

PHYLOGENETIC REALTIONSHIP BETWEEN PRIMATES AND SCADENTIA BY FLOW SORTING AND RECIPROCAL CHROMOSOME PAINTING

F. Dumas¹, F. Bigoni², L. Sineo¹, R. Stanyon²

¹Palermo University, Department of Animal biology "G. Reverberi", via Archirafi 18, 90123 Palermo, Italy,

²Firenze University, Department of Evolutionary Biology "Leo Pardi", via del Proconsolo 12, 50122 Firenze, Italy.

Presenter's Email: fdumas@unipa.it

Comparative molecular cytogenetic facilitates mapping chromosomal homology between species and clarifies phylogenomic relationships by tracing chromosome evolution. Here we report on reciprocal chromosome painting using both human (HSA) and tree shrew (*Tupaia minor*-TMI 2n=68 order Scandentia) chromosome specific painting probes derived by fluorescence-activated flow sorting. This study clarifies previous molecular cytogenetics reports on tree shrews and primates.(There is a lack of a sentence!! Please cut it) Twelve syntenic associations of human chromosome segments (HSA) were detected in the TMI genome: 1/18, 2/21, 3/21, 4/8 (twice), 7/10, 7/16, 11/20, 12/22 (twice), 14/15, and 16/19. Reverse painting of TMI paints onto human chromosomes confirmed the results by independent hybridizations. Our results were then compared with data from *Tupaia belangeri* (TBE 2n=62, Müller et al., 1999). Apparently in the report on TBE some syntenic associations were missed (1/18, 4/8 twice and 10/7/16). We conclude that the two karyotypes differ only by two inversions, possibly centromeric shift (evolutionary new centromeres), and three Robertsonian transformations, which could be fissions or fusions depending on the direction of change. Two inversions or centromeric shifts involve TMI chromosomes homologous to HSA syteny 14/15 and 3/21/2. Two fissions form new segments of human syteny 3 and 4 in TMI. Lastly, a fission spit HSA syteny association 9/10 in TMI giving one chromosome covered by human syteny 9 and another covered by 10/7/16. (There is a lack of a sentence!!Please cut it) The study of Scadentia is relevant because it results an appropriate outgroup for primates in phylogenomic comparisons.

Keywords: Phylogeny, Molecular cytogenetics, Primates, Scadentia