

ers by FISH showed a small variation of 5S rDNA sites and the occurrence of interstitial telomeric sites (ITS) traces in a metacentric (M) chromosome pair of karyomorph B, indicating a Robertsonian fusion and a numeric reduction to  $2n = 54$ . Two populations of *R. latirostris* (Laranjinha and Barra Grande Rivers) had  $2n = 46$  and the same karyotype organization. Even keeping the diploid number, the analysis of rDNAs and (TTAGGG)<sub>n</sub> sequences using FISH mapping indicated that Robertsonian fusion events occurred in the evolutionary history of this species. In populations of *R. latirostris*, the occurrence of 1 large M chromosome pair carrying 18S rDNA and 1 large M chromosome pair carrying 5S rDNA collocated with (TTAGGG)<sub>n</sub> sequences, in addition to a third large M chromosome pair carrying ITS vestiges, all with centromeric location, may indicate fusions between subtelocentric or acrocentric chromosome pairs. These results support that numerous fusion events occurred in the karyotype differentiation within this species. Therefore, in this study, we assessed the telomeric instability, chromosomal breaks, and rearrangements due to ITS vestiges detection, in addition to the probable role of rDNAs in chromosome fusions in karyotype diversification of this group.

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### III.33

#### A Centromeric Repeat of *Solanum chomatophilum* and Its Dynamics in Natural Populations

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The centromere is an essential chromosome locus since it is responsible for organizing the kinetochore, a proteinaceous structure where the spindle fibers attach to promote chromosome segregation. A variant of histone H3, named CenH3, is found in centromeres in all eukaryotes studied so far and is considered as a mark for centromeric function. Centromeres usually contain repetitive DNA and retrotransposons, which often diverge rapidly and can differ among closely related species. Centromeric DNA of *Solanum chomatophilum* ( $2n = 2x = 24$ , genome P, the closest to genome A of potato – *S. tuberosum*) was isolated by ChIP (chromatin immunoprecipitation) and sequenced using Illumina platform. Centromeric repeats were identified using RepeatExplorer pipeline. A highly repetitive DNA element, Sc83, was identified, cloned, and sequenced. FISH mapping of Sc83 was performed in *S. chomatophilum* and several other diploid *Solanum* species, including *S. tuberosum* group Phureja (DM1-3516R44, genome A), *S. verrucosum* (genome A), *S. jamesii* (genome B), *S. palustre* (genome E), and *S. lycopersicum* (genome T). Repeat Sc83 is exclusively present in the centromeres of chromosome 3 of *S. chomatophilum*. However, Sc83 was detected in a nonidentified chromosome in some plants. Intraspecific variation of this repeat was examined in 80 different plants; 55 contained only the signals on chromosome 3, and 25 contained the third signal. Sc83 was also consistently found in 8 and 6 chromosomes in *S. verrucosum* and

*S. palustre*, respectively, but was not detected in the remaining species. These results show a recent origin of the Sc83 repeat and a highly dynamic evolution of the centromeres in *Solanum* species.

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### III.34

#### Cytogenetic Analysis of the Genome in *Brachiaria* (Poaceae) Species and Its Interspecific Hybrids

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The grass genus *Brachiaria* (Poaceae) comprises species showing different ploidy levels and reproduction modes. Despite the great economic and agronomic importance of forage species used in genetic breeding, studies on genomic constitution and relationship within the genus are limited. Accordingly, molecular cytogenetic analyses can help us understand genomes and their differentiation and the species' phylogenetic relationships. The objective of this study was to investigate the genomic relationships among *B. ruziziensis*, *B. decumbens*, *B. brizantha*, and interspecific hybrids by means of GISH, FISH, and meiosis, and nuclear genome quantification by flow cytometry. The hybrid 1863 (*B. ruziziensis* × *B. brizantha*) presented  $2n = 36$ , 3.24 pg of nuclear DNA, and 4 and 7 sites of 45S and 5S rDNA, respectively. The hybrid Mulato II [(*B. ruziziensis* × *B. decumbens*) × *B. brizantha*] presented  $2n = 36$ , 4 and 7 sites of 45S and 5S rDNA, respectively, and an increase in DNA content (3.83 pg) compared to the average content of the parents (3.43 pg). The hybrid 963 (*B. ruziziensis* × *B. decumbens*) showed  $2n = 38$  in all metaphases, exceeding 2 chromosomes compared to the expected number and an increase of 0.29 pg (9%) of DNA, considering the average DNA content of the parents (3.33 pg) and the presence of 5 sites of 45S rDNA and 7 sites of 5S rDNA. GISH, using total nuclear DNA, performed in *B. decumbens*, *B. brizantha*, and *B. ruziziensis* showed variations in the hybridized genome percentage and in the chromosome region of this hybridization. Chromosomal rearrangements were observed as well as differences in the contribution of parent genomes in the constitution of the hybrids. GISH results associated to chromosomal pairing in meiosis of the interspecific hybrids confirmed that parental species are closely related, and they share similarities between chromosomes/genomes, which were considered homeologous.

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**July 10–13, Foz do Iguaçu, Brazil**

## **21st International Chromosome Conference (ICC)**

*A venue that offers a diversity of scientific approaches to chromosome biology and a diversity of wildlife in Iguaçu National Park*

The International Chromosome Conferences (ICC) originated from the Oxford Chromosome Conferences, inaugurated by C.D. Darlington and K.R. Lewis in 1964 and held subsequently in England in 1967 and 1970. The Chromosome Conference grew to an international event with its fourth meeting, held in Jerusalem, Israel in 1972, heralding the beginning of 40 years of technological advances that have expanded our understanding of chromosome biology in model and non-traditional biological systems. Having been hosted in Europe and the United States 16 times since then, this year the ICC will be held across the equator in Foz do Iguaçu, Brazil, on July 10–13, 2016. The event will bring scientists from across the globe to a biannual meeting focused on modern advances in chromosome biology, technology and theory. The Iguaçu National Park, a UNESCO World Heritage Centre, includes the Iguaçu Falls and has been chosen as one of the 'New Natural Seven Wonders of the World'. Home to an

amazing diversity of life, including over 2,000 species of vascular plants, exotic mammals such as tapirs, giant anteaters, howler monkeys, ocelots, and jaguars, in addition to hundreds of different bird species and thousands of different insects, the choice of Foz is an excellent analogy for the diverse approaches and systems chromosome biologists explore, and that will be emphasized throughout this conference.

The 2016 ICC program offers seven sessions, beginning with a session on **Chromosome Structure and Nuclear Architecture**, highlighting the influences and interactions chromosomes have on the three-dimensional space of the nucleus. Session II will focus on **Specialized Chromosomes**, such as sex chromosomes and B chromosomes, whose structure and behavior are often distinguished from that of autosomal chromosomes. **Population and Evolutionary Chromosome Biology**, the third session, covers a synthesis of chromosome biology and