

IN-SILICO MINING OF THE OPOSSUM GENOME FOR CYTOKINE GENES

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Cytokines are small proteins that are the core in communication between immune cells. Immune genes are known to evolve quickly. Past studies have demonstrated that the isolation of marsupial cytokine genes is difficult, due to their low levels of similarity to eutherian sequences. Hence, only three different marsupial cytokine gene types have been previously identified from four species.

A combination of prediction tools and database searching were used to identify 32 cytokines and receptors never found before in opossum (*Monodelphis domestica*). BLAST, syntenic genes and HMMER were used to search for homologous cytokine sequences in the opossum genome. GenomeScan was used to predict the exon-intron structure of genes, and phylogenetic trees were constructed to verify orthologous relationships with known eutherian cytokine genes.

Our findings included IL-2, IL-4, IL-6 and IL-13 with 41.8%, 30.8%, 36.4% and 36.7% protein identity to humans orthologs, respectively. Comparison of opossum cytokines with vertebrate cytokines from other lineages allows us to trace the evolution of these immune genes. The predictive tools used here were extremely useful in locating genes with low similarity to known homologues, and we suggest that the techniques described here will be valuable in identifying other divergent genes in organisms other than the opossum.