Phylogenetic analysis of recent Species of the genus *Homo*: Contributions to understanding Human Evolution in Asia

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Phylogenetic relationships among species of the genus *Homo* are highly debated, yet resolving them is crucial for understanding human evolution over the past million years. The "recent" discoveries of *Homo floresiensis*, Denisovans, and *Homo luzonensis* have added complexity to an already poorly understood history. In light of these new challenges, we propose two areas of investigation.

The first focuses on revisiting methods for studying dental fossils within a phylogenetic framework to better understand intra-taxonomic variation. The second area emphasizes the use of postcranial characteristics in phylogenetic analysis, a dataset traditionally excluded from such studies.

The results from these two lines of analysis provide complementary insights into the phylogenetic relationships of recent species within the genus *Homo*. Dental analysis groups many contemporary Denisovan fossils into the same lineage as Denisovans themselves, while postcranial analysis suggests a close relationship between this lineage and the Neanderthal lineage. Furthermore, the postcranial analysis indicates that *Homo floresiensis* is derived relative to *Homo erectus sensu lato* and not related to older taxa.

While these hypotheses about taxonomic relationships are not entirely new, our analyses provide a demonstration based on morphology within the conceptual framework of cladistics. Additionally, these findings validate two essential aspects of our approach: (1) effective methods can incorporate known intra-taxonomic variation into phylogenetic analysis, and (2) the postcranial skeleton carries a phylogenetic signal.

Integrating all anatomical elements into phylogenetic analysis represents the next step toward a comprehensive assessment of hominin relationships.