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## **ARTICLE DETAILS**

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Title of article: The evolution of human synteny 4 in Primates

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Article category, e.g. Editorial, Article, Review: Article

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Paste your <u>abstract</u> in here:

Comparative cytogenetic data concerning the ortholog to human chromosome 4 in primates shows that this chromosome is conserved between humans and non-human primates. However, the degree of conservation is not as high as previously estimated. In primates it is as a rule a large submetacentric chromosome but many exceptions are known especially in

taxa characterized by a high level of chromosomal rearrangements. The rearrangements that have been visualized by chromosome painting so far, which are mostly interchromosomal changes, are in fact only a fraction of the actual chromosomal changes that have occurred during evolution. Intrachromosome changes can be analyzed through classical cytogenetic approach or by mapping sub-chromosomal specific probes. In order to study human synteny 4 evolution we mapped diverse subchromosomal specific probes on chromosomes of representative species of the main primates taxa, with the aim to verify markers order conservation along the orthologs to human chromosome 4 allowing us the detection of possible intra-chromosomal rearrangements. The mapping of these probes permitted us to test previous cytogenetic hypothesis on human synteny 4 evolution, and to show a markers order conservation between orthologs to human synteny 4 in Catarrhini and Platyrrhini, but with a different position of the centromeres. This data permitted us to hypothesize the occurrence of a new centromeres evolution in one of the two lineages. Moreover we analysed literature data regarding HSA4 homologous in Primates with particular attention to Platyrrhini allowing us the reconstruction of the changes that synteny 4 has undergone during evolution. Lastly we highlight the value of the subchromosomal specific probes mapping approach in the detection of intrachromosomal rearrangements that can be crucial for a more refined comparative mapping and for phylogenetic reconstruction.

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