

Minimal ProtoHox cluster inferred from bilaterian and cnidarian Hox complements

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Abstract

Bilaterian animals have a Hox gene cluster essential for patterning the main body axis, and a ParaHox gene cluster. Comparison of Hox and ParaHox genes has led workers to postulate that both clusters originated from the duplication of an ancient cluster named ProtoHox, which contained up to four genes with at least the precursors of anterior and posterior Hox/ParaHox genes^{1,2,3}. However, the way in which genes diversified within the ProtoHox, Hox and ParaHox clusters remains unclear because no systematic study of non-bilaterian animals exists. Here we characterize the full Hox/ParaHox gene complements and genomic organization in two cnidarian species (*Nematostella vectensis* and *Hydra magnipapillata*), and suggest a ProtoHox cluster simpler than originally thought on the basis of three arguments. First, both species possess bilaterian-like anterior Hox genes, but their non-anterior genes do not appear as counterparts of either bilaterian central or posterior genes; second, two clustered ParaHox genes, *Gsx* and a gene related to *Xlox* and *Cdx*, are found in *Nematostella vectensis*; and third, we do not find clear phylogenetic support for a common origin of bilaterian *Cdx* and posterior genes, which might therefore have appeared after the ProtoHox cluster duplication. Consequently, the ProtoHox cluster might have consisted of only two anterior genes. Non-anterior genes could have appeared independently in the Hox and ParaHox clusters, possibly after the separation of bilaterians and cnidarians.

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