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Evolutionary Biology, Genetics and Genomics

A broad mutational target explains a fast rate of phenotypic evolution

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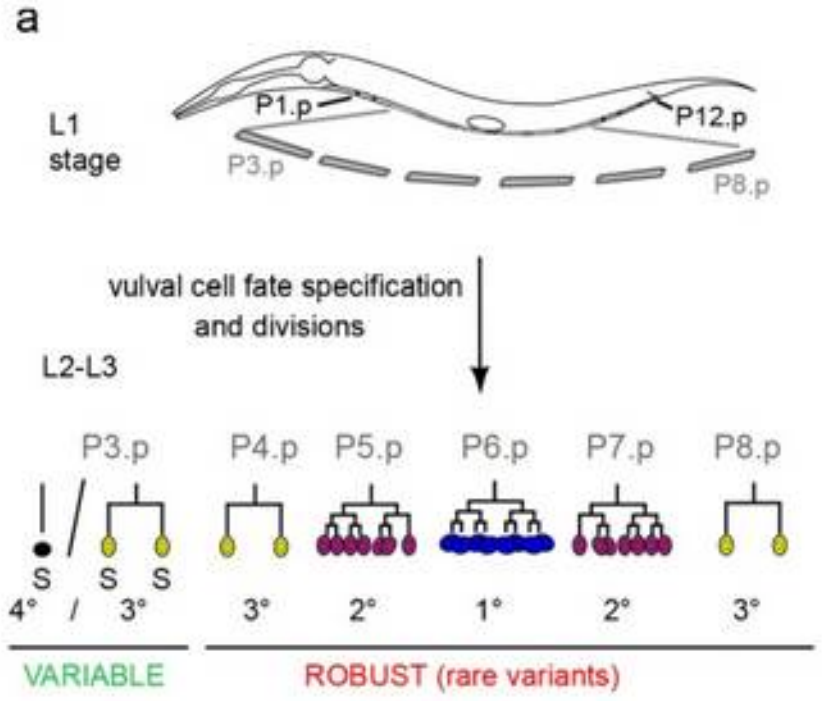
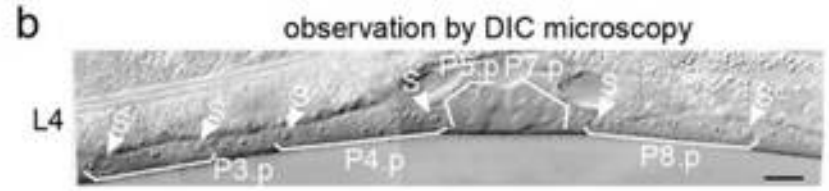
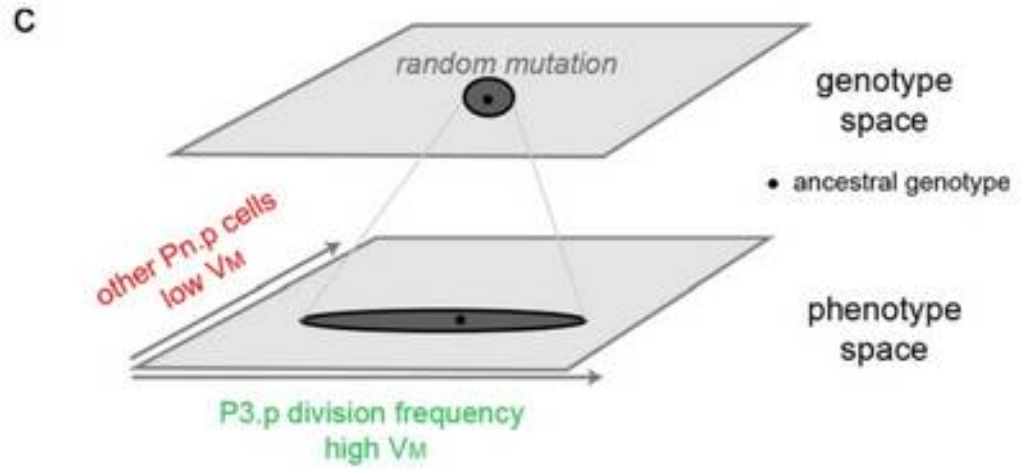
Research Article · Aug 27, 2020

Previous studies have shown that one of *C. elegans'* six cells of the reproductive system evolves faster than the others. To investigate this further, Besnard, Picao-Osorio et al. analysed the genetic mutations driving change in this cell in 250 worm generations. The results showed that five mutations in five different genes – all responsible for different processes in the cells – were behind the supercharged evolution of this particular cell. This suggests that fast evolution results from natural selection acting upon a collection of genes, rather than one gene, and that many genes and pathways shape this trait.







d

	P3.p 4°/3°	P(4-8).p 3° 2° 1° 2° 3°
Among species	EVOLUTIONARY TREND	STASIS
Within species	high V_G	low V_G
Mutation accumulation	high V_M	low V_M

?

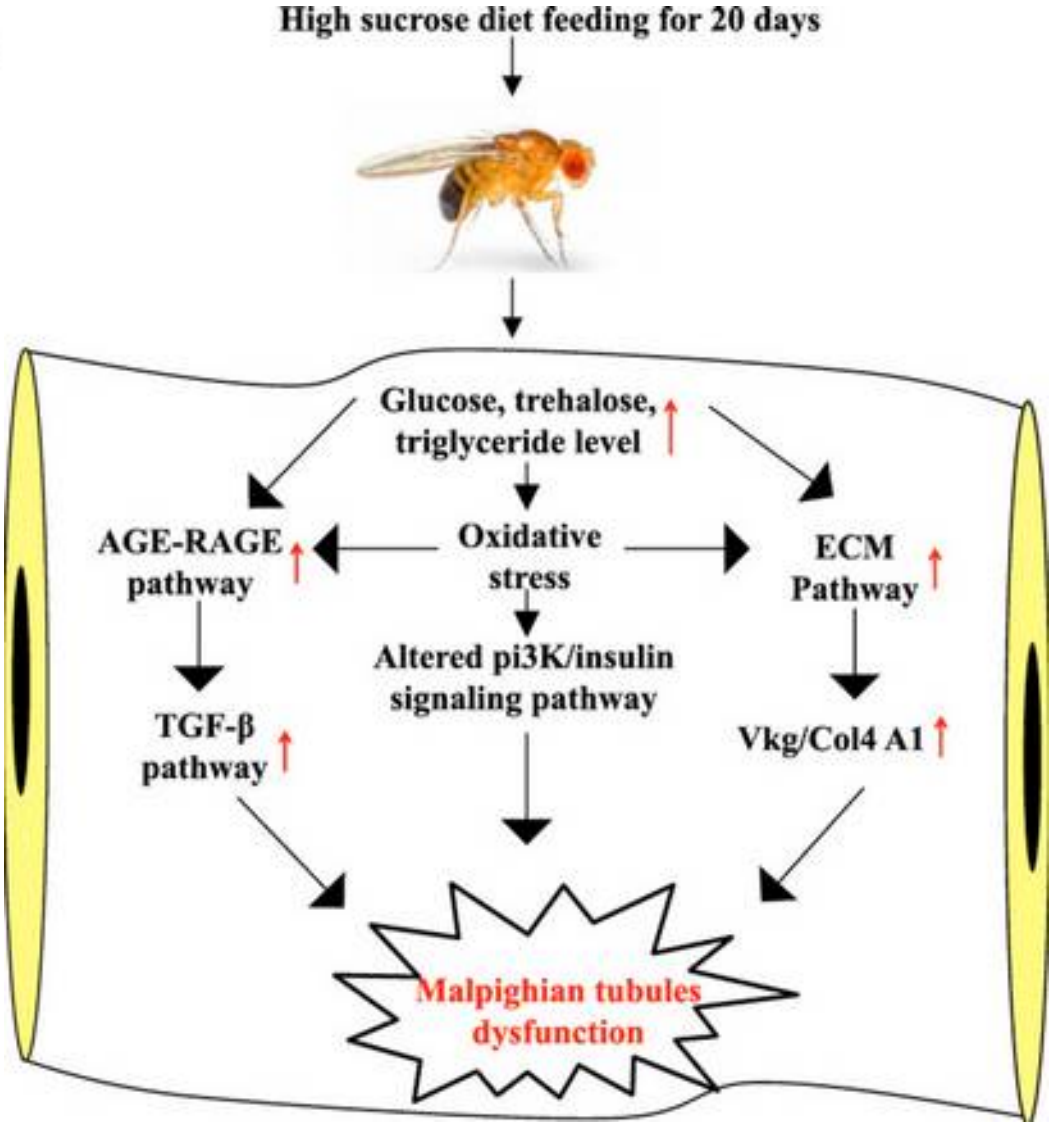
Hypothesis 1
Highly mutable loci

Hypothesis 2
Broad mutational target

> Insect Biochem Mol Biol. 2020 Oct;125:103441. doi: 10.1016/j.ibmb.2020.103441.
Epub 2020 Jul 29.

High sucrose diet induces morphological, structural and functional impairments in the renal tubules of Drosophila melanogaster: A model for studying type-2 diabetes mediated renal tubular dysfunction

Lavi Rani [1], Sanjay Saini [2], Neha Shukla [3], Debapratim Kar Chowdhuri [1], Naveen Kumar Gautam [4]



> Genome Biol Evol. 2020 Aug 1;12(8):1407-1418. doi: 10.1093/gbe/evaa145.

Contributions of cis- and trans-Regulatory Evolution to Transcriptomic Divergence across Populations in the Drosophila mojavensis Larval Brain

Kyle M Benowitz [1], Joshua M Coleman [1 2], Carson W Allan [1], Luciano M Matzkin [1 3 4]

Affiliations + expand

PMID: 32653899 PMCID: PMC7495911 DOI: 10.1093/gbe/evaa145

Free PMC article

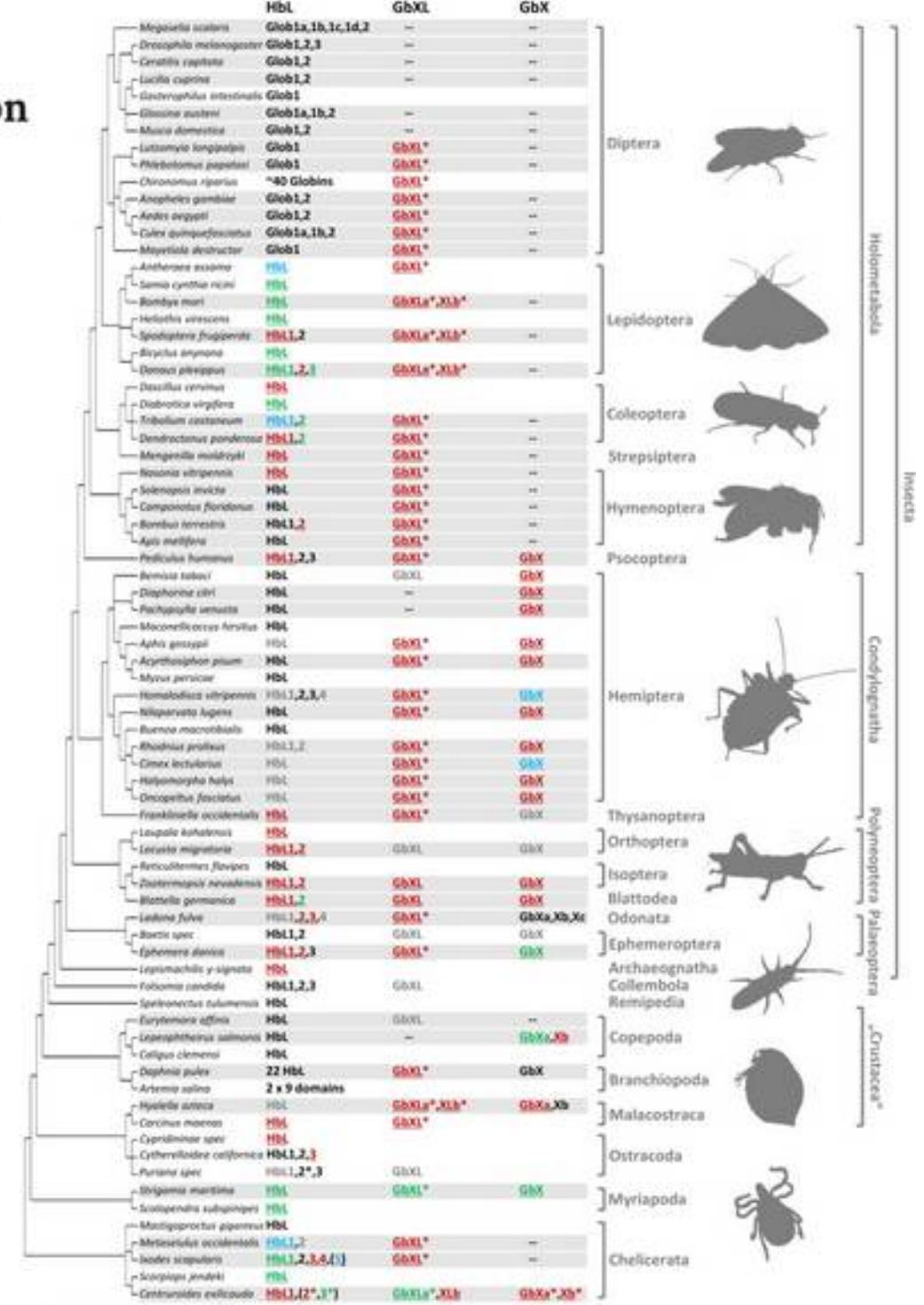
Abstract

Natural selection on gene expression was originally predicted to result primarily in cis- rather than trans-regulatory evolution, due to the expectation of reduced pleiotropy. Despite this, numerous studies have ascribed recent evolutionary divergence in gene expression predominantly to trans-regulation. Performing RNA-seq on single isofemale lines from genetically distinct populations of the cactophilic fly Drosophila mojavensis and their F1 hybrids, we recapitulated this pattern in both larval brains and whole bodies. However, we demonstrate that improving the measurement of brain expression divergence between populations by using seven additional genotypes considerably reduces the estimate of trans-regulatory contributions to expression evolution. We argue that the finding of trans-regulatory predominance can result from biases due to environmental variation in expression or other sources of noise, and that cis-regulation is likely a greater contributor to transcriptional evolution across D. mojavensis populations. Lastly, we merge these lines of data to identify several previously hypothesized and intriguing novel candidate genes, and suggest that the integration of regulatory and population-level transcriptomic data can provide useful filters for the identification of potentially adaptive genes.

> Front Genet. 2020 Aug 13;11:858. doi: 10.3389/fgene.2020.00858. eCollection 2020.

The Globin Gene Family in Arthropods: Evolution and Functional Diversity

Andreas Prothmann [1], Federico G Hoffmann [2 3], Juan C Opazo [4 5], Peter Herbener [1], Jay F Storz [6], Thorsten Burmester [7], Thomas Hankeln [1]



› Evolution. 2020 Aug 26. doi: 10.1111/evo.14089. Online ahead of print.

Plastic male mating behavior evolves in response to the competitive environment

Alice A Dore [1], Wayne G Rostant [1], Amanda Bretman [2], Tracey Chapman [1]

Affiliations + expand

PMID: 32844404 DOI: 10.1111/evo.14089

Free article

Abstract

Male reproductive phenotypes can evolve in response to the social and sexual environment. The expression of many such phenotypes may also be plastic within an individual's lifetime. For example, male Drosophila melanogaster show significantly extended mating duration following a period of exposure to conspecific male rivals. The costs and benefits of reproductive investment, and plasticity itself, can be shaped by the prevailing sociosexual environment and by resource availability. We investigated these ideas using experimental evolution lines of D. melanogaster evolving under three fixed sex ratios (high, medium, and low male-male competition) on either rich or poor adult diets. We found that males evolving in high-competition environments evolved longer mating durations overall. In addition, these males expressed a novel type of plastic behavioral response following exposure to rival males: they both significantly reduced and showed altered courtship delivery, and exhibited significantly longer mating latencies. Plasticity in male mating duration in response to rivals was maintained in all of the lines, suggesting that the costs of plasticity were minimal. None of the evolutionary responses tested were consistently affected by dietary resource regimes. Collectively, the results show that fixed behavioral changes and new augmentations to the repertoire of reproductive behaviors can evolve rapidly.

Keywords: Courtship; experimental evolution; mating duration; sex ratio; sexual selection.

> Mol Ecol. 2020 Aug;29(15):2840-2854. doi: 10.1111/mec.15531. Epub 2020 Jul 13.

Genetic architecture of a body colour cline in Drosophila americana

Lisa L Sramkoski [1], Wesley N McLaughlin [2], Arielle M Cooley [2], David C Yuan [1], Alisha John [1], Patricia J Wittkopp [1 2]

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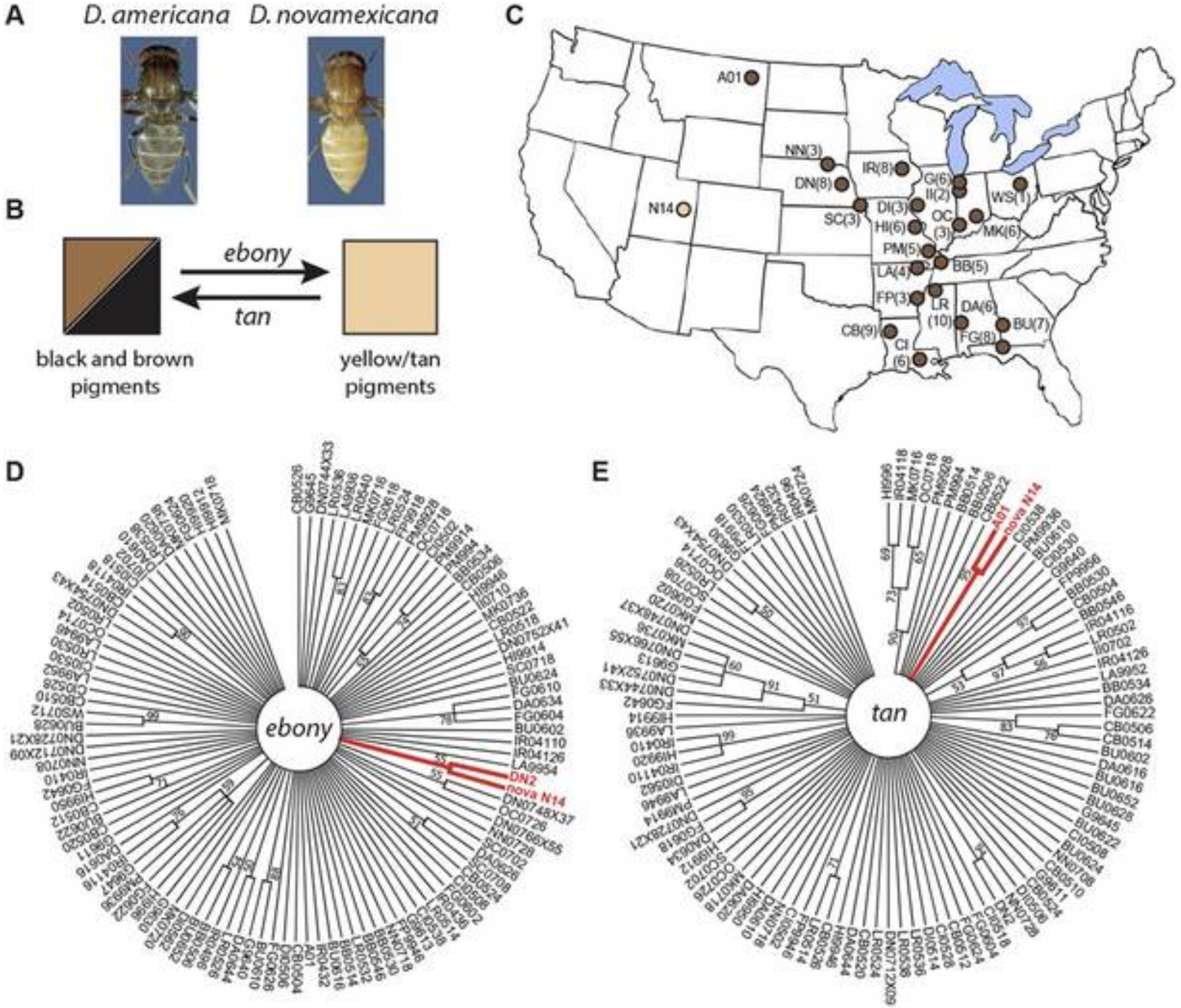
PMID: 32603541 PMCID: PMC7482988 DOI: 10.1111/mec.15531

Free PMC article

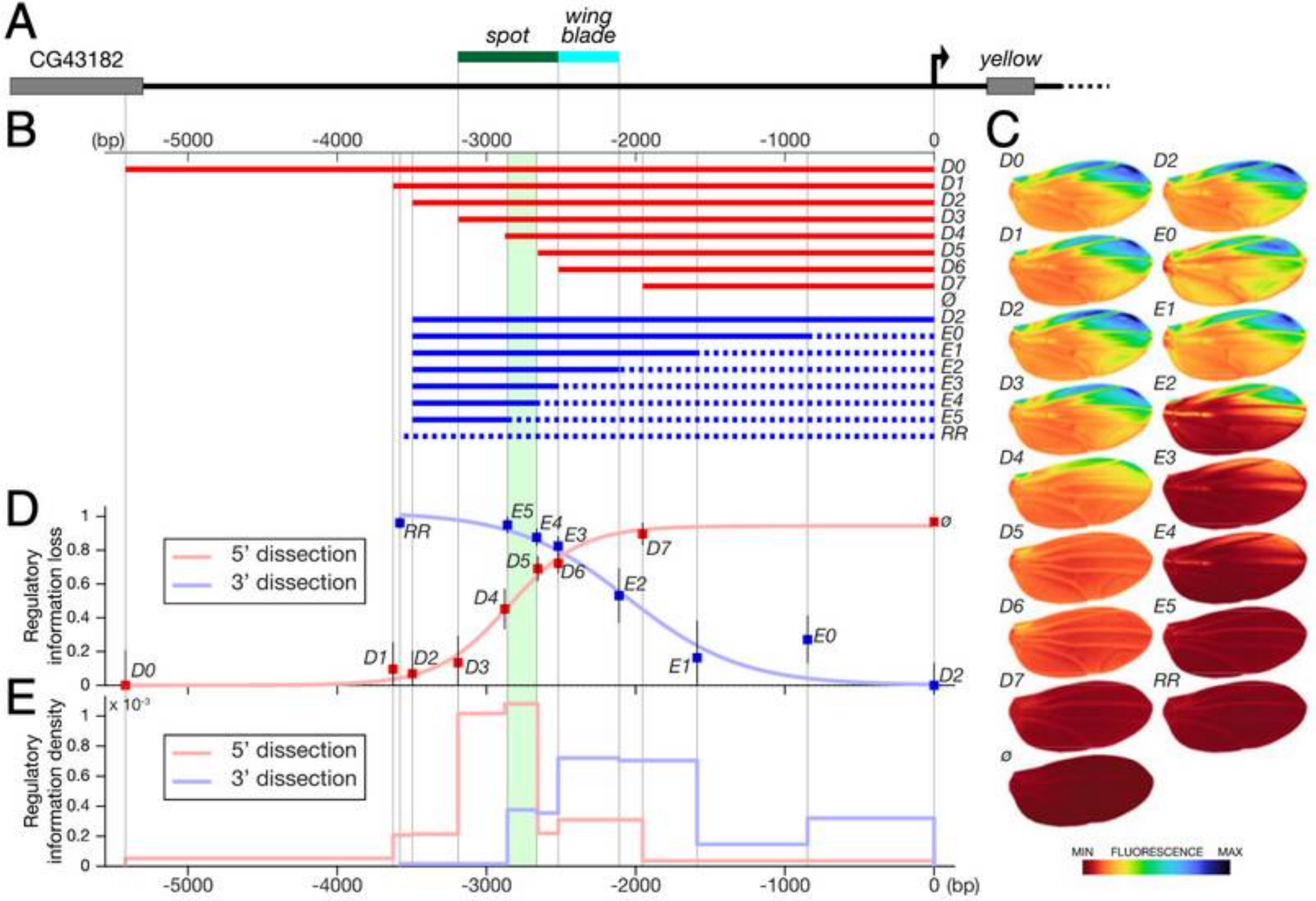
Abstract

Phenotypic variation within a species is often structured geographically in clines. In Drosophila americana, a longitudinal cline for body colour exists within North America that appears to be due to local adaptation. The tan and ebony genes have been hypothesized to contribute to this cline, with alleles of both genes that lighten body colour found in D. americana. These alleles are similar in sequence and function to the allele fixed in D. americana's more lightly pigmented sister species, Drosophila novamexicana. Here, we examine the frequency and geographic distribution of these D. novamexicana-like alleles in D. americana. Among alleles from over 100 strains of D. americana isolated from 21 geographic locations, we failed to identify additional alleles of tan or ebony with as much sequence similarity to D. novamexicana as the D. novamexicana-like alleles previously described. However, using genetic analysis of 51 D. americana strains derived from 20 geographic locations, we identified one new allele of ebony and one new allele of tan segregating in D. americana that are functionally equivalent to the D. novamexicana allele. An additional 5 alleles of tan also showed marginal evidence of functional similarity. Given the rarity of these alleles, however, we conclude that they are unlikely to be driving the pigmentation cline. Indeed, phenotypic distributions of the 51 backcross populations analysed indicate a more complex genetic architecture, with diversity in the number and effects of loci altering pigmentation observed both within and among populations of D. americana. This genetic heterogeneity poses a challenge to association studies and genomic scans for clinal variation, but might be common in natural populations.


A
D. americana
D. novamexicana
B
ebony
tan
black and brown pigments
yellow/tan pigments
C
A01
N14
NN(3)
DN(8)
IR(8)
G(6)
II(2)
WS(1)
SC(3)
DI(3)
OC (3)
MK(6)
HI(6)
PM(5)
BB(5)
LA(4)
FP(3)
LR (10)
DA(6)
BU(7)
CB(9)
CI (6)
FG(8)
D
ebony
DN2
nova N14
E
tan
A01
nova N14

Ancestral and derived transcriptional enhancers share regulatory sequence and a pleiotropic site affecting chromatin accessibility

Yaqun Xin[a,1], Yann Le Poul[a,1], Liucong Ling[a], Mariam Museridze[a], Bettina Mühling[a], Rita Jaenichen[a], Elena Osipova[a], and Nicolas Gompel[a,2]


A
CG43182
spot
wing blade
yellow
B
(bp)
-5000
-4000
-3000
-2000
-1000
0
D0
D1
D2
D3
D4
D5
D6
D7
Ø
D2
E0
E1
E2
E3
E4
E5
RR
C
D0
D2
D1
E0
D2
E1
D3
E2
D4
E3
D5
E4
D6
E5
D7
RR
ø
MIN
FLUORESCENCE
MAX
D
Regulatory information loss
5' dissection
3' dissection
RR
E5
E4
E3
D7
ø
D5
D6
E2
D4
E0
D1
D2
D3
E1
D0
D2
E
Regulatory information density
x 10-3
5' dissection
3' dissection
-5000
-4000
-3000
-2000
-1000
0 (bp)