

Modeling Pathfinding and Target Recognition in the Olfactory System

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The formation of a functional nervous system requires billions of neurons to find and synapse with their appropriate partners. The molecular mechanisms that underlie this problem of axon guidance and target recognition in the mouse olfactory system are still poorly characterized. In particular, the role of the target tissue itself, the olfactory bulb, is unknown. We assumed that molecular cues must exist within the olfactory bulb to guide neurons to their targets, and that these cues are restricted in expression within the bulb. These differential expression patterns would collectively form a spatial map that would guide neurons to their targets. The goal of the CRCNS award was to use molecular biological, statistical, and computational approaches to study connectivity in the olfactory system. In the first two years of the grant, laser microdissection, amplification techniques, and microarrays were used to obtain samples of RNA from various regions of the bulb. Novel statistical approaches were developed to analyze this data, and identify candidate genes. Consistent with our initial hypothesis, we identified ~15 genes that are differentially expressed within the bulb. Currently, computational approaches are being used to analyze the function of these genes in connectivity, and to build a three-dimensional model of gene expression within the bulb. This award has therefore produced insight into this process of target recognition, and has also generated several tools that can be used by other scientists pursuing microarray studies.

Publications

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