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Study of Skates and Sharks Questions Assumptions About 'Essential' Genes

ScienceDaily (Dec. 15, 2011) — Biologists have long assumed that all animals with jaws and spinal columns possess nearly identical genes that regulate critical aspects of their embryological development. But a paper in the December 16 issue of *Science* by Benjamin King of the Mount Desert Island Biological Laboratory (MDIBL) and three of his colleagues shows that a class of fishes that includes skates and sharks lack genes that were formerly thought to be essential for their development.

"Ben's work shows that there are still surprises to be found by studying a broad variety of organisms," says MDIBL Director Kevin Strange. "This paper will make scientists take a closer look at something we thought we had already figured out."

Genes are sequences of genetic material found on the chromosomes contained in every living cell. As an animal develops from a single cell, certain genes become active at different times and control particular stages of development, such as the definition of limbs or organs. A group of genes named "*Hox*" is instrumental in the correct arrangement of cells during development. *Hox* genes have been found in every "bilateral" animal, that is, every animal that has a top and a bottom and a back and a front.

Hox genes can be critically important for the correct formation of limbs or appendages. When one of the *Hox* genes in fruit flies is mutated, for example, legs will grow where antenna should be. In mammals, *Hox* genes are required for the proper development of vertebrae and ribs. *Hox* genes intrigue scientists because the order in which they appear among the entire set of an organism's genes corresponds to the order in which they become active as an embryo develops from head to toe.

There is a remarkable similarity among *Hox* genes between broad classes of animals. When scientists take a *Hox* gene from a chicken and put it in the *Hox* location in a fruit fly, for example, the fly will develop normally.

Fruit flies have one cluster of *Hox* genes. In all the jawed vertebrates previously studied, scientists always found four copies of the *Hox* cluster. These clusters, named *HoxA*, *HoxB*, *HoxC*, and *HoxD*, are present in humans, who have roughly 10 genes in each cluster (39 in all). Prior to King's study, it was thought that all jawed vertebrates needed at least one gene from each of the four clusters for successful development. However, King's paper calls that fundamental assumption into question by demonstrating that at least two kinds of fish from a subclass called "elasmobranchs," which have cartilage instead of bones, lack the *HoxC* cluster.

King looked at the genes that were active in the later stages of embryonic development in the little skate (*Leucoraja erinacea*) and the dogfish shark (*Scyliorhincus canicula*) and did not find any *HoxC* genes. He

also searched the entire set of DNA sequences of the skate's genome without finding any *HoxC* genes. For comparison, he confirmed the presence of *HoxC* genes in the elephant shark (*Callorhincus milii*) that is from a subclass of cartilaginous fishes that are separate from elasmobranchs.

All of these studies used modern, high-throughput sequencing technology that enables researchers to characterize all genes in a sample rapidly. This technology has made it possible to sequence a human genome for less than ten thousand dollars and is ushering in an era of personalized medicine.

King says his work shows the importance of studying all kinds of organisms, including elasmobranchs, to understand evolution. "A goal of the field of evolutionary developmental biology is to learn how developmental processes evolved by comparing many organisms with one another," says King. "Our work illustrates the value of studying elasmobranch fishes such as skates and sharks to gain new insights. If elasmobranchs do not need *HoxC* genes to develop properly, we must consider the possibility that there is more flexibility in the role of the various *Hox* clusters than we previously thought."

Heather Carlisle and Randall Dahn from MDIBL and Andrew Gillis from Cambridge University co-authored the *Science* article with King. Their work was supported by the Maine INBRE, a federally-financed network of Maine laboratories, colleges, and universities led by MDIBL with the goal of strengthening Maine's capacity to conduct competitive biomedical research. King and colleagues from similar INBRE networks in Vermont and Delaware are currently collaborating to sequence the entire skate genome.

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1. B. L. King, J. A. Gillis, H. R. Carlisle, R. D. Dahn. **A Natural Deletion of the *HoxC* Cluster in Elasmobranch Fishes.** *Science*, 2011; 334 (6062): 1517 DOI: [10.1126/science.1210912](https://doi.org/10.1126/science.1210912)

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