



The SBE meeting 2021's Book of Abstracts

Edited by the SBE meeting 2021's organizing committee

June, 2021

II Virtual Meeting of Systematics, Biogeography, and Evolution: The Research of Biodiversity and the Diversity of Researchers

www.sbemeeting.com

June 19–23, 2021

Time Zone: UTC-4



License: Creative Commons License 4.0 CC-BY-NC-SA
DOI: 10.5281/zenodo.5109989 (new version published on July 16, 2021)

Why tropical plants can have small genomes? Genome size evolution in Cactaceae is shaped by geographically structured polyploidy

June 21
12:00 PM
Session 5

Rodríguez P.E.¹, Almeida E.¹, Costa L.¹, Amorim B.S.², Guignard M.S.³,
Carvalho-Sobrinho J.⁴, Sader M.A.^{1,*}, Lopes S.⁵, Mota L.⁵, Loureiro J.⁵, Leitch
I.J.³ & Souza G.^{1,*}

¹Laboratório de Citogenética e Evolução Vegetal, Universidade Federal de Pernambuco, Brasil. ²Museu da Amazônia, MUSA, 69099-415 Manaus, Amazonas, Brazil. ³Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, UK ⁴Laboratory of Plant Cytogenetics, Department of Biology, Federal Rural University of Pernambuco, Recife, Brazil. ⁵Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Calçada Martim de Freitas, 3000-456 Coimbra, Portugal. *Correspondence: lgrsouza@hotmail.com.

Genome size (GS) displays a broad variation across land plants. Although it is considered to be influenced by selection pressures depending on different environmental conditions and life-history strategies, the underlying drivers of GS variation across lineages remain elusive. Latitude gradients of GS tend to show contrasting patterns among different plant groups, sampling and statistical approaches. A recent analysis suggested that niche conservatism in dry environments may be associated with bigger GS increase at higher latitudes. However, it is not clear how the extreme ecological conditions in these dry environments might play a role in driving GS evolution. We investigated GS evolution in the dry-climate specialized family Cactaceae, aiming to explore the relationship between GS and latitude as well as a range of cytogenetic and climatic variables. We used flow cytometry to generate original GS data for *Melocactus* and *Pereskia* species which together with GSs compiled from previous publications, resulted in data for 344 species belonging in 63 genera, including representatives in all the main Cactaceae lineages. 1C-values varied 14.31-fold, with high variability of GS was observed at the genus level for representatives of the Cactoideae II and Opuntioideae clades. Our comparative analysis revealed that these clades contain most of the Cactaceae polyploids that have been identified. Molecular clock analysis revealed that the Opuntioideae polyploid lineages are older than those in Cactoideae II, which is correlated with low monoploid GS (1Cx) values in the Opuntioideae paleopolyploids. A positive correlation was observed between 1C-values and latitude, with a tendency for species with larger genomes to occur more frequently at higher latitudes, associated to higher levels of polyploidy (up to 22x) in temperate regions. In contrast, the 1Cx vs. latitude relationship showed the complete opposite result, with a decrease in monoploid GS at higher latitudes, indicating that in the temperate regions the polyploids (mainly of Opuntioideae) have smaller amounts of DNA per monoploid chromosome set. Surprisingly, correlations between tested environmental variables and GS in the Cactaceae seem to be, in general, low. We believe that endoreduplication, such as in the epidermis, can enable diploid plants to physiologically act as a polyploid in certain tissues, masking the correlations between GS and temperature/ precipitation traits. Our data suggest that polyploidy (associated with processes such as gene duplication, asexual reproduction, nucleotype effects etc.), have played a role in contributing to the geographic distribution and diversification of Cactaceae lineages.