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paniculata, Litchi chinensis, Pometia tomentosa, Sapindus mukorossi, Xanthoceras sorbifolium. We also reconstructed a plastome-based phylogeny involving 16 species of Sapindaceae and 7 other species as outgroups. We aligned the protein-coding genes using Mafft, to concatenate the alignments was performed in the Sequence Matrix and filtered alignment using GBlocks. The phylogeny was reconstructed using the IQ-TREE program with 1000 replicates. The chloroplast genome of *S. erecta* has a size of 159,297 bp, a quadripartite structure with two regions of single copy, the small single copy (SSC) and large single copy (LSC), divided by two inverted repeat regions (IRa and IRb). We identified a total of 132 genes and 2 pseudogenes (infA and ycf1), 87 of which are protein-coding genes, 37 tRNAs and 8 rRNAs. Among the genomes evaluated in the comparative analysis, the size ranged from 163,258 bp (*K. paniculata*) and 155,871 bp (*A. wangii*) and the number of genes between 132 (subfamilies Sapindoideae and Xanthoceratoideae) and 128 (*A. buergerianum* and *A. wangii*). The genes rpl22, rps3, rps19 are duplicated in the subfamily Sapindoideae which increased the size of the IRs in this group. In addition, the rps2 gene is pseudogenized in the subfamilies Hippocastanoideae and Xanthoceratoideae. The phylogenetic tree had well supported nodes within Sapindaceae and *Serjania* formed a clade with *Sapindus*, *Litchi*, *Dimocarpus*, and *Pometia* genera. The results obtained in this study provide the assembly and annotation of the chloroplast genome of *S. erecta*, the first annotation of a species of the genus. It also provides an idea of how chloroplast genomes evolved in the Sapindaceae family.

The mitochondrial genome of holoparasites of the family Balanophoraceae has been severely impacted by horizontal gene transfer

June 21
5:00 PM
Session 6

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Plant vascular connections established in a host-parasite relationship allow the passage of water, nutrients, and nucleic acids. This intimate contact promotes the exchange of genetic information between unrelated species, a process named Horizontal Gene Transfer (HGT). Plant mitochondrial genomes (mtDNAs) are frequently impacted by HGT. We deciphered the mtDNA of the holoparasitic angiosperm *Lophophytum leandri* (Balanophoraceae). This plant grows in Argentina, parasitizing roots of the mimosoid legume *Parapiptadenia rigida* (Fabaceae). The *L. leandri* mtDNA is 806,114 bp long and has a multichromosomal structure consisting of 50 circular chromosomes (5-72 kb in length). This multipartite genome was recently described in the relatives *L. mirabile* and *Ombrophytum subterraneum*. Similarity searches revealed 46.37% of shared regions between the mtDNA of *L. mirabile* and *L. leandri*. The *L. leandri* mtDNA carries 3 ribosomal RNA genes, 6 transfer RNA genes, and 35 protein-coding genes that represent 7.25% of the genome and are distributed across 23 chromosomes. The remaining 27 chromosomes are devoid of any identifiable coding region. Comprehensive phylogenetic analyses showed that L. leandri harbors 5 foreign and 15 chimeric mitochondrial protein-coding genes as a result of HGT from its legume hosts. To unveil the overall impact of HGT in the *L. leandri* mtDNA, we performed BLASTn searches against angiosperm mtDNAs. The *L. leandri* mtDNA presents 48.3% foreign sequences acquired from legumes and 31.9% native DNA, while 19.6% remains undetermined, as it is not similar to any other angiosperm mtDNA. The availability of the *L. leandri* mtDNA permitted a genus-wide evolutionary assessment. The analyses uncovered the presence of 19 chimeric genes in *L. mirabile*, representing almost half (43.18%) of the protein-coding genes. Besides, we found evidence for ancient HGT events in which foreign mitochondrial genes or regions were acquired before the divergence of *L. mirabile* and *L. leandri.*