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Combining molecular information on chromatin organisation with eQTLs and evolutionary conservation provides strong candidates for the evolution of gene regulation in mammalian brains

Marc Robinson-Rechavi

Department of Ecology and Evolution, University of Lausanne -- Lausanne, Switzerland
marc.robinson-rechavi@unil.ch
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A recommendation of

Novo FJ. 2017. **Evolutionary analysis of candidate non-coding elements regulating neurodevelopmental genes in vertebrates**. *BioRxiv*, 150482, ver. 4 of 29th September 2017. doi: 10.1101/150482

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In this manuscript [1], Francisco J. Novo proposes candidate non-coding genomic elements regulating neurodevelopmental genes.

What is very nice about this study is the way in which public molecular data, including physical interaction data, is used to leverage recent advances in our understanding to molecular mechanisms of gene regulation in an evolutionary context. More specifically, evolutionarily conserved non coding sequences are combined with enhancers from the FANTOM5 project, DNAse hypersensitive sites, chromatin segmentation, ChIP-seq of transcription factors and of p300, gene expression and eQTLs from GTEx, and physical interactions from several Hi-C datasets. The candidate regulatory regions thus identified are linked to candidate regulated genes, and the author shows their potential implication in brain development.

While the results are focused on a small number of genes, this allows to verify features of these candidates in great detail. This study shows how functional genomics is increasingly allowing us to fulfill the promises of Evo-Devo: understanding the molecular mechanisms of conservation and differences in morphology.

References

[1] Novo, FJ. 2017. Evolutionary analysis of candidate non-coding elements regulating neurodevelopmental genes in vertebrates. bioRxiv, 150482, ver. 4 of Sept 29th, 2017. doi: 10.1101/150482

Appendix

Reviews by Marc Robinson-Rechavi and Charles Danko: http://dx.doi.org/10.24072/pci.evolbiol.100035