Abstract presented at the 75th Annual Meeting
of the Society of Vertebrate Paleontology;
Dallas, TX, October 2015
Meeting Program and Abstracts, SVP 2015, p. 222

Symposium 3 (Saturday, October 17, 2015, 9:30 AM)

ADDING PHYLOGENETIC TREES TO IMPROVE VIRTUAL RETRODEFORMATION: CERCOPITHECIDAE AS A TEST CASE

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Three-dimensional shape analysis is increasingly used to answer questions about functional morphology, paleoecology, and phylogeny of fossil taxa. Diagenetic shape change is a major obstacle for the use of geometric morphometrics (as well as more standard analytical approaches). Retrodeformation is the process of returning a deformed fossil to its antemortem-or "pre-death"-shape. The techniques of simple reflection and averaging and the more recently published approach of algorithmic symmetrization both adjust for asymmetrical deformation. Symmetrical deformation, however, remains a problem. Here we present a potential solution for addressing symmetrical deformation in fossil crania using three-dimensional morphometric data in combination with assumed phylogenetic relationships to create hypotheses for antemortem shape.

Dense patches of semilandmarks were collected on surface scans of the crania of undeformed extant and fossil cercopithecids and mapped onto a composite molecular phylogenetic tree with estimated divergence dates. Hypothetical landmark configurations representing all ancestral nodes and transformations along branches were calculated using a squared-change parsimony model of (Brownian-motion) evolution. Two mechanically deformed casts of *Papio hamadryas kindae* crania of known antemortem shape were first retrodeformed with algorithmic symmetrization (as in our previous work) and then fit onto the tree by finding the place-or places-where Procrustes distance was minimized. Three-dimensional models were generated based on the landmark configurations at those places and were used as templates to further correct the symmetrical deformation present in the crania, yielding a series of hypothetical reconstructions of antemortem shape. Principal component analyses of a broad sample of extant cercopithecids indicate that the hypothetical reconstructions fall within the range of extant variation of *P. h. kindae.* Permutation tests of pairwise Procrustes distances among the extant taxa and retrodeformed models indicate that the retrodeformed specimens are significantly more similar to other *P. h. kindae* than to members of any other taxon.