Bridging molecular evolution and phenotypic evolution

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Some phenotypic traits, such as sociality, feeding behavior, breeding behavior, are less polymorphic within species compared with inter-species diversity. We developed a method to estimate the genetic background behind these life history traits by associating them with molecular evolutionary rates. The neutral theory of molecular evolution asserts that among mutations fixed to the population, advantageous mutations are rare. Therefore, the molecular evolution rate is expressed as the product of the mutation rate and the ratio of the mutation which is neutral. By extending this theory to genome evolution, the branch lengths of the multi-loci phylogenetic trees can be decomposed into gene effect, branch effect, and gene-branch interaction. The gene effect represents a difference in preservability of the genes. The branch effect expresses the fluctuation of the product of mutation rates and evolutionary times, making it possible to robustly estimate the divergence times and the variation of the genomic mutation rates. Since the gene-branch interaction expresses the fluctuation of functional constraints on genes, it has a high potential as a feature for association analysis with traits. Analysis of the genomes form 89 placental mammals implied that the placental mammalian ancestors did not make groups, had seasonality in breeding, fed insects and were nocturnal. Genes involved in the brain and nervous system were detected for the trait of sociality, and the genes associated with seasonality in reproductive behaviors include those involved in meiosis, embryonic stem cell plasticity and sex hormone synthesis. These results imply that the genetic background of the trait polymorphisms in the human population can be consistent with those inferred by association of the long-term inter-species variation of molecular evolutionary rate. Comprehensive analysis of inter-species evolution and that of within-species polymorphism may improve our understanding of our diversity.