Press Report

January 2019

Flora Borne

Nature. January 2019

TOOLBOX

3D PRINTING IN THE LAB

As the cost of 3D printers tumbles, researchers have begun using them to make everything from bespoke equipment for experiments to realistic models of human organs.

Equipment on the go
Build a full light microscope using 3D-printing components.
-> Build on the field, repair quickly

Share models: Thingiverse, MyMiniFactory

Life-like organs
Design and build the exact replicate of an organ to practice robot-assisted surgery.
-> Very realistic and adapted to specific patients

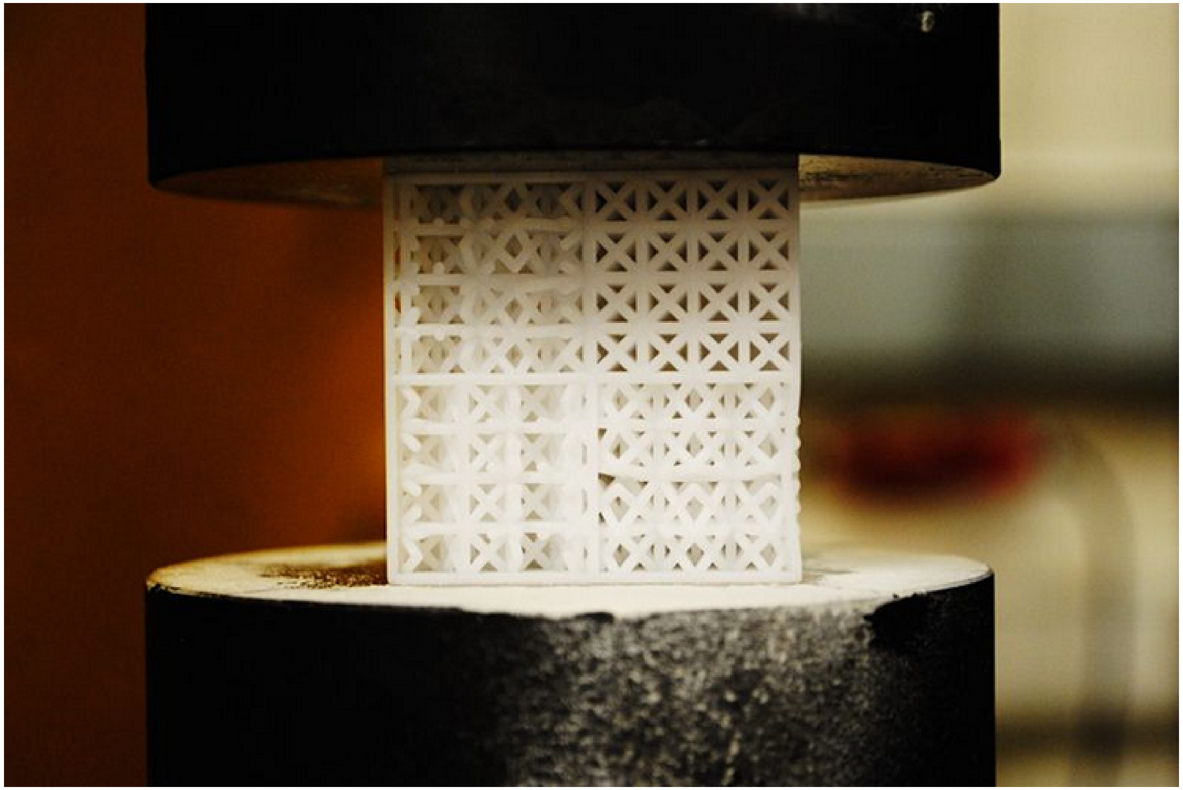
Replicate rocks
-> Create the most realistic rocks to study liquid-flow properties for oil and gas extraction

Nature. January 2019

Damage-tolerant architected materials inspired by crystal microstructure

Minh-Son Pham[1]*, Chen Liu[1], Iain Todd[2] & Jedsada Lertthanasarn[1]

Create complex network structures using 3D printing technologies to obtain the same properties as metallic materials



A new generation of 3D printed materials mimic metals. Credit: M.-S. Pham *et al./Nature*

BMC Genomics. January 2019

Genomic changes associated with adaptation to arid environments in cactophilic *Drosophila* species

Rahul V. Rane[1,2]*, Stephen L. Pearce[1], Fang Li[3], Chris Coppin[1], Michele Schiffer[2], Jennifer Shirriffs[2], Carla M. Sgrò[4], Philippa C. Griffin[2], Goujie Zhang[3,5], Siu F. Lee[1,2], Ary A. Hoffmann[2] and John G. Oakeshott[1]

Goal

Investigate gene gains and positive selection in 5 species from the *depleta* group:

- desert-adapted and non desert-adaptive species
- cactophilic and non cactophilic species

Results

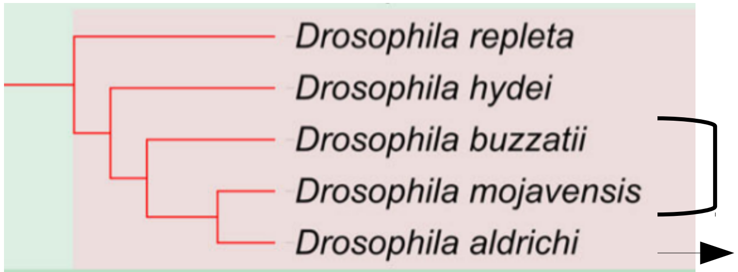
Assembly and annotation of 3 species (*D. repleta, D. buzzatii, D. aldrichi*)

Produce a new phylogeny using 19 *Drosophila* species

High rates of gene gains in internal branches in the species' phylogeny (metabolism)

D. aldrichi, also shows high rates of both gene gains and positive selection (developmental genes)

Rapid genomic changes are associated with both host use and heat and dessication tolerance



cactus use

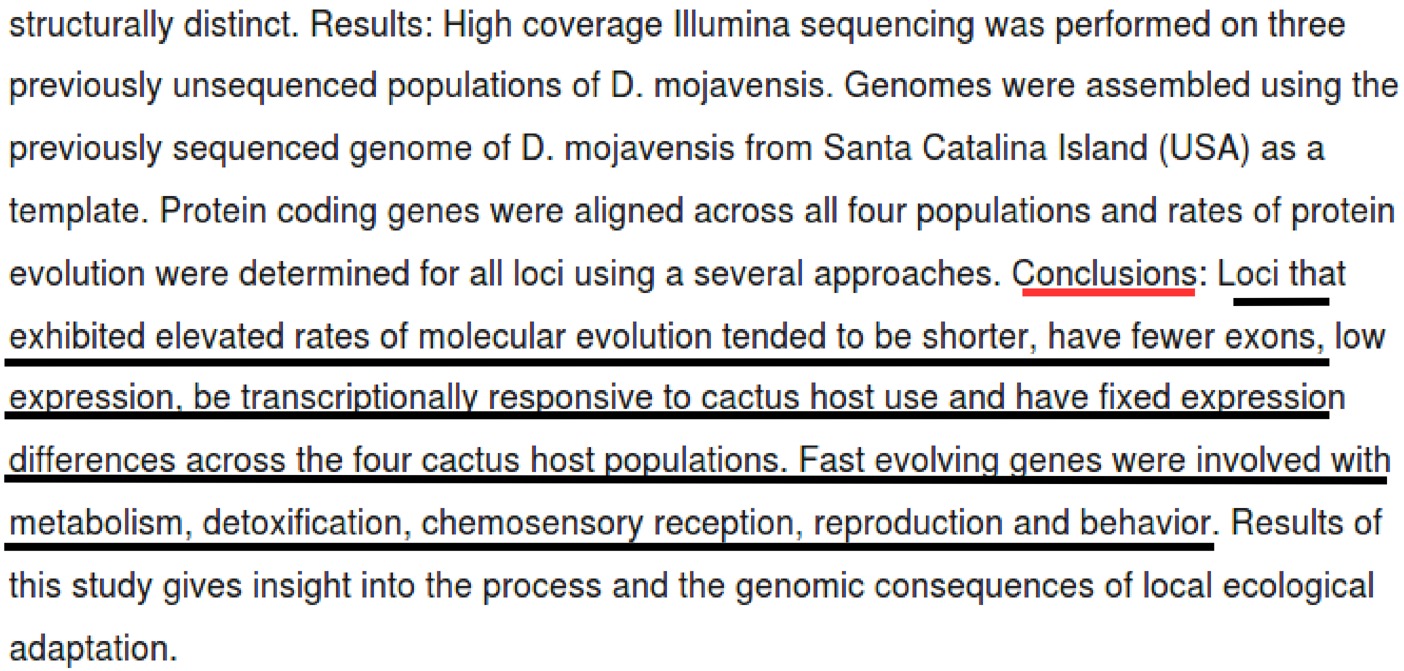
cactus specialisation

Biorxiv. January 2019

Genomic analysis of the four ecologically distinct cactus host populations of Drosophila mojavensis

Carson W Allan, Luciano Matias Matzkin

doi: https://doi.org/10.1101/530154



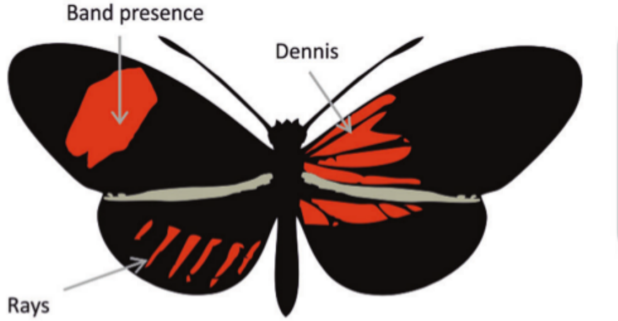
structurally distinct. Results: High coverage Illumina sequencing was performed on three previously unsequenced populations of D. mojavensis. Genomes were assembled using the previously sequenced genome of D. mojavensis from Santa Catalina Island (USA) as a template. Protein coding genes were aligned across all four populations and rates of protein evolution were determined for all loci using a several approaches. Conclusions: Loci that exhibited elevated rates of molecular evolution tended to be shorter, have fewer exons, low expression, be transcriptionally responsive to cactus host use and have fixed expression differences across the four cactus host populations. Fast evolving genes were involved with metabolism, detoxification, chemosensory reception, reproduction and behavior. Results of this study gives insight into the process and the genomic consequences of local ecological adaptation.

Heredity. January 2019

The genetic architecture of adaptation: convergence and pleiotropy in *Heliconius* wing pattern evolution

Jake Morris[1] · Nicolas Navarro[2,3] · Pasi Rastas[4] · Lauren D. Rawlins[5] · Joshua Sammy[1] · James Mallet[6] ·
Kanchon K. Dasmahapatra[1]

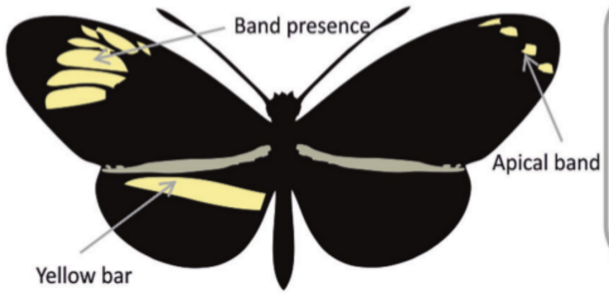
3 main locus control the majority of pattern variation in *Heliconius* species



optix (LG 18)

Locus synonyms: *B/D, D, Br/G*

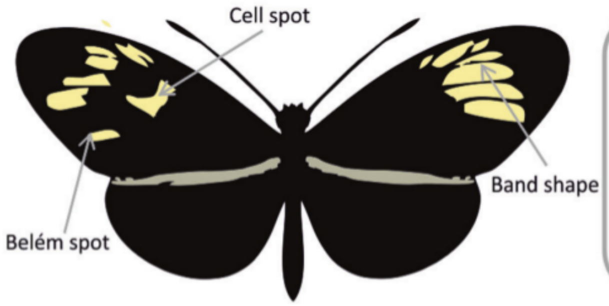
- Red band presence = *H. erato, H. melpomene*
- Dennis patch = *H. erato, H. melpomene*
- Rays = *H. erato, H. melpomene*
- Red/brown patterning in other *Heliconius* species



cortex (LG 15)

Locus synonyms: *Yb/Sb/N/P*

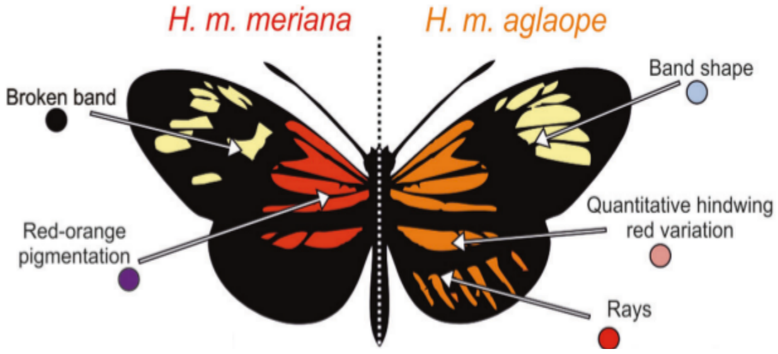
- Yellow band presence = *H. erato, H. melpomene*
- Apical band = *H. hecale*
- Yellow bar = *H. erato, H. melpomene*
- Found within the *H. numata* supergene P



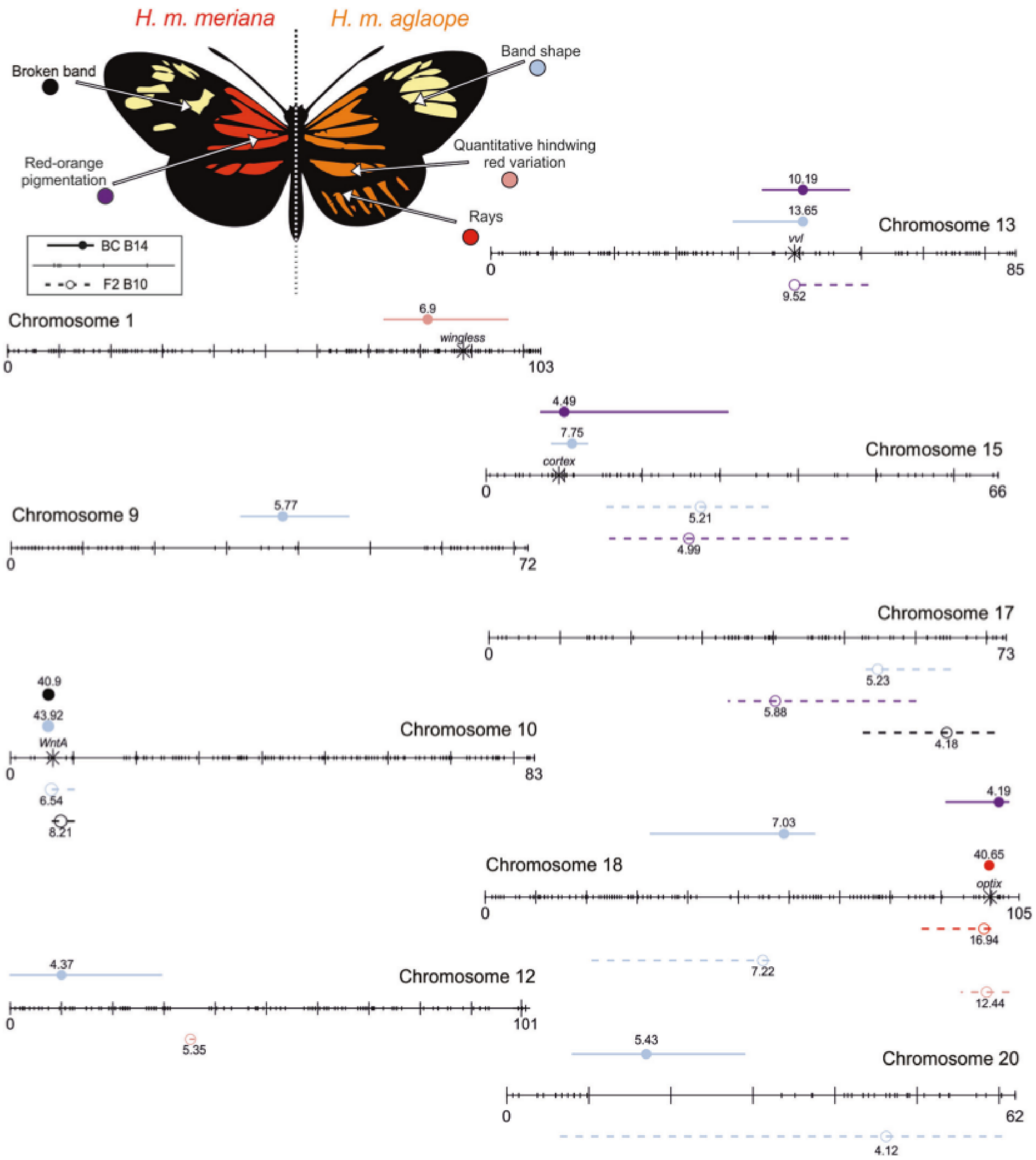
WntA (LG 10)

Locus synonyms: *Ac, Sd*

- Yellow band shape = *H. erato*
- Red band shape = *H. erato, H. melpomene*
- Dumbbell/Cell spot = *H. erato, H. cydno*
- Belém spot = *H. erato*
- Quantitative forewing black variation = *H. hecale*



→ QTL mapping on crosses of *Heliconius melpomene*



- already known genes
- pleiotropy

→ discussion about pleiotropy and adaptive constraint

chr 13:
- mapping *Or* locus near *vvl*
- close to *Ro* locus in *H. erato* but not homologous

→ convergent evolution in *Heliconius* species

Genetics. early online. January 2019

The genetics of mating song evolution underlying speciation: linking quantitative variation to candidate genes for behavioral isolation

Mingzi Xu, Kerry L. Shaw

Here, we investigate the genetic and genomic basis of natural variation in pulse rate (the inverse of pulse duration, Figure 1) of the male mating song of the endemic Hawaiian cricket *Laupala*. In *Laupala*, a rapid radiation has resulted in 38 morphologically and ecologically similar, but acoustically distinctive species (Otte 1994; Mendelson and Shaw 2005). Similar to most crickets, males sing long-range "calling" songs to attract females. Male songs of *Laupala* are characterized by simple trains of pulses delivered at species-specific rates (Otte 1994, Shaw 2000). Evidence shows that divergent pulse rate partially mediates mate choice (Shaw and Herlihy 2000, Oh and Shaw 2013) and constitutes a reproductive barrier between species (Mendelson and Shaw 2002).

We focus on two closely related species, the slow calling *L. paranigra* (0.71 pulse per second, pps) and the fast calling *L. kohalensis* (3.72 pps, Shaw et al. 2007, Figure 1),

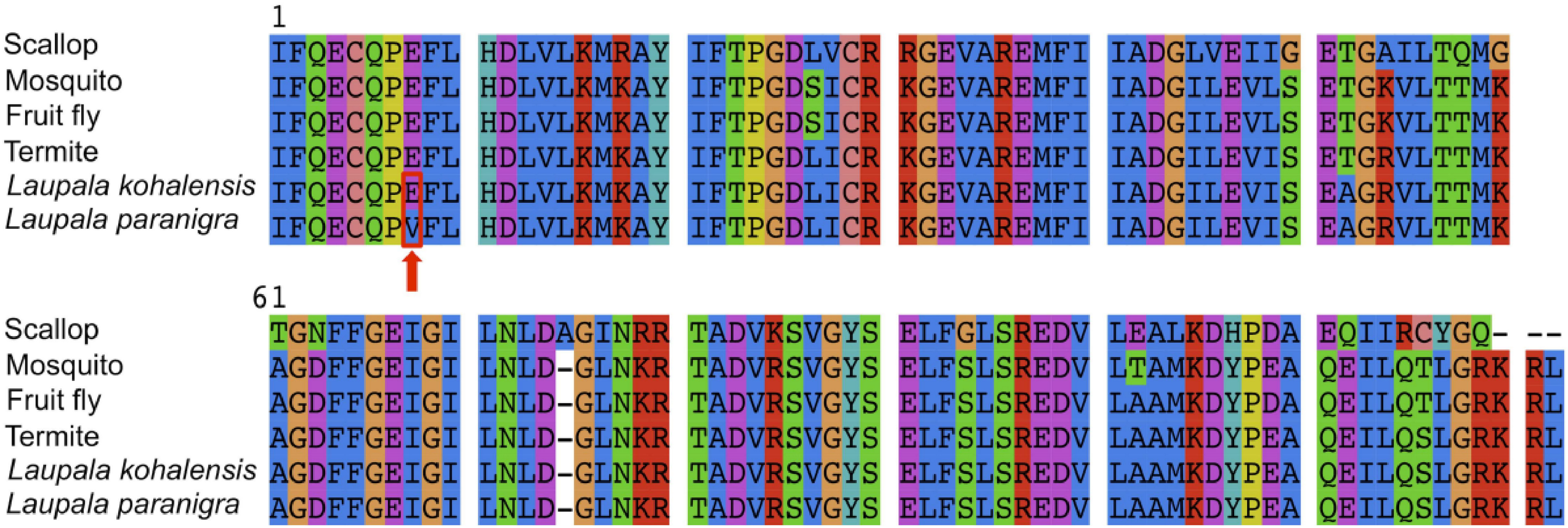
QTL mapping

Map one large effect QTL

No QTL contains homologs of *D. melanogaster* genes involved in courtship song

One candidate causal gene: cyclic nucleotide-gated ion channel-like gene (Cngl)

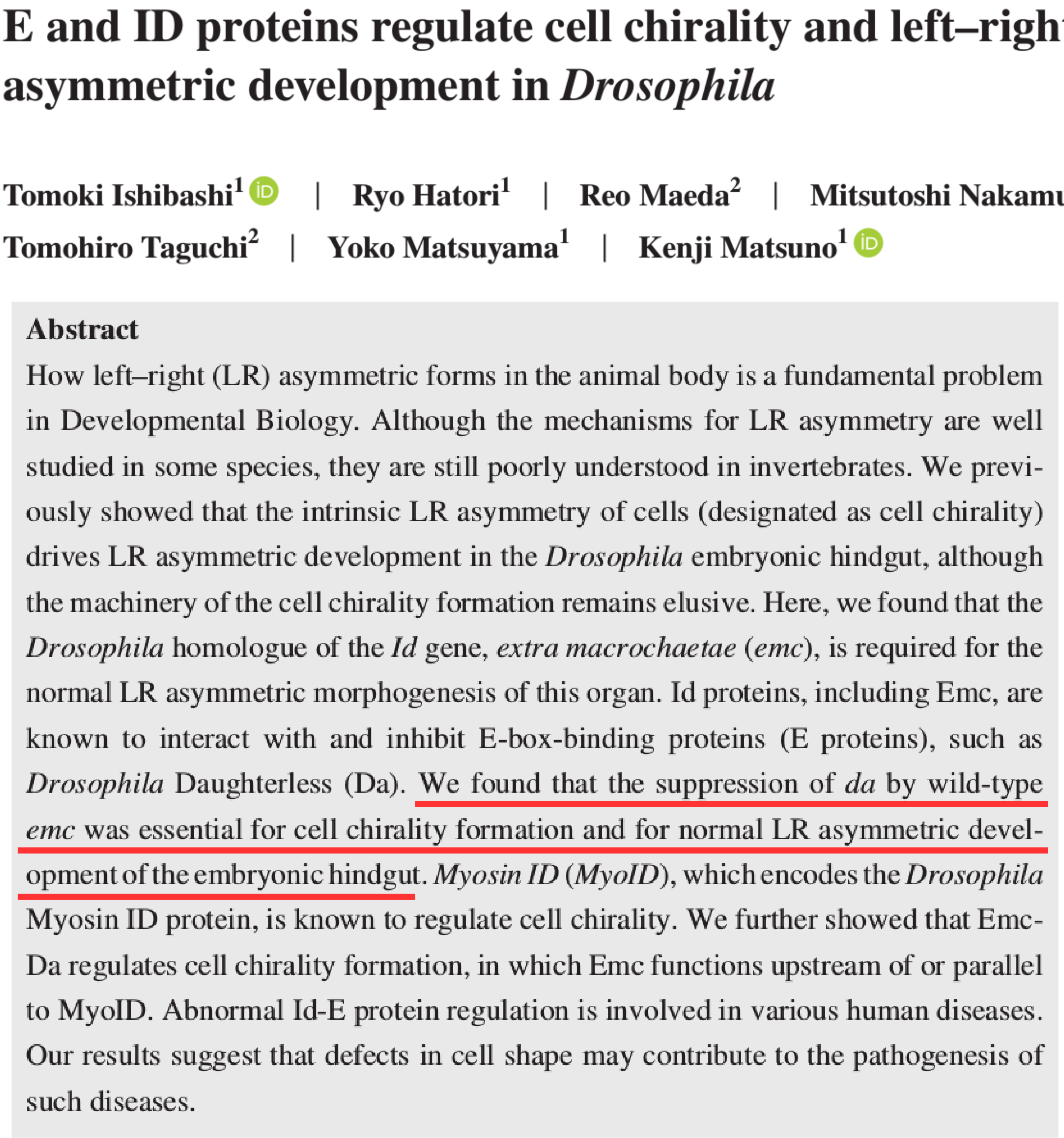
- ion channels gated by cyclic-nucleotides are known to be involved in rhythm generation
- a non-synonymous SNP in the exon coding one highly conserved binding domain



	1					
Scallop	IFQECQPEFL	HDLVLKMRAY	IFTPGDLVCR	RGEVAREMFI	IADGLVEIIG	ETGAILTQMG
Mosquito	IFQECQPEFL	HDLVLKMKAY	IFTPGDSICR	KGEVAREMFI	IADGILEVLS	ETGKVLTTMK
Fruit fly	IFQECQPEFL	HDLVLKMKAY	IFTPGDSICR	KGEVAREMFI	IADGILEVLS	ETGKVLTTMK
Termite	IFQECQPEFL	HDLVLKMKAY	IFTPGDLICR	KGEVAREMFI	IADGILEVIS	ETGRVLTTMK
Laupala kohalensis	IFQECQPEFL	HDLVLKMKAY	IFTPGDLICR	KGEVAREMFI	IADGILEVIS	EAGRVLTTMK
Laupala paranigra	IFQECQPVFL	HDLVLKMKAY	IFTPGDLICR	KGEVAREMFI	IADGILEVIS	EAGRVLTTMK

	61						
Scallop	TGNFFGEIGI	LNLDAGINRR	TADVKSVGYS	ELFGLSREDV	LEALKDHPDA	EQIIRCYGQ-	--
Mosquito	AGDFFGEIGI	LNLD-GLNKR	TADVRSVGYS	ELFSLSREDV	LTAMKDYPEA	QEILQTLGRK	RL
Fruit fly	AGDFFGEIGI	LNLD-GLNKR	TADVRSVGYS	ELFSLSREDV	LAAMKDYPDA	QEILQTLGRK	RL
Termite	AGDFFGEIGI	LNLD-GLNKR	TADVRSVGYS	ELFSLSREDV	LAAMKDYPEA	QEILQSLGRK	RL
Laupala kohalensis	AGDFFGEIGI	LNLD-GLNKR	TADVRSVGYS	ELFSLSREDV	LAAMKDYPEA	QEILQSLGRK	RL
Laupala paranigra	AGDFFGEIGI	LNLD-GLNKR	TADVRSVGYS	ELFSLSREDV	LAAMKDYPEA	QEILQSLGRK	RL

Genes to Cells. January 2019



E and ID proteins regulate cell chirality and left–right asymmetric development in *Drosophila*

Tomoki Ishibashi[1] | **Ryo Hatori**[1] | **Reo Maeda**[2] | **Mitsutoshi Nakamura**[1] | **Tomohiro Taguchi**[2] | **Yoko Matsuyama**[1] | **Kenji Matsuno**[1]

Abstract

How left–right (LR) asymmetric forms in the animal body is a fundamental problem in Developmental Biology. Although the mechanisms for LR asymmetry are well studied in some species, they are still poorly understood in invertebrates. We previously showed that the intrinsic LR asymmetry of cells (designated as cell chirality) drives LR asymmetric development in the *Drosophila* embryonic hindgut, although the machinery of the cell chirality formation remains elusive. Here, we found that the *Drosophila* homologue of the *Id* gene, *extra macrochaetae* (*emc*), is required for the normal LR asymmetric morphogenesis of this organ. Id proteins, including Emc, are known to interact with and inhibit E-box-binding proteins (E proteins), such as *Drosophila* Daughterless (Da). We found that the suppression of *da* by wild-type *emc* was essential for cell chirality formation and for normal LR asymmetric development of the embryonic hindgut. *Myosin ID* (*MyoID*), which encodes the *Drosophila* Myosin ID protein, is known to regulate cell chirality. We further showed that Emc-Da regulates cell chirality formation, in which Emc functions upstream of or parallel to MyoID. Abnormal Id-E protein regulation is involved in various human diseases. Our results suggest that defects in cell shape may contribute to the pathogenesis of such diseases.

- Hypoxic and Cold Adaptation Insights from the Himalayan Marmot Genome. iScience, January 2019.

- A potential role for the gut microbiota in the specialisation of Drosophila sechellia to its toxic host noni (Morinda citrifolia). Biorxiv, January 2019.

- Eco-evolutionary dynamics of sexual selection and sexual conflict. Heredity, January 2019.

- Evolutionary Quantitative Genetics of Genomic Imprinting. Genetics, January 2019.

- Transforming insect population control with precision guided sterile males with demonstration in flies. Nature Communication, January 2019.

- Insights from genomes into the evolutionary importance and prevalence of hybridization in nature. Review. Nature Ecology and Evolution, January 2019.

- Imaging flyes by fluorescence microscopy: principles, technologies and applications. Genetics. Flybook methods. January 2019