

Studying genomic changes in mammals shaped by the evolution of distinct phenotypic traits

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Changes in mammalian genomes reflect the evolution of distinct phenotypic traits. For instance, these phenotypic traits comprise adaptations to different habitats, diets, and morphological changes. Such changes can lead to the loss of protein-coding genes that do not serve advantageous or essential functions for the corresponding species. Our group previously developed a method for accurately detecting inactivating mutations in protein-coding genes, which render a protein-coding gene non-functional, referred to as gene loss. Using a forward genomics principle combined with selection rate analysis, we identified gene losses in independent lineages that relate to the convergent evolution of phenotypic traits. In this context, we identified gene losses related to the transition to an aquatic environment, the loss of tooth enamel and an herbivorous or carnivorous diet. Morphological traits such as the absence of specific bones, however, are less likely to be reflected by gene loss, but are more likely to exhibit changes in non-coding gene regulatory elements. To address this aspect, we computed an alignment of 120 mammalian genomes specifically geared towards an improved coverage of non-coding elements. This 120way genome alignment allows us to study genomic changes related to a wide-range of morphological traits over a broad phylogeny of mammalian species.

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