



XIII Congresso de ECOLOGIA

III International Symposium of Ecology and Evolution

Múltiplas ecologias: evolução e diversidade

08 a 12 de outubro de 2017 • UFV - VIÇOSA | MG

PHYLOGEOGRAPHY OF BROMELIAD SPECIES ENDEMIC FROM MIDWEST OF BRAZIL IN COMPARISON WITH WIDESPREAD CONGENER

Camila de Aguiar Melo¹, Camila Martini Zanella^{1,2}; Gecele Matos Paggi³; Luiza Domingues Hirsch¹,
Fernanda Bered^{1*}

1.Universidade Federal do Rio Grande do Sul, Instituto de Bociências, Departamento de Genética, Avenida Bento Gonçalves 9500, P.O. Box 15053, 91501-970, Porto Alegre, RS, Brazil. 2.The John Bingham Laboratory, National Institute of Agricultural Botany (NIAB), Huntingdon Road, CB30LE, Cambridge, UK. 3.Universidade Federal do Mato Grosso do Sul, Laboratório de Genética e Biodiversidade, Ciências Biológicas, Campus Pantanal, P.O Box 252, 79304-902, Corumbá, MS, Brazil. *Correspondence to fernanda.bered@ufrgs.br

Tema/Meio de apresentação: Filogeografia/ Pôster

Bromeliaceae is one of the most diverse morphological and ecologically neotropical family, which suffered one extensive adaptative radiation that allowed this species spread and inhabit xeric to mesic environments. The family comprises more than 3000 species and is divided in eight subfamilies. *Dyckia* genus belongs to Pitcairnioideae subfamily, and is characterized by the absence of a "tank" that accumulates water, enabling these species to inhabit environments with extreme drought conditions, such as "the dry diagonal" in the center of South America. Mato Grosso do Sul state harbour to Midwest of Brazil, that is located in dry diagonal and comprises four biomes (Cerrado, Pantanal, Chaco and Atlantic Forest), being one interesting area for phylogeographic studies. The aim of this study was to estimate genetic diversity within and among five restricted *Dyckia* species endemic to the Cerrado and the Pantanal/Chaco biomes, comparing with a congener species with wide geographical distribution through a phylogeographic approach, using two plastid markers (*rpl32-trnL* and *rps16-trnK*) and one nuclear (*phyC*). The results from cpDNA showed that restricted distributed species had low genetic diversity in comparison with the widely distributed species, however the diversity presented by the widely distributed species was not considered high. The nuDNA revealed high genetic diversity and a slightly structured network, indicating that pollen dispersal has been more effective than seeds. The cpDNA genetic relationship showed by haplotype network revealed three haplogroups, one formed by widespread species, other by species that occur in Cerrado and another by Pantanal/Chaco species, indicating that the biogeographic history of these biomes may have influenced the speciation process of this group of species. The endemism and lower genetic diversity of this species indicated the necessity of conservation efforts of these biomes that have been suffering with intensive anthropogenic impacts.

The authors thank CNPq (CNPq 457698/2014-4 and Ação Transversal nº6/2011- Casadinho/Procad); Fundect (11/2014 – Universal-MS),PPGBM-UFRGS, and C.A.M received fellowship from CNPq.