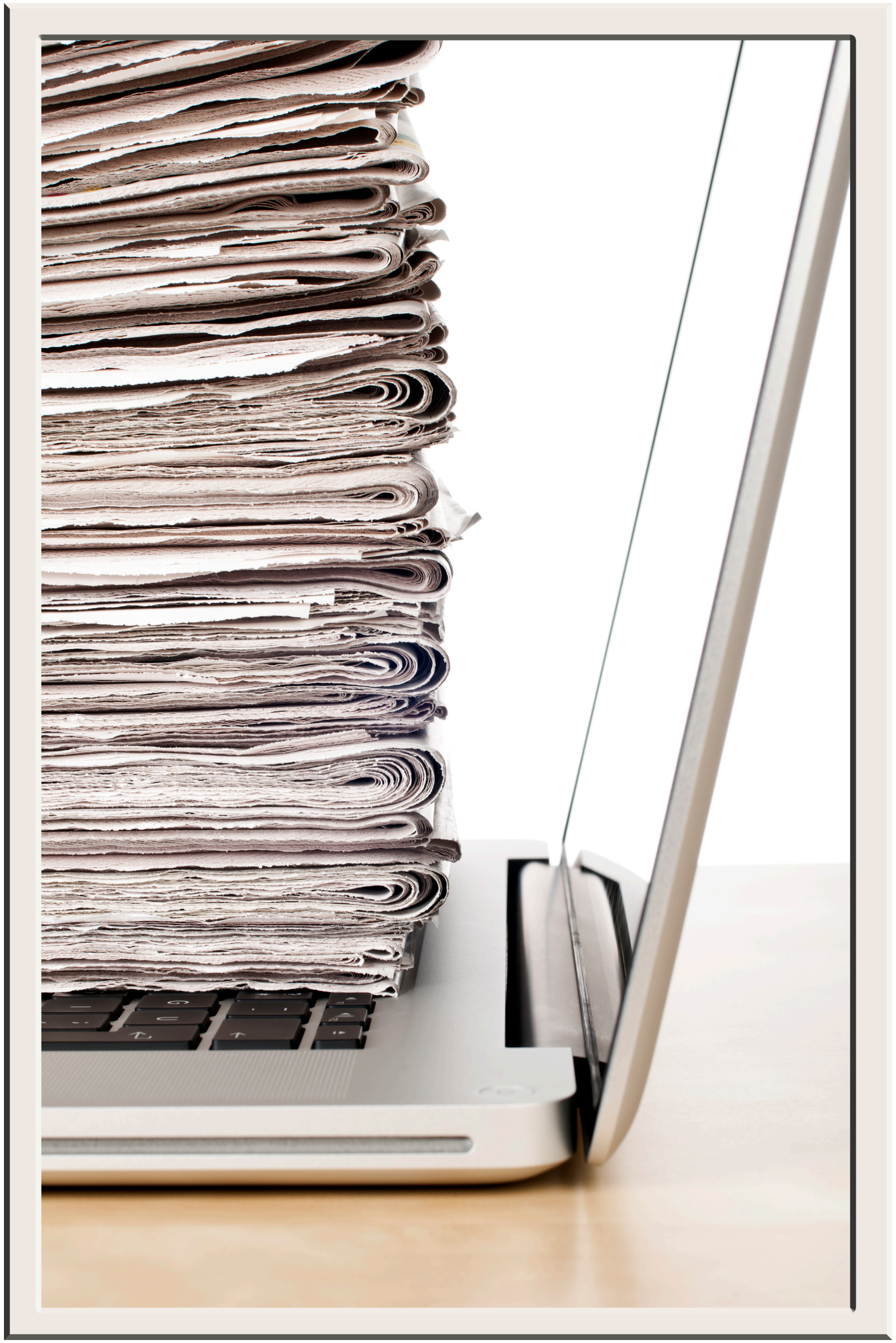
Press report

April 2015

Alexandre Peluffo
Orgogozo Lab

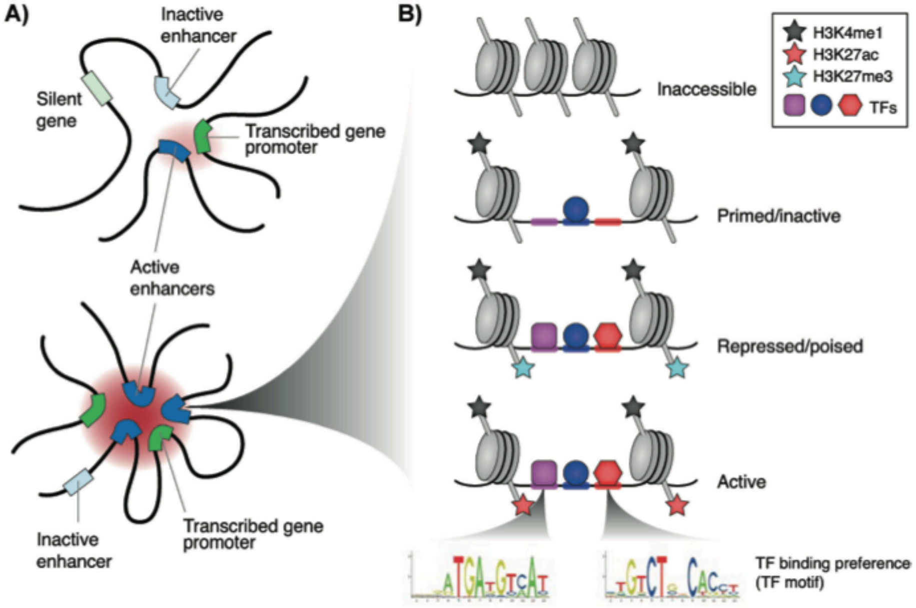


Prospects & Overviews

Problems & Paradigms

Promoter or enhancer, what’s the difference? Deconstruction of established distinctions and presentation of a unifying model

Robin Andersson



The 3D Organization of Chromatin Explains Evolutionary Fragile Genomic Regions

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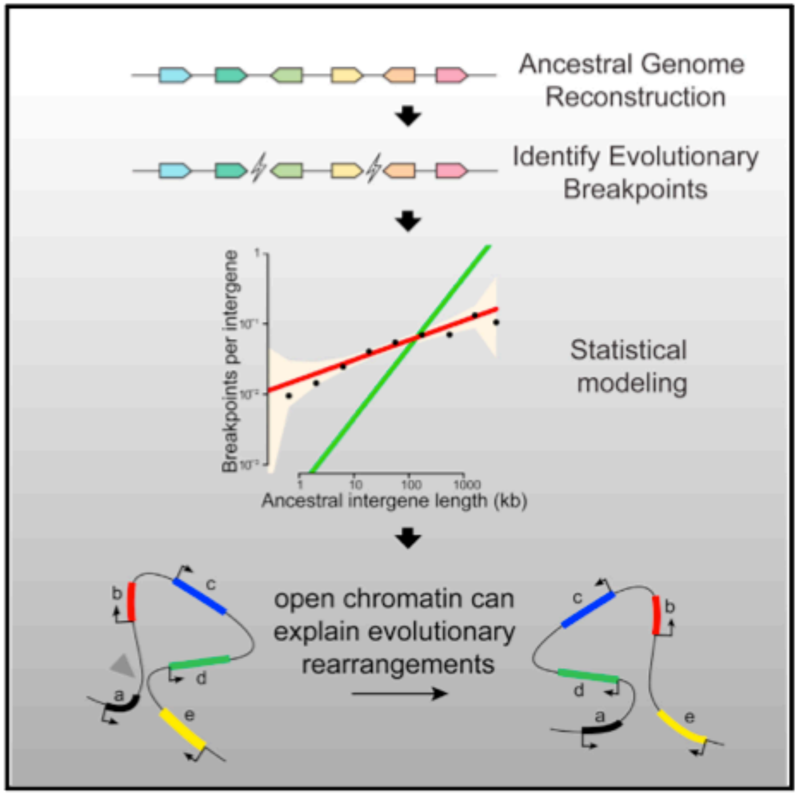
Graphical Abstract



JOURNAL OF Evolutionary Biology

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Molecular evolution of candidate genes involved in post-mating-prezygotic reproductive isolation

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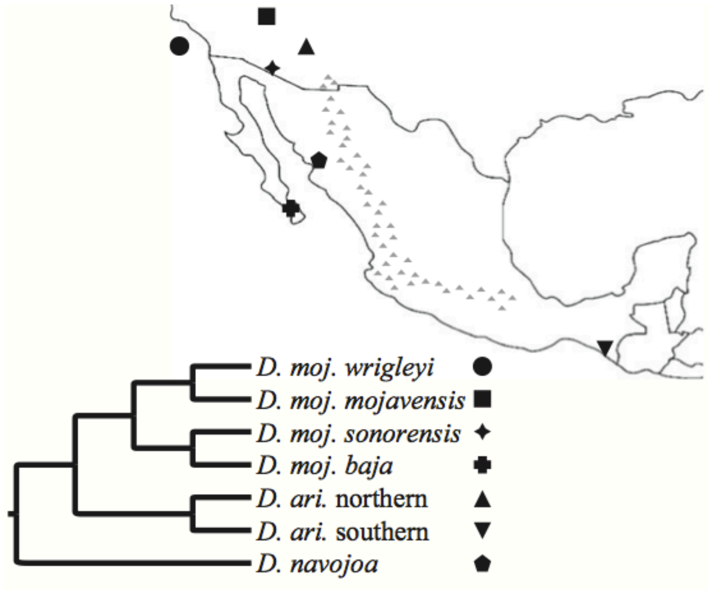

Abstract

Traits involved in post-copulatory interactions between the sexes may evolve rapidly as a result of sexual selection and/or sexual conflict, leading to post-mating-prezygotic (PMPZ) reproductive isolating barriers between diverging lineages. Although the importance of PMPZ isolation is recognized, the molecular basis of such incompatibilities is not well understood. Here, we investigate molecular evolution of a subset of *Drosophila mojavensis* and *Drosophila arizonae* reproductive tract genes. These include genes that are transcriptionally regulated by conspecific mating in females, many of which are misregulated in heterospecific crosses, and a set of male genes whose transcripts are transferred to females during mating. As a group, misregulated female genes are not more divergent and do not appear to evolve under different selection pressures than other female reproductive genes. Male transferred genes evolve at a higher rate than testis-expressed genes, and at a similar rate compared to accessory gland protein genes, which are known to evolve rapidly. Four of the individual male transferred genes show patterns of divergent positive selection between *D. mojavensis* and *D. arizonae*. Three of the four genes belong to the sperm-coating protein-like family, including an ortholog of *antares*, which influences female fertility and receptivity in *Drosophila melanogaster*. Synthesis of these molecular evolutionary analyses with transcriptomics and predicted functional information makes these genes candidates for involvement in PMPZ reproductive incompatibilities between *D. mojavensis* and *D. arizonae*.

PLOS | GENETICS

RESEARCH ARTICLE

The Evolutionary Origination and Diversification of a Dimorphic Gene Regulatory Network through Parallel Innovations in *cis* and *trans*

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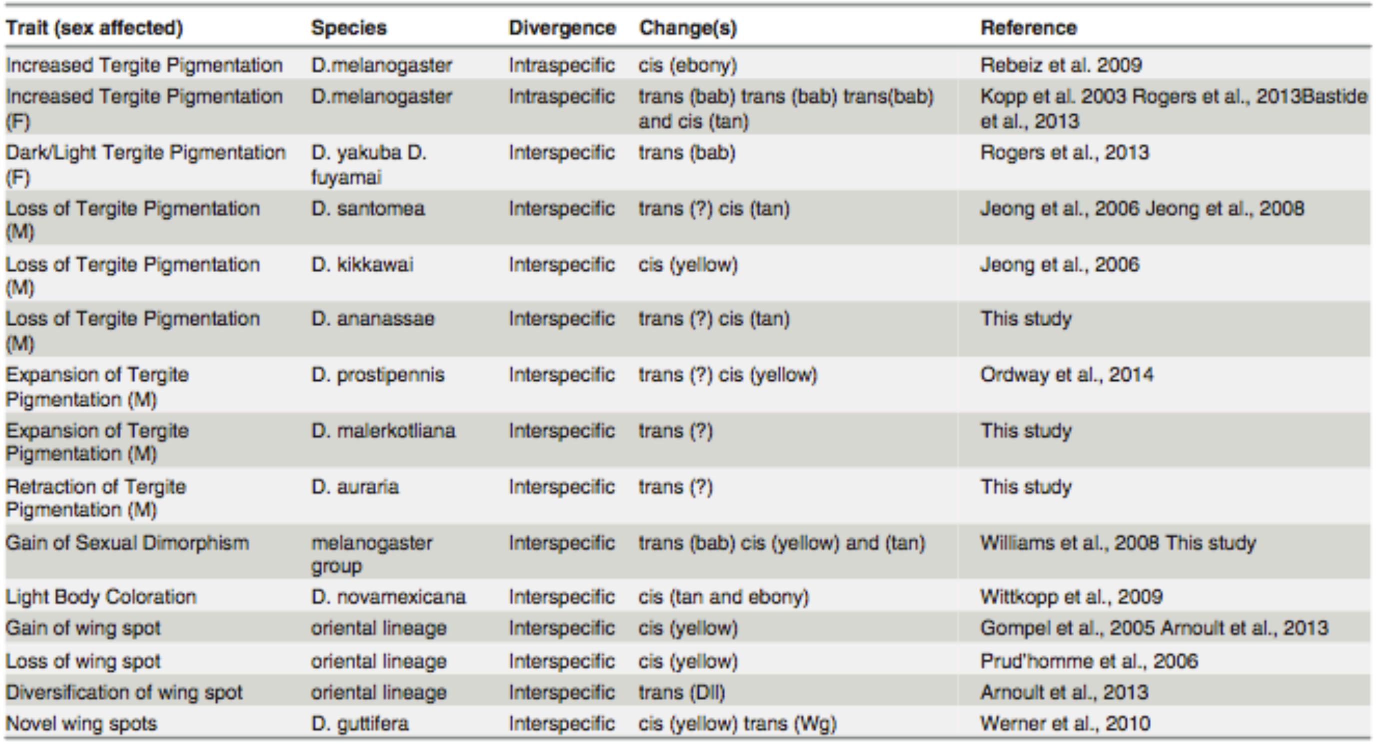
Table 1. A pigmentation enzyme gene perspective of network evolution.



Trait (sex affected)	Species	Divergence	Change(s)	Reference
Increased Tergite Pigmentation	D.melanogaster	Intraspecific	cis (ebony)	Rebeiz et al. 2009
Increased Tergite Pigmentation (F)	D.melanogaster	Intraspecific	trans (bab) trans (bab) trans(bab) and cis (tan)	Kopp et al. 2003 Rogers et al., 2013Bastide et al., 2013
Dark/Light Tergite Pigmentation (F)	D. yakuba D. fuyamai	Interspecific	trans (bab)	Rogers et al., 2013
Loss of Tergite Pigmentation (M)	D. santomea	Interspecific	trans (?) cis (tan)	Jeong et al., 2006 Jeong et al., 2008
Loss of Tergite Pigmentation (M)	D. kikkawai	Interspecific	cis (yellow)	Jeong et al., 2006
Loss of Tergite Pigmentation (M)	D. ananassae	Interspecific	trans (?) cis (tan)	This study
Expansion of Tergite Pigmentation (M)	D. prostipennis	Interspecific	trans (?) cis (yellow)	Ordway et al., 2014
Expansion of Tergite Pigmentation (M)	D. malerkotliana	Interspecific	trans (?)	This study
Retraction of Tergite Pigmentation (M)	D. auraria	Interspecific	trans (?)	This study
Gain of Sexual Dimorphism	melanogaster group	Interspecific	trans (bab) cis (yellow) and (tan)	Williams et al., 2008 This study
Light Body Coloration	D. novamexicana	Interspecific	cis (tan and ebony)	Wittkopp et al., 2009
Gain of wing spot	oriental lineage	Interspecific	cis (yellow)	Gompel et al., 2005 Arnoult et al., 2013
Loss of wing spot	oriental lineage	Interspecific	cis (yellow)	Prud'homme et al., 2006
Diversification of wing spot	oriental lineage	Interspecific	trans (Dll)	Arnoult et al., 2013
Novel wing spots	D. guttifera	Interspecific	cis (yellow) trans (Wg)	Werner et al., 2010

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Notes & Tips

Microwave-mediated enzymatic modifications of DNA

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ABSTRACT

Here we report microwave-induced specific cleavage, ligation, dephosphorylation, and phosphorylation of nucleic acids catalyzed by restriction endonucleases, T4 DNA ligase, T4 polynucleotide kinase, and calf intestinal alkaline phosphatase. The microwave-mediated method has dramatically reduced the reaction time to 20 to 50 s. In control experiments, the same reactions failed to give the desired reaction products when carried out in the same time periods but without microwave irradiation. Because the microwave method is rapid, it could be a useful alternative to the time-consuming conventional procedure for enzymatic modification of DNA.

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FEATURE ARTICLE

THE NATURAL HISTORY OF MODEL ORGANISMS

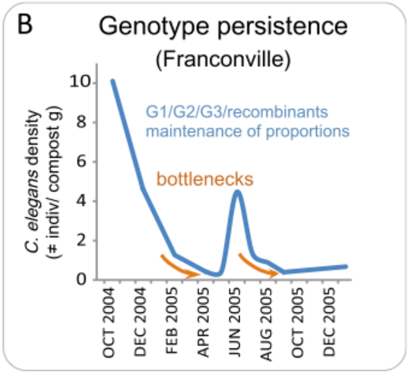
THE NATURAL HISTORY OF MODEL ORGANISMS

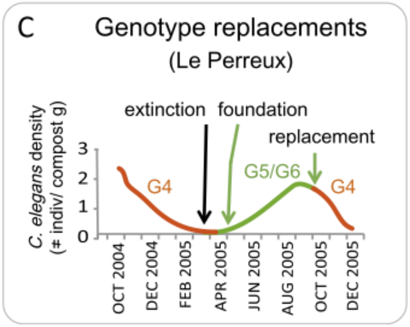
C. elegans outside the Petri dish

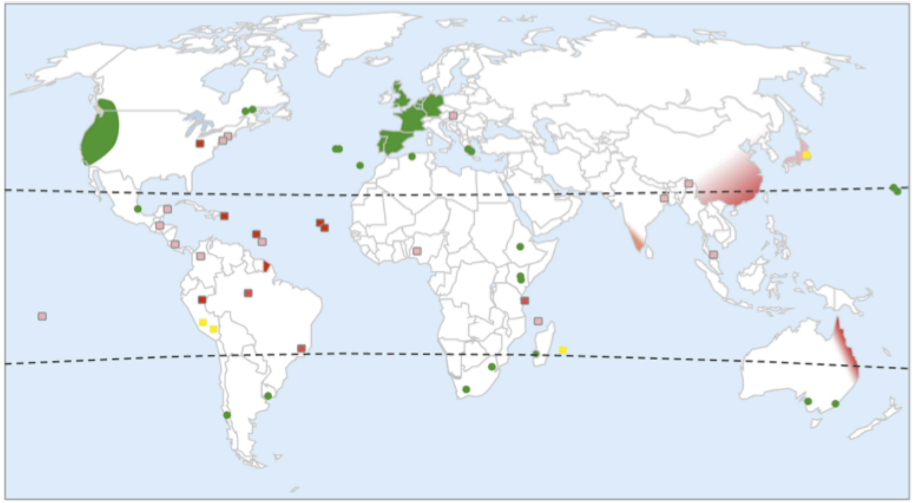
Abstract The roundworm *Caenorhabditis elegans* has risen to the status of a top model organism for biological research in the last fifty years. Among laboratory animals, this tiny nematode is one of the simplest and easiest organisms to handle. And its life outside the laboratory is beginning to be unveiled. Like other model organisms, *C. elegans* has a boom-and-bust lifestyle. It feasts on ephemeral bacterial blooms in decomposing fruits and stems. After resource depletion, its young larvae enter a migratory diapause stage, called the dauer. Organisms known to be associated with *C. elegans* include migration vectors (such as snails, slugs and isopods) and pathogens (such as microsporidia, fungi, bacteria and viruses). By deepening our understanding of the natural history of *C. elegans*, we establish a broader context and improved tools for studying its biology.

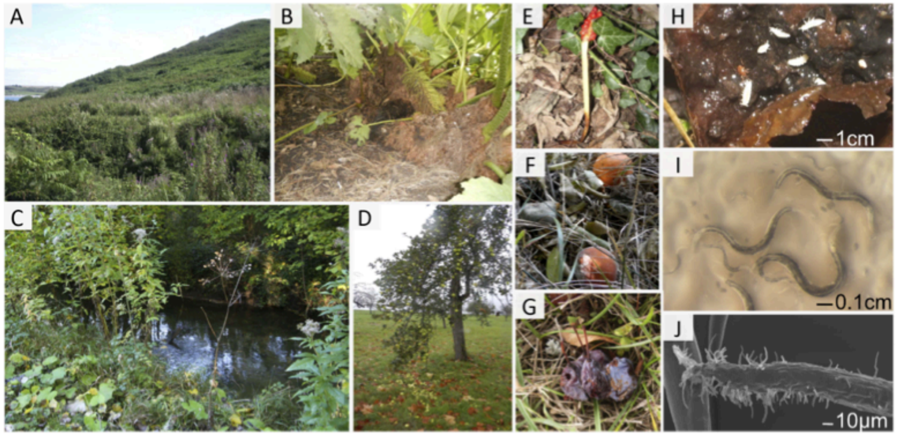
DOI: 10.7554/eLife.05849.001

LISE FRÉZAL* AND MARIE-ANNE FÉLIX*









Evolution: Tinkering within Gene Regulatory Landscapes

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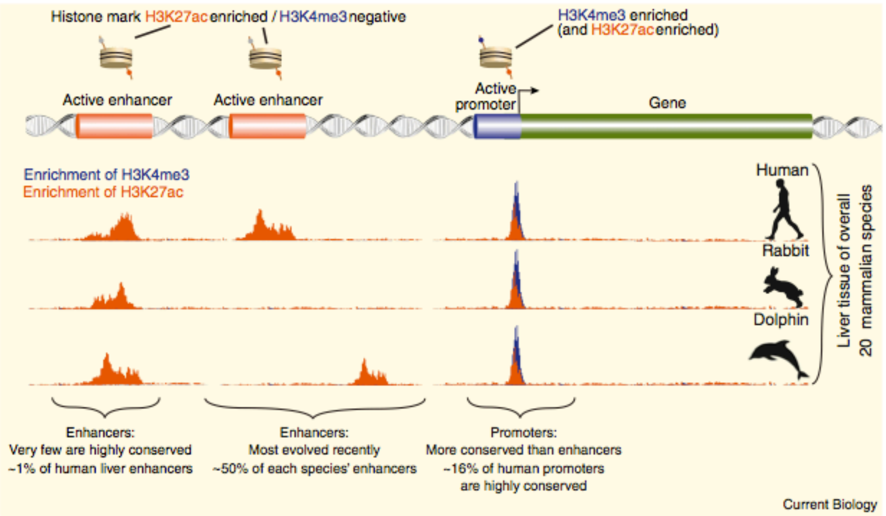
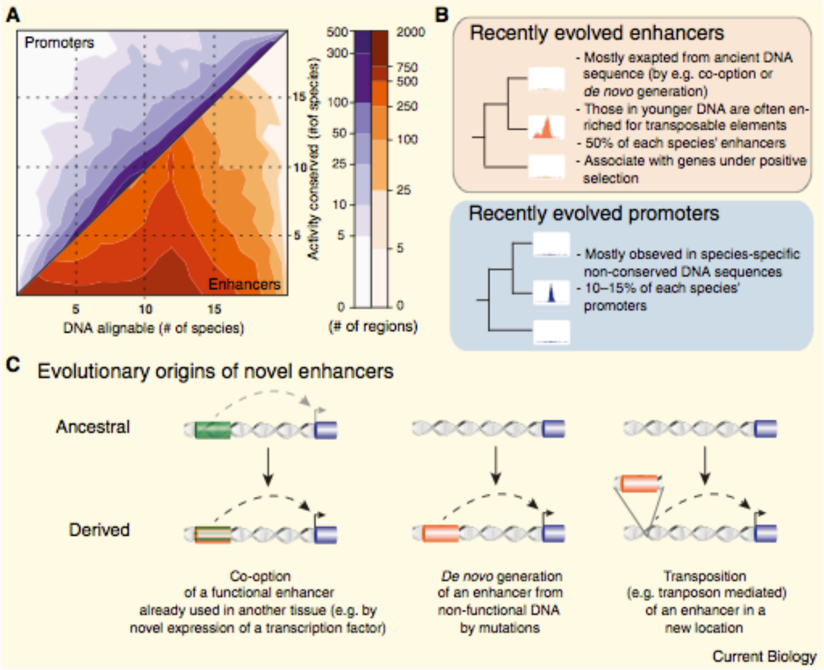
Recently evolved enhancers dominate mammalian gene regulatory landscapes. Mostly exapted from ancestral DNA sequences, many are linked to genes under positive selection. Just as RNA-seq some years ago, unbiased enhancer mapping is on the verge of changing evolutionary research.



Current Biology



Current Biology

Enhancer Evolution across 20 Mammalian Species

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