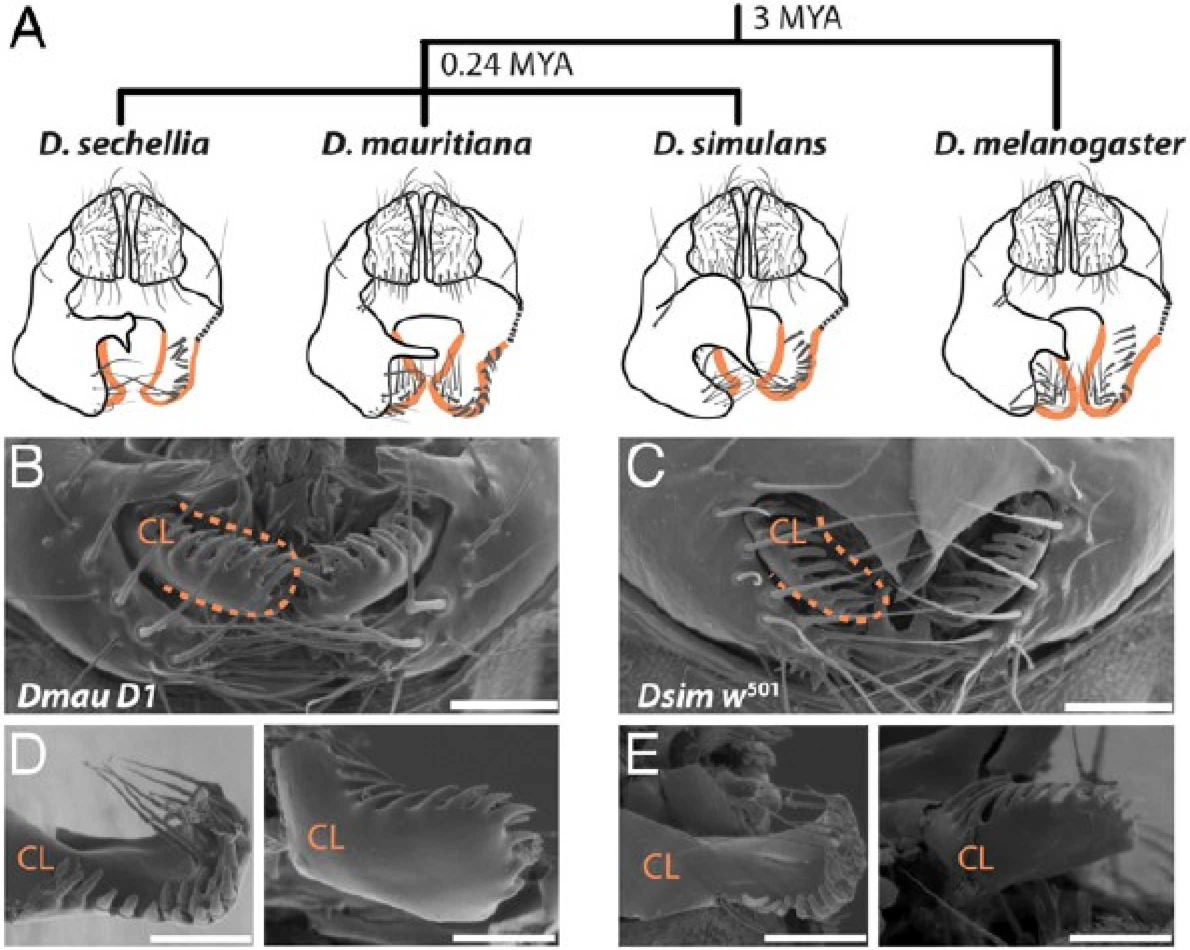
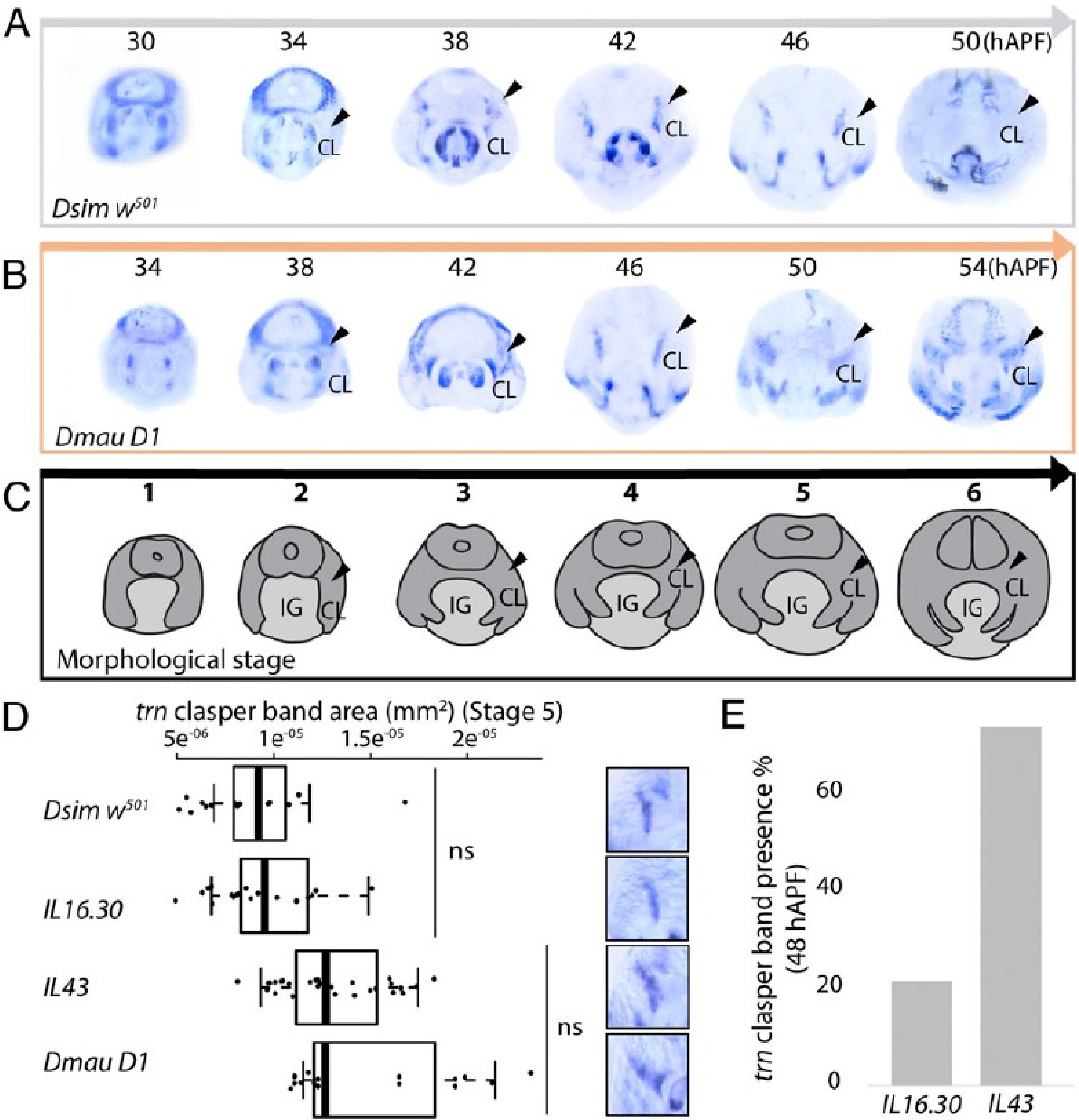
Press Report
September 2019
Virginie

tartan underlies the evolution of *Drosophila* male genital morphology

Joanna F. D. Hagen[a], Cláudia C. Mendes[a,1], Amber Blogg[a], Alexander Payne[a,2], Kentaro M. Tanaka[a,3], Pedro Gaspar[a], Javier Figueras Jimenez[a], Maike Kittelmann[a], Alistair P. McGregor[a,b,4], and Maria D. S. Nunes[a,b,4]

insects. Here, we show that divergence in clasper size and bristle number between *Drosophila mauritiana* and *Drosophila simulans* is caused by evolutionary changes in *tartan* (*trn*), which encodes a transmembrane leucine-rich repeat domain protein that mediates cell–cell interactions and affinity. There are no fixed amino acid differences in *trn* between *D. mauritiana* and *D. simulans*, but differences in the expression of this gene in developing genitalia suggest that cis-regulatory changes in *trn* underlie the evolution of clasper morphology in these species. Finally, analyses of reciprocal hemizygotes that are genetically identical, except for the species from which the functional allele of *trn* originates, determined that the *trn* allele of *D. mauritiana* specifies larger claspers with more bristles than the allele of *D. simulans*. Therefore, we have identified a gene underlying evolutionary change in the size of a male genital organ, which will help to better understand not only the rapid diversification of these structures, but also the regulation and evolution of organ size more broadly.

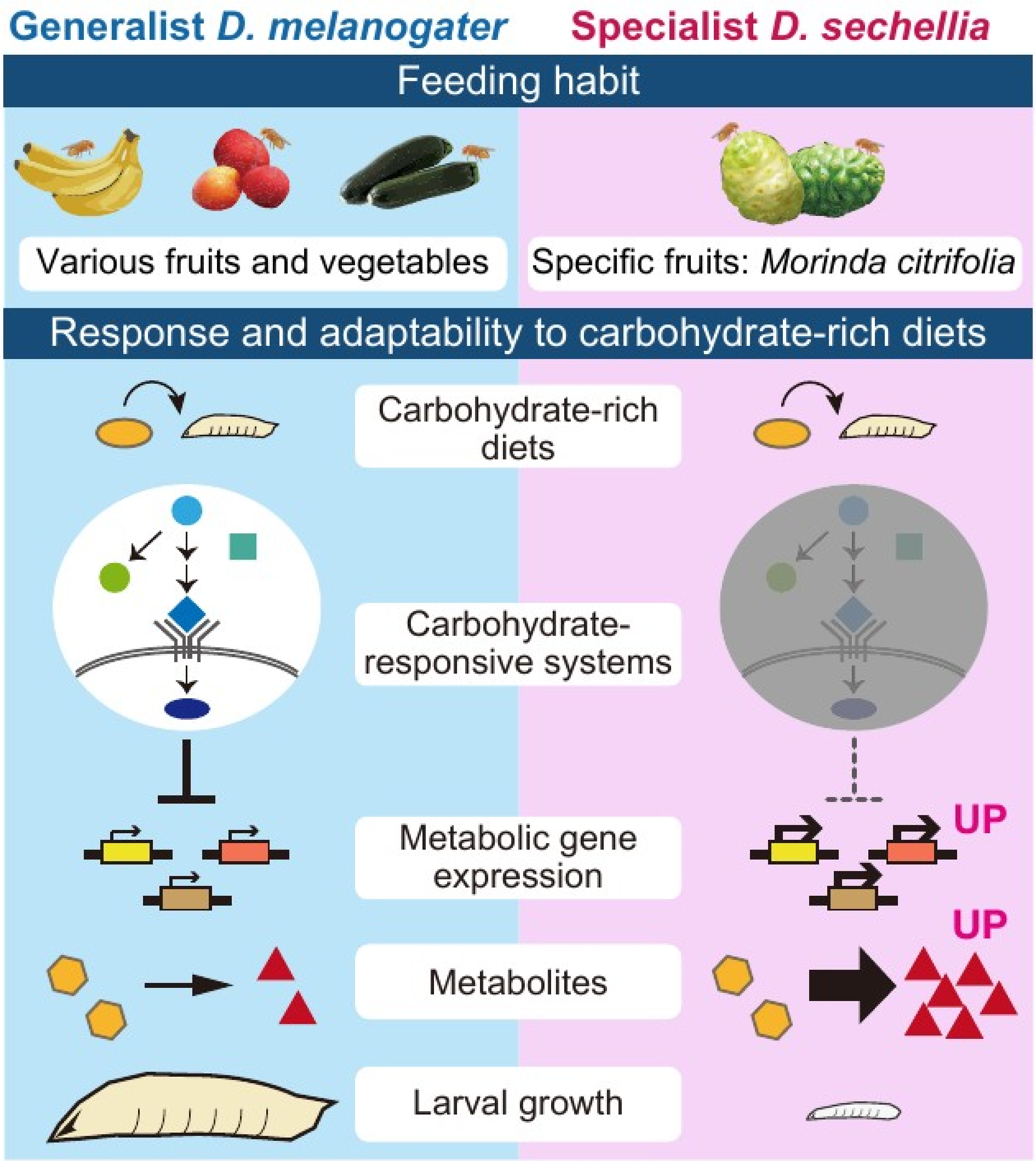

A
3 MYA
0.24 MYA
D. sechellia
D. mauritiana
D. simulans
D. melanogaster
B
CL
Dmau D1
C
CL
Dsim w501
D
CL
CL
E
CL
CL

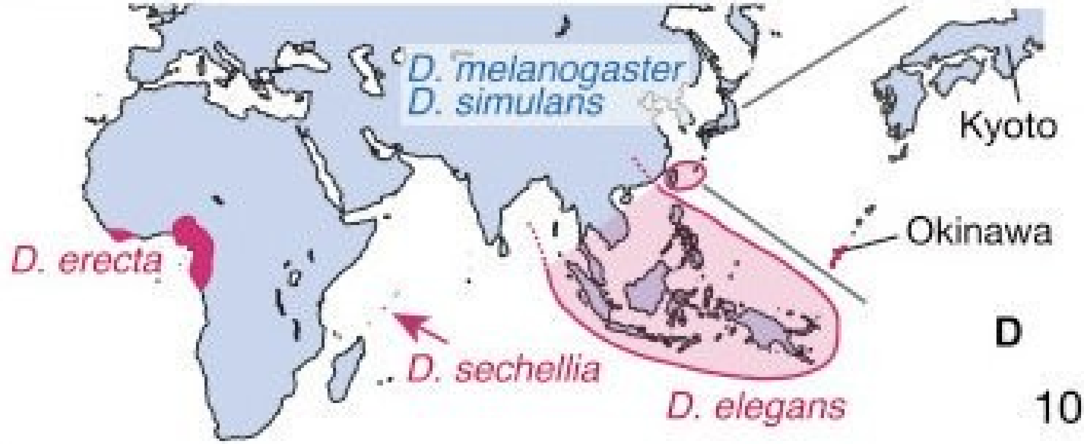

A
30
34
38
42
46
50(hAPF)
CL
Dsim w501
B
34
38
42
46
50
54(hAPF)
CL
Dmau D1
C
1
2
3
4
5
6
IG
CL
Morphological stage
D
trn clasper band area (mm²) (Stage 5)
5e-06
1e-05
1.5e-05
2e-05
Dsim w501
IL16.30
IL43
Dmau D1
ns
ns
E
trn clasper band presence % (48 hAPF)
0
20
40
60
IL16.30
IL43

Carbohydrate-Responsive Systems among Drosophila Species

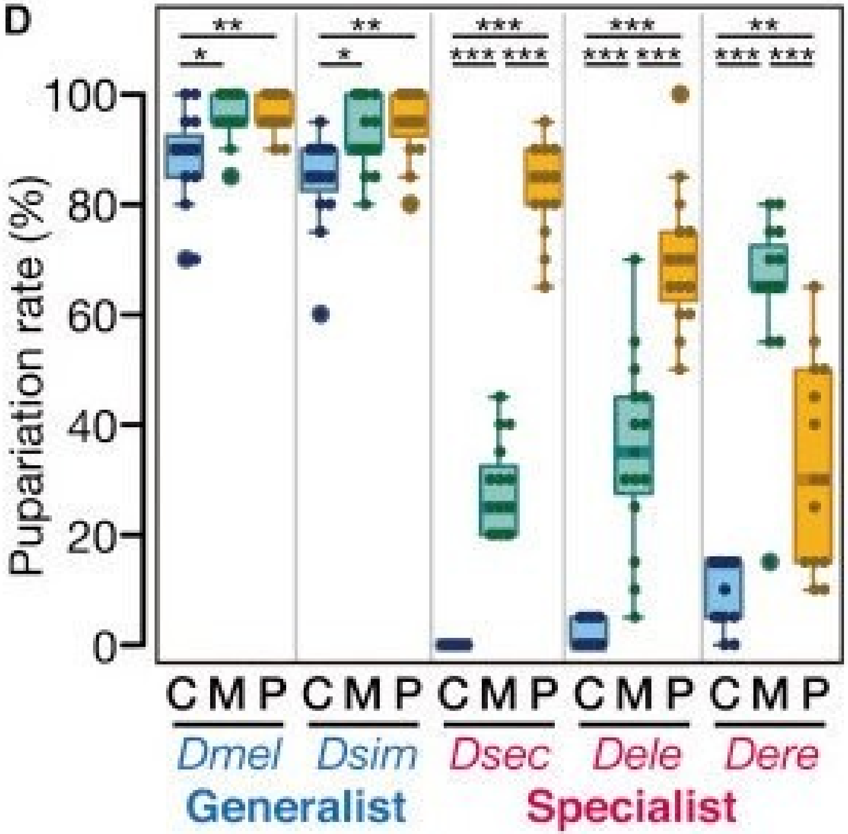
Cell Reports

Watanabe et al. uncover robust carbohydrate-responsive regulatory systems, including TGF-β/Activin signaling, which allow larvae of a generalist *Drosophila melanogaster* to adapt to various nutrient balances. In contrast, a specialist *D. sechellia* is defective in the systems and no longer maintains metabolic homeostasis, culminating in reduced adaptation to carbohydrate-rich diets.





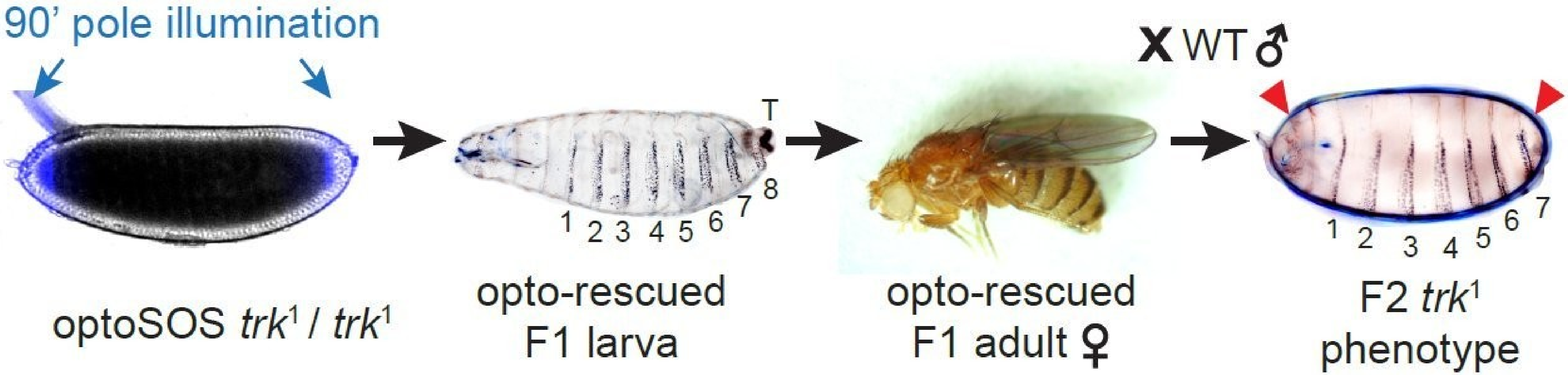
C diet: high carbohydrates
M diet: medium
P diet: high protein



Optogenetic rescue of a developmental patterning mutant

Heath E. Johnson, Stanislav Y. Shvartsman, Jared E. Toettcher

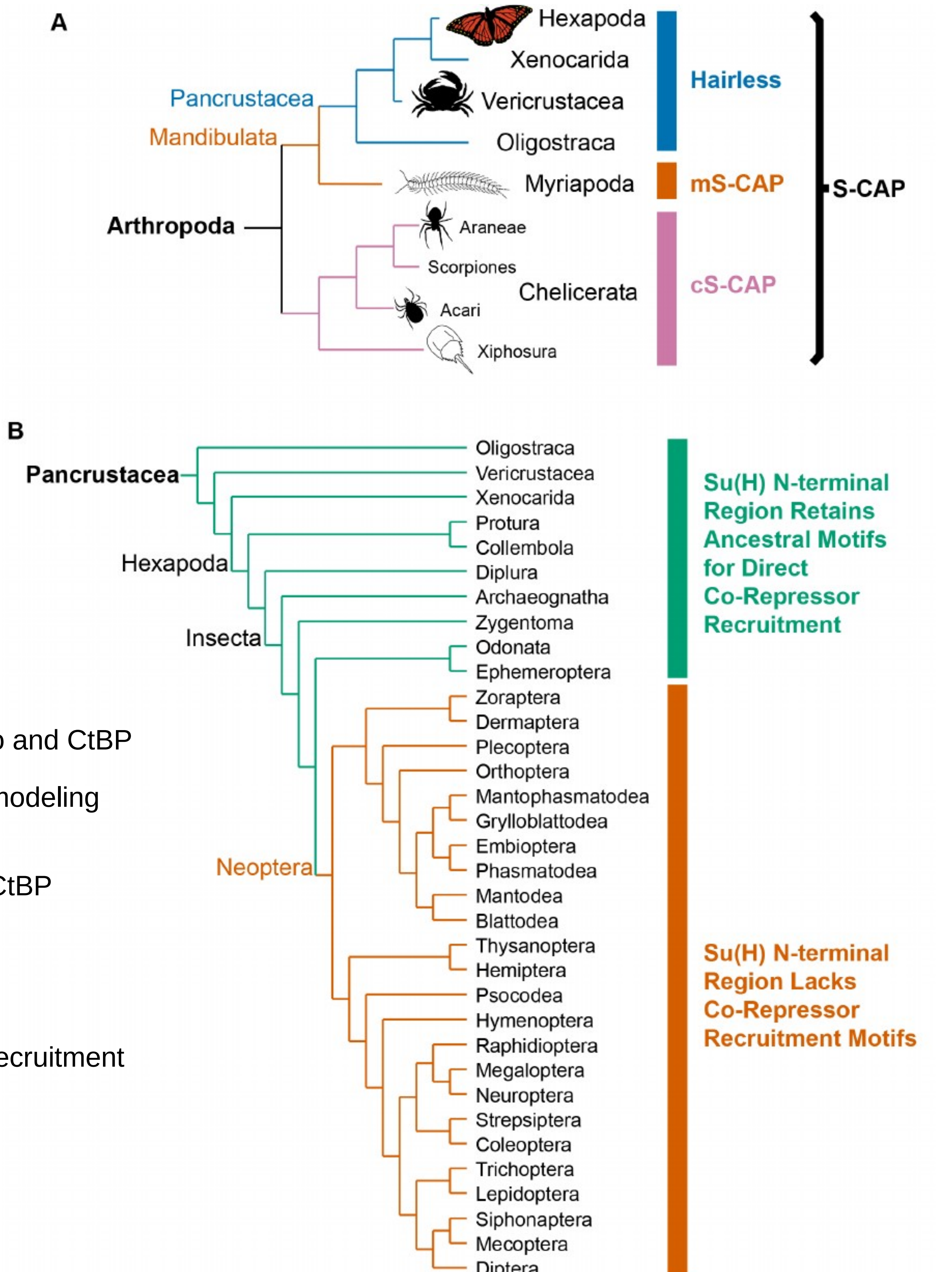
BioRxiv



Evolutionary emergence of Hairless as a novel component of the Notch signaling pathway

Steven W Miller, Artem Movsesyan, Sui Zhang, Rosa Fernández, James W Posakony

BioRxiv



Molluscs, Annelids, Myriapods: Su(H) directly recruits Gro and CtBP

Crustaceans, Hexapoda: duplication of a nucleosome remodeling gene

-> Hairless which can bind to Su(H) and recruit Gro and CtBP

-> loss of the Gro- and CtBP recruitment motifs in Su(H)

Crabs and even some insects (dragonflies) retain direct recruitment AND have Hairless. Transitional intermediates

Population genomics on the fly: recent advances in *Drosophila*

BioRxiv – book chapter

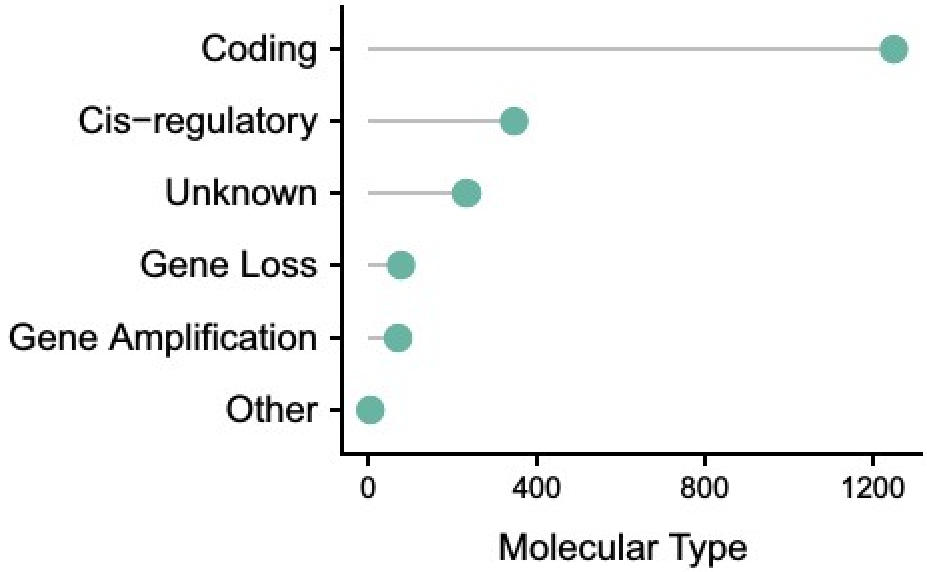
Annabelle Haudry[1]*, Stefan Laurent[2], Martin Kapun[3]

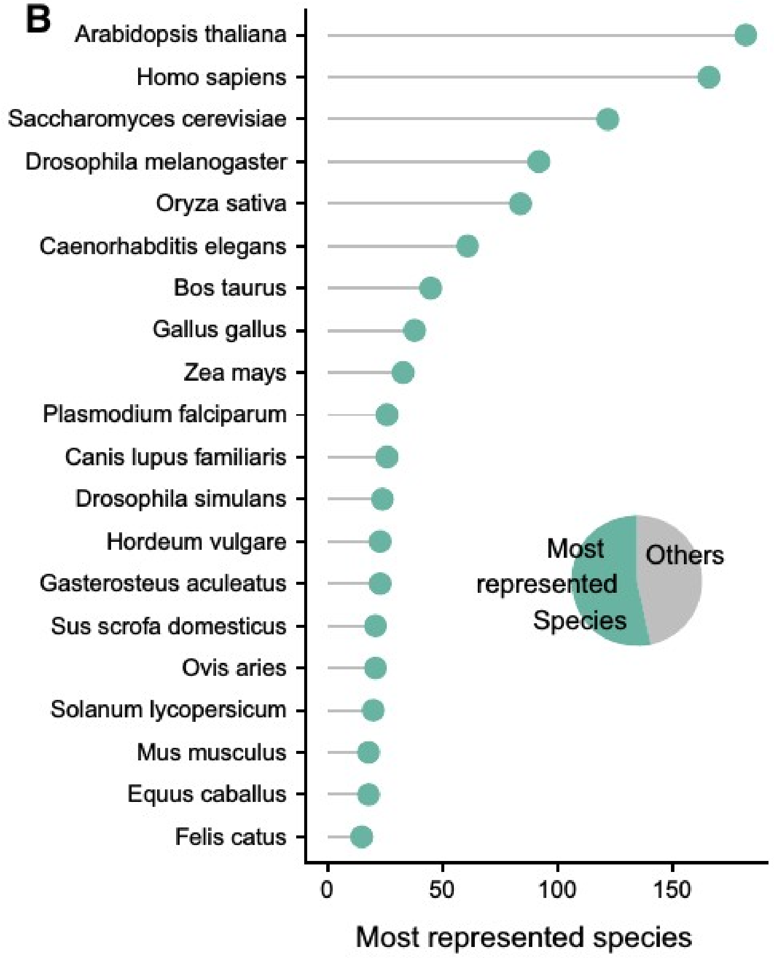
advances during the genomic era. After describing different types and sources of genomic data, we discuss mechanisms of neutral evolution including the demographic history of *Drosophila* and the effects of recombination and biased gene conversion. Then, we review recent advances in detecting genome-wide signals of selection, such as soft and hard selective sweeps. We further provide a brief introduction to background selection, selection of non-coding DNA and codon usage and focus on the role of structural variants, such as transposable elements and chromosomal inversions, during the adaptive process. Finally, we discuss how genomic data helps to dissect neutral and adaptive evolutionary mechanisms that shape genetic and phenotypic variation in natural populations along environmental gradients. In summary, this book chapter serves as a starting point to *Drosophila* population genomics and provides an introduction to the system and an overview to data sources, important population genetic concepts and recent advances in the field.

Nucleic Acids Research, 2019 **1**
doi: 10.1093/nar/gkz796

Gephebase, a database of genotype–phenotype relationships for natural and domesticated variation in Eukaryotes

Virginie Courtier-Orgogozo[1,*], Laurent Arnoult[1], Stéphane R. Prigent[1], Séverine Wiltgen[2] and Arnaud Martin[3,*]





Experimental Evidence

3 categories, each with biases

	Candidate Gene	Linkage Mapping	Association Mapping
Experimental Principle	**Reverse Genetics**: looking for sequence differences and trait effects based on previous studies of a given gene	**Forward Genetics**: trait mapping in hybrids obtained from laboratory crosses, using recombination over a few generations	**Forward Genetics**: statistical SNP/character state association in large cohorts, using recombination over many generations
Example	66 cases of color variation associated to *MC1R* coding mutations in vertebrates	F2 crosses between melanic and amelanic phenotypes in cavefish : identification of *MC1R* and *Oca2* alleles in distinct cave populations	GWAS of human pigmentation (skin, hair, eyes): identification and confirmation of causal variants at >15 genes including *Oca2* p.His615Arg in Eastern Asia
Ascertainment Bias on Locus Identification	**High**	**Low to Intermediate** (depending on resolution / cross size)	**Low**
Molecular Type Bias	Favors identification of **coding mutations**	Little molecular bias	Can miss structural variants (short read genotyping)
Trait Type Bias	Favors traits with small molecular targets, large-effect size	Amenable to dissection of complex traits with small-effect size (large crosses, multiparental families)	Most common approach for complex traits with small-effect size
Taxonomic Breadth	**Large**	**Narrow**, limited to interfertile lineages (populations or sister species)	**Very narrow**, limited to polymorphic or intermixing populations

Evaluating the Probability of CRISPR-based Gene Drive Contaminating Another Species

Virginie Courtier-Orgogozo[1], Antoine Danchin[2], Pierre-Henri Gouyon[3] and Christophe Boëte[4]

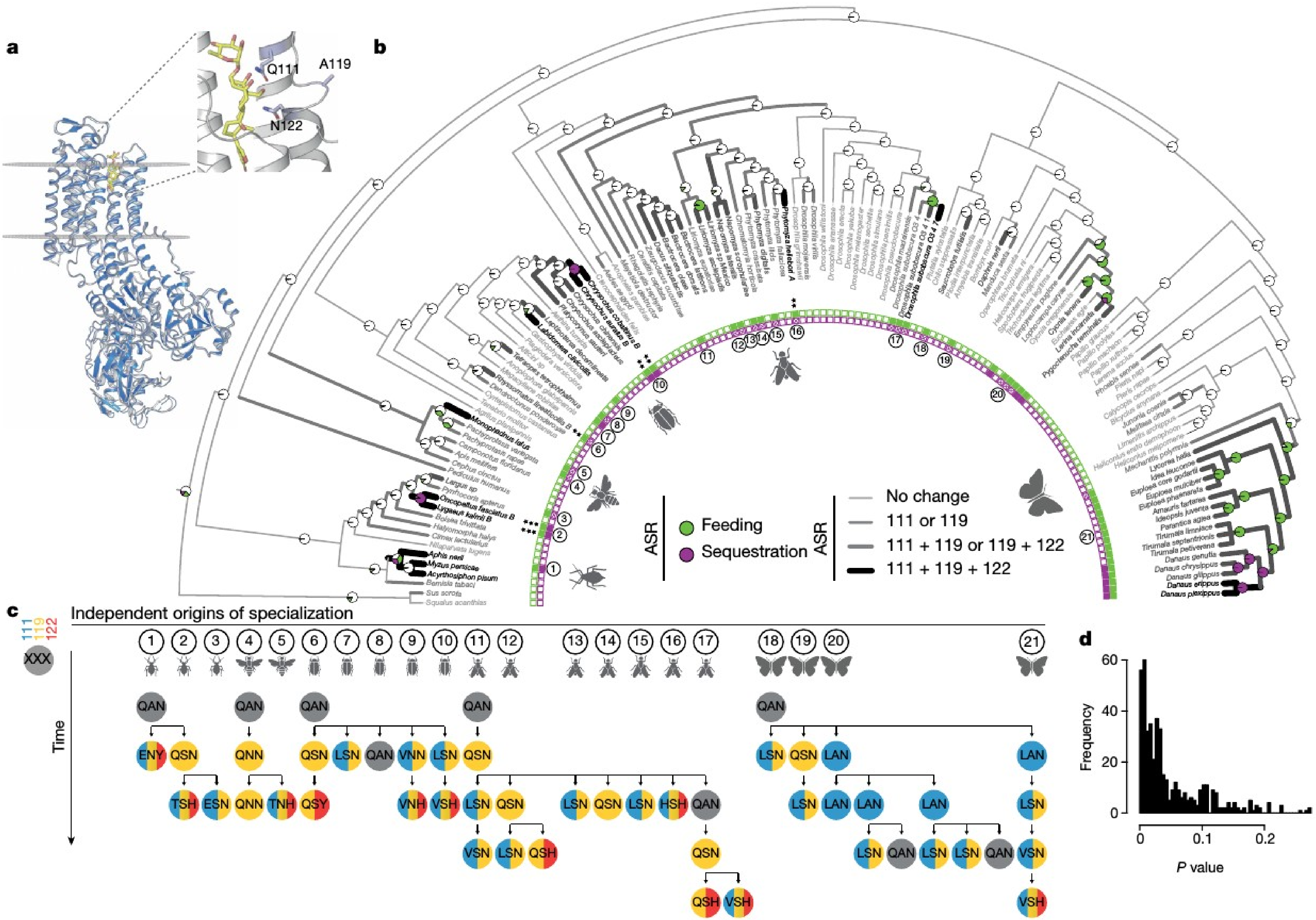
BioRxiv

Adaptive substitutions underlying cardiac glycoside insensitivity in insects exhibit epistasis in vivo

Andrew M Taverner[1], Lu Yang[2], Zachary J Barile[3,4], Becky Lin[3,4], Julie Peng[1], Ana P Pinharanda[5], Arya S Rao[5], Bartholomew P Roland[3,4], Aaron D Talsma[3,4], Daniel Wei[3,4], Georg Petschenka[6], Michael J Palladino[3,4]*, Peter Andolfatto[5]*

Genome editing retraces the evolution of toxin resistance in the monarch butterfly

Marianthi Karageorgi[1,8], Simon C. Groen[1,2,8], Fidan Sumbul[3], Julianne N. Pelaez[1], Kirsten I. Verster[1], Jessica M. Aguilar[1], Amy P. Hastings[4], Susan L. Bernstein[1], Teruyuki Matsunaga[1], Michael Astourian[1], Geno Guerra[5], Felix Rico[3], Susanne Dobler[6], Anurag A. Agrawal[4,7] & Noah K. Whiteman[1]*


a
Q111
A119
N122
b
ASR
Feeding
Sequestration
ASR
No change
111 or 119
111 + 119 or 119 + 122
111 + 119 + 122
Sus scrofa
Squalus acanthias
Bemisia tabaci
Acyrthosiphon pisum
Myzus persicae
Aphis nerii
Nilaparvata lugens
Cimex lectularius
Halyomorpha halys
Boisea trivittata
Lygaeus kalmii B
Oncopeltus fasciatus B
Pyrrhocoris apterus
Largus sp
Pediculus humanus
Cephus cinctus
Apis mellifera
Camponotus floridanus
Pachyprotasis rapae
Pachyprotasis variegata
Monophadnus latus
Agrilus planipennis
Tenebrio molitor
Cyrtepistomus castaneus
Dendroctonus ponderosae
Rhyssomatus lineaticollis B
Megacyllene robiniae
Anoplophora glabripennis
Tetraopes tetrophthalmus
Altica sp
Plagiodera versicolora
Gastrophysa viridula
Leptinotarsa decemlineata
Labidomera clivicollis
Aethina tumida
Platycorynus peregrinus
Chrysochus asclepiadeus
Chrysochus chinensis
Chrysochus auratus B
Chrysochus cobaltinus B
Ceratitis capitata
Bactrocera dorsalis
Bactrocera oleae
Zeugodacus cucurbitae
Dacus ciliatus
Liriomyza trifolii
Liriomyza sativae
Napomyza lateralis
Chromatomyia horticola
Phytomyza digitalis
Phytomyza ilicis
Phytomyza fallaciosa
Phytomyza hellebori A
Drosophila virilis
Drosophila mojavensis
Drosophila grimshawi
Drosophila willistoni
Drosophila pseudoobscura
Drosophila subobscura O3 4
Drosophila subobscura O3 4 7
Scaptomyza flava
Plutella xylostella
Chilo suppressalis
Bombyx mori
Daphnis nerii
Manduca sexta
Operophtera brumata
Trichoplusia ni
Helicoverpa armigera
Spodoptera frugiperda
Empyreuma pugione
Cycnia tenera
Euchaetes egle
Pygarctia roseicapitis
Lertha incarnata
Papilio glaucus
Papilio polytes
Papilio machaon
Papilio xuthus
Phoebis sennae
Pieris napi
Pieris rapae
Calycopis cecrops
Bicyclus anynana
Junonia coenia
Melitaea cinxia
Limenitis archippus
Heliconius erato demophoon
Heliconius melpomene
Mechanitis polymnia
Lycorea halia
Idea leuconoe
Euploea core godartii
Euploea mulciber
Euploea phaenareta
Amauris tartarea
Ideopsis juventa
Parantica aglea
Tirumala limniace
Tirumala septentrionis
Tirumala petiverana
Danaus genutia
Danaus chrysippus
Danaus gilippus
Danaus eresimus
Danaus plexippus
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21
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111
119
122
XXX
Time
Independent origins of specialization
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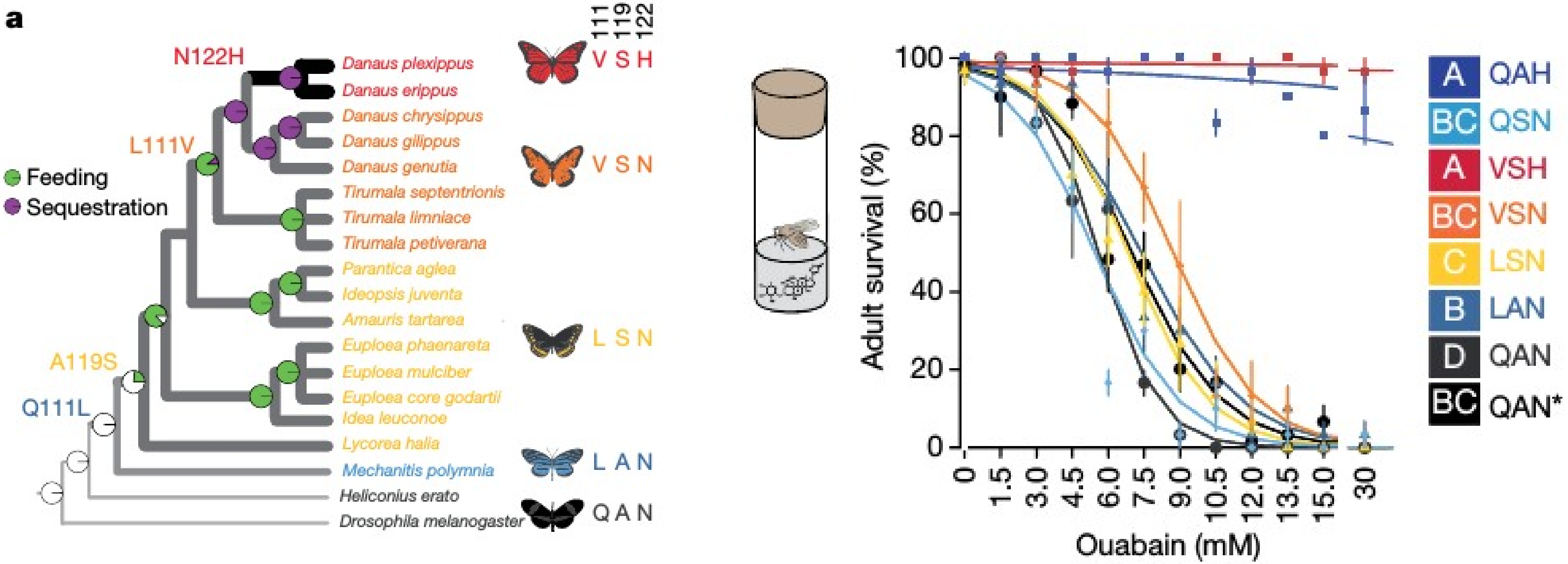
QAN
QAN
QAN
ENY
QSN
QNN
QSN
LSN
QAN
VNN
LSN
QSN
LSN
QSN
LAN
LAN
TSH
ESN
QNN
TNH
QSY
VNH
VSH
LSN
QSN
LSN
QSN
LSN
HSH
QAN
LSN
LAN
LAN
LAN
LSN
VSN
LSN
QSH
QSN
LSN
QAN
LSN
LSN
QAN
VSN
QSH
VSH
VSH
d
Frequency
0
20
40
60
0
0.1
0.2
P value


a
111
119
122
N122H
L111V
A119S
Q111L
Feeding
Sequestration
Danaus plexippus
Danaus erippus
Danaus chrysippus
Danaus gilippus
Danaus genutia
Tirumala septentrionis
Tirumala limniace
Tirumala petiverana
Parantica aglea
Ideopsis juventa
Amauris tartarea
Euploea phaenareta
Euploea mulciber
Euploea core godartii
Idea leuconoe
Lycorea halia
Mechanitis polymnia
Heliconius erato
Drosophila melanogaster
V S H
V S N
L S N
L A N
Q A N
Adult survival (%)
100
80
60
40
20
0
0
1.5
3.0
4.5
6.0
7.5
9.0
10.5
12.0
13.5
15.0
30
Ouabain (mM)
A QAH
BC QSN
A VSH
BC VSN
C LSN
B LAN
D QAN
BC QAN*

Cooption of the pteridine biosynthesis pathway underlies the diversification of embryonic colors in water striders

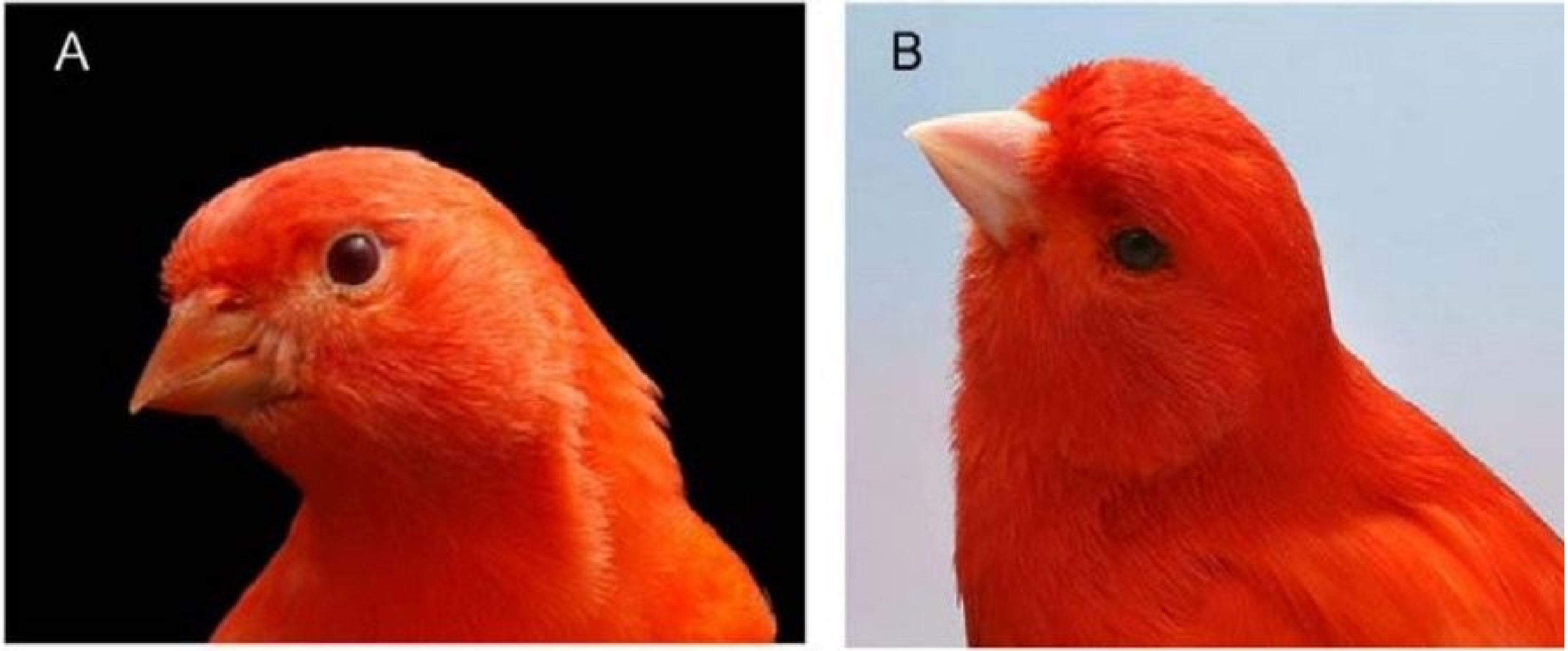
Aidamalia Vargas-Lowman, David Armisen, Carla Fernanda Burguez Floriano, Isabelle da Rocha Silva Cordeiro, Séverine Viala, Mathilde Bouchet, Marie Bernard, Augustin Le Bouquin, M. Emilia Santos, Alexandra Berlioz-Barbier, Arnaud Salvador, Felipe Ferraz Figueiredo Moreira, François Bonneton, and Abderrahman Khila

PNAS

Genetic Basis of De Novo Appearance of Carotenoid Ornamentation in Bare-Parts of Canaries

Małgorzata Anna Gazda, Matthew B. Toomey, Pedro M. Araújo, Ricardo J. Lopes, Sandra Afonso, Connie A. Myers, Kyla Serres, Philip D. Kiser, Geoffrey E. Hill, Jos

BioRxiv



The carotenoid gatekeeper (BCO2) gene is a great example for students:
1) repeated evolutionary changes in carotenoid content in 5 species, same gene

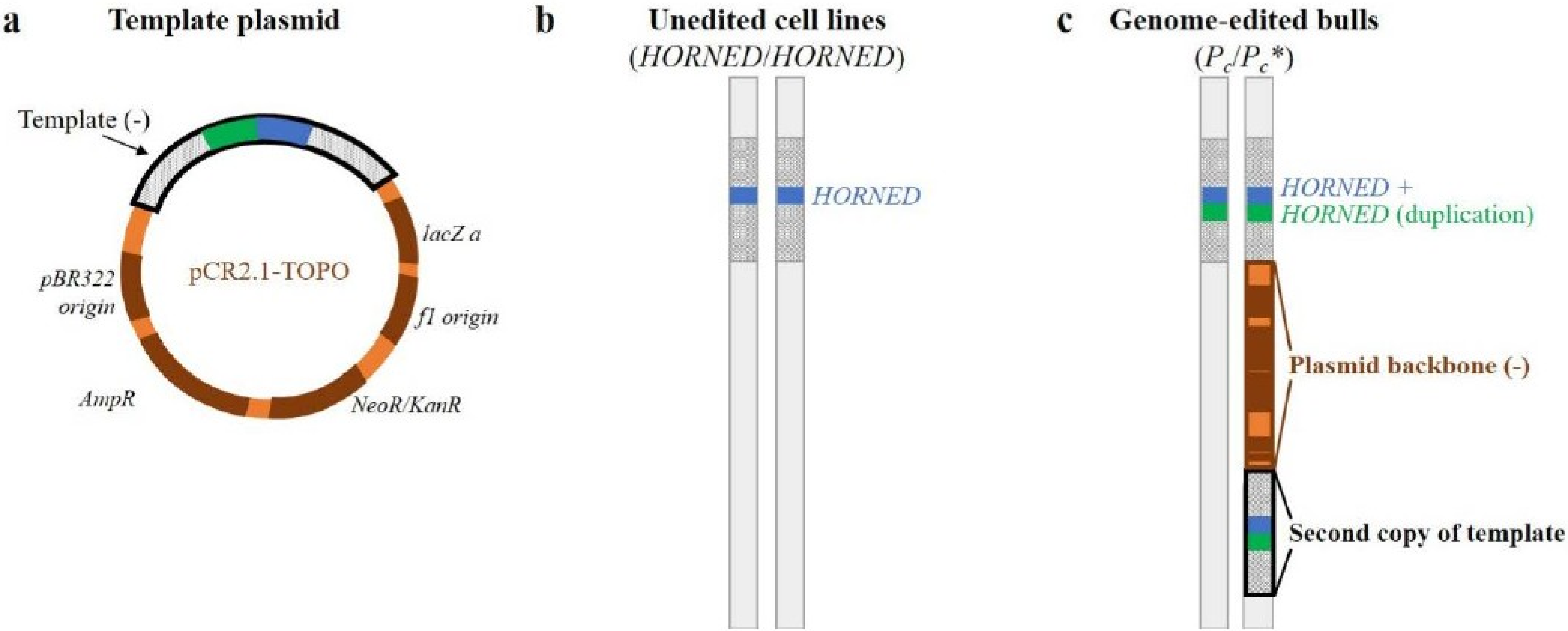
2) domesticated species (cattle, sheep, canari)=coding mutations whereas natural evolution (junglefowl, warbler)=cis-reg

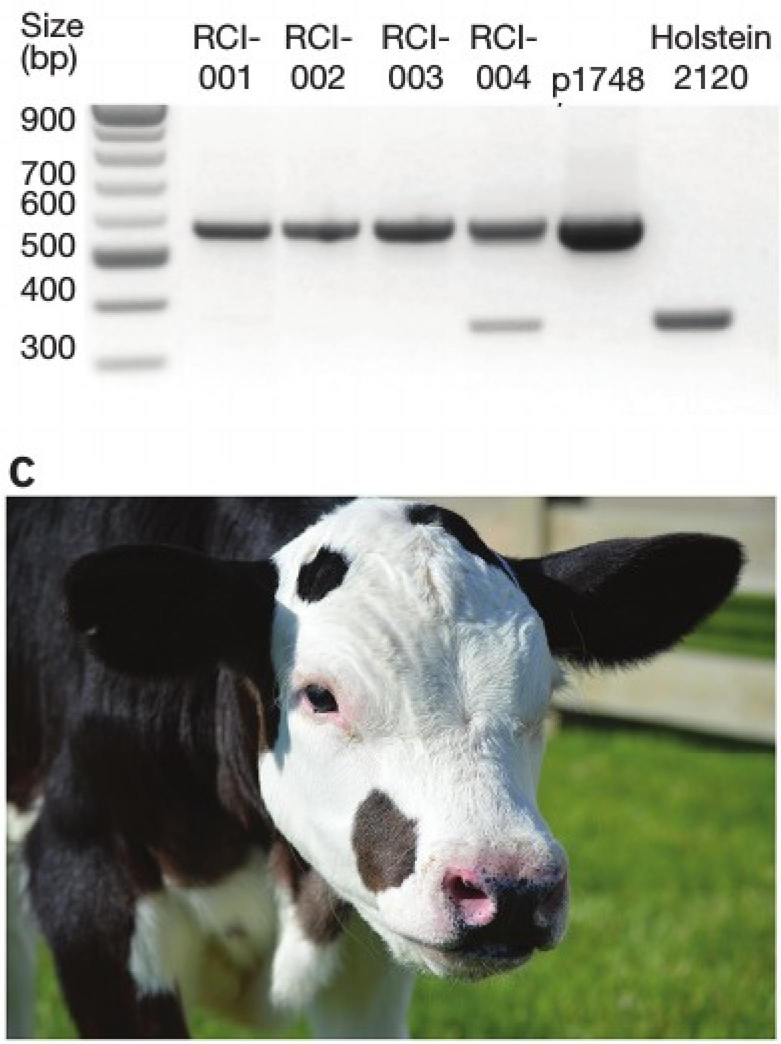
Template plasmid integration in germline genome-edited cattle.

Alexis L. Norris[1*], Stella S. Lee[1*], Kevin J. Greenlees[1], Daniel A. Tadesse[1], Mayumi F. Miller[1], Heather Lombardi[1†]

[1] Center for Veterinary Medicine, Food and Drug Administration, Rockville, MD 20855

BioRxiv



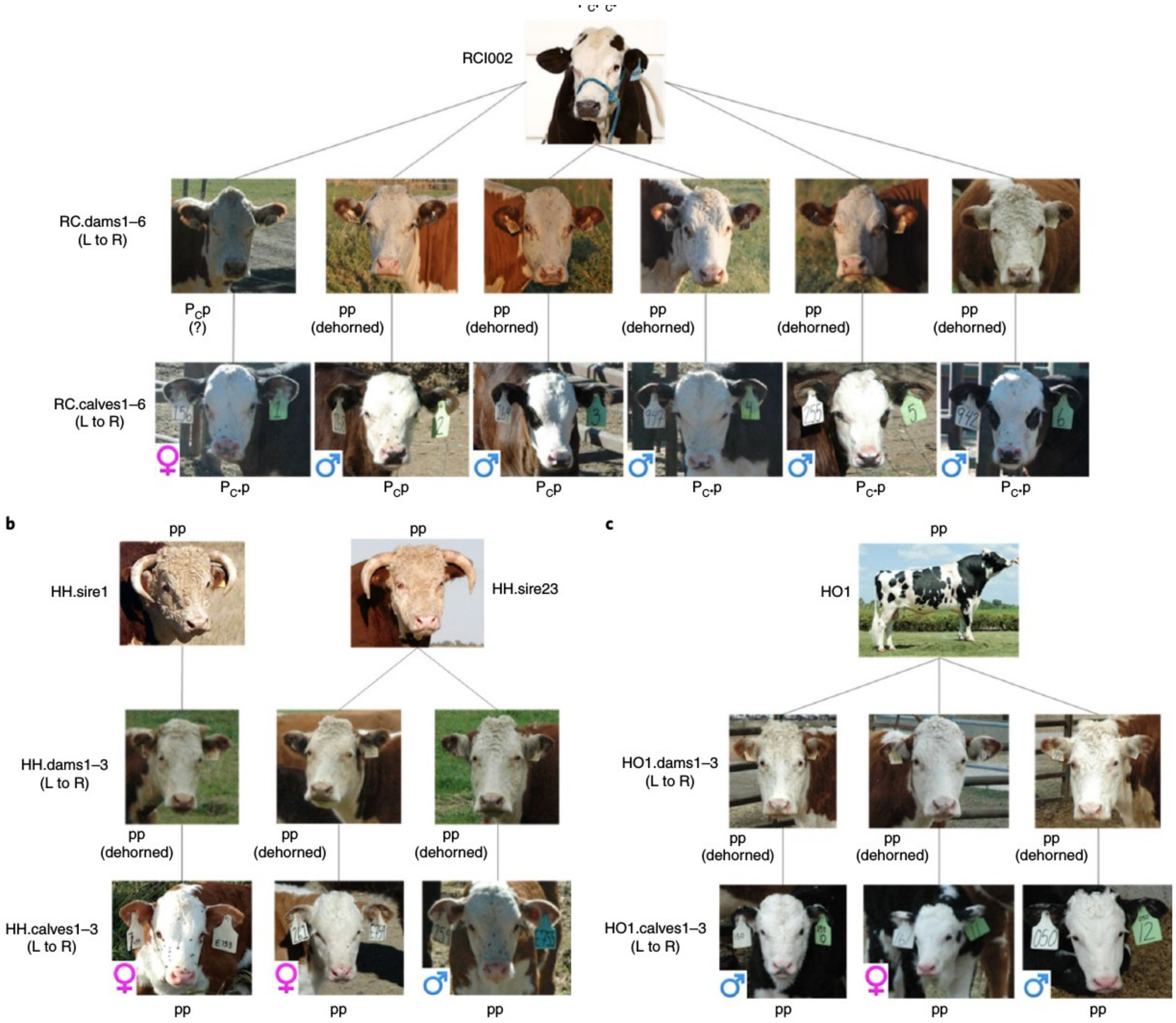


2016
Nature Biotechnologies

Production of hornless dairy cattle from genome-edited cell lines

Genomic and phenotypic analyses of six offspring of a genome-edited hornless bull

Amy E. Young[1], Tamer A. Mansour[2,3], Bret R. McNabb[3], Joseph R. Owen[1], Josephine F. Trott[1], C. Titus Brown[3] and Alison L. Van Eenennaam[1*]



SCIENTIFIC REPORTS
natureresearch

OPEN

Transgenic *Aedes aegypti* Mosquitoes Transfer Genes into a Natural Population

y 2019
2019
September 2019

Benjamin R. Evans[1], Panayiota Kotsakiozi[1], Andre Luis Costa-da-Silva[2,3], Rafaella Sayuri Ioshino[2,3], Luiza Garziera[3], Michele C. Pedrosa[2,3,4], Aldo Malavasi[4], Jair F. Virginio[4], Margareth L. Capurro[2,3] & Jeffrey R. Powell[1]

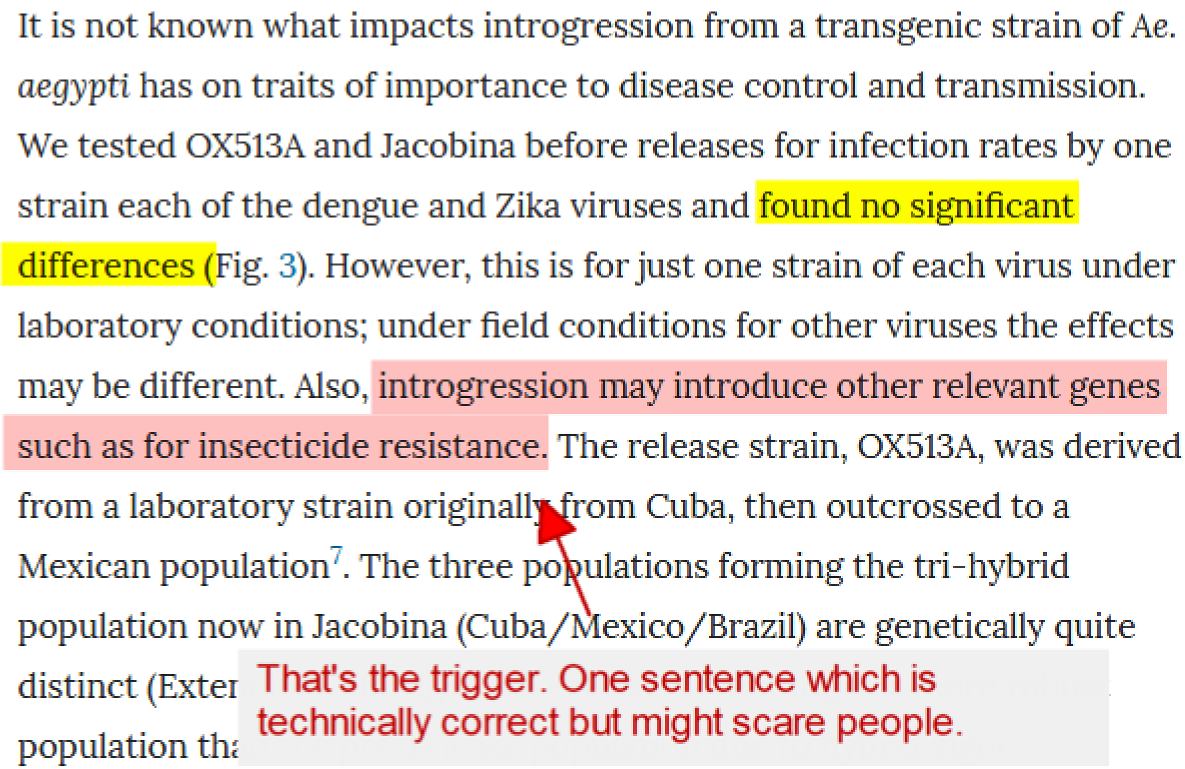
Genetically modified mosquitoes, such as these being released in Brazil, could combat infectious diseases. PAULO FRIEDMAN

Study on DNA spread by genetically modified mosquitoes prompts backlash

Science

By **Kelly Servick** | Sep. 17, 2019 , 4:50 PM

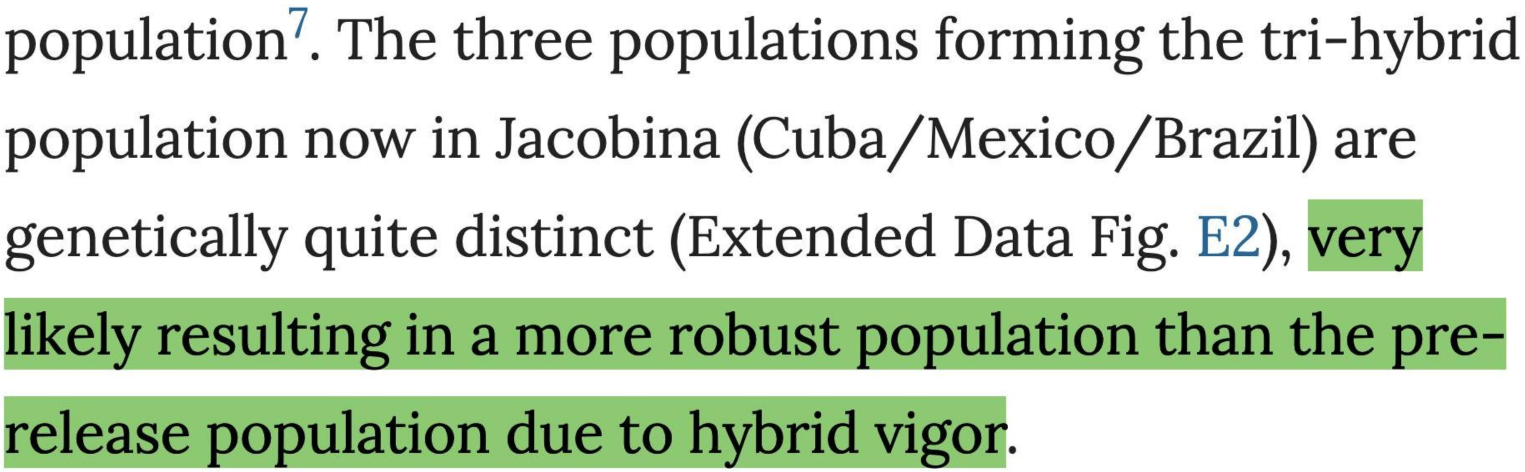
in nature. The release strain was developed using a strain originally from Cuba, then outcrossed to a Mexican population. Thus, Jacobina *Ae. aegypti* are now a mix of three populations. It is unclear how



It is not known what impacts introgression from a transgenic strain of *Ae. aegypti* has on traits of importance to disease control and transmission. We tested OX513A and Jacobina before releases for infection rates by one strain each of the dengue and Zika viruses and found no significant differences (Fig. 3). However, this is for just one strain of each virus under laboratory conditions; under field conditions for other viruses the effects may be different. Also, introgression may introduce other relevant genes such as for insecticide resistance. The release strain, OX513A, was derived from a laboratory strain originally from Cuba, then outcrossed to a Mexican population[7]. The three populations forming the tri-hybrid population now in Jacobina (Cuba/Mexico/Brazil) are genetically quite distinct (Exter

population tha

That's the trigger. One sentence which is technically correct but might scare people.



population[7]. The three populations forming the tri-hybrid population now in Jacobina (Cuba/Mexico/Brazil) are genetically quite distinct (Extended Data Fig. E2), very likely resulting in a more robust population than the pre-release population due to hybrid vigor.