A CLADISTIC APPROACH TO TESTING PHYLOGENOMIC EVOLUTION IN STREPSIRHINES

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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 belangieri* (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