

ALCOHOL DEHYDROGENASE (ADH) GENE CLUSTER IN PRIMATES

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By increasing the number of genes, gene duplication allows gain of new functions and properties, and is one of the most important mechanisms for genome evolution. The alcohol dehydrogenase (ADH) gene family exists widely in the genomes of many organisms, and provides a fine model for evolution of gene families. The seven human ADH genes are classified into five classes based on nucleotide/amino acid sequence similarity. Mice have six ADH genes in the same order as humans. One of the most interesting differences between humans and mice is that mice have only one Class I gene. The three Class I genes (*ADH1A*, *ADH1B*, *ADH1C*) in humans show very high nucleotide similarity both in exons (> 90%) and introns (> 70%), suggesting duplication events occurred probably after primates diverged from rodents. We have proposed a hypothesis that the primates' frugivorous behavior has maintained the duplicated genes because of the necessity of digesting ethanol generated by fermentation of fruit sugar. To test the hypothesis, we are screening the BAC clone libraries of 11 primates, and sequencing the ADH cluster clones in order to obtain nucleotide sequence information for the whole region of the gene cluster in the primates. Initial analyses of the three Class I genes suggest that the Class I genes have evolved without concerted evolution. Here we present the progress of the sequencing on the ADH gene cluster evolution in primate lineage.

Keywords: ADH, duplicated gene, clone-by-clone method, primates diet