

## A sneak peek into chromosome and genome size evolution among *Sisyrinchium* taxa (Iridaceae: Iridoieae)

Burchardt, P.<sup>1</sup>; Souza-Chies, T.T.<sup>1,2</sup>; Brioslara-Corrêa L.<sup>1</sup>;  
Chauveau, O.<sup>3</sup>; Inácio, C.D.<sup>3</sup>; Eggers, L.<sup>2,3</sup>; Siljak-Yakovlev, S.<sup>5</sup>;  
Campos, J.M.S.<sup>6</sup>; Kaltchuk-Santos, E.<sup>1,4</sup>

### Abstract/Resumo

Iridaceae is one of the largest Asparagales families with over 2030 species. Besides a wide morphological variation, this family presents great karyological variation including many polyploid taxa. *Sisyrinchium* is restricted to the New World and it holds a large amount of cytological data. Despite its importance in providing critical evidence to understand processes involved in genome evolution, cytological data is lacking for most of South American species of *Sisyrinchium*. Therefore, the present work aims to identify and characterize chromosome evolutionary trends among *Sisyrinchium* taxa of sect. *Viperella*. Chromosome numbers and genome sizes (GS) were determined for 16 and 17 taxa, respectively, from sect. *Viperella*; all reported here for the first time, except for *S. alatum*. Meiotic behavior, tetrad normality, pollen viability and morphology were also analyzed and revealed regular meiosis, high meiotic indexes and pollen viability (> 87%), except for *Sisyrinchium* sp. nov. aff. *alatum* (22.70%). The GS and chromosome number obtained were plotted onto a phylogenetic frame to identify transitions between character states and to locate where these transitions occurred throughout this group's evolution. Based on our results, we suggest that the ancestral chromosome number for sect. *Viperella* is  $2n = 18$  and two independent polyploidization events occurred. Lower DNA content ( $2.17 \leq 2C \leq 2.97$  pg) was the ancestral condition from which six major events took place towards GS increase. Despite the stability in base chromosome number ( $x = 9$ ), evolutionary changes in karyotypes of this section involve primarily variation in DNA amount regardless of ploidy level, and secondly polyploidy and variation in chromosome size. Combining GS and chromosome number with molecular phylogeny, our data provides the first scenario for karyotype and genome evolution in *Sisyrinchium*, sect. *Viperella*, allowing us to suggest that mechanisms other than polyploidy were responsible for GS increase among these taxa.

Keyword/Palavras-chave: Ancestral chromosome number; DNA content; meiotic behavior; pollen viability; polyploidy

1 Programa de Pós-Graduação em Genética e Biologia Molecular, UFRGS, Porto Alegre, RS, Brazil, [paula.burchardt@hotmail.com](mailto:paula.burchardt@hotmail.com)

2 Departamento de Botânica, Instituto de Biociências, UFRGS, Brazil.

3 Programa de Pós-Graduação em Botânica, Instituto de Biociências, UFRGS, Brazil.

4 Departamento de Genética, Instituto de Biociências, UFRGS, Brazil.

5 Ecologie Systématique Evolution, Univ. Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, 91405 Orsay Cedex, France.

6 Departamento de Biologia, Instituto de Ciências Biológicas, UFJF, Juiz de Fora, MG, Brazil