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Evolutionary perspective of the genus *Homo*: new approaches

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Evolutionary perspective of the genus *Homo*: new approaches

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1 No consensus exists in human evolution research regarding the definition of genus *Homo* and its mode of evolution. Based on a database that comprises more than 350 characters scored on 22 hominin species from Late Miocene to Holocene, we address methodologically these two questions with a quantitative taxonomic approach that combines Maximum Parsimony (MP) phylogenetic reconstruction with a Phylogenetic Networks method. Based on tree-based MP, we identify three *Homo* most parsimonious definitions, with cumulative distinguishing feature changes in support of hypothetical last common ancestors for each definition highlighted by a novel graphical elliptic representation. We analyze the complexity of hominin evolutionary processes by means of a Phylogenetic Networks method. For the late Miocene-Pliocene taxa up to Au. africanus, the reading of the reticulate network shows no evidence of diffuse ancestral radiations but rather directional adaptive changes with uncertain cladogeneses. More importantly, we show the probable web-like reticulate mode of evolution of the *Homo* genus that gave rise to the emergence of the only surviving paleospecies, *Homo sapiens*. Our results confirm a paradigm shift in the study of human evolution in favor of reticulation, in accord with recent paleogenomic findings of introgressive hybridization in the genus *Homo*.

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