**PlantFUNCO: integrative functional genomics database reveals clues into duplicates divergence evolution**

Víctor Roces1, Sara Guerrero1, Ana Álvarez1, Jesús Pascual1, Mónica Meijón1\*

1 Plant Physiology, Department of Organisms and Systems Biology, Faculty of Biology and Biotechnology Institute of Asturias, University of Oviedo, Asturias, Spain

\* Correspondence: [meijonmonica@uniovi.es](mailto:meijonmonica@uniovi.es)

# Abstract

Evolutionary epigenomics, and more generally evolutionary functional-genomics, is an exciting emerging field studying how non-DNA encoded alterations in gene expression regulation are an important form of plasticity and epigenetic adaptation. Previous evidence analyzing plants evolutionary functional-genomics has mostly been focused on compare same assay matched experiments, missing the power of heterogeneous datasets for conservation inference. To fill this gap, we introduced PlantFUN(nctional)CO(nservation) database which is derived from two resources, inter-species chromatin states and functional genomics conservations scores, presented and analysed in this work for three well-established plant models. Overall, both resources can elucidate evolutionary information in terms of cross-species functional agreement. Therefore, PlantFUNCO could complement other comparative-genomics sources to asses evolutionary studies. In order to illustrate potential applications of the database, we replicated two previously published models predicting genetic redundancy in *A. thaliana* and found that chromatin states are a determinant of paralogs degree of functional divergence. These predictions were validated based on the phenotypes of mitochondrial alternative oxidases knockout mutants under two different stresses. Taken all together, PlantFUNCO aim to leverage data diversity and extrapolate molecular mechanisms findings from different model organisms to determine the extent of functional conservation, thus, deepen our understanding of how plants phenotypic plasticity has fascinatingly evolved. PlantFUNCO database is available at <https://rocesv.github.io/PlantFUNCO>.

**Keywords**: evolutionary epigenomics, functional genomics, integrative approach, database, genome evolution.