2

lolal Is an Evolutionarily New Epigenetic Regulator of dpp Transcription during Dorsal-Ventral Axis Formation.

Quijano JC, Wisotzkey RG, Tran NL, Huang Y, Stinchfield MJ, Haerry TE, Shimmi O, Newfeld SJ

show author affiliations

Mol Biol Evol. 2016 Oct; 33(10):2621-32

Recommendations:

Very Good **10 Jan 2017**

Manyuan Long

F1000 Genomics & Genetics

University of Chicago, Chicago, IL, USA.

NEW FINDING

DOI: 10.3410/f.726500532.793526924

The fate of new genes, duplicates of existing genes, is often elimination by natural selection. In some cases, these genes provide a novel function or more efficiently execute an existing function, offering the organism a selective advantage and are maintained. Yet how a new gene with a novel function becomes integrated into an existing genetic network is not well known. The distribution of these events across the phylogenetic landscape is also unknown.

The same group of authors has produced a pair of comparative experimental studies of the genetic network underlying the formation of the dorsal-ventral body axis during development in Drosophila and vertebrates. First, they found that a new gene unique to vertebrates, a Ring class ubiquitin ligase called TRIM33, had replaced an older gene called Nedd4, a Hect class ubiquitin ligase, that was common to both phyla {1}. Those experiments revealed that the vertebrate dorsal-ventral pathway, until then considered universally conserved with Drosophila, was able to incorporate a new gene.

The current paper nicely complements that analysis by demonstrating that a new gene in the fly lineage, called Lolal has been incorporated into the conserved dorsal-ventral patterning network. Lolal is present only in insects and crustaceans, yet it functions as part of a multiprotein complex that maintains the expression of Dpp - a key signaling molecule in dorsal-ventral axis formation that is absolutely conserved as vertebrate BMP2/4. The authors predict that while Lolal itself is not present in vertebrates, its function in the maintenance of BMP2/4 expression almost certainly is. They suggest several candidates and await the outcome.

Overall, these two studies demonstrate the new genes are capable of incorporation into existing, highly conserved genetic networks across phyla. From a larger perspective, they reveal that the dorsal-ventral pattern formation pathway functioning in all Bilateria has both highly conserved components and species-specific components, an advance on the current model of monolithic conservation.

References

1. **New gene evolution in the bonus-TIF1-γ/TRIM33 family impacted the architecture of the vertebrate dorsal-ventral patterning network.**
Wisotzkey RG, Quijano JC, Stinchfield MJ, Newfeld SJ. Mol Biol Evol. 2014 Sep; 31(9):2309-21
PMID: 24881051 DOI: 10.1093/molbev/msu175

Disclosures

None declared

Add a comment

Abstract:

ABSTRACT

Secreted ligands in the Dpp/BMP family drive dorsal-ventral (D/V) axis formation in all Bilaterian species. However, maternal factors regulating Dpp/BMP transcription in this process are largely unknown. We identified the BTB domain protein longitudinals lacking-like (lolal) as a modifier of decapentaplegic (dpp) mutations. We show that Lolal is evolutionarily related to the Trithorax group of chromatin regulators and that lolal interacts genetically with the epigenetic factor Trithorax-like during Dpp D/V signaling. Maternally driven Lolal(HA)... more »
is found in oocytes and translocates to zygotic nuclei prior to the point at which dpp transcription begins. lolal maternal and zygotic mutant embryos display significant reductions in dpp, pMad, and zerknullt expression, but they are never absent. The data suggest that lolal is required to maintain dpp transcription during D/V patterning. Phylogenetic data revealed that lolal is an evolutionarily new gene present only in insects and crustaceans. We conclude that Lolal is the first maternal protein identified with a role in dpp D/V transcriptional maintenance, that Lolal and the epigenetic protein Trithorax-like are essential for Dpp D/V signaling and that the architecture of the Dpp D/V pathway evolved in the arthropod lineage after the separation from vertebrates via the incorporation of new genes such as lolal.

DOI: 10.1093/molbev/msw132

RECOMMENDATIONS 1 | ABSTRACT | COMMENTS expand all

Library of Medicine and the National Institutes of Health.

Comments:

COMMENTS add a comment

F1000 Faculty Reviews are comprehensive, open access, topical reviews written by members of the prestigious **F1000 Faculty**. These peer reviewed articles provide context on emerging themes in biology and medicine.

view all

Developmental Biology | Evolutionary Biology | Genomics & Genetics | Ecology

From Darwin's Origin of Species toward a theory of natural history

Ferdinando Boero
F1000Prime Reports 2015 7:(49) *(12 May 2015)*

Full text | PDF | Abstract on PubMed

Bioinformatics & Computational Biology | Biotechnology | Developmental Biology | Evolutionary Biology | Genomics & Genetics | Molecular Biology | Neuroscience | Structural Biology | Cell Biology | Biochemistry | Physiology

Post-transcriptional regulation of early embryogenesis

Timothy T. Weil
F1000Prime Reports 2015 7:(31) *(03 Mar 2015)*

Full text | PDF | Abstract on PubMed

Librarian Resources
Press Office
F1000 Specialists
F1000 Updates
About/Contact

Article Recommendations
F1000Prime Reports
F1000Prime Faculty
Blog
Subscribe
F1000 Mobile
About
FAQs
Contact

Work
FAQ
Contact

Articles
Advisory Panel
Blog
Submit
Author Guidelines
Register
About
Contact

Download the mobile app today