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PRIMATE CRANIAL MORPHOGENETICS AND THE ROLE OF REPEAT POLYMORPHISMS

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Abstract

As molecular genetics becomes increasingly sophisticated, analyses of DNA sequences throughout the living world are often used to help decipher evolutionary phylogenies, diagnose pathological conditions, and unlock the ongoing mysteries of gene structure, function, and interaction. Based on such studies in modern purebred dogs, workers have recently hypothesized that variations in coding tandem repeat regions of several genes may account for at least some of the phenotypic variation in cranial evolution. In this paper, I attempted to examine orthologous repeat regions in three genes that are believed to be involved in craniofacial development (RUNX-2, DLX-2, and TWIST-1) to see if similar sequence variations to those observed in dogs exist in primates, and, if so, whether they indicate any direct correlation with craniofacial shape. While I did not see evidence of the enormous allelic variation observed in *Canis familiaris*, I did observe a very modest correlation between RUNX-2 total allele length and midface length in several Old World Monkey taxa. Accordingly, tandem repeat variation does appear to affect morphology; very generally, longer repeats are correlated with longer measurements. However, in the absence of artificially selective breeding (such as exists in modern dog breed) tandem repeat variation likely alters morphology over great periods of evolutionary time, rather than in a few dozen generations. It is possible that the mechanisms of change are similar in both artificial and natural selection, but the time scales are literally millennia apart. While I did not measure any statistical correlations between shape and either DLX-2 or TWIST-1 repeat sequences, the variation (or lack thereof, in DLX-2) in primate taxa was quite different from previous observations in dogs, also suggesting different genetic implications of short-term controlled breeding versus evolution by natural selection over geological time.