A Phylogenetic Networks perspective on reticulate human evolution

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Résumé

No consensus exists in human evolution research regarding the definition of genus *Homo* and its mode of evolution. We present a methodological phylogenetic reconstruction approach combining Maximum Parsimony and Phylogenetic Networks methods applied to phenotypic craniodental characters of 22 hominin species from Late Miocene to Holocene. The approach consists in selecting and validating first a tree-like most parsimonious scenario out of several parsimony runs based on various numerical constraints. We identify three *Homo* genus definitions based on various cumulative distinguishing apomorphies in support of last common ancestors (LCAs), and highlight the results by a novel graphical elliptic representation. An intermediate step is implemented by running an analysis with a reduced apomorphous character dataset that generates multiple parsimonious trees. These most parsimonious trees are in turn used as input for a Phylogenetic Networks analysis that produces consensus and reticulate networks. We show that the phylogenetic tree-like definition of the genus Homo is a relative concept linked to craniodental characters in support of hypothetical LCAS of the most parsimonious scenario. For the late Miocene-Pliocene taxa up to *Au. africanus*, the Phylogenetic Networks method shows no evidence of diffuse ancestral radiations but rather directional adaptive changes with uncertain cladogeneses. But more importantly, the method comes in support of a probable web-like reticulate mode of evolution of the genus *Homo* that gave rise to the emergence of the only surviving paleospecies, *Homo* sapiens. Our results related to the *Homo* reticulate network concords with recent findings in paleogenomic research regarding its mode of evolution.

Mots-Clés: Genus Homo definitions and mode of evolution, Maximum Parsimony, Phylogenetic Networks.

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