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Review

The Hox Paradox: More Complex(es) Than Imagined

Victoria E. Prince1

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Abstract

An understanding of the origin of different body plans requires knowledge of how the genes and genetic pathways that control embryonic development have evolved. The Hox genes provide an appealing starting point for such studies because they play a well-understood causal role in the regionalization of the body plan of all bilaterally symmetric animals. Vertebrate evolution has been characterized by gene, and possibly genome, duplication events, which are believed to have provided raw genetic material for selection to act upon. It has recently been established that the Hox gene organization of ray-finned fishes, such as the zebrafish, differs dramatically from that of their lobe-finned relatives, a group that includes humans and all the other widely used vertebrate model systems. This unusual Hox gene organization of zebrafish is the result of a duplication event within the ray-finned fish lineage. Thus, teleosts, such as zebrafish, have more Hox genes arrayed over more clusters (or “complexes”) than do tetrapod vertebrates. Here, I review our understanding of Hox cluster architecture in different vertebrates and consider the implications of gene duplication for Hox gene regulation and function and the evolution of different body plans.

Keywords

Hox genes; Hox clusters; gene duplication; vertebrate evolution; teleosts; zebrafish; hindbrain

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1 Fax: (773) 702-0037. E-mail: vprince@midway.uchicago.edu.