

The freewill of evolution in the structuring of Rodentia genomes

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Two rodent species, the common hamster *Cricetus cricetus*, and the cactus mouse *Peromyscus eremicus* (Rodentia: Cricetidae), displaying diploid chromosome numbers of 22 and 48 chromosomes respectively, were studied. *C. cricetus* encloses a nearly meta/submetacentric karyotype, whose constitutive heterochromatin (CH) seems to be greatly found at the (peri)centromeric regions, exhibiting the majority of the chromosomes two very large blocks at this location. *P. eremicus* exhibits a very distinct karyotype organization, solely constituted by submetacentric chromosomes. This karyotype also displays great amounts of CH, being the p-arms of the majority of the chromosomes almost entirely heterochromatic. The index genome *Rattus rattus* allowed deciphering the different genomic architecture of these two genomes. Comparative Chromosome Painting illuminated the evolutionary pathways that created these two genomes of species belonging to the same family. As more Rodentia species are thoroughly analyzed, the evolutionary events in this order seem to have been more complex.

Acknowledgements

This work was supported by the project POCI/BIA-BCM/58541/2004 and the PosDoc and PhD grants SFRH/BPD/32661/2006, SFRH/BD/25813/2005 and SFRH/BD/41942/2007 of Portugal FCT. We are deeply grateful to Dr. Vitaly Volobouev for providing the Rodentia cell cultures.