## Discussion

We introduced PlantFUNCO, a database to allow the community further inspection of the crosstalk between evolution and phenotypic plasticity in terms of epigenomics/functional-genomics. This database is derived from two resources presented and analysed in this work for three well-established plant models. On one hand, we generated inter-species CS using hiHMM. While this flexible framework provides a consistent definition of CS across multiple genomes, making easier direct comparison between them, the stack approach allows the understanding of the potential epigenomic regulation over several tissues/conditions such as differentiating constitutively active/repressive regions (Vu & Ernst, 2022). CS link with different types of evolutionary information established a foundation for the epigenomics inter-species perspective. It should be noted that all the approaches have trade-offs so the resource should be considered complementary to and not a replacement to other single-species/condition annotations. On the other hand, we obtained functional genomics conservation scores using LECIF. In accordance to the abovementioned framework, LECIF can handle very diverse datasets and take advantage of it to quantify functional conservation. Plants LECIF-score elucidated functional-genomics cross-species agreement without being correlated with other comparative-genomics sources. Hence, probably reflecting a complementary side of the evolution. Despite the greater diversity in plants vs metazoan models (Ho et al., 2014; Kwon & Ernst, 2021), both resources results are coungruent with a higher plant epigenomic/functional complexity probed by more states with species-specific features and lower values of LECIF-scores.

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CS application to modelling, models far of being perfect … Use for predicting genomic elements and mechanisms. Functional translatation of the predictions and resource to explain complex biological mechanisms; diferencia de intensidad de estreses, con el estres AOX1C insensitive, lio con otras referencias, additional care; DFD values partial redundancy of aox1d con aox1a pero no al reves, aox1c almost stress insentitive. Stress promotes neofunctions. exploiting that our approach could differ between constituvely active and repressive states.

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Diversidad de datos perdida de oportunidad para entender conservacion. DB and future of evolutionary epigenomics. Hypotehsiis unificar conclusions y ver como fascinanemente ha evolucionar la diversidad molecular. Con el increment de track Genome Era etc. Further expansion to other well know models.

wide range of genomic prediction properties for the community.. Deep and narrow vs shallow and broad

Previous works analyzing inter-species functional genomics were focused on comparing same assay matched experiments missing the power of diverse datasets for conservation inference .integrative features needed for genomic elements and patterns discovery.

Therefore, simplifying genome annotation across tissues/species through a single segmentation.

Paralog ancestral function hypothesis