



ABSTRACT BOOK

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PS-P-1679 Chromosome evolution in *Passiflora*: from chromosome numbers to single-copy and repetitive DNA sequences

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Passiflora L. has around 500 species mainly distributed in the Neotropics. The genus shows different basic chromosome numbers associated to different subgenus ($x = 6, 9$ and 12) and high variation in genome size. In order to investigate karyotype evolution in this group, we generated a time-calibrated phylogeny including 102 taxa with known chromosome number and tested the relative importance of polyploidy and dysploidy. We established comparative cytogenetic maps using BACs (bacterial artificial chromosomes) and ribosomal DNA (rDNA) as probes in fluorescent in situ hybridization (FISH) to investigate conservation of synteny among species with $n = 9$. We also generated low-coverage, whole-genome data from species with different genome sizes to investigate composition and abundance of its repetitive DNA with RepeatExplorer and Satminer. The ancestral basic chromosome number of the genus was $x = 6$, and a recent diversification in the *Passiflora* subgenus (~ 25.94 Mya, Miocene) correlated to genome size increase and chromosome change from $n = 6$ to $n = 9$ by ascending dysploidy. Single-copy BACs suggest conservation of synteny among species with $n = 9$ (*P. edulis*, *P. alata* and *P. watsoniana*), although an extra 35S DNAr site was detected in *P. watsoniana*. Repeat content differed markedly between *P. quadrangularis* ($2n = 18$; $2C = 2.680$ pg), *P. cincinnata* ($2n = 18$; 2.202 pg) and *P. organensis* ($2n = 12$; 0.404 pg). While *P. quadrangularis* and *P. cincinnata* (*Passiflora* subgenus) showed high proportions of Ty1-copia LTR-retrotransposons from the Angela lineage, it was not among the most abundant clusters in the small *P. organensis* genome (*Decaloba* subgenus). On the other hand, satellite DNA (satDNA) diversity and abundance was higher in *P. organensis*. Altogether, structural rearrangements that caused dysploidy to $n = 9$ in the *Passiflora* subgenus did not further reshaped genomes during its diversification, but some transposable elements have contributed to increased genome size.

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