Analysis of Expressed Sequence Tags (ESTs) from Cat Cerebrum and Cerebellum cDNA Libraries

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The cat is an attractive candidate for an animal model for human disease, genome evolution, comparative research for several reasons. Although mouse and rat have been powerful models to examine molecular mechanisms of human hereditary disorders. We believe that there are cogent rationales for development of a carnivore animal model. Domestic cats are subject to epidemics of two viruses, FeLV and FIV, that cause immunodeficiencies and neoplasias, providing a powerful animal model for leukemia and AIDS. These viruses and other feline pathogens provide a good opportunity to investigate the interaction of host immune response and fatal infectious disease.

The generation of expressed sequence tags (ESTs) has proven to be a rapid and economical approach by which to identify and characterize expressed genes. We constructed cDNA libraries from cat brain cerebrum and cerebellum and generated a total of 10,000 ESTs of high quality. Of these, 57.6% matched to known human or other mammalian coding sequences, 14.2% matched only to other ESTs, and 27.8% showed no match to any ESTs or known genes in the data base. Clustering of all ESTs identified 458 unique clusters comprising 4677 ESTs, whereas the remaining 5323 ESTs did not cluster. This estimates the number of unique genes identified in the data set to be approximately 5781.

The most redundant connective tissue-related genes with the exception of mitochondrial genes were Mbp, GLUL, EEF1A2, SNAP25, HSPCA, GPI, ENO2, SPARC and so on. This effort provides the first partial list of genes expressed in cat brain. Identification of genes expressed in the cat brain contributes to our understanding of human neurobiology, and potentially provides positional candidate genes for neurodegeneration such as or Alzheimer's disease.