## Introduction

A fundamental question in biology is how complex patterns of gene expression are determined to explain different phenotypes (Schmitz, Grotewold, & Stam, 2022; Marand et al., 2023). Nowadays, is largely known that genome function is dynamically regulated in part by chromatin organization, which consists of the histones, non-histone proteins and RNA molecules that package DNA (Ho et al., 2014). In this sense, the generation of comprehensive chromatin state maps, defined as the homogeneous co-existance of multiple epigenetic marks at the whole genome level, provide valuable information for annotating coding and non-coding genome features, including the identification of various types of regulatory elements. Chromatin states can facilitate our understanding of regulatory elements and variants that are associated to core life-processes such as development, disease and stress response (Liu et al., 2018). Great efforts have been made by the plant research community to contribute to the comprehension of chromatin mechanisms using different models (Zhao et al., 2020; Jamge et al., 2023), but an universal annotation which allows the extrapolation and unification of earlier conclusions across species/conditions still needs to be adressed.

Evolutionary theory has been dominated by the ideas that selection proceeds by changes in allele frequencies within-between populations and mutations occur randomly with respect to their consequences. Last theoretical and experimental advances in the field point to phenotypic plasticty as an adaptative trait subjected to natural selection, ergo, similar genotypes that develop different and appropiate phenotypes without sequence change could be equally responsible of evolutionary changes (Ashe, Colot, & Oldroyd, 2021; Monroe et al., 2022). This bring us to evolutionary epigenomics, and more generally, evolutionary functional-genomics, an exciting emerging field studying how non-DNA encoded alterations in protein functions for multiple generations are an important form of plasticity and epigenetic adaptation. For that reason, regulatory elements states started to be considered major targets of evolution because their diversity is critical for phenotypic variance in all organisms to adapt to various environment niches (Yocca & Edger, 2022). Although relevant research in plants has lagged behind animals species (Schmitz et al., 2022), some of the most controversial findings in evolutionary biology, for example mutations occur less often in functionally constrained regions and epimutations are located in hotspots with specific chromatin features, used plant models (Hazarika et al., 2022; Monroe et al., 2022). These findings supported the clear importance of the plant kingdom in evolutionary functional-genomics. Plants present a series of interesting molecular features that allow same-sequence different-functions scenarios, like epigenetic states are more easily transmitted intergenerationally due to soft epigenetic reset during meiosis and early development, epialleles are quite common and relative high rate of duplication events so multiple original exact gene copies with distinct selection pressures in response to the enviroment could exist (Ashe et al., 2021; Cusack et al., 2021). Many comparative-genomics studies interrogate sequence-conserved loci of interest across a wide range of species and its function is determined by perturbing their homologous in a single model organism. In this context, a maze of opportunities and challenges appeared to systematically and confidently determine the extent of conservation at the functional genomics level between model species (Kwon & Ernst, 2021).

Little previous evidence analyzing evolutionary functional-genomics has mostly been focused on compare same assay matched experiments (Maher et al., 2018; Lu et al., 2019). These works have been crucial for in-depth study of molecular machinery, but missed the power of diverse datasets for conservation inference. In contrast to this narrow but deep knowledge bottleneck, we adopted a broad but shallow approach using heterogeneous functional-genomics to directly search simple large-scale answers that we would never have contemplated asking based on our understanding of single-assay/species information (Kliebenstein, 2019). In the current Earth Biogenome era there are more and more genomes and functional tracks becoming available (Exposito-alonso et al., 2020), thus, highlighting the urge of using integrative tools that consider the vast diversity of biological strategies and enable wide genomic elements chracterization. In the present study, taking into account the abovementioned knowledge trade-off, we introduced PlantFUN(ctional)CO(nservation) an integrative functional-genomics database constituted by several tools and two main resources, inter-species chromatin states and functional genomics conservation scores, for the well-known plant models *Arabidopsis thaliana*, *Oryza sativa* and *Zea mays*. Overall, both resources can elucidate evolutionary information in terms of cross-species functional agreement, therefore PlantFUNCO can complement other comparative-genomics sources to asses conservation and diversity. To illustrate how results derived from the resources generated could be functionally relevant, we developed an application of the database and found that chromatin state information improved paralogous degree of functional divergence predictions. Lastly, we validated the redundancy predictions based on phenotypic effects of alternative oxidases genes knockout mutants under several stres conditions.

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