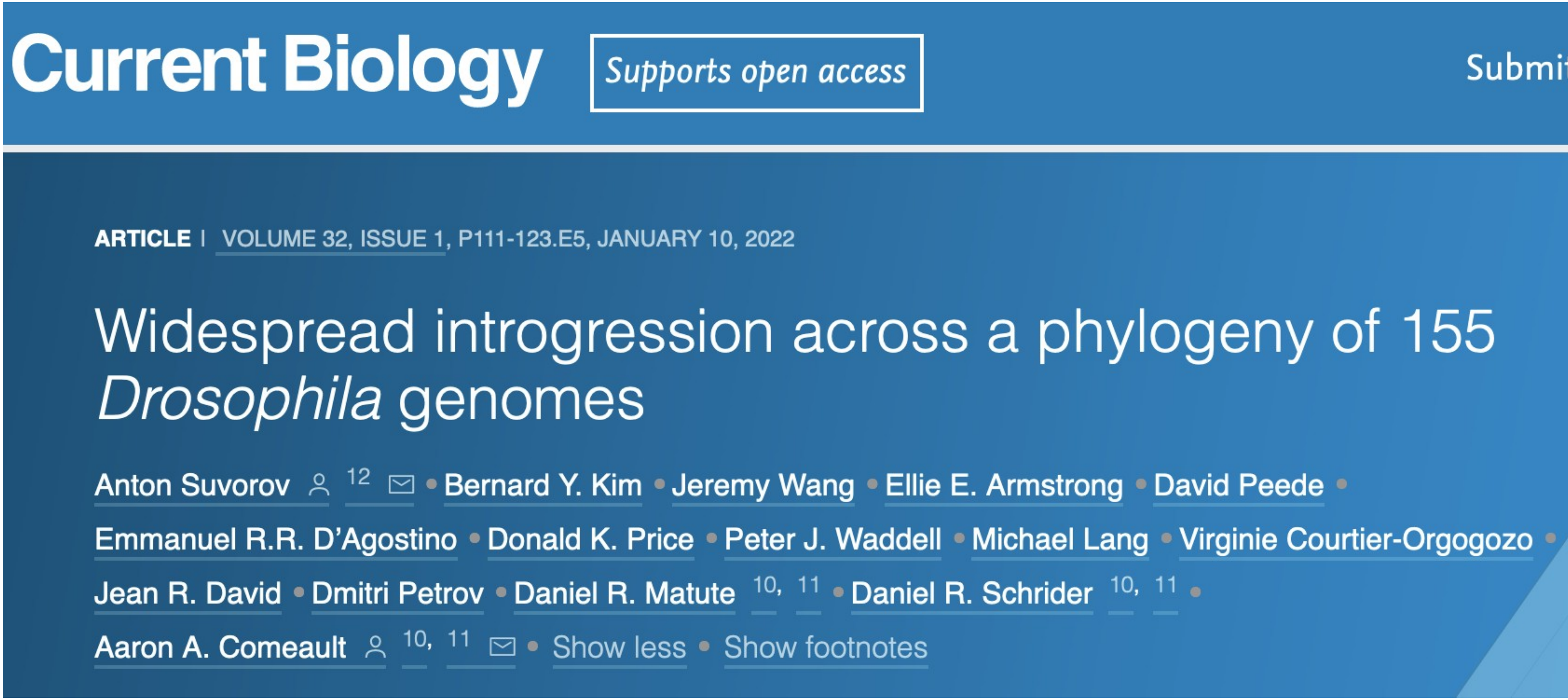
Press Report
November 2022
Virginie



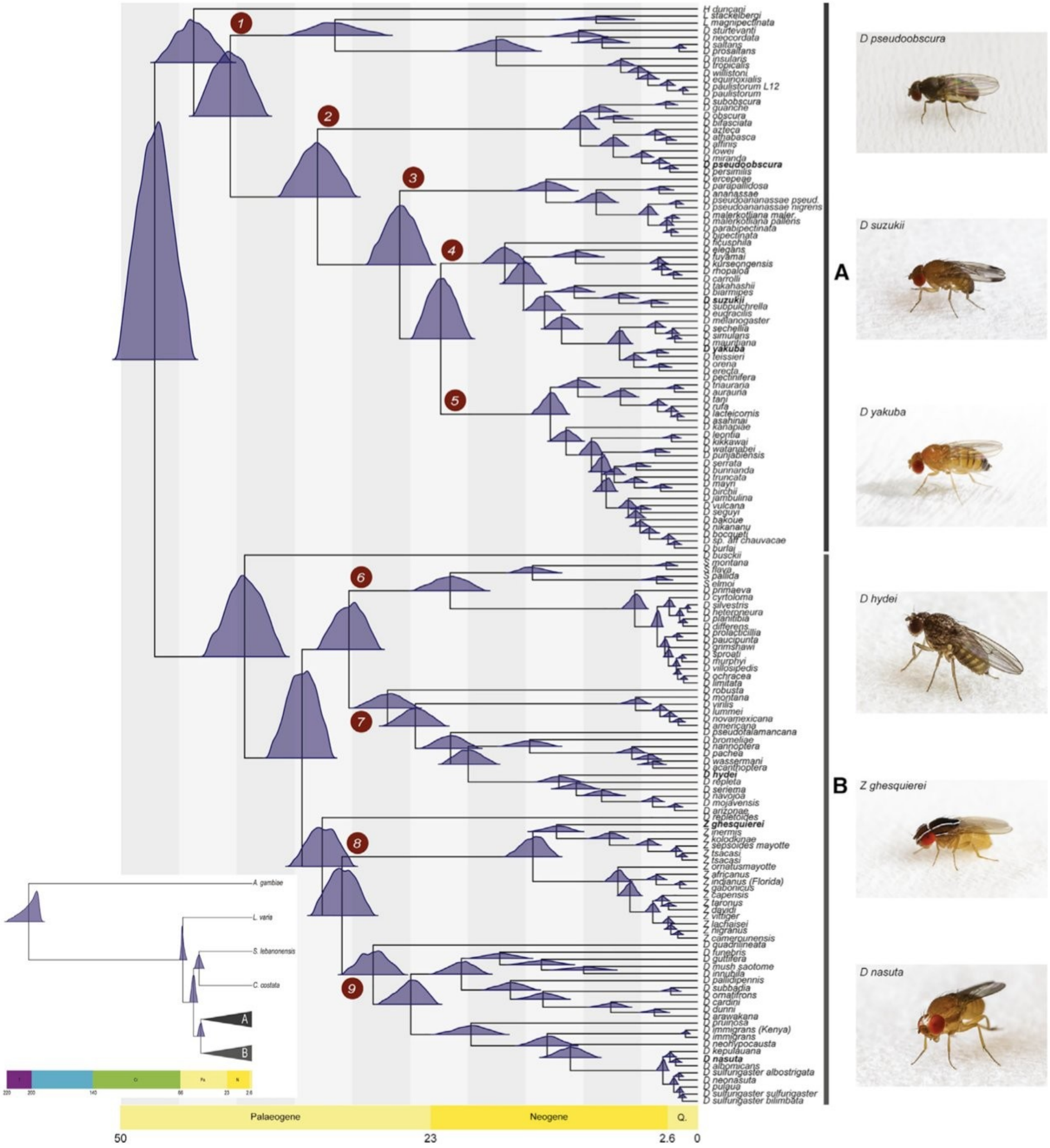
Current Biology

ARTICLE | VOLUME 32, ISSUE 1, P111-123.E5, JANUARY 10, 2022

Widespread introgression across a phylogeny of 155 *Drosophila* genomes

Anton Suvorov [12] • Bernard Y. Kim • Jeremy Wang • Ellie E. Armstrong • David Peede • Emmanuel R.R. D'Agostino • Donald K. Price • Peter J. Waddell • Michael Lang • Virginie Courtier-Orgogozo • Jean R. David • Dmitri Petrov • Daniel R. Matute [10, 11] • Daniel R. Schrider [10, 11] • Aaron A. Comeault [10, 11]

https://www.cell.com/current-biology/fulltext/S0960-9822(21)01496-2#relatedArticles



https://www.cell.com/current-biology/fulltext/S0960-9822(21)01496-2#relatedArticles

GBE

Glue Genes Are Subjected to Diverse Selective Forces during Drosophila Development

Flora Borne[1], Rob J. Kulathinal[1,2], and Virginie Courtier-Orgogozo[1,*]

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[2]Department of Biology, Temple University, USA

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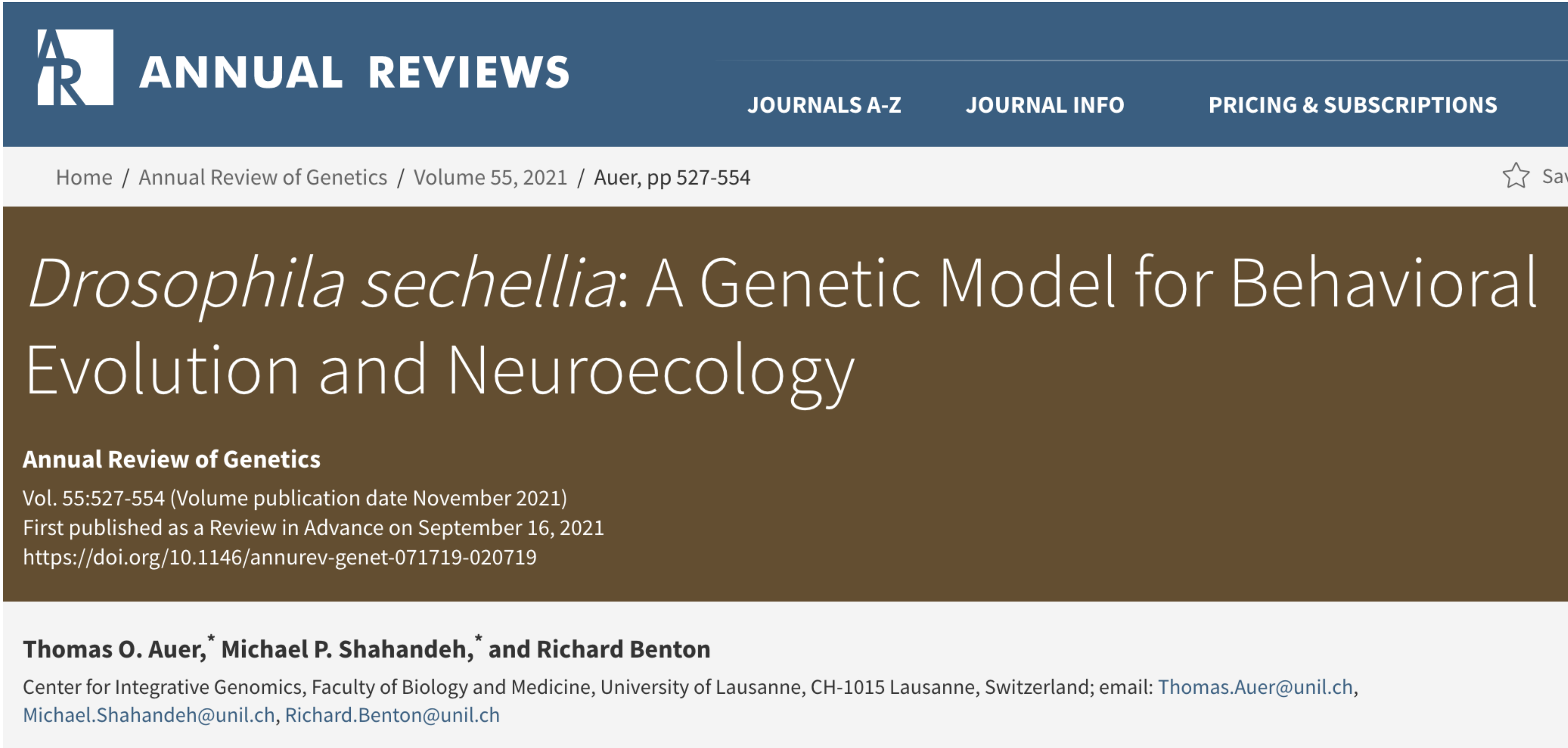
Accepted: 30 October 2021



ANNUAL REVIEWS

JOURNALS A-Z JOURNAL INFO PRICING & SUBSCRIPTIONS

Home / Annual Review of Genetics / Volume 55, 2021 / Auer, pp 527-554 ☆ Sa

Drosophila sechellia: A Genetic Model for Behavioral Evolution and Neuroecology

Annual Review of Genetics

Vol. 55:527-554 (Volume publication date November 2021)
First published as a Review in Advance on September 16, 2021
https://doi.org/10.1146/annurev-genet-071719-020719

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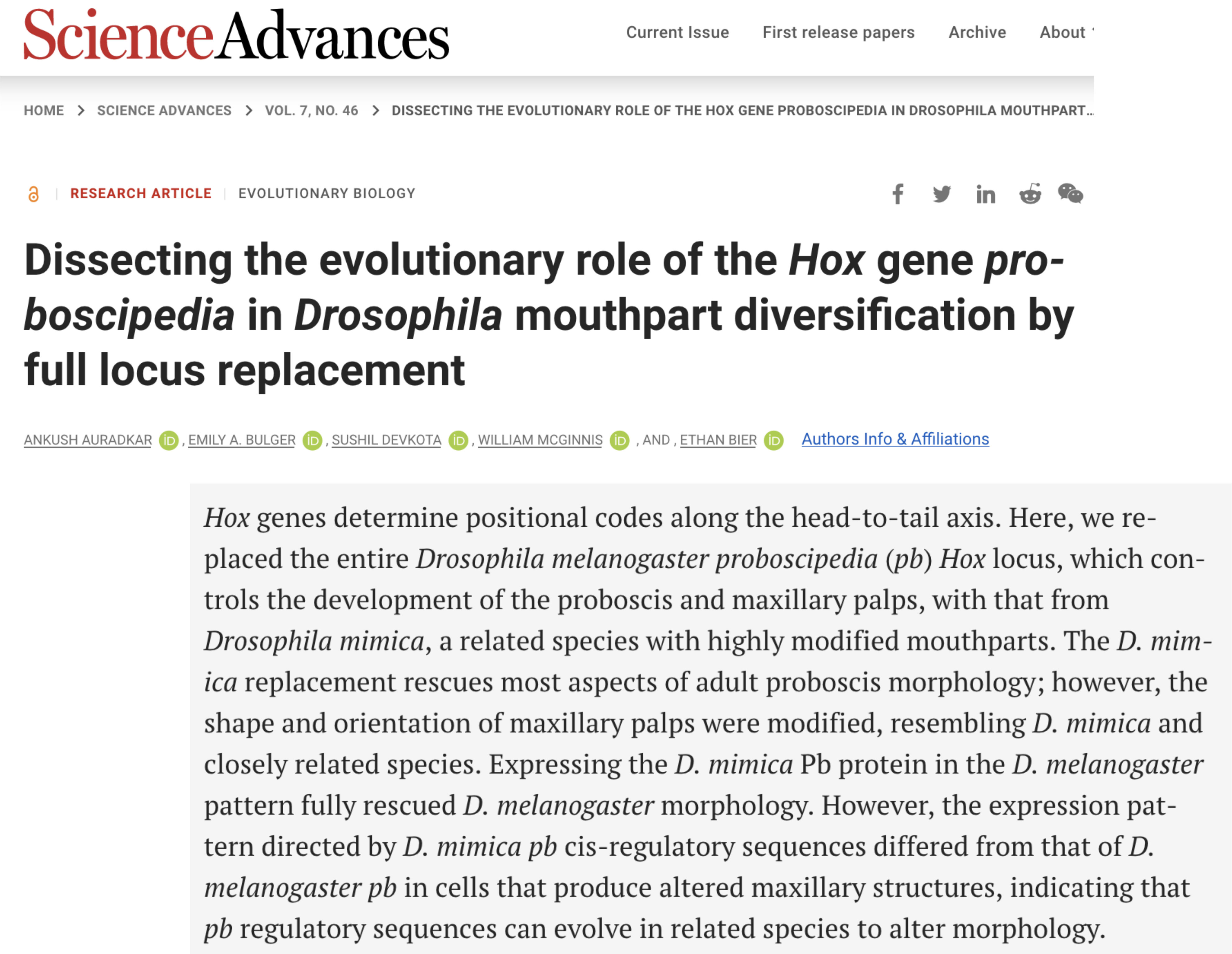
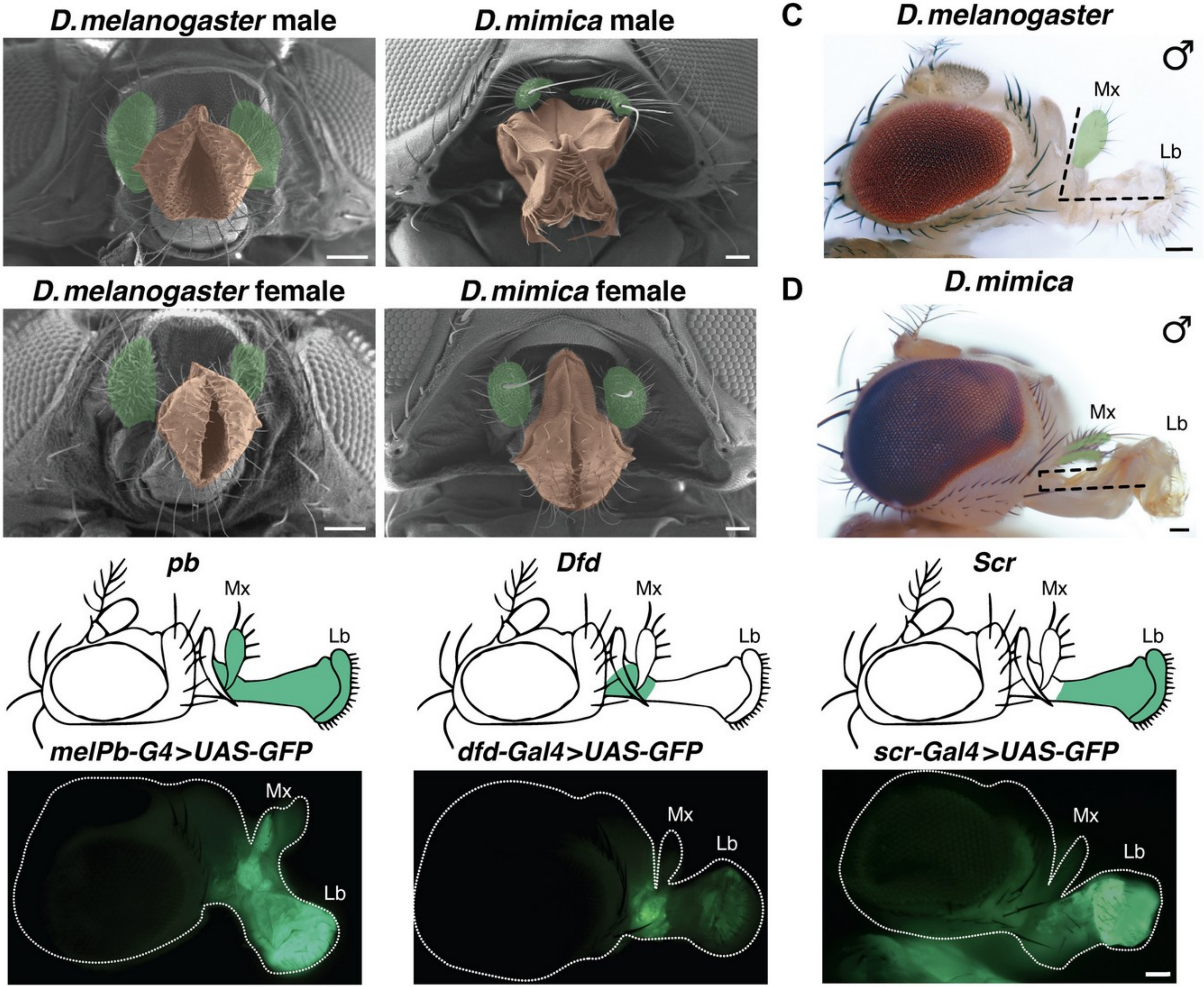


RESEARCH ARTICLE | EVOLUTIONARY BIOLOGY

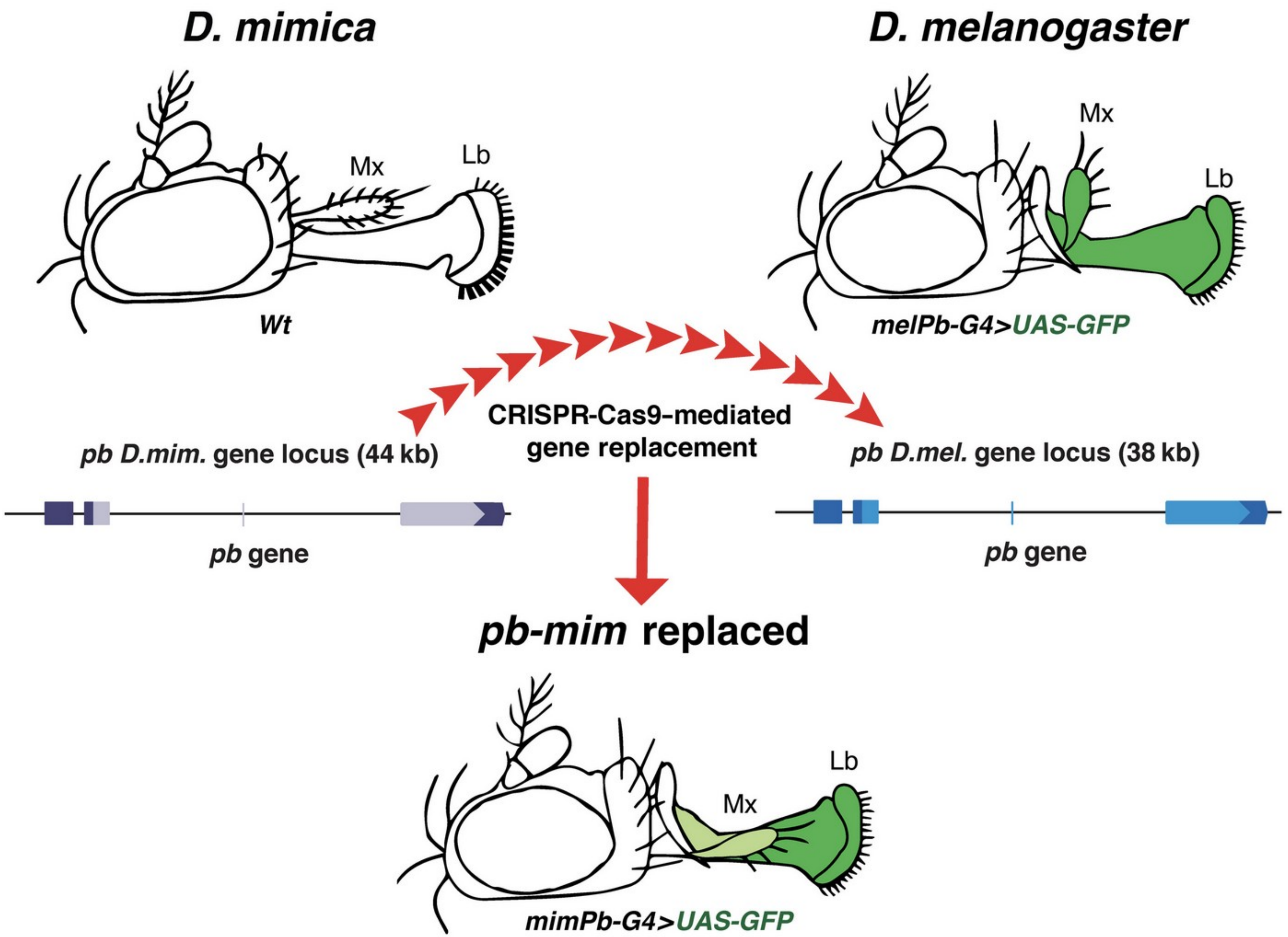
Dissecting the evolutionary role of the *Hox* gene *proboscipedia* in *Drosophila* mouthpart diversification by full locus replacement

ANKUSH AURADKAR, EMILY A. BULGER, SUSHIL DEVKOTA, WILLIAM MCGINNIS, AND, ETHAN BIER Authors Info & Affiliations

Hox genes determine positional codes along the head-to-tail axis. Here, we replaced the entire *Drosophila melanogaster proboscipedia* (*pb*) *Hox* locus, which controls the development of the proboscis and maxillary palps, with that from *Drosophila mimica*, a related species with highly modified mouthparts. The *D. mimica* replacement rescues most aspects of adult proboscis morphology; however, the shape and orientation of maxillary palps were modified, resembling *D. mimica* and closely related species. Expressing the *D. mimica* Pb protein in the *D. melanogaster* pattern fully rescued *D. melanogaster* morphology. However, the expression pattern directed by *D. mimica pb* cis-regulatory sequences differed from that of *D. melanogaster pb* in cells that produce altered maxillary structures, indicating that *pb* regulatory sequences can evolve in related species to alter morphology.


D. melanogaster male
D. mimica male
C
D. melanogaster
♂
Mx
Lb
D. melanogaster female
D. mimica female
D
D. mimica
♂
Mx
Lb
pb
Mx
Lb
Dfd
Mx
Lb
Scr
Mx
Lb
melPb-G4>UAS-GFP
Mx
Lb
dfd-Gal4>UAS-GFP
Mx
Lb
scr-Gal4>UAS-GFP
Mx
Lb

HOX gene replacement



D. mimica

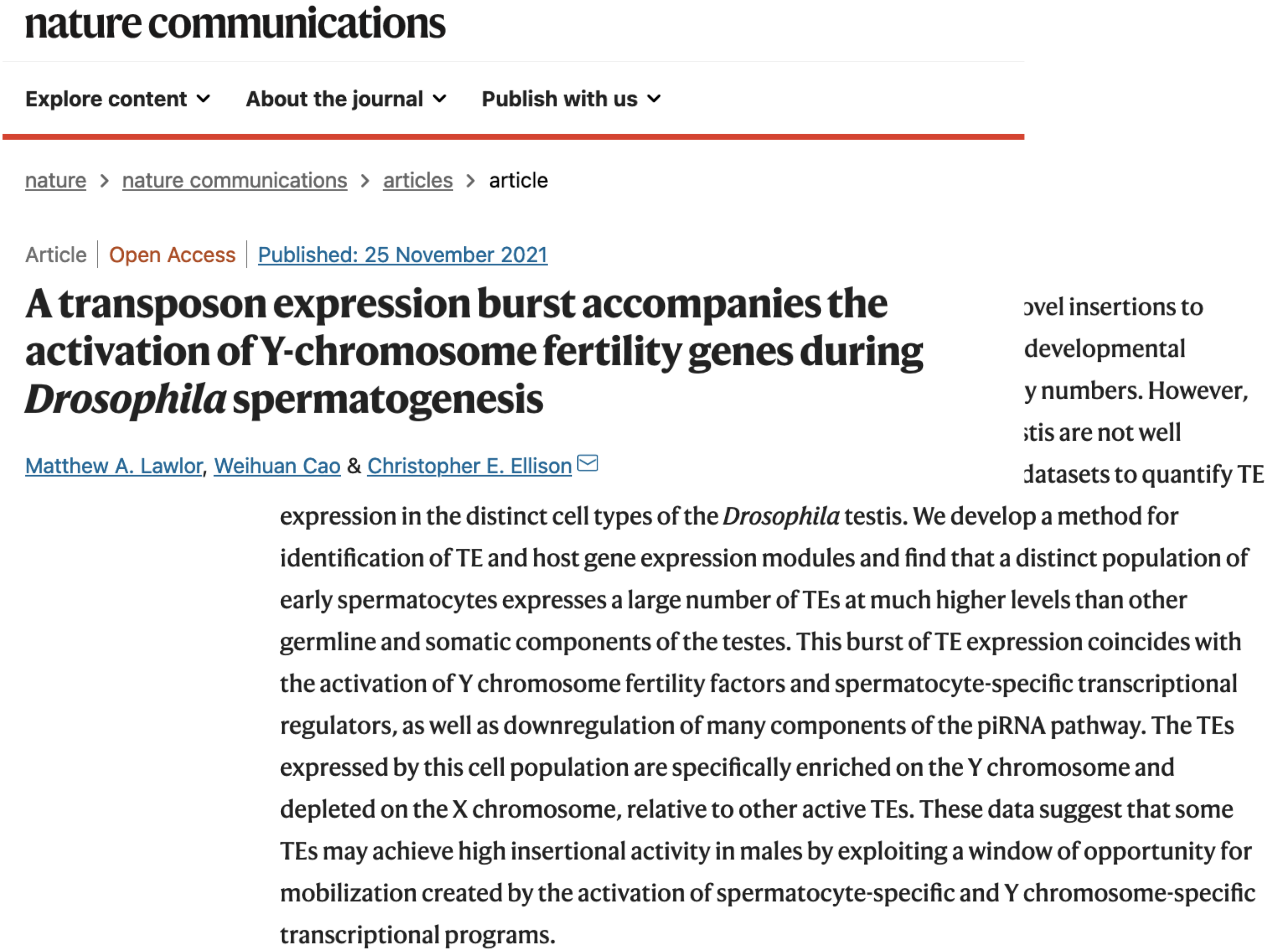
D. melanogaster

CRISPR-Cas9-mediated gene replacement

***pb D.mim.* gene locus (44 kb)**

***pb D.mel.* gene locus (38 kb)**

***pb-mim* replaced**



Article | Open Access | Published: 25 November 2021

A transposon expression burst accompanies the activation of Y-chromosome fertility genes during *Drosophila* spermatogenesis

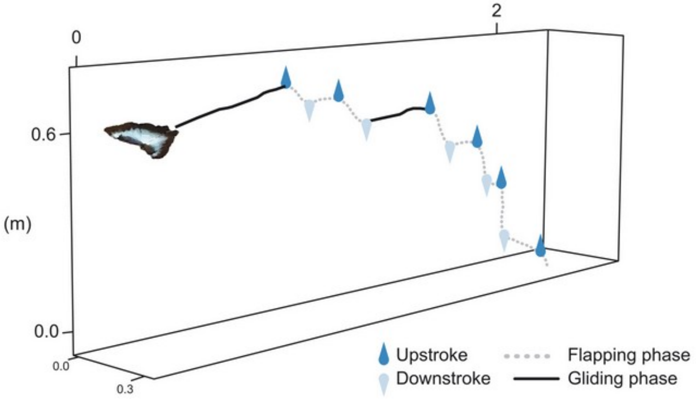
Matthew A. Lawlor, Weihuan Cao & Christopher E. Ellison

ovel insertions to
developmental
y numbers. However,
stis are not well
datasets to quantify TE
expression in the distinct cell types of the *Drosophila* testis. We develop a method for identification of TE and host gene expression modules and find that a distinct population of early spermatocytes expresses a large number of TEs at much higher levels than other germline and somatic components of the testes. This burst of TE expression coincides with the activation of Y chromosome fertility factors and spermatocyte-specific transcriptional regulators, as well as downregulation of many components of the piRNA pathway. The TEs expressed by this cell population are specifically enriched on the Y chromosome and depleted on the X chromosome, relative to other active TEs. These data suggest that some TEs may achieve high insertional activity in males by exploiting a window of opportunity for mobilization created by the activation of spermatocyte-specific and Y chromosome-specific transcriptional programs.

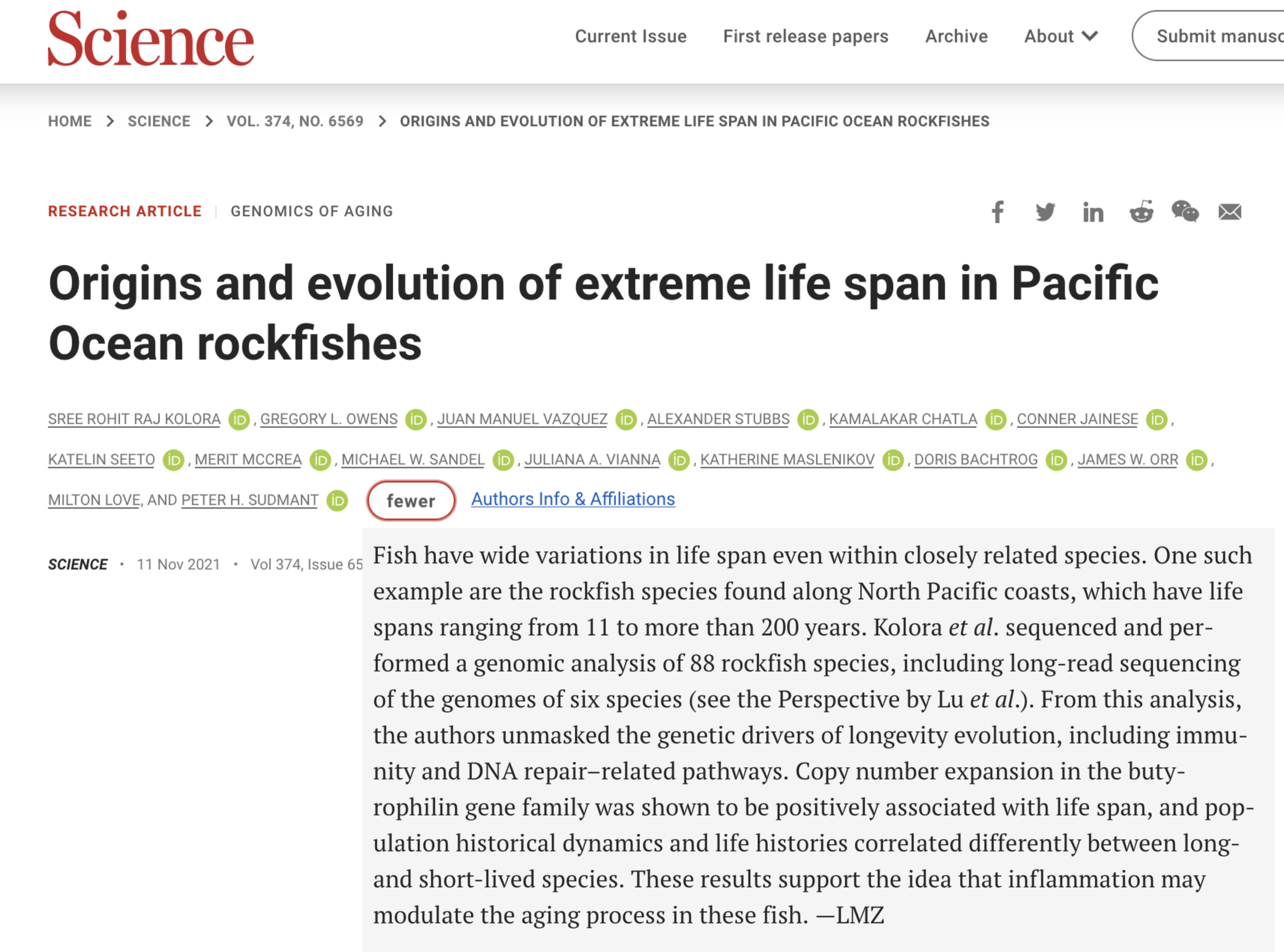
REPORT | ADAPTIVE FLIGHT

Adaptive evolution of flight in *Morpho* butterflies

CAMILLE LE ROY, DARIO AMADORI, SAMUEL CHARBERET, JAAP WINDT, FLORIAN T. MUIJRES, VIOLAINE LLAURENS, AND VINCENT DEBAT



The diversity of flying animals suggests that countless combinations of flight morphologies and behaviors have evolved with specific lifestyles, thereby exploiting diverse aerodynamic mechanisms. How morphology, flight behavior, and aerodynamic properties together diversify with contrasting ecology remains to be elucidated. We studied the adaptive codivergence in wing shape, flight behavior, and aerodynamic efficiency among *Morpho* butterflies living in different forest strata by combining high-speed videography in the field with morphometric analyses and aerodynamic modeling. By comparing canopy and understory species, we show that adaptation to an open canopy environment resulted in increased glide efficiency. Moreover, this enhanced glide efficiency was achieved by different canopy species through distinct combinations of flight behavior, wing shape, and aerodynamic mechanisms, highlighting the multiple pathways of adaptive evolution.



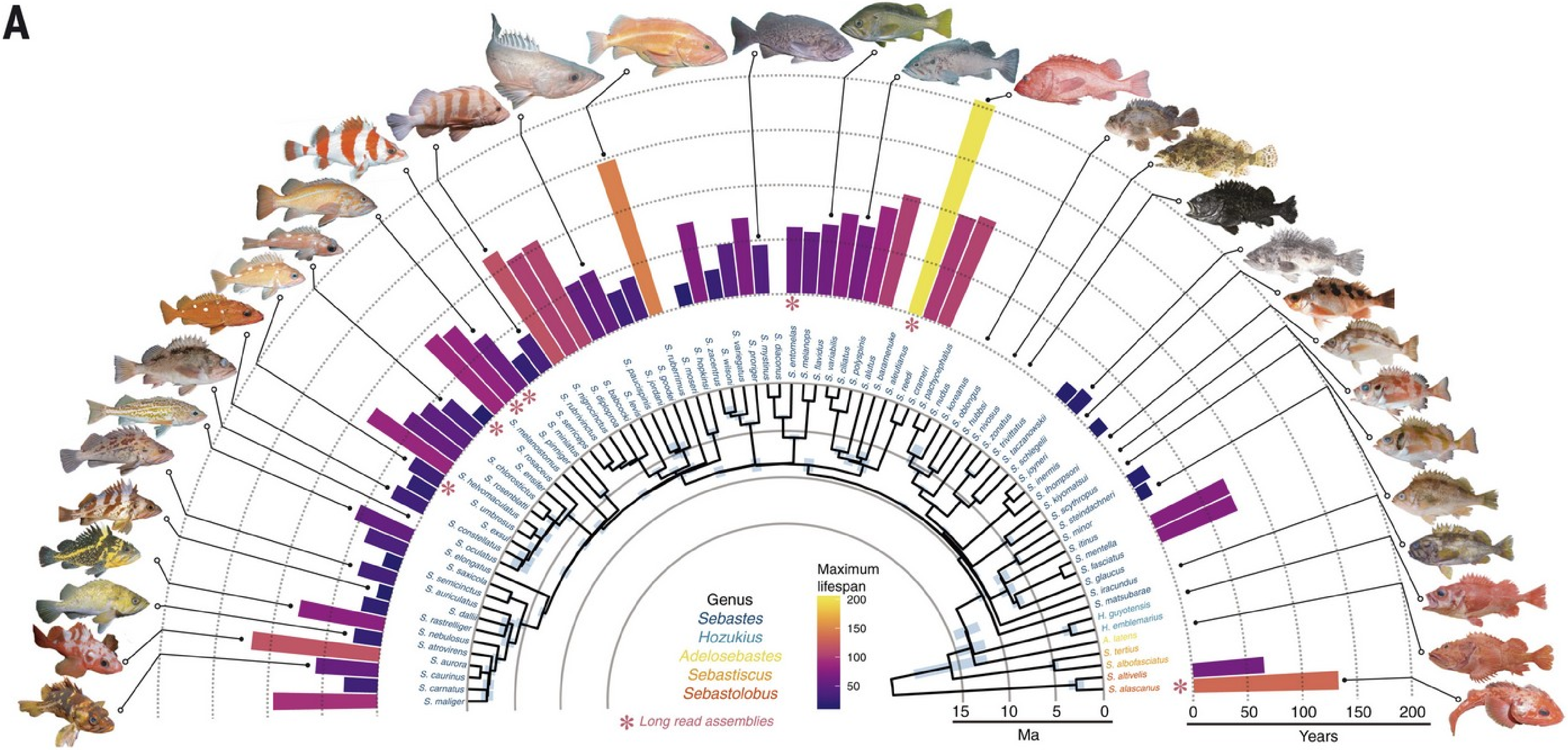
RESEARCH ARTICLE | GENOMICS OF AGING

Origins and evolution of extreme life span in Pacific Ocean rockfishes

SREE ROHIT RAJ KOLORA, GREGORY L. OWENS, JUAN MANUEL VAZQUEZ, ALEXANDER STUBBS, KAMALAKAR CHATLA, CONNER JAINESE, KATELIN SEETO, MERIT MCCREA, MICHAEL W. SANDEL, JULIANA A. VIANNA, KATHERINE MASLENIKOV, DORIS BACHTROG, JAMES W. ORR, MILTON LOVE, AND PETER H. SUDMANT

SCIENCE • 11 Nov 2021 • Vol 374, Issue 65

Fish have wide variations in life span even within closely related species. One such example are the rockfish species found along North Pacific coasts, which have life spans ranging from 11 to more than 200 years. Kolora *et al*. sequenced and performed a genomic analysis of 88 rockfish species, including long-read sequencing of the genomes of six species (see the Perspective by Lu *et al*.). From this analysis, the authors unmasked the genetic drivers of longevity evolution, including immunity and DNA repair–related pathways. Copy number expansion in the butyrophilin gene family was shown to be positively associated with life span, and population historical dynamics and life histories correlated differently between long- and short-lived species. These results support the idea that inflammation may modulate the aging process in these fish. —LMZ


A
S. maliger
S. carnatus
S. caurinus
S. aurora
S. atrovirens
S. nebulosus
S. rastrelliger
S. dallii
S. auriculatus
S. semicinctus
S. saxicola
S. elongatus
S. oculatus
S. constellatus
S. exsul
S. umbrosus
S. helvomaculatus
S. rosenblatti
S. chlorostictus
S. ensifer
S. rosaceus
S. melanostomus
S. pinniger
S. miniatus
S. serriceps
S. rubrivinctus
S. nigrocinctus
S. diploproa
S. babcocki
S. levis
S. paucispinis
S. jordani
S. goodei
S. ruberrimus
S. moseri
S. hopkinsi
S. zacentrus
S. wilsoni
S. variegatus
S. proriger
S. mystinus
S. diaconus
S. entomelas
S. melanops
S. flavidus
S. variabilis
S. ciliatus
S. polyspinis
S. alutus
S. baramenuke
S. aleutianus
S. reedi
S. crameri
S. pachycephalus
S. nudus
S. koreanus
S. oblongus
S. hubbsi
S. nivosus
S. zonatus
S. trivittatus
S. taczanowskii
S. schlegelii
S. joyneri
S. inermis
S. thompsoni
S. kiyomatsui
S. scythropus
S. steindachneri
S. minor
S. itinus
S. mentella
S. fasciatus
S. glaucus
S. iracundus
S. matsubarae
H. guyotensis
H. emblemarius
A. latens
S. tertius
S. albofasciatus
S. altivelis
S. alascanus
Genus
Sebastes
Hozukius
Adelosebastes
Sebastiscus
Sebastolobus
Maximum lifespan
200
150
100
50
* Long read assemblies
15
10
5
0
Ma
0
50
100
150
200
Years

GBE

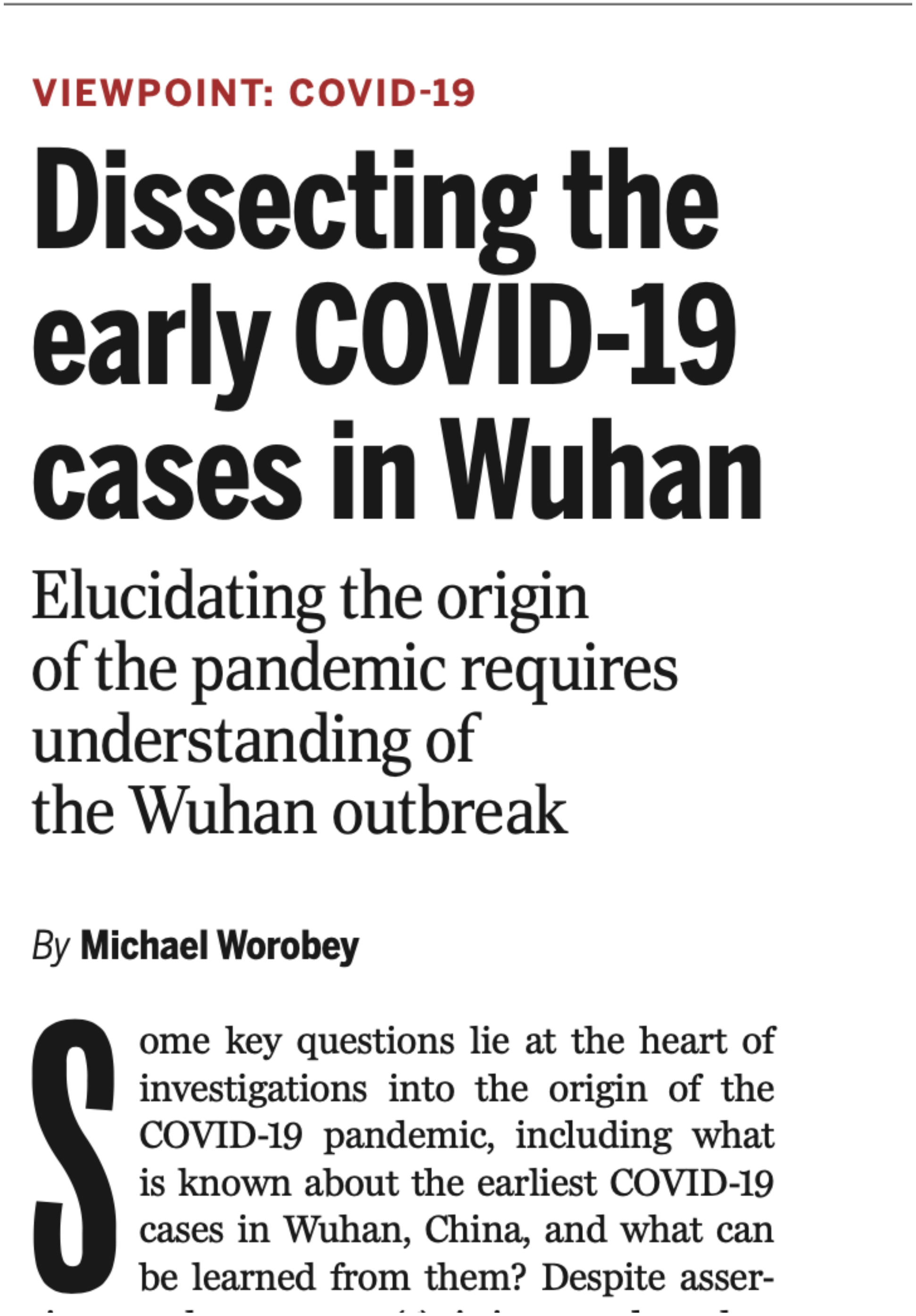
The Birth-and-Death Evolution of Cytochrome P450 Genes in Bees

Kathy Darragh ✉, David R Nelson, Santiago R Ramírez

Genome Biology and Evolution, Volume 13, Issue 12, December 2021, evab261,
https://doi.org/10.1093/gbe/evab261

Published: 30 November 2021 **Article history ▾**

Science



VIEWPOINT: COVID-19

Dissecting the early COVID-19 cases in Wuhan

Elucidating the origin of the pandemic requires understanding of the Wuhan outbreak

By **Michael Worobey**

Some key questions lie at the heart of investigations into the origin of the COVID-19 pandemic, including what is known about the earliest COVID-19 cases in Wuhan, China, and what can be learned from them? Despite asser-