

Recurrent specialization on a toxic fruit in *Drosophila*: a population genomics perspective



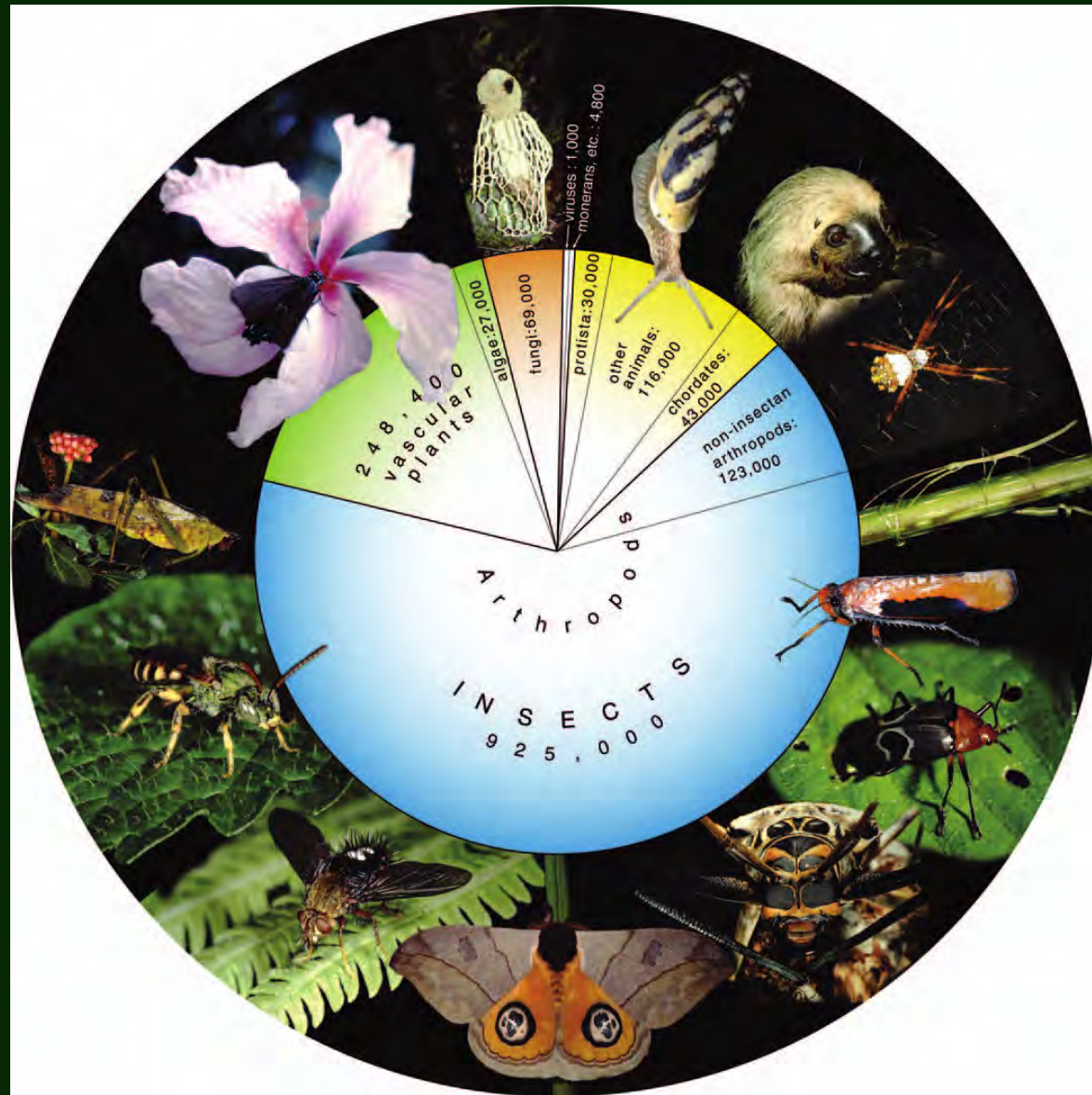
Amir Yassin

Institut Systématique Evolution Biodiversité (ISyEB) – UMR7205

Centre National de la Recherche Scientifique (CNRS)

Muséum National d'Histoire Naturelle (MNHN)

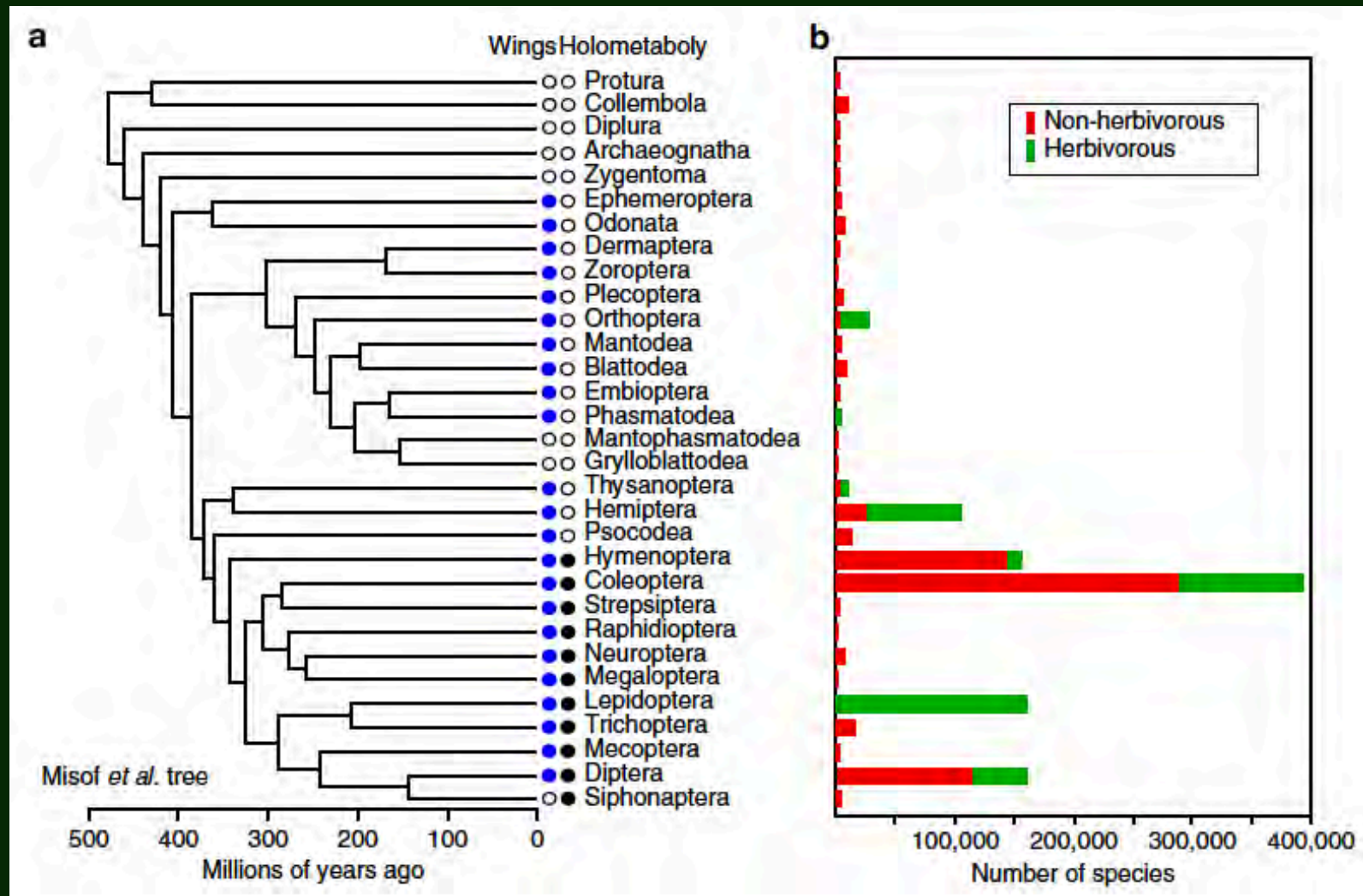
An inordinate fondness for insects



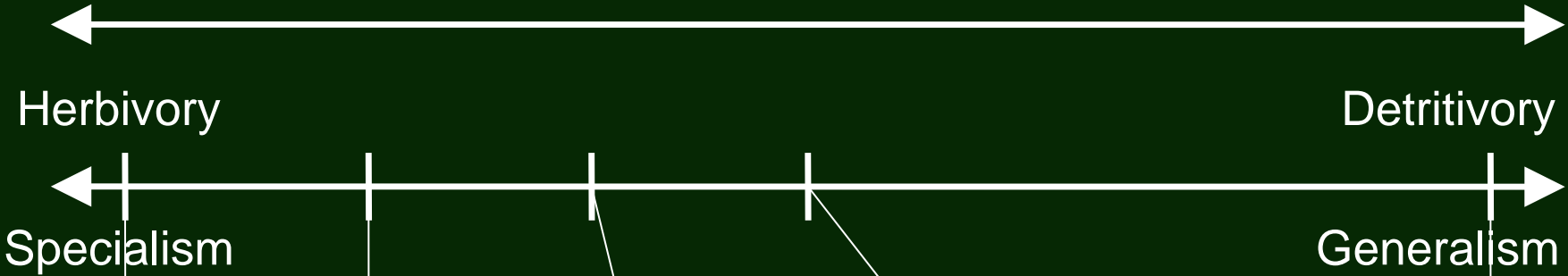
1.3 The diversity of life shown as proportions of named species

Grimaldi & Engels (2005) *Evolution of the Insects*

A role of herbivory in diversification



Herbivory gradient in the Drosophilidae



Scaptomyza nigrita



D. pachea



D. sechellia

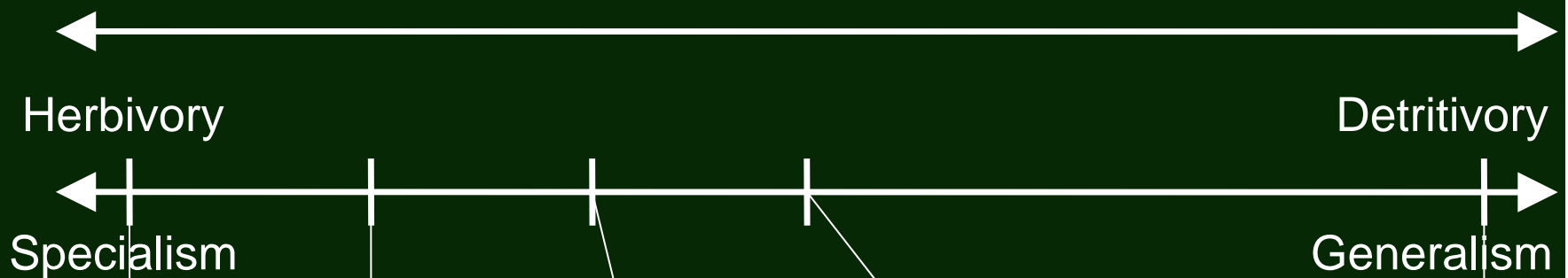


D. suzukii



D. melanogaster

Transition from generalism to specialism



Scaptomyza nigrita

D. pachea

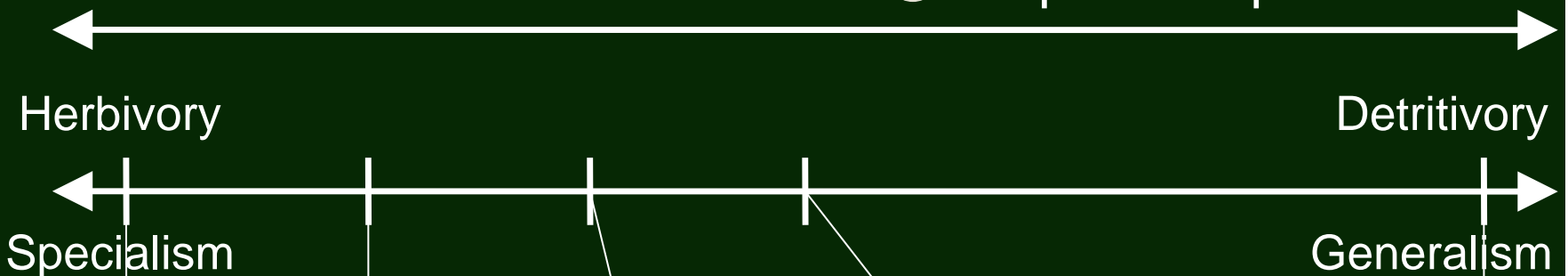
D. sechellia

D. suzukii

D. melanogaster

Transition from generalism to specialism

- 1 Long-range attraction
- 2 Tolerance of plant defensive toxins
- 3 Digestion of ingested ripe plant material
- 4 Oviposition preference



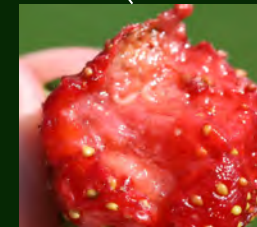
Scaptomyza nigrita



D. pachea



D. sechellia

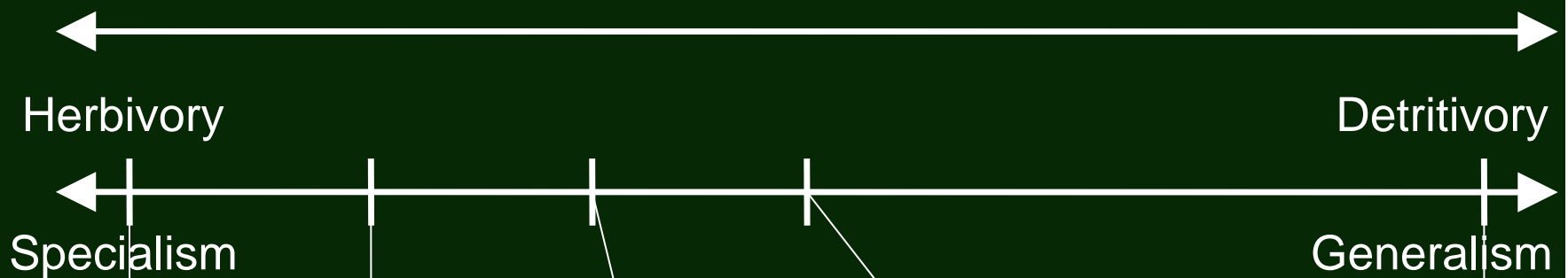


D. suzukii



D. melanogaster

Transition from generalism to specialism



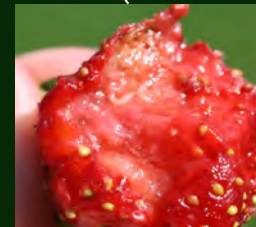
Scaptomyza nigrita



D. pachea



D. sechellia



D. suzukii

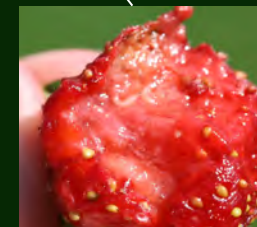
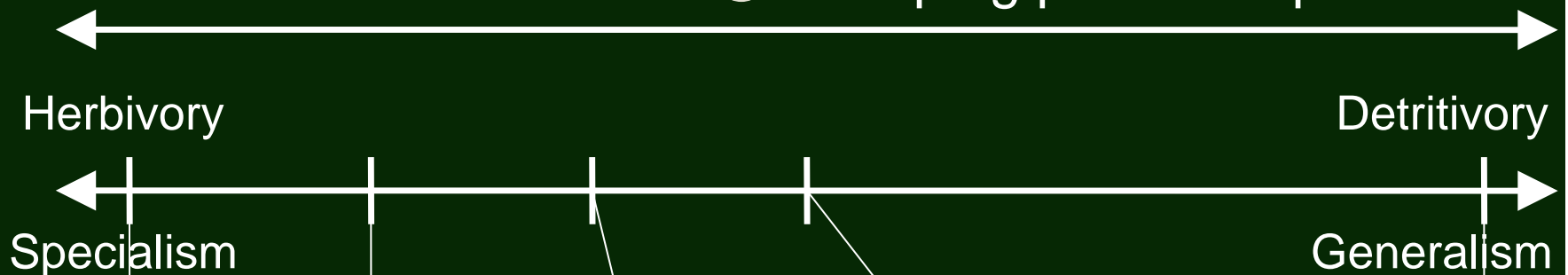


D. melanogaster

Transition from generalism to specialism



- 1 Ecological predictability
- 2 Inter-specific competition
- 3 Genetic constraints
- 4 Escaping predators/parasites



Scaptomyza nigrita

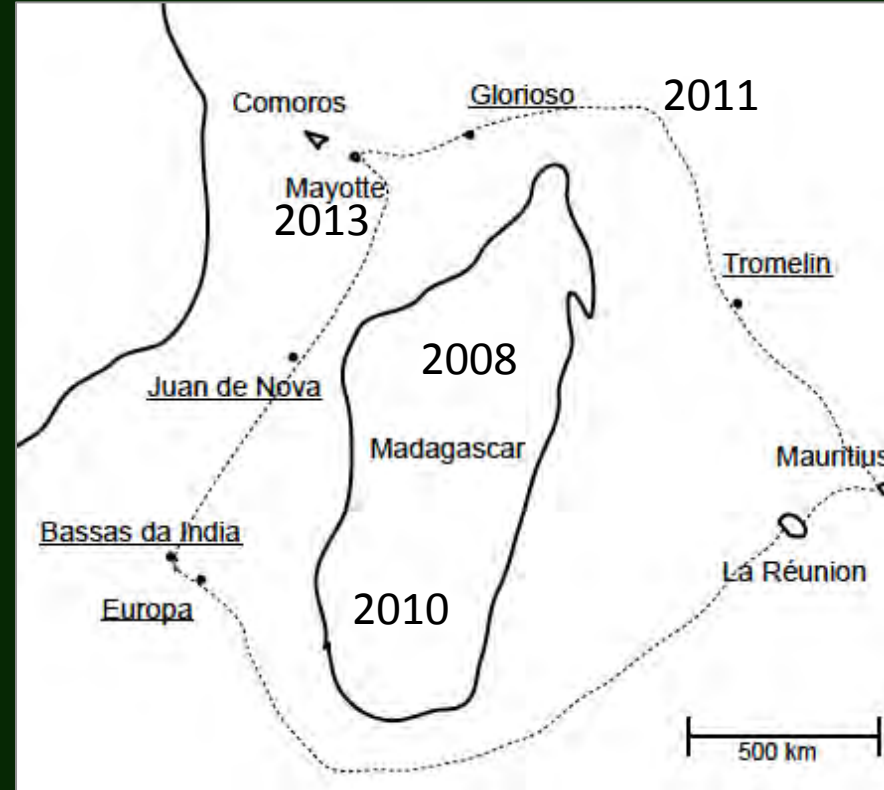
D. pachea

D. sechellia

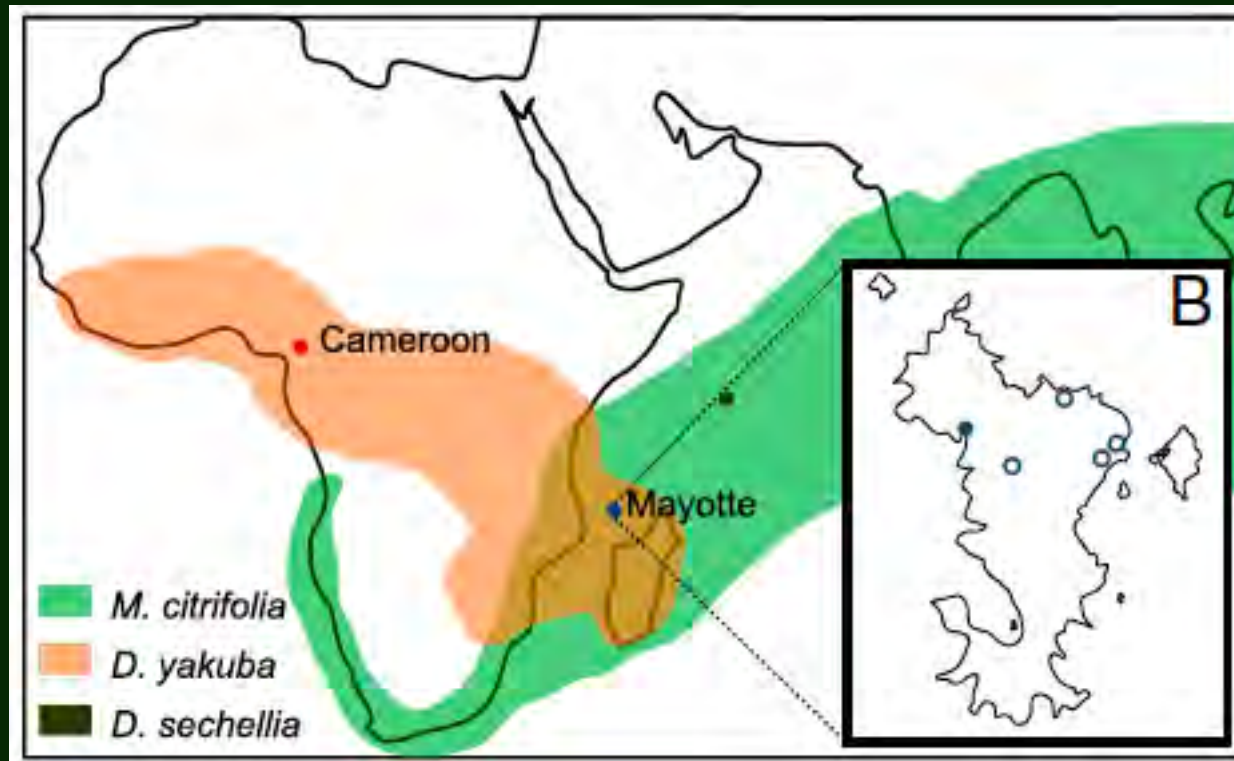
D. suzukii

D. melanogaster

Drosophilids collection in the Indian Ocean



Drosophila yakuba is strictly associated with noni on Mayotte



Drosophila yakuba is strictly associated with noni on Mayotte

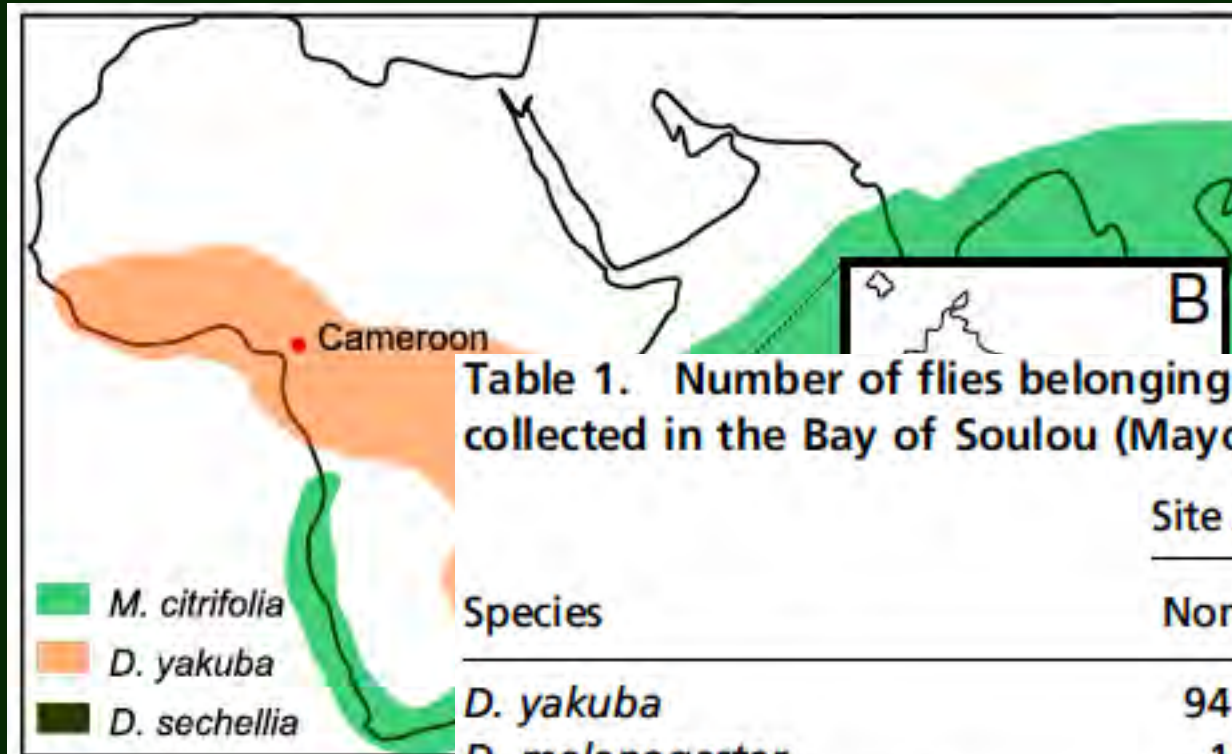
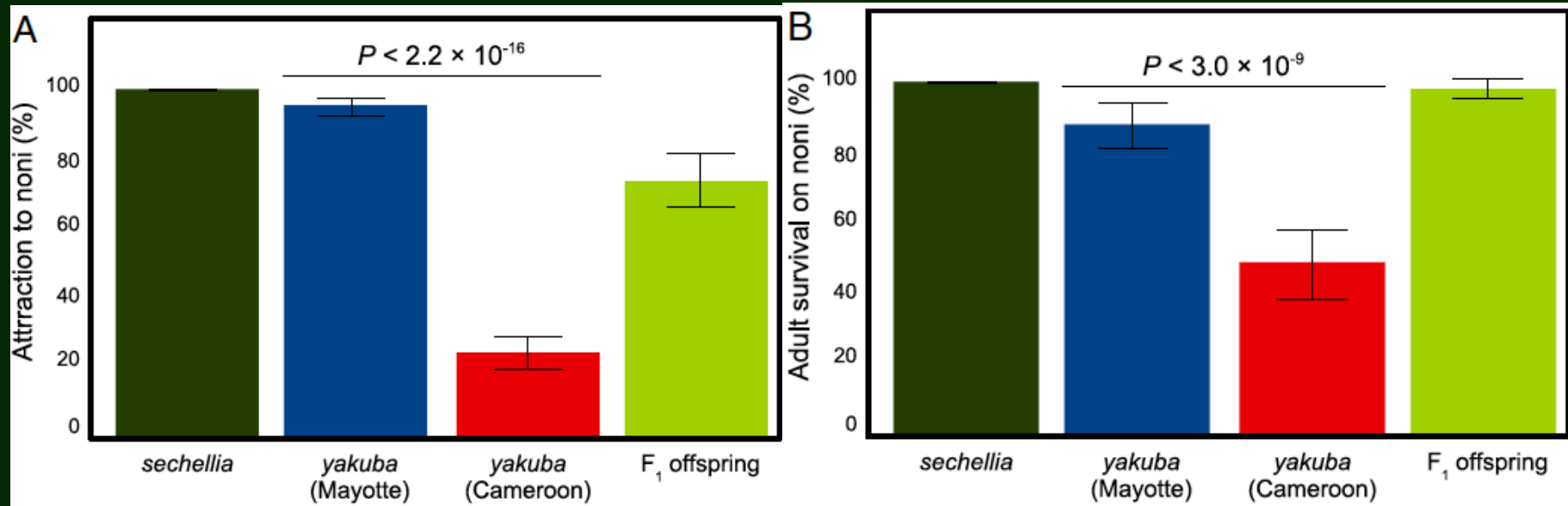


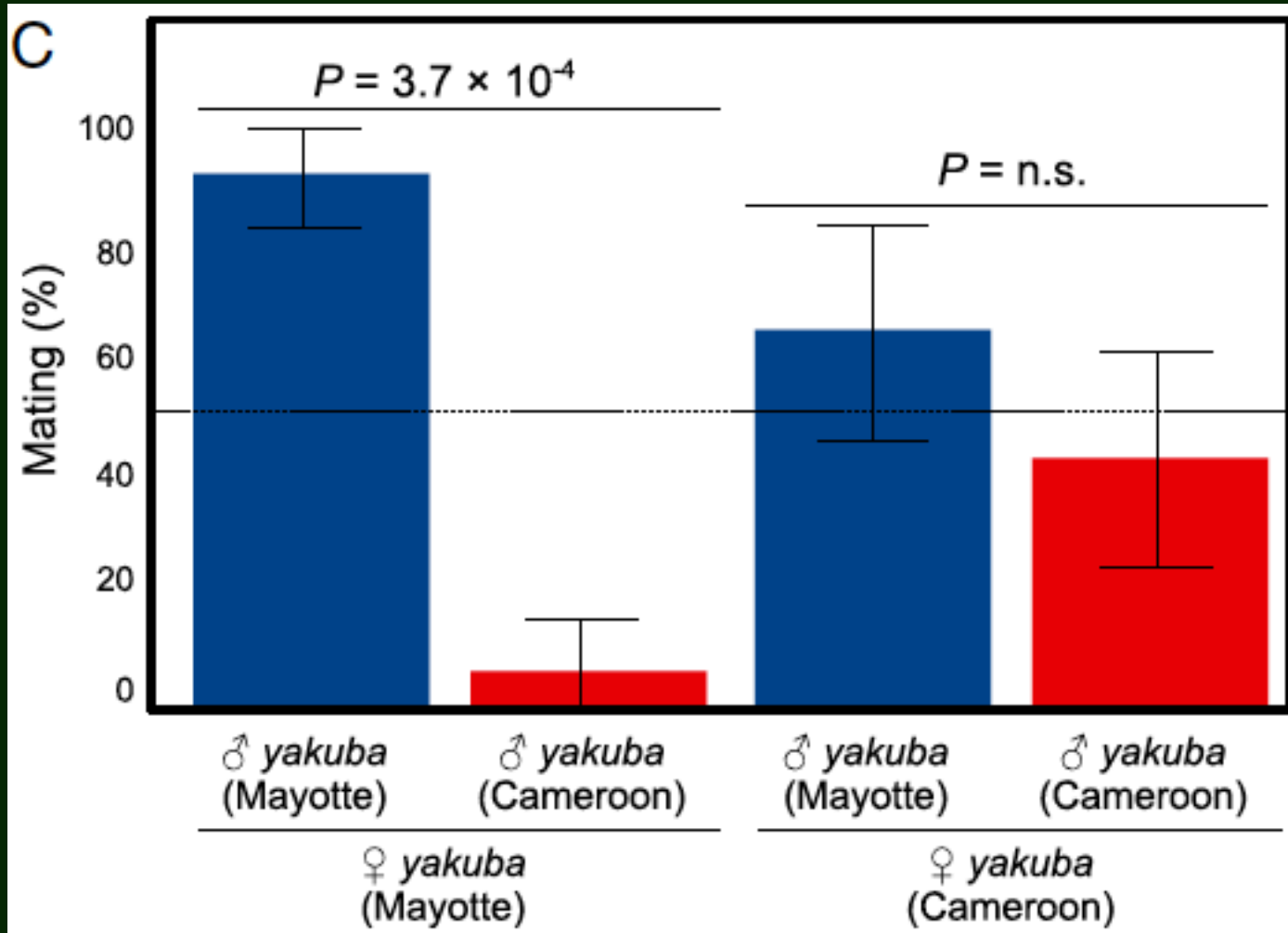
Table 1. Number of flies belonging to different species collected in the Bay of Soulou (Mayotte)

Species	Site A	Site B		Emergence from noni
	Noni	Noni	Jackfruit	
<i>D. yakuba</i>	94	331	2	44
<i>D. melanogaster</i>	1	0	0	0
<i>Drosophila malerkotliana</i>	71	129	151	30
<i>Drosophila nasuta</i>	5	39	11	12
<i>Scaptodrosophila latifasciaeformis</i>	0	10	227	0
<i>Zaprionus indianus</i>	0	8	1	0
<i>Zaprionus tuberculatus</i>	5	105	24	8

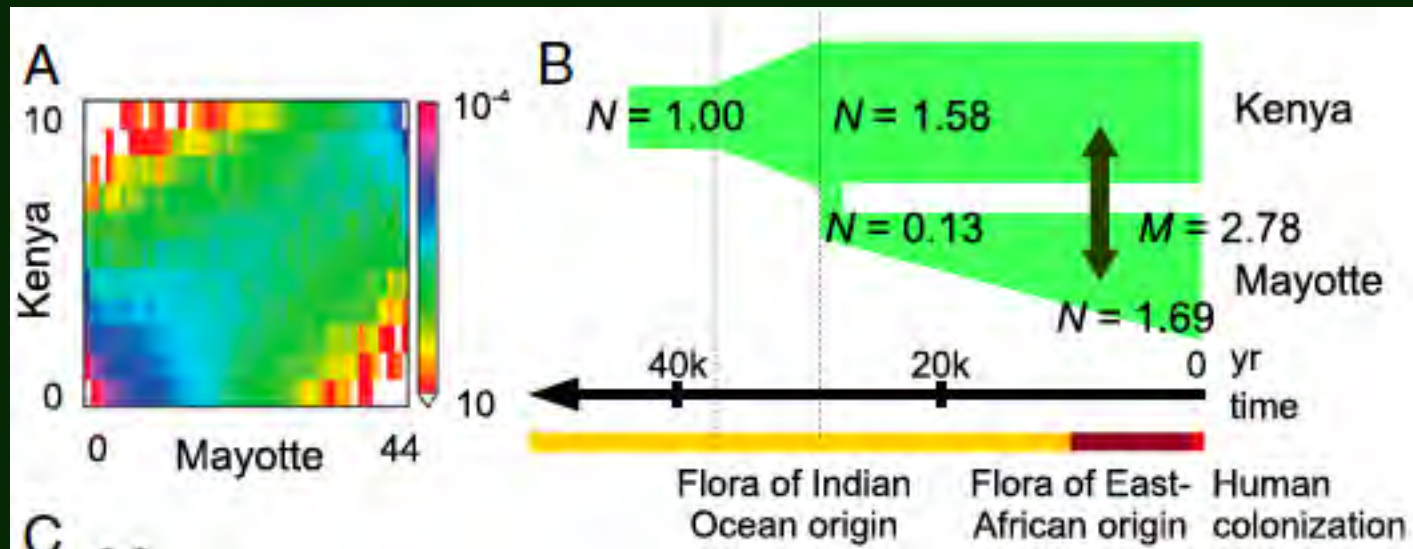
Laboratory experiments



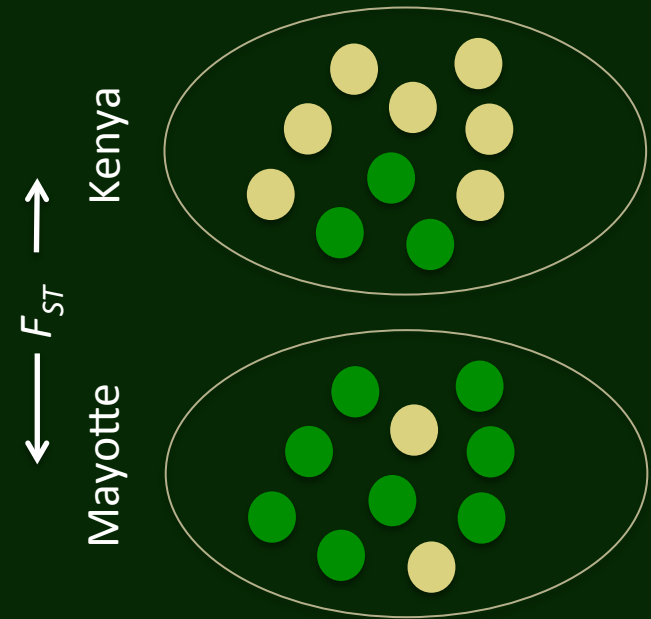
Assortative mating



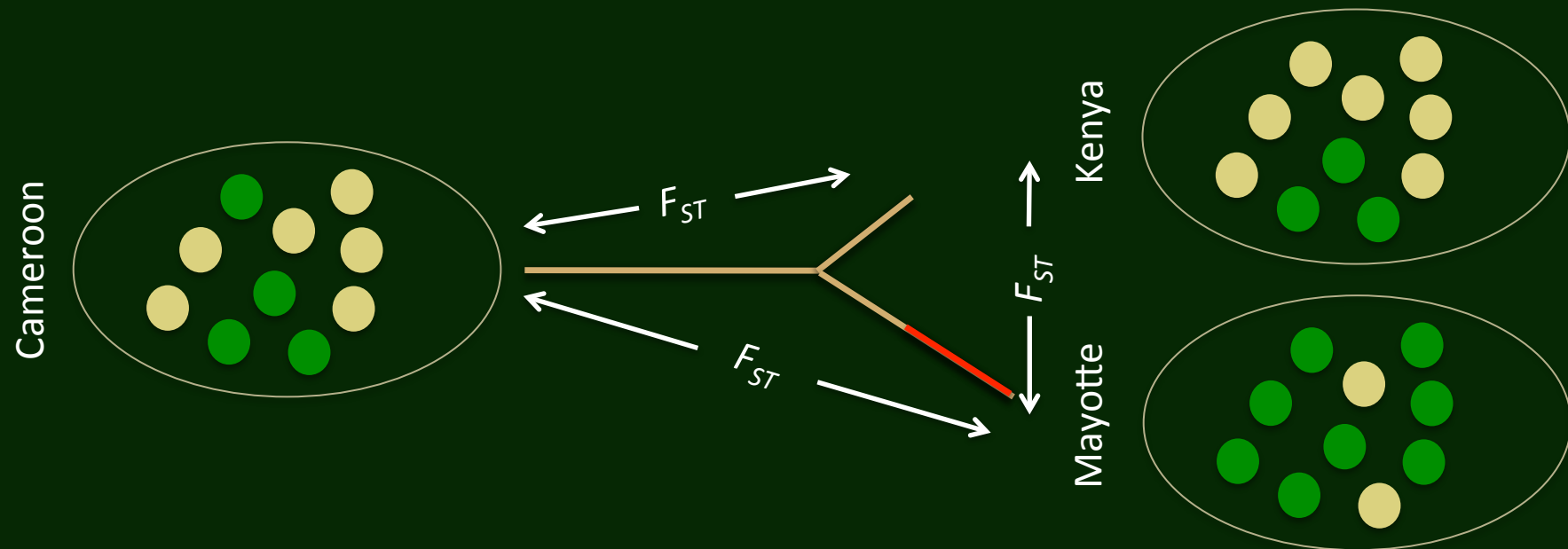
Demographic history



« Population Branch Excess »



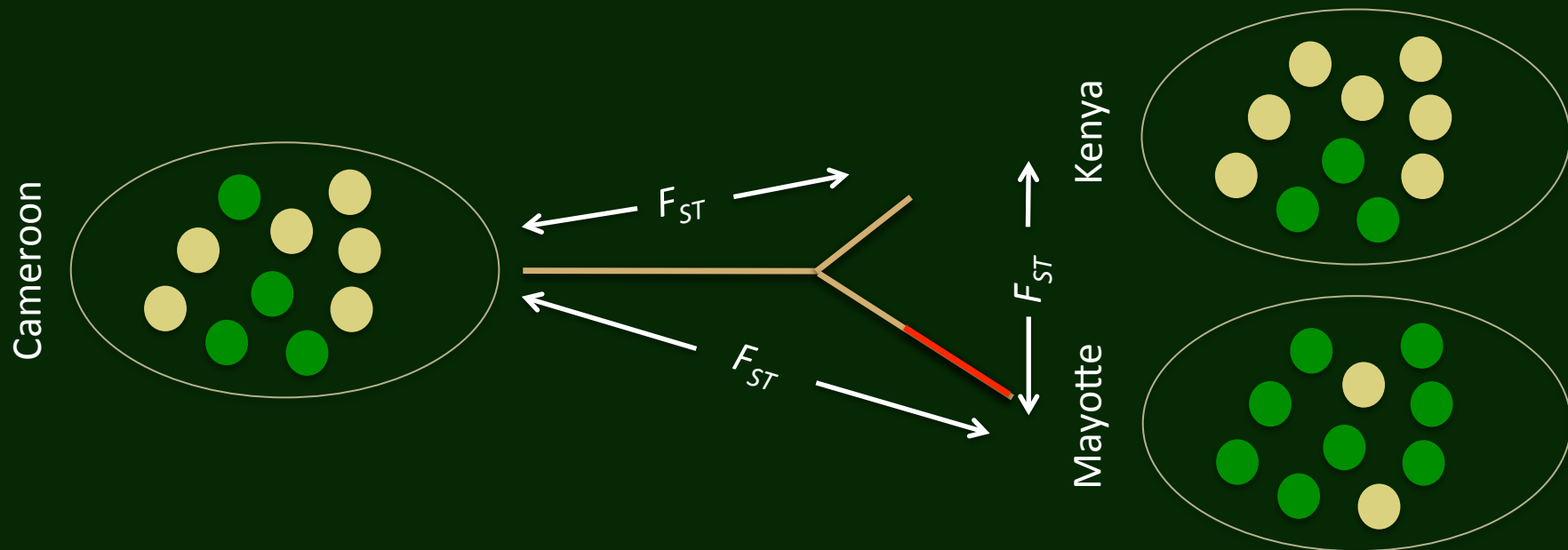
« Population Branch Excess »



$$PBS = [-\log (1-F_{ST_{MK}}) - \log (1-F_{ST_{MC}}) + \log (1-F_{ST_{KC}})] / 2$$

Yi et al. (2010) *Science*

« Population Branch Excess »



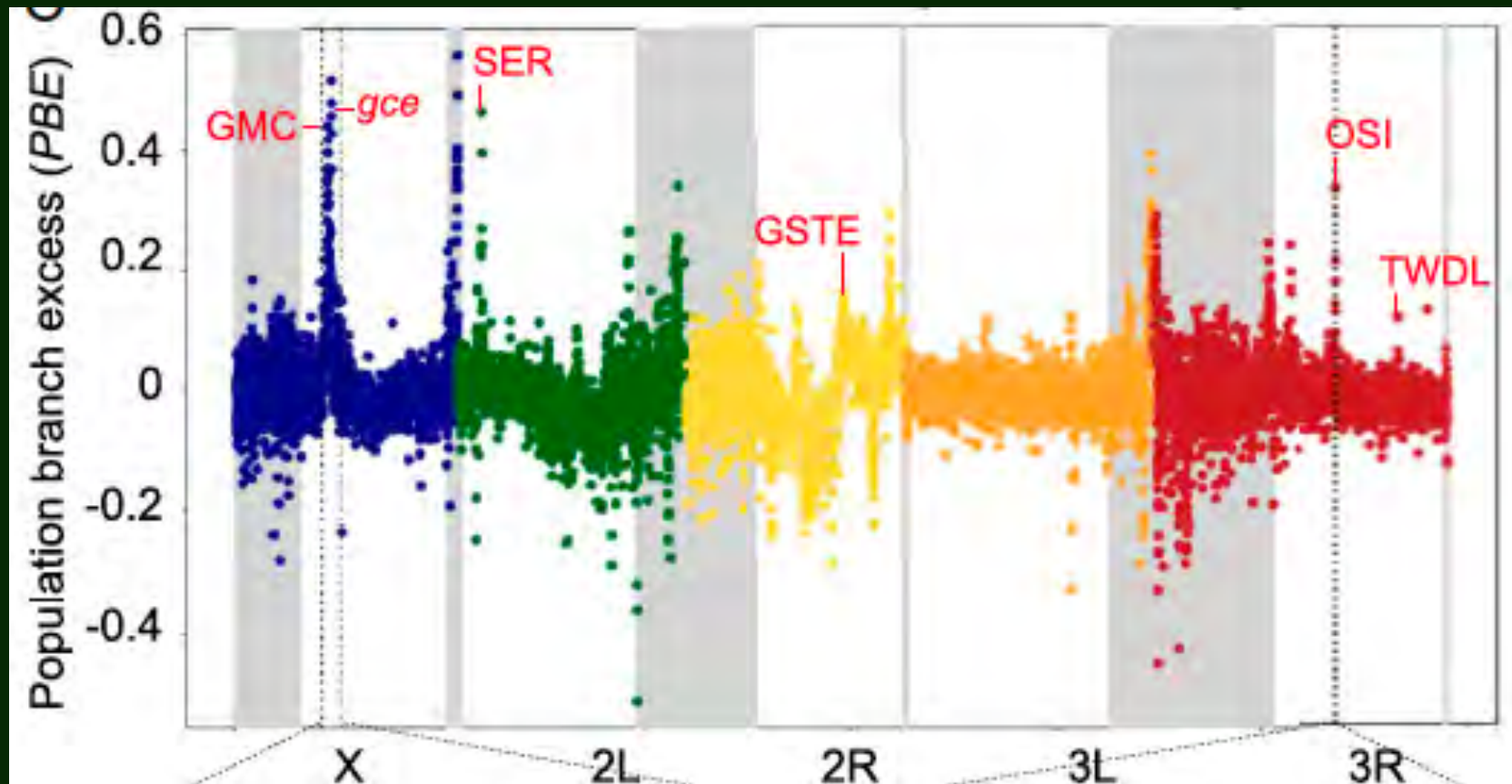
$$PBS = [-\log(1-F_{ST_{MK}}) - \log(1-F_{ST_{MC}}) + \log(1-F_{ST_{KC}})] / 2$$

Yi et al. (2010) *Science*

$$PBE = PBS_{obs} - PBS_{exp} = PBS - [-\log(1-F_{ST_{KC}}) \times (PBS_{med} / \{-\log(1-F_{ST_{KC}})\}_{med})]$$

Yassin et al. (2016) *PNAS*

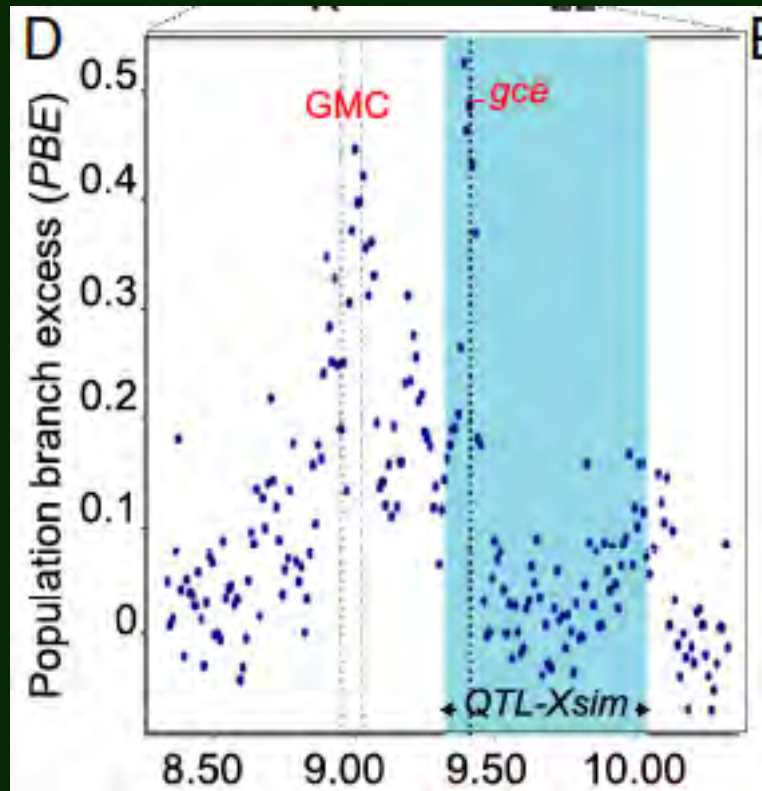
« Population Branch Excess »



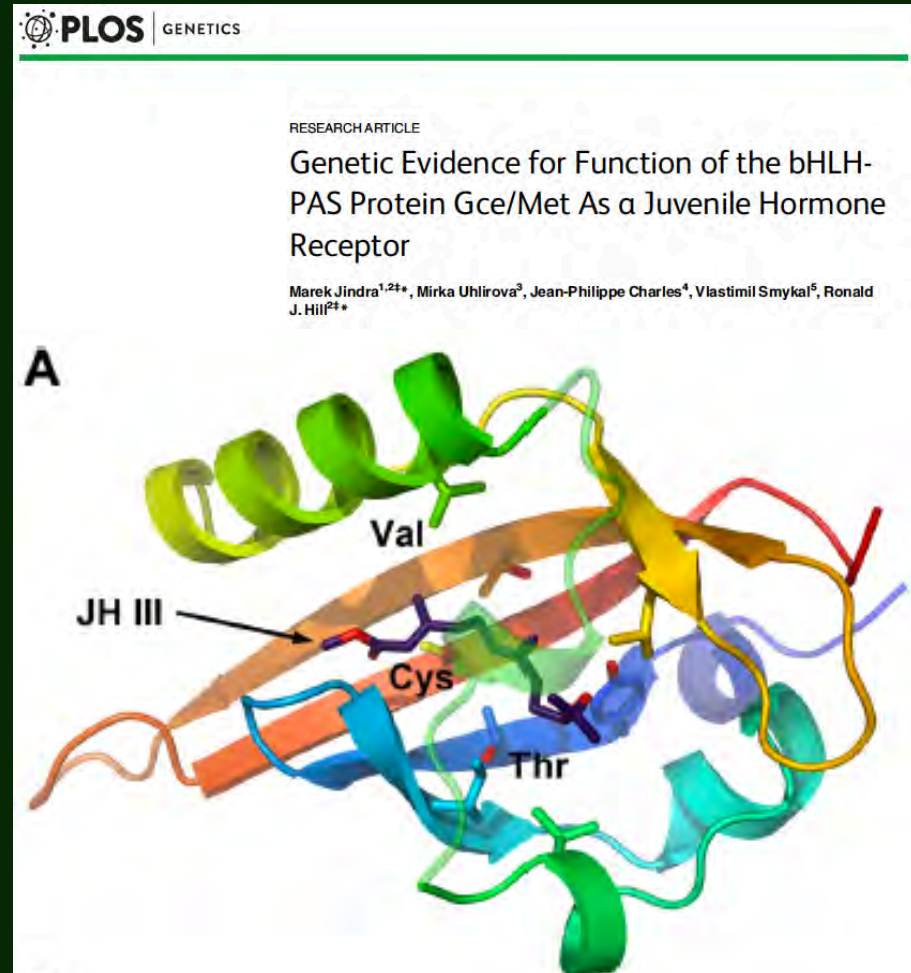
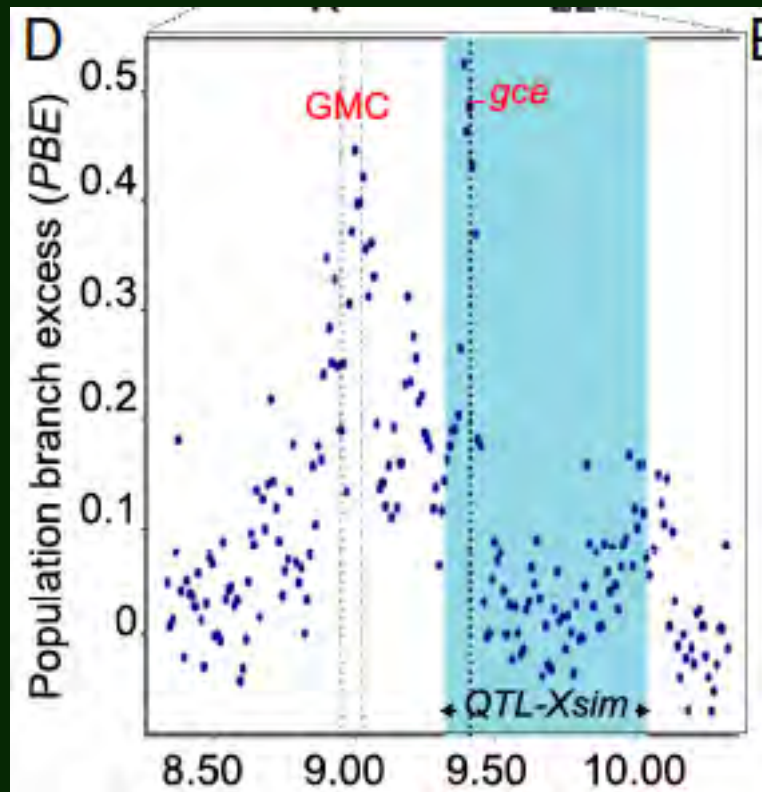
Grey areas = low recombining regions (telomeres, centromeres)

GMC = glucose-methanol-choline oxidoreductases, *gce* = *germ cell elongation*, SER = serine endopeptidases, GSTE = Glutathamine S transferases, OSI = Osiris, TWDL = *Tweedle*

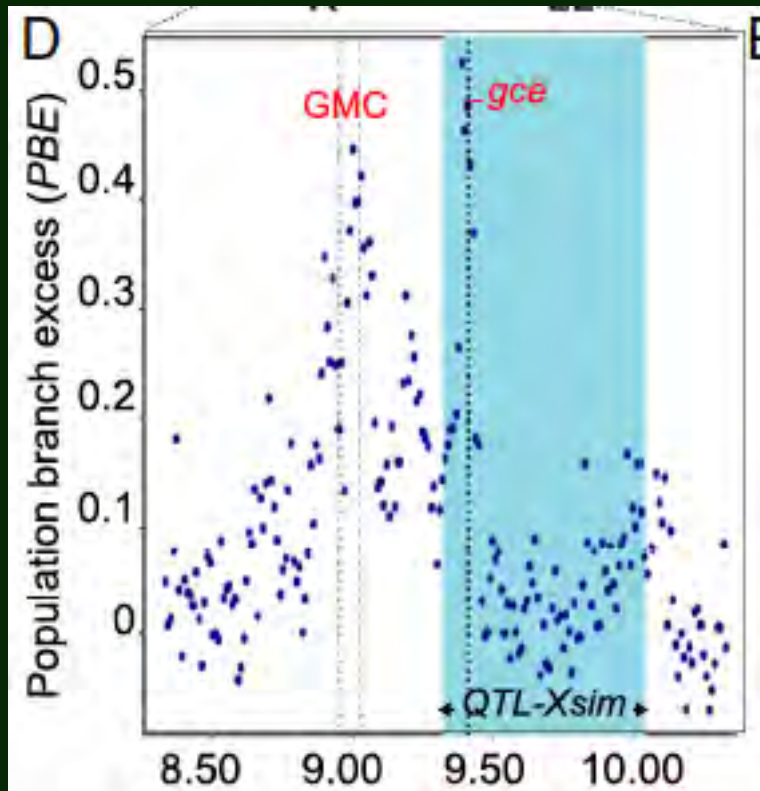
Candidate region 1: *gce*



Candidate region 1: *gce*



Candidate region 2: GMC, *Flo2*



BMC Evolutionary Biology

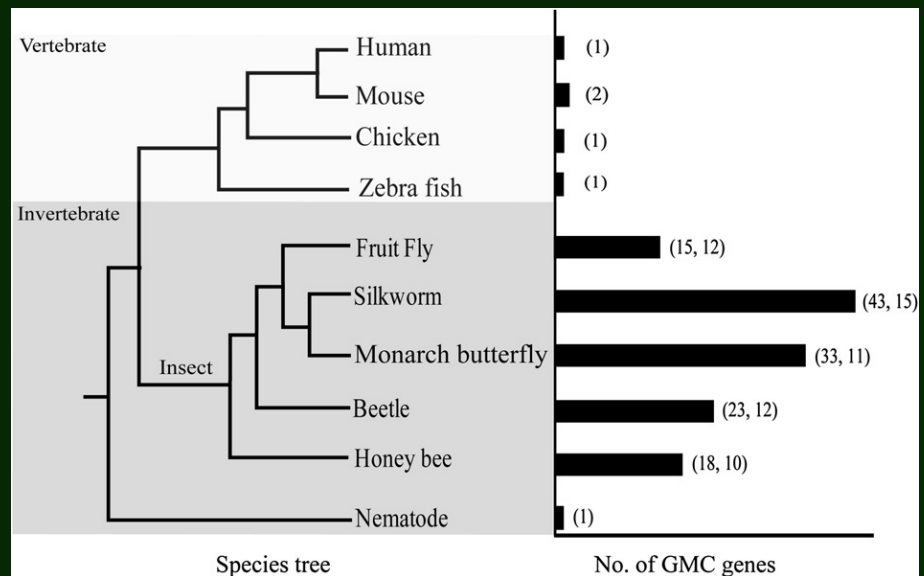
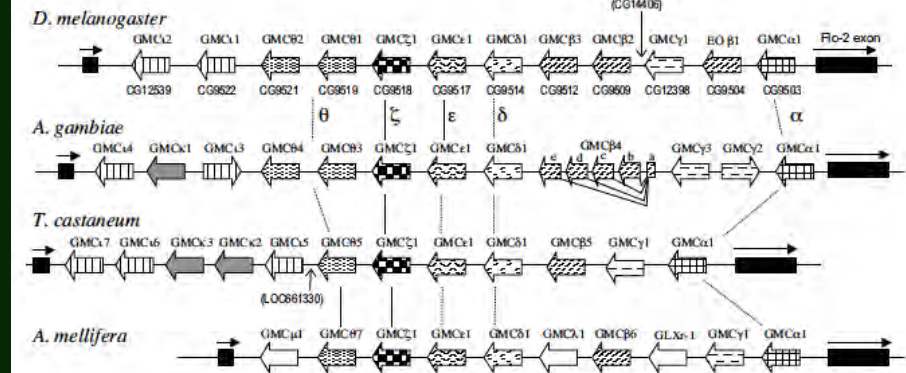


Research article

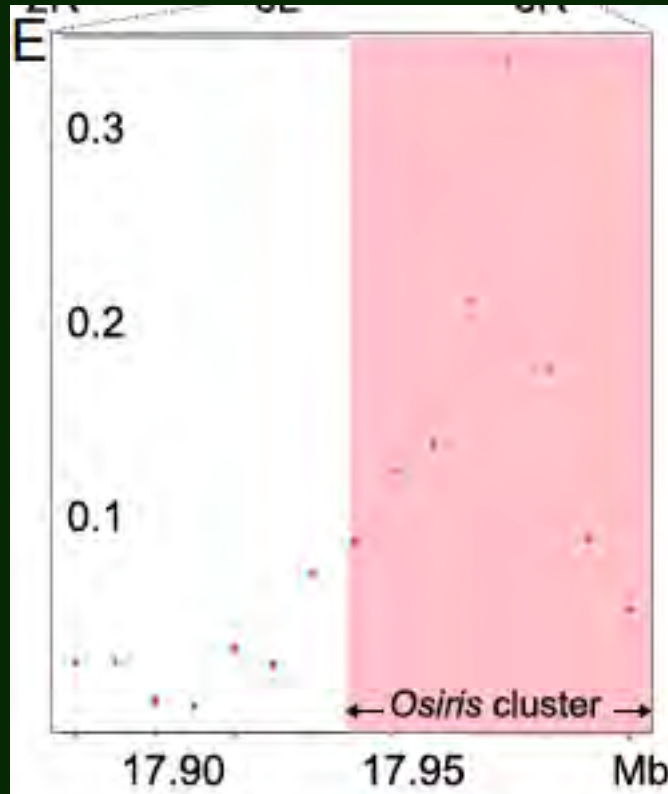
Open Access

Expansion and evolution of insect GMC oxidoreductases

Kaori Iida¹, Diana L Cox-Foster², Xiaolong Yang², Wen-Ya Ko and Douglas R Cavener*¹



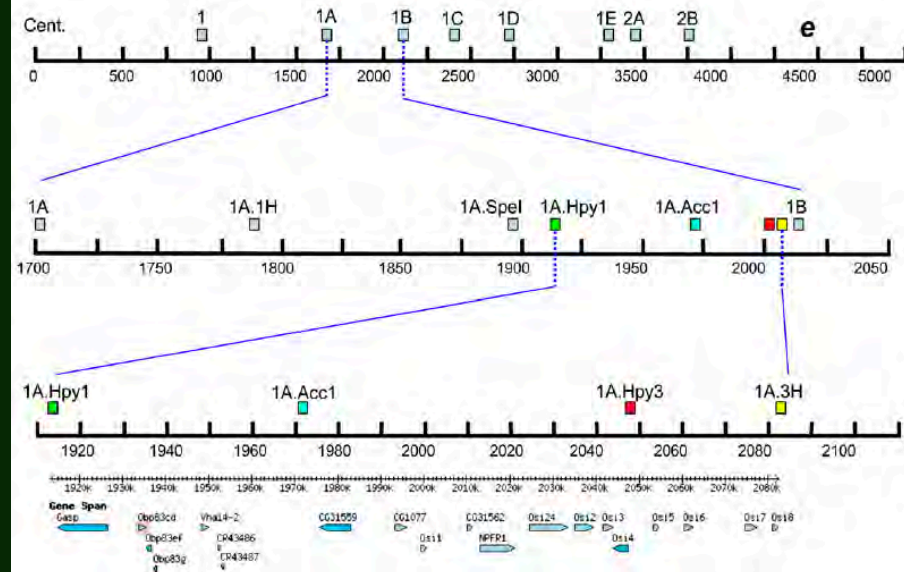
Candidate region 3: *Osiris*



A Locus in *Drosophila sechellia* Affecting Tolerance of a Host Plant Toxin

Eric A. Hungate,* Eric J. Earley,† Ian A. Boussy,‡ David A. Turissini,* Chau-Ti Ting,§ Jennifer R. Moran,* Mao-Lien Wu,* Chung-I Wu,* and Corbin D. Jones*¹

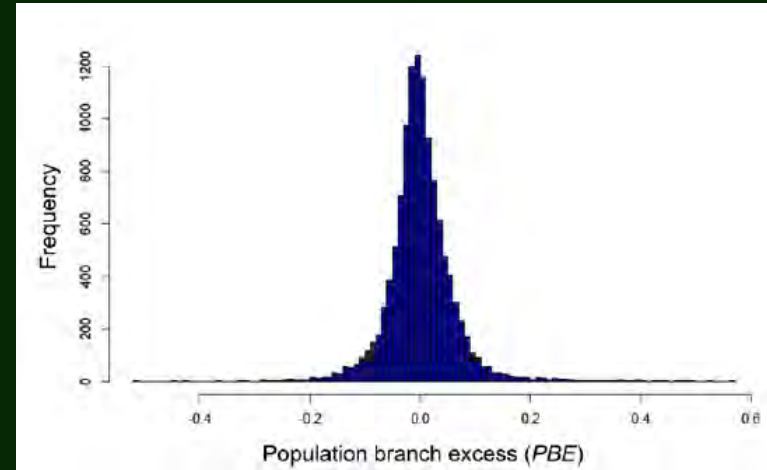
*Department of Ecology and Evolution, University of Chicago, Chicago, Illinois 60637, †Department of Biology, University of North Carolina, Chapel Hill, North Carolina 27599, ‡Department of Biology, Loyola University, Chicago, Illinois 60660, and § Department of Life Science, National Taiwan University, Taipei, 10617 Taiwan



Tolerance region harbors several candidate loci

Of the 18 genes in this region, two gene families represented two-thirds of the total and only three remain unnamed. A cluster of nine *Osiris* genes was present, along with three *Obps*. None of these 18 genes, however, showed a strong signature of positive selection that may be expected for a gene contributing to *D. sechellia* adaptation to its host.

Genomic parallelism with *D. sechellia*



- Larval tolerance to octanoic acid (Huang & Erezyilmaz 2015 *G3*)
 - 4 of 9 QTLs ($P = 0.013$)
- Adult tolerance to octanoic acid (Hungate et al. 2013 *Genetics*)
 - 1 of 1 QTL ($P = 0.008$)
- Adult attraction to noni volatiles (Earley & Jones 2011 *Genetics*, C. B. Jones, pers.)
 - 3 of 13 QTLs ($P = 0.200$)

Conclusions: an 'ecological speciation continuum'

- Specialization on noni occurred twice on independent islands:
 - *D. sechellia*, 250000 ya, large QTLs (~2 Mb), pre- and post-zygotic isolation
 - *D. yakuba*, 29000 ya, small windows (~20 kb), pre-zygotic isolation
- Similar detoxification genes strongly selected for
- Different genes or weak selection on preference genes
- Similar pathways may involved other *Drosophila* and herbivorous species

Acknowledgements

Jean R. David
(CNRS, Gif-sur-Yvette)

John E. Pool
Héloïse Bastide
(University of Wisconsin-Madison, Madison)

Vincent Debat
Nelly Gidaszewski
(MNHN, Paris)

