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Bioinformatic and evolutionary analysis of chemoreceptors and related proteins in a grapevine pest

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Drosophila suzukii is an invasive pest of fruits such as grapevine, berries and cherries. *D. suzukii* lays eggs on ripening, unwounded fruits, while most other Drosophila oviposit on rottening fruits. This switch in ecological behaviour is reflected by morphological adaptations such as a serrated ovipositor, but should also include adaptations for tracking the odor of fresh fruits. In *Drosophila*, like in all other insects, odor(chemo) reception is mediated by multi-gene families of olfactory and gustatory receptors (Ors, IRs and GRs) sometimes assisted by two diverse protein families, odorant binding and chemosensory proteins (OBPs and CSPs). Knowledge of these genes may not only help in developing agricultural controlling strategies, but also offer an interesting model for the study of evolution of behavioral innovation. We extensively blasted the newly sequenced genome of *D. suzukii*, identified its likely full set of chemosensory receptors, and conducted a comparative genomic analyses of these genes in various sister species. Results show that repertoire of chemosensory genes in *D. suzukii* is different to that of sister species, but that this variation follows a likely birth death process as in other Drosophilas. Exception is the OBP family where the gene loss is significantly higher in *D. suzukii* than in sister species. Our results reveal some specific gene gains and losses in *D. suzukii* that may be responsible for its innovative behavior.

Evidence of disruptive selection in the adaptation of two closely related species of tropical trees

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Amazonian forest is highly diverse and the presence of closely related species still exchanging genes is not rare involving that gene flow may play a significant role in the speciation processes. Here, we present a population-genomic approach, using both AFLP and SNP genome scans, to analyze the genetic differentiation between the tree species *Symphonia globulifera* and its closely related species *S. sp1*. We first demonstrated the significant role of disruptive selection at a small proportion of AFLP loci at both the population and the regional level. In addition, we showed that at least one AFLP locus was linked to environmental features related to the water soil content. Secondly, we present the first results of the high-throughput AFLP sequencing which permitted to obtain more than 15000 contigs for 40 individuals (20 per morphotypes). We will see how the inter-species genetic differentiation is distributed in the genome and we will discuss the possible role of key genes in adaptation to the environment.

Structure, transcription and variability of metazoan mitochondrial genome: perspectives from an unusual mitochondrial inheritance system

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Despite its functional conservation, mtDNA presents strikingly different features among eukaryotes, such as size, rearrangement frequency, and amount of intergenic regions. The reasons beyond this diversity have been object of extensive studies that have investigated the correlation between different mtDNA evolutionary patterns and body mass, metabolic rate, reactive oxygen species production, lifespan, etc. The fundamental role