

## **Comparative analysis of two *Cricetus cricetus* chromosomes with *Mus musculus* and *Rattus norvegicus* using chromosome painting**

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One of the aims of analyzing mammalian genome architecture is to weave their evolutionary history. Such knowledge enables making a phylogenetic analysis of mammalian species, to establish a possible structure of ancestral karyotype for genus, families and higher taxa, and to infer probable evolutionary chromosomal rearrangements. This information is useful to evolutionary studies but also in biomedical research (e.g. to choose representative model animals to specific genetic disorders). One of the methods commonly used to make this kind of study is Comparative Chromosome Painting, which is based on chromosomal homology between genomes. Almost half of the extant mammalian species belongs to the order Rodentia, being Muroidea (where are included the index species mouse and rat) the larger and most diverse rodent superfamily. The evolutionary success of these rodents is reflected by the extensive chromosome polymorphisms (wide variation in diploid numbers, heterochromatin nature, localization and amount, etc). As more Muroidea species are analyzed, more unraveled are the evolutionary events in this taxon. Common hamster *Cricetus cricetus* (Rodentia, Muroidea, Cricetidae) has a diploid number of 22 chromosomes, mainly composed by metacentric/sub-metacentric chromosomes, with constitutive heterochromatin preferentially located at the (peri)centromeric regions. To establish chromosomal homologies between *Cricetus cricetus* (CCR), mouse (*Mus musculus*, MMU, 2n=40) and rat (*Rattus norvegicus*, RNO, 2n=42) (Rodentia, Muroidea, Muridae), we conducted Comparative Chromosome Painting with mouse and rat chromosome-specific painting probes. Here we present the results regarding two CCR chromosomes (CCR1 and CCR2). MMU paint probes produced a higher segmentation in *Cricetus cricetus* chromosomes. Cricetinae, Cricetidae and Muroidea

specific syntenic associations were revealed. These are preliminary results of an ongoing CCR genomic architecture analysis.