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SRC Abstract

Retinal Expression of key players in the growth cone collapse pathway

During embryonic brain development, axonal movement in response to attractive and repulsive guidance cues is essential for proper patterning of the central nervous system. During retraction, microtubules depolymerize in the growth cone periphery. This reorganization is the result of signaling cascades that are initiated inside of the cell upon receptor activation. Semaphorins are a class of guidance cues that have long been implicated in growth cone collapse. Sema3A is a secreted protein that promotes cytoskeletal reorganization, and has been found to bind to Neuropilin-1/Plexin-A1 receptor complexes. Phosphorylation of these co-receptors has not been widely studied, but could have potential implications in the initiation of signal transduction. CRMPs, or collapsin response mediator proteins, are a class of proteins that have been shown to be involved downstream of this receptor complex. Several residues have been shown to be phosphorylated in the five different CRMP isoforms. Furthermore, phosphorylation of some of these residues has been shown to reduce the protein's ability to bind to tubulin heterodimers, thereby accelerating growth cone collapse in the migrating neuron. Protein expression of key players involved in the growth cone collapse pathway will be visualized using the zebrafish model system, including Sema3A, NP1, PlexA1, CRMP1, and CRMP2. *In situ* hybridizations have been performed in fish at 24, 48, and 72 hours post fertilization to determine the expression pattern of these proteins in the retinal tract of the zebrafish, an area whose development is known to involve multiple guidance cues including semaphorins.