

Evidencing genome downsizing as a result of multiple robertsonian translocations in the subfamily allioideae (Amararyllidaceae)

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Abstract/Resumo

Large genomes and a history of chromosome rearrangements have made the subfamily Allioideae an interesting model to understand chromosome evolution. The majority of its genera show high karyotype diversity mainly due to polyploidy and Robertsonian translocations (RT) events. The three lineages of Allioideae present different levels of RT, evidenced by metacentric-rich karyotypes observed in Allieae and Tulbaghieae, and a variable proportion between metacentric/acrocentrics in Gilliesieae. Extreme condition of centric fissions occurs in the genera *Ipheion*, *Zoellnerallium* and *Miersia*, whose results in karyotypes formed almost exclusively by acrocentric chromosomes. In this work we investigate how RT drives genome size and chromosome number variation in species of Allioideae. For this, we estimated the genome size by flow cytometry and compiled chromosome number data for 37 species of Allioideae. We employed comparative phylogenetic methods in a Bayesian tree based on ITS1-5.8S-ITS2 sequences. Genome size ranged from $1C = 9.03$ picograms (pg) in *Ipheion uniflorum* to $1C = 54.97$ pg in *Leucocoryne ixioides*. Our analyses revealed that metacentric-rich karyotype is the plesiomorphic state in the subfamily Allioideae and RT as a driving force in genome size variation. This is demonstrated in the relationships *Leucocoryne* ($2n = 14M+4A$) / *Zoellnerallium* ($2n = 8M+16A$) and *Tristagma* ($2n = 6M+2A$) / *Ipheion* ($2n = 14A$) with a strong reduction of DNA content (49.5% and 61.47%, respectively) associated to multiple fissions. These changes in *Zoellnerallium* and *Ipheion* genomes occurred independently around 12 myr. This relationship was not observed in the Chilean species *Speea humilis* ($2n = 8M+2SM+2A$) / *Miersia chilensis* ($2n = 2SM+18A$) with recent differentiation (5 mya), suggesting that multiple centric fusions may require additional evolutionary time to decrease genome size. Our phylogenetic independent contrast analysis of genome size and chromosome number revealed that these traits have a negative correlation ($r^2=0.18$ and $p=0.01$). This corroborates a tendency of decrease in genome size after events that increase chromosome number such as fissions. Possibly, changes in chromosome linkage may increase meiotic recombination frequency, which might lead to higher probability of unequal crossing over. This mechanism could associate the loss of repetitive sequences to centric fission, explaining downsizing in Allioideae acrocentric-rich genomes.

Keyword/Palavras-chave: Allioideae; Genome size, Robertsonian translocations

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