Measuring Primate Gene Expression Variation with Linear Mixed Model

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Abstract

An emerging issue in evolutionary genetics is whether it is possible to use gene expression profiling to identify genes that are associated with morphological, physiological, or behavioral divergence between species and whether these genes have undergone positive selection. Some of these questions were addressed in a study (Enard et al. 2002) of the difference in gene expression among human, chimp, and orangutan, which suggested an accelerated rate of divergence in gene expression in the human brain relative to liver. Reanalysis of the Affymetrix data set using analysis of variance methods to quantify the contributions of individuals and species to variation in expression of 12,600 genes indicates that as much as one-quarter of the genome shows divergent expression between primate species at the 5% level. However, biases inherent to short oligonucleotide microarray technology may account for some of the tissue and species effects. At high significance levels, more differences were observed in the liver than in the brain in each of the pairwise species comparisons, so it is not clear that expression divergence is accelerated in the human brain. Further, there is an apparent bias toward upregulation of gene expression in the brain in both primates and mice, whereas genes are equally likely to be up- or downregulated in the liver when these species diverge. A small subset of genes that are candidates for adaptive divergence may be identified on the basis of a high ratio of interspecific to intraspecific divergence.