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Chromosomal Mapping of Microsatellites $(GATA)_n$ and Transposable Element Mariner Sequences in *Characidium* (Characiformes: Crenuchidae)

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The *Characidium* (Characiformes) may present a ZZ/ZW sex chromosome system, varying in the degree of differentiation. These heteromorphic sex chromosomes are absent in some species, while in others they are found with different heterochromatinization and morphology patterns, some presenting 45S rDNA sites. The heteromorphic sex chromosome differentiation is based on recombination supression, chromosomal rearrangements, heterochromatinization, and accumulation of repetitive DNA. In this study, we mapped the microsatellite $(GATA)_n$ and the transposable element Mariner in the genomes of *C. gomesi*, *C. heirmostigmata*, and *C. zebra*, highlighting the location of these repeats and their possible role in the evolution of sex chromosomes. The probe for $(GATA)_n$ sequences showed hybridization signals on all autosomes, especially on the terminal region. In *C. gomesi* the same probe showed hybridization signals only on the short arm of the W chromosome. The probe for Mariner sequences interestingly revealed the same pattern distribution as the $(GATA)_n$ sequences, even in the W chromosomes of *C. gomesi* and in the W pericentric region of *C. heirmostigmata*. The $(GATA)_n$ repeat is considered a motif for GATA-binding proteins related to decondensation of the genic regions, where there are genes related to the oocyte development, especially in heterochromatic regions of heteromorphic sex chromosomes. That the GATA motif was detected only in the short arm of the W chromosome of *C. gomesi* may indicate the existence of coding genes in this region. The absence of these repeats in the major portion of the W chromosomes may represent the lack of coding genes. The transposable element Mariner presented a distribution pattern similar to the $(GATA)_n$ sequence. Transposable elements are able to shape both genic regions and even the entire genome. In the *Characidium* karyotypes, the distribution of $(GATA)_n$ sequence and the transposable element Mariner is not involved with W chromosome gene erosion and differentiation.

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V.18

Ionizing Irradiation Does Not Promote Chromosomal Breakages in the Fragile Sites 45S rDNA of the *Lolium multiflorum*

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In *Lolium*, 45S rDNA sites have shown high decondensation in metaphase chromosomes, constituting regions slightly stained with DAPI. These regions are denominated fragile sites (FSs) that have been widely studied in humans. FSs might be prone to form chromosomal fragments and rearrangements, unless repair mechanisms such as homologous recombination (HR) or non-homologous end joining (NEJH) play a role at the DNA break-site. Thus, this study aimed at investigating if such sites are hotspots for the occurrence of breakages induced by X-ray in *Lolium multiflorum*. *Hordeum vulgare* was used as a comparative model. Seedlings of both species were irradiated with 50Gy X-ray and evaluated 1 day following the irradiation and thereafter at 7-day intervals for a 28-day period using FISH with 45S rDNA and telomere probes. *H. vulgare* did not survive after a few days of irradiation due to the increased rate of chromosomal abnormalities. Chromosomes of *L. multiflorum* exhibited abnormalities such as deletions, fusions, translocations, and chromosomal fragments with and without 45S rDNA sequences, yet over the 28-day trial, it had a decrease in the rate of chromosomal damage. Despite being considered to be FSs, the 45S rDNA sites of *L. multiflorum* are not hotspots to chromosomal breakages after the induction with X-ray. The lack of fragments with 45S rDNA can be explained by the absence of double-strand DNA breaks (DSBs) in these sequences, not being necessarily the genome sites where the irradiation interacts or due to DSBs in 45S rDNA that were more efficiently repaired by mechanisms like HR or NEJH compared to other chromosomal regions where the breakages have also occurred.

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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

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