Pecha Kucha Presentation Session 3, Saturday 16:40-17:55

A new multi-approach method for taxonomically identifying isolated hominin teeth from the Omo, Ethiopia

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One of the longest-studied hominin-bearing fossil sites in eastern Africa is the Omo Basin of Ethiopia, prominently investigated from 1967-1976 [1] and more recently since 2006 [2]. Sediments exposed by the Omo River produce an abundant fossil record of ca. 3.5 to 1 million-year-old terrestrial faunas. These 2.5-million years represent a particularly interesting time in human evolution because they capture the early evolution of the genus *Homo* and the first appearance of the eastern African robust hominins. However, fossils from the Omo tend to be highly fragmentary, with isolated teeth being among the most common elements recovered.

While teeth are often the most diagnostic element for vertebrate paleontological taxonomy, teeth in isolation are much less informative. Previous studies have taken on the challenge of identifying the taxonomic affinities of isolated teeth from the Omo [e.g., 3]. We revisited the taxonomic identification of isolated teeth from the Omo for two reasons. First, there have been discoveries that dramatically alter and improve our understanding of hominid evolution since those previous studies were conducted, such as *Ardipithecus ramidus*, *Australopithecus garhi*, *Au. deyiremeda*, *Homo erectus* from Dmanisi, and *Au. sediba*. And second, with the Omo Group Research Expedition's renewed fieldwork in the Omo [2], dozens of new hominin specimens have been recovered, demonstrating that the Omo localities (and their proclivity to yield isolated teeth) will continue to contribute evidence of human evolution during this particularly intriguing time period. Consequently, we need to continue to improve our ability to infer taxonomy from isolated teeth.

We developed a four-pronged approach that produces most-likely taxonomic identifications based on the external crown morphology of postcanine hominid teeth. For the first component, we ran linear discriminant analyses of linear crown dimensions on a comparative dataset of 464 hominid teeth (with well-established taxonomic identifications) that were then used to predict the classification of 114 crowns from 94 specimens from the Omo (including 22 new specimens). For the second and third components, we ran a cluster analysis on the morphological scores and on the 2-dimensional cusp areas for subsets of the study sample. The fourth part of our approach was a comparison of the three analytical methods to reach a final decision on taxonomic identification.

Our results demonstrate a significant amount of overlap in size and morphology between the isolated postcanine teeth of *Au. afarensis* and *H. habilis*. This *afarensis/habilis* group dominates the dental assemblage in the earliest part of the Omo stratigraphic sequence, with the robust lineage gradually increasing in proportion. By 2.27 million years ago, we see clear evidence of teeth from genus *Homo* alongside those from the robust lineage. Near the top of the sequence, between 1.38 and 1.09 million years ago, we only find isolated teeth of *Homo*. This tooth-by-tooth analysis also offers insight to the modularity of hominid dental evolution, which will be discussed in the presentation.

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