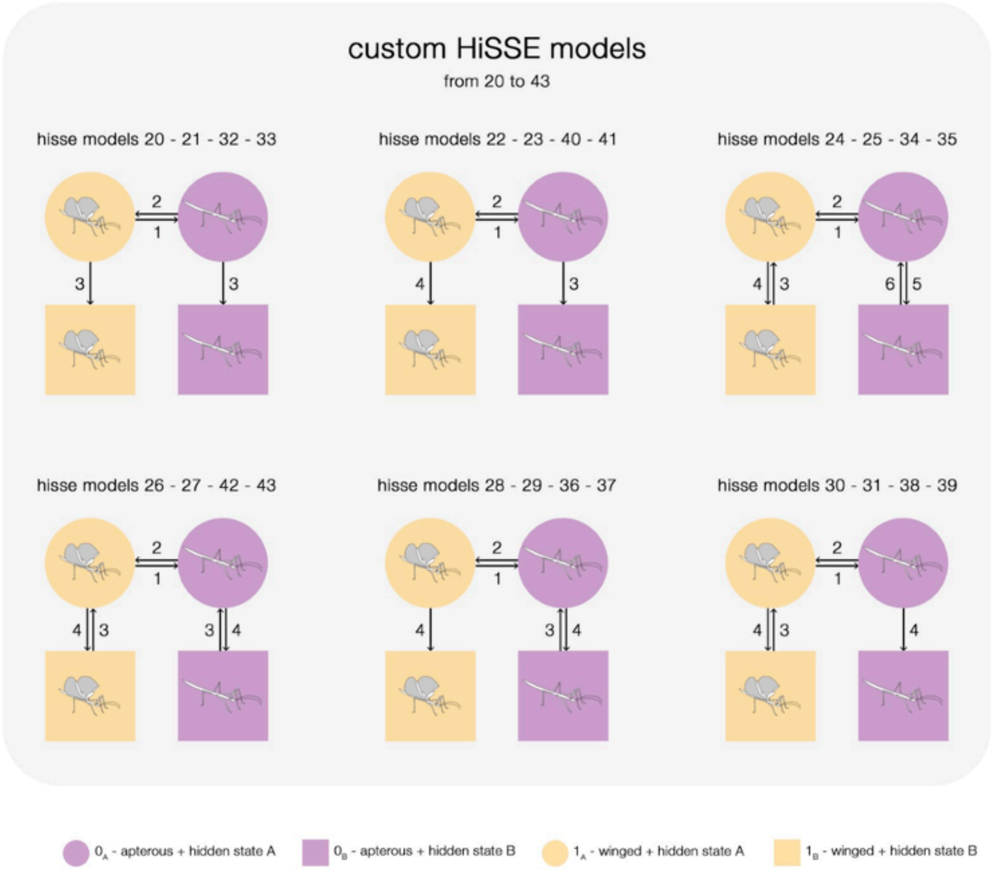
[1]*Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy*
[2]*Department of Agricultural and Environmental Sciences, University of Milan, Milano, Italy*
[3]*The Natural History Museum, Cromwell Road, London, UK*
[4]*School of Life and Environmental Sciences, The University of Sydney, Sydney NSW 2006, Australia*

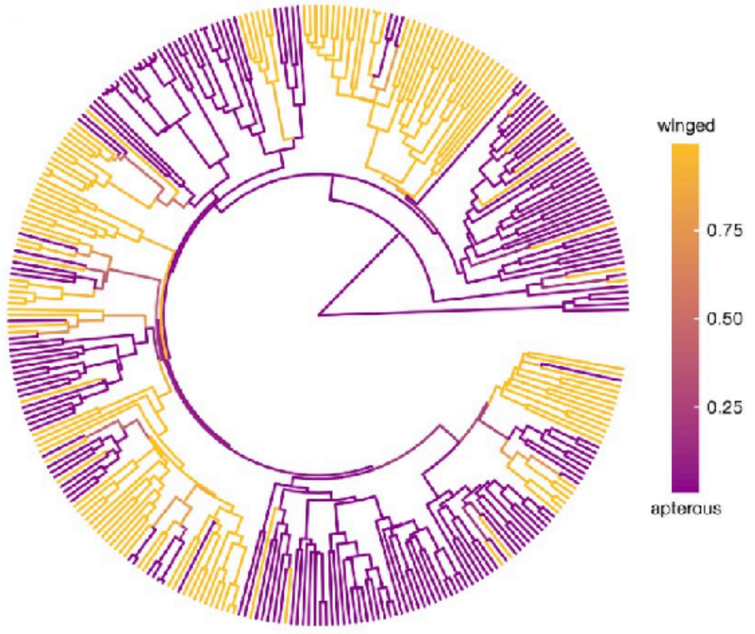
Received 18 March 2022; revised 4 July 2022; accepted for publication 8 August 2022



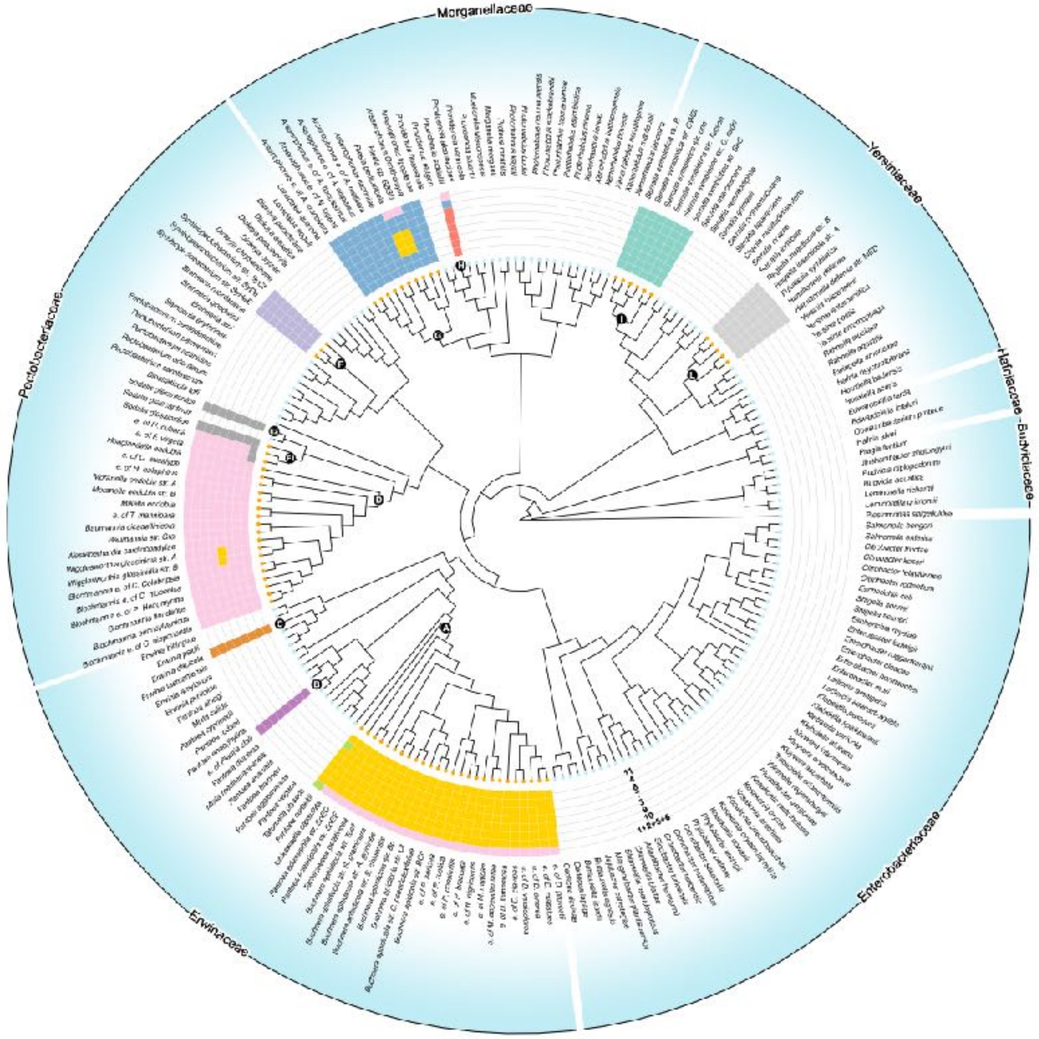


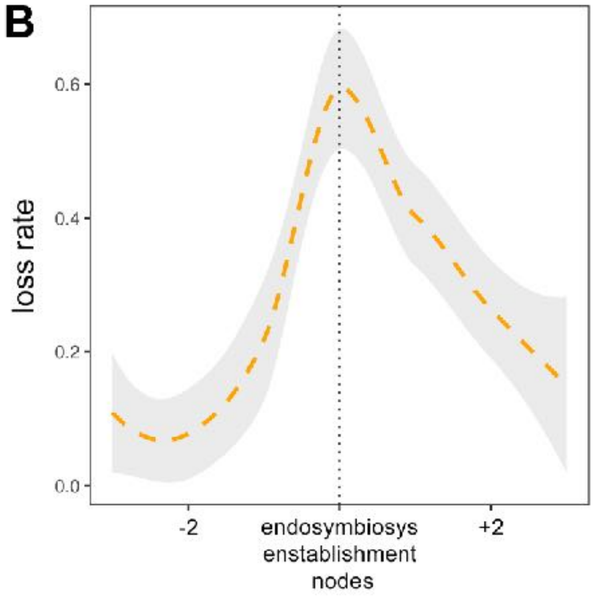
MY RESEARCH

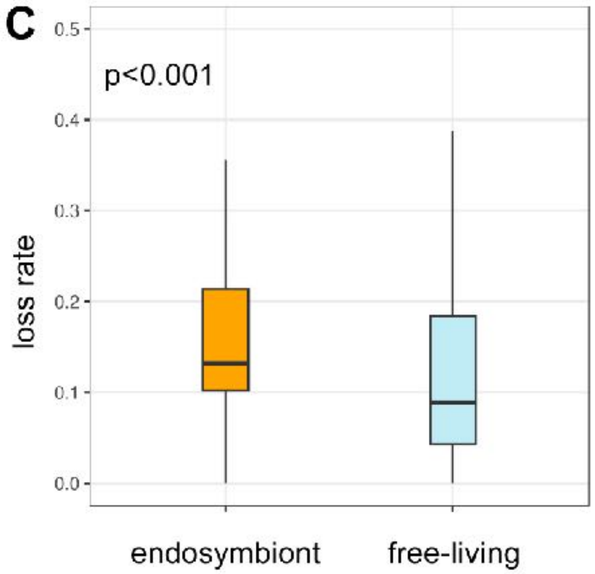

custom HiSSE models
from 20 to 43
hisse models 20 - 21 - 32 - 33
hisse models 22 - 23 - 40 - 41
hisse models 24 - 25 - 34 - 35
hisse models 26 - 27 - 42 - 43
hisse models 28 - 29 - 36 - 37
hisse models 30 - 31 - 38 - 39
0A - apterous + hidden state A
0B - apterous + hidden state B
1A - winged + hidden state A
1B - winged + hidden state B


winged
0.75
0.50
0.25
apterous

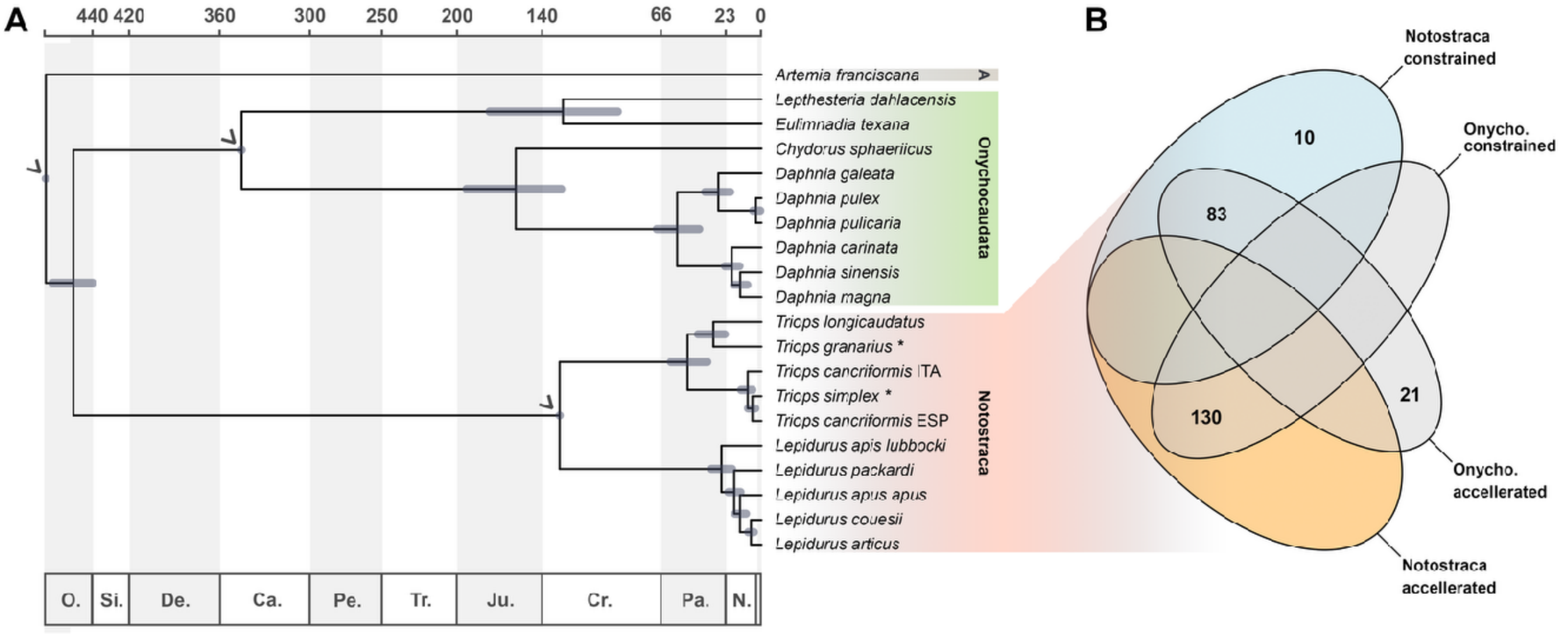
MY RESEARCH


Morganellaceae
Yersiniaceae
Hafniaceae
Budviciaceae
Enterobacteriaceae
Erwiniaceae
Pectobacteriaceae


B
loss rate
0.0
0.2
0.4
0.6
-2
endosymbiosys
enstablishment
nodes
+2


C
p<0.001
loss rate
0.0
0.1
0.2
0.3
0.4
0.5
endosymbiont
free-living

MY RESEARCH



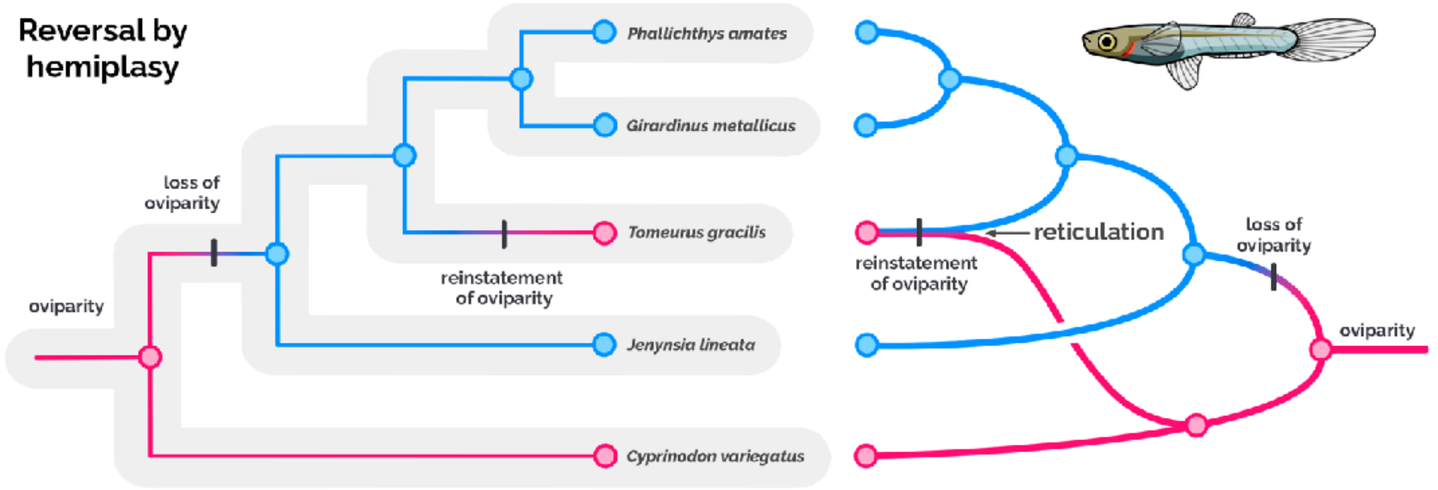
C

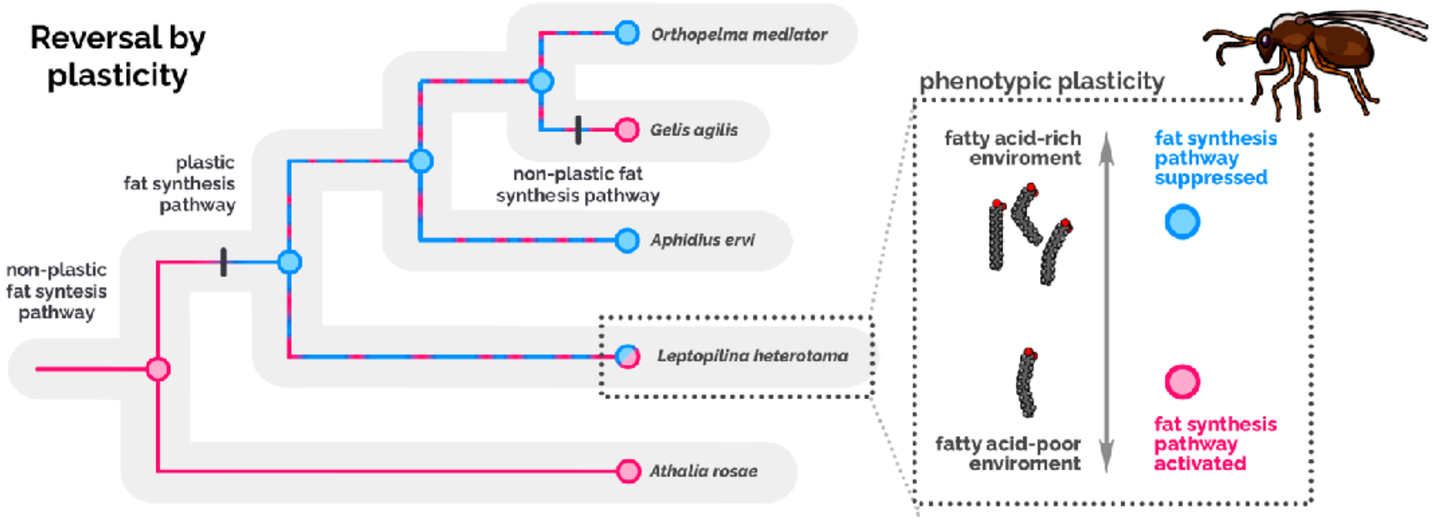
	constrained genes terms	*p*	significant / expected
GO:0007249	I-kappaB kinase/NF-kappaB signaling	0.00217	11.54
GO:0006357	regulation of transcription by RNA polym...	0.00384	2.37
GO:0006470	protein dephosphorylation	0.00784	5.06
GO:0006355	regulation of transcription, DNA-templat...	0.00819	1.93
GO:1903506	regulation of nucleic acid-templated tra...	0.00819	1.93

D

	accelerated genes terms	*p*	significant / expected
GO:0010466	negative regulation of peptidase activit...	0.0024	10.71
GO:0006397	mRNA processing	0.0024	2.36
GO:0016071	mRNA metabolic process	0.0029	2.48
GO:0097193	intrinsic apoptotic signaling pathway	0.0072	7.32
GO:0050684	regulation of mRNA processing	0.0077	5.06

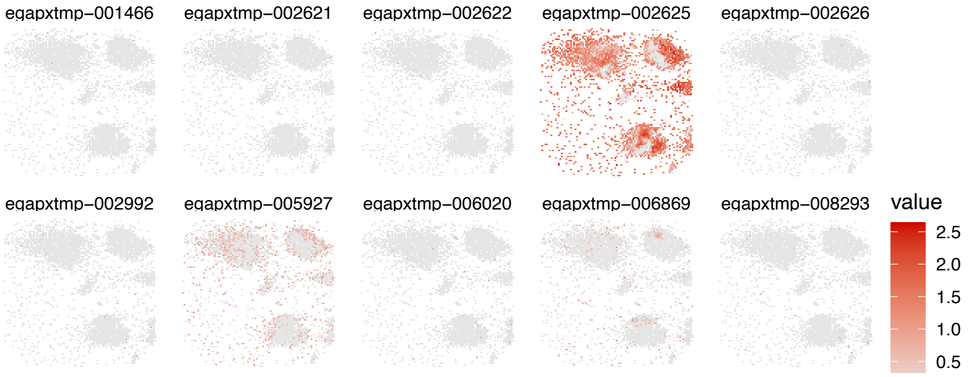
MY RESEARCH

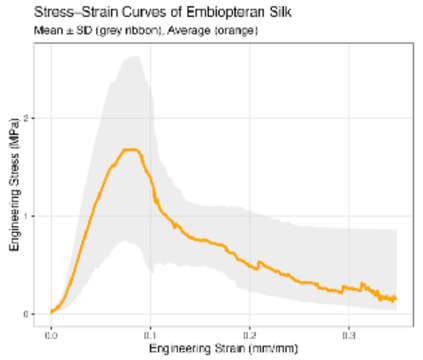

Reversal by hemiplasy
Phallichthys amates
Girardinus metallicus
loss of oviparity
Tomeurus gracilis
reinstatement of oviparity
oviparity
Jenynsia lineata
Cyprinodon variegatus
reticulation
reinstatement of oviparity
loss of oviparity
oviparity


Reversal by plasticity
Orthopelma mediator
Gelis agilis
plastic fat synthesis pathway
non-plastic fat synthesis pathway
Aphidius ervi
non-plastic fat syntesis pathway
Leptopilina heterotoma
Athalia rosae
phenotypic plasticity
fatty acid-rich enviroment
fat synthesis pathway suppressed
fatty acid-poor enviroment
fat synthesis pathway activated

MY RESEARCH


HV
10.00 kV
curr
0.18 nA
det
ETD
WD
8.7 mm
HFW
31.9 µm
mag
6 500 ×
pressure
5.24E-4 Pa
10 µm


egapxtmp–001466
egapxtmp–002621
egapxtmp–002622
egapxtmp–002625
egapxtmp–002626
egapxtmp–002992
egapxtmp–005927
egapxtmp–006020
egapxtmp–006869
egapxtmp–008293
value
2.5
2.0
1.5
1.0
0.5


Stress–Strain Curves of Embiopteran Silk
Mean ± SD (grey ribbon), Average (orange)
Engineering Stress (MPa)
Engineering Strain (mm/mm)

FINISH