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A MORPHOMETRIC ANALYSIS OF HOMININ TEETH ATTRIBUTED TO DIFFERENT SPECIES OF *AUSTRALOPITHECUS, PARANTHROPUS* AND *HOMO*

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ABSTRACT

Teeth are the most common element in the fossil record and play a critical role in taxonomic assessments. Size, relative width and cusp arrangements on enamel crown surfaces are used to help assess relationships between specimens. In this exploratory study, a model is developed for the placement of landmarks on images of lower first molars to maximise key information from crown surfaces of molars of African Plio-Pleistocene hominin fossils representing species of *Australopithecus, Paranthropus* and *Homo*. Lower first molar data of four extant species (*Pan paniscus, Pan troglodytes, Gorilla* and *Homo sapiens*) are visualised in a principal components analysis to detect whether landmark placements are adequate to identify species groupings and overlaps and patterns indicative of sexual dimorphism. The role of size as a differentiator between extant species is visualised using Procrustes Form Space as the basis for the analysis. A series of analyses, including linear diameter plots, Procrustes averaging, principal components analyses, discriminant function analyses and log se_m (based on regression analyses) are used to test whether species groupings agree with currently accepted taxonomic classifications of thirty-six African Plio-Pleistocene hominin lower

first molars. Specimens in the sample that consistently fail to group with current species designations are flagged as "anomalous". Six specimens are identified as anomalous and these are ultimately removed from the analyses. The resultant principal components plot of the fossil specimens appears to show distinctions between currently accepted species groups. The statistical regression analyses (log se_m) confirm the results from the geometric morphometric analyses, and are associated with an average log se_m value of -1.61 for conspecific pairwise comparisons. The log se_m value of -1.61 has been proposed by Thackeray (2007a) as an approximation of a biological species constant (T), based on pairwise comparisons of modern vertebrate taxa, using cranial data. The anomalies confirm the hypothesis that certain specimens from the sample may have been misclassified, and that certain species groups as currently defined may comprise more than one morphotype.