# *Paramecium* as a model to study ciliary function

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SUMMARY

Cilia are eukaryotic organelles that protrude from the cell surface. They are composed of a complex cytoskeleton, the axoneme, and surrounded by an extension of the cell membrane. Ion channels, receptors and other signaling proteins in the cell membrane control the bending of the axoneme for motility or for sensing chemicals and mechanical stimuli. Cilia can be motile (e.g. causing movement of mucous or cerebral-spinal fluid), or sensory (as in olfactory neurons and kidney cells). Failure of cilia to develop or perform their function leads to developmental problems, and numerous human genetic diseases have been traced to ciliary dysfunction. Genes that affect cilia can be identified through the human disease phenotype and often have functions that remain elusive. Because the organization, composition and function of cilia are highly conserved throughout evolution, we propose to provide unique insights into human diseases related to cilia using *Paramecium* as a model. We have begun to identify genes that encode proteins that may possibly be related to ciliary structure, biogenesis or function using comparative genomics and proteomics. Several of these genes are now under study in our laboratory using the RNAi feeding method and analysis of the phenotypes.