

Exploring evolutionary trends, and testing developmental hypotheses, in the Multituberculata

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The extinct multituberculates had the longest existence of any mammalian order known. They were the most diverse and abundant mammals for the majority of the Jurassic, Cretaceous and Paleocene, before becoming extinct in the late Eocene, some 130 million years after they first appeared. Considered to have been the rodents of their day, they are superficially similar in skull and dental morphology to living rodents.

In the first part of this talk, I will show results suggesting that multituberculates underwent an adaptive radiation some 20 million years before the extinction of non-avian dinosaurs, and continuing across the Cretaceous-Paleogene boundary (Wilson et al 2012). Measures of diversity, disparity in body size and disparity in dental complexity (which reflects diet, Laakkonen et al 2014) all rose sharply through this period, while large increases in maximum dental complexity and body size indicate evolutionary shifts towards herbivory in a number of lineages. This radiation tracked the ecological rise of angiosperms, suggesting resources used by multituberculates were relatively unaffected by the Cretaceous-Paleogene mass extinction.

Secondly, I will discuss ongoing work to test developmental biology macroevolutionary hypotheses in the fossil record using the dentitions of multituberculates as an example. Recent experimental genetic and developmental studies (Harjunmaa et al 2014) have shown that it is possible to engineer ancestral rodent characteristics in growing mouse teeth, and determine character linkages and signaling thresholds. However, experimentally increasing dental complexity or tooth cusp number is considerably more difficult than decreasing it. This leads to the hypotheses that in evolution, there may be a developmental constraint on the evolution of high dental complexity, that small complexity increases may be as common as small decreases, but that large complexity increases may be less common than large decreases. I will show pilot data testing these hypotheses against the evolutionary patterns of multituberculates.

References

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