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exchange (homologous recombination) between closely related viruses. In phylogenetics, recombination may be revealed through incongruence of trees in regions of genomes with occurrence of recombination. Reticulate evolution refers to the origination of lineages through the complete or partial merging of ancestor lineages. Networks may be used to represent lineage independence events in non-treelike phylogenetic processes. In terms of information through reticulate evolution, genetic recombination entails the splitting and rejoining of two unrelated or distantly related DNA to form a new DNA. As the recombinant sequence is a merger of two evolutionary histories, such a process cannot be modeled by trees. Instead, a phylogenetic network representation of a recombination event is needed. The methodology for reconstructing networks is still in development. Here we explore two methods for reconstructing unrooted phylogenetic networks, PhyloNetworks and Phylonet, which employ computationally expensive and time consuming algorithms. The construction of phylogenetic networks follows a coordinated processing flow of data sets analyzed and processed by the coordinated execution of a set of different programs, packages, libraries or pipelines, called workflow activities. In view of the complexity in modeling network experiments, the present work introduces a workflow for phylogenetic network analyses coupled to be executed in High-Performance Computing (HPC) environments. The workflow aims to integrate well-established software, pipelines and scripts, implementing a challenging task since these tools do not consistently profit from the HPC environment, leading to an increase in the expected makespan and idle computing resources. At first, we draw a straightforward workflow without optimization to create phylogenetic networks aiming to observe the performance of the employed tools. Parsl -a scalable parallel programming library for Python- was used to orchestrate the flow activities. This integration shows overperformed result executions of the workflow, also with better management of HPC resources, enabling us to scale our phylogenetic studies.

Native and foreign proteins conform the OXPHOS complexes of *Lophophytum mirabile* (Balanophoraceae)

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Session 8

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The intimate contact between the holoparasitic plant *Lophophytum mirabile* (Balanophoraceae) and its host plant (Mimosoideae, Fabaceae) facilitates the exchange of genetic information, increasing the frequency of horizontal gene transfer (HGT). *Lophophytum* has revealed the unprecedented acquisition of a large number of mitochondrial genes from its legume host that replaced the native homologs. These foreign genes are functional and encode proteins that form multi-subunit enzyme complexes together with proteins of nuclear origin. For all these reasons, *Lophophytum* is an interesting model to study the evolution of multiprotein complexes in the mitochondria, the impact of HGT in the nuclear genome, and its co-evolution with the mitochondrial genome. Given the presence of foreign mitochondrial proteins in

Lophophytum, it is proposed that nuclear genes that encode proteins involved in these complexes are also foreign, minimizing the incompatibilities in the assembly and functioning of these multiprotein complexes. Multiple alignments were generated from nucleotide sequences of 25 angiosperms to infer the phylogenetic relationships of 75 nuclear genes (obtained from the *Lophophytum* transcriptome) involved the oxidative phosphorylation system (OXPHOS) of *Lophophytum*. Maximum likelihood phylogenetic analyses were ran with RAxML 8.2.11 using GTRGAMMA models along with 1,000 rapid bootstrapping pseudo-replicates. To examine gene conversion events within genes we used Geneconv. Based on these results, we infer that 74 subunits are native and one is foreign (SDH3) as a result of HGT from mimosoid hosts. These results reflect that the OXPHOS of *Lophophytum* is exceptional due to the presence of foreign (mostly encoded in the mitochondrial genome) and native (mostly encoded in the nuclear genome) subunits, generating new questions about the evolution and physiology of this parasitic plant. It is possible that the interactions between native and foreign proteins do not generate incompatibilities in the assembly and functioning of OXPHOS due to the low rate of evolution of mitochondrial genes in angiosperms. In contrast, the higher divergence among angiosperm nuclear genes would cause a negative effect on OXPHOS activity if foreign genes replace the native homologs.

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Phylogenomics of Hemidontidae (Ostariophysi: Characiformes)

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The South American characiform family Hemiodontidae comprises five genera and 33 species. The family lacks comprehensive phylogenetic hypotheses resolving its monophyly and most of its intra-familial relationships. The few studies that addressed these questions exhibited a narrow taxon sampling and/or used single-locus markers. Even so, well-known morphological traits in some members of the family have been used to propose interrelationships among taxa. Therefore, here we used ultraconserved elements (UCEs) to provide the first molecular phylogenetic hypothesis for hemiodontids encompassing all its genera and most species (26 out of 33). We surveyed a total of 1,286,841 base pairs (bp) and 2,508 UCE loci with mean locus size of 513 bp (range = 100–1,577). We generated matrices of 70% and 90% UCEs completeness to explore the role of missing data on phylogenetic reconstruction. Phylogenetic inferences were based on maximum likelihood, Bayesian and species tree analyses on both complementary matrices. We used nine species from related characiform families as outgroups. In all phylogenetic methods on both complementary matrices we recovered the monophyly of Hemiodontidae, as well as the genera *Argonectes* and *Bivibranchia*, with maximum statistical support.