Phylogenetic relationships among strepsirhines are enigmatic. Comparative chromosome painting using Zoo-FISH techniques can provide independent verification of phylogenetic trees derived from classical or molecular data. We compared chromosomal features of 11 representative species (8 within Lemuriformes and 3 from both lineages of Lorisiformes) using parsimony. Chromosomal syntenies were used to build a binary matrix of characters in PAUP 4.0b1, and subsequently analyzed by the bootstrap method. The chromosome complement of Tupaia belangeri (Scandentia) was used as the outgroup. An exhaustive search retrieved 8 equally parsimonious trees. Four characters ancestral for eutherians (HSA3+21, 7+16, 12+22 and 14+15) have been retained in all strepsirhine species, and one ancestral eutherian association (HSA16+19) was unique to Daubentonia madagascariensis. Among lorisiforms and other lemuriforms, chromosomes 16 and 19 have undergone different, and presumably successive, associations. The analysis also revealed a large number of autapomorphies (i.e. HSA1+5, 3+7, 8+11, 16+22) for most of the families investigated here. Three of the remaining associations (HSA1+7, 6+14, 12+19) shared by at least two species within the same family, are considered to be convergent in our chromosomal phylogeny. Most, but not all, molecular phylogenies reconstruct D. madagascariensis as the basal divergence of the Malagasy lemurs, and nested within the living strepsirhines. Under this interpretation, the 16+19 association, shared with non-primate mammals, would be considered a convergent autapomorphy. However, the morphological peculiarities that characterize this species, and a few molecular phylogenies, allow the possibility that this association is an ancient retention.

Keywords: Strepsirrhines, phylogenetic evolution, chromosomes, syntenic associations