

Identification and Expression of ParaHox Genes in the annelid *Perionyx excavatus* during Embryonic Development

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Hox and ParaHox genes arose by tandem duplications of a ProtoHox gene cluster are thought to have a key role in pattern formation and evolution of development. Both Hox genes and ParaHox genes known as 'dispersed' Hox-like genes contain equally homeobox and ParaHox cluster is also believed to be the evolutionary sister of the Hox cluster. ParaHox cluster has a spatial colinearity and inverted temporal colinearity with respect to the pattern in the Hox cluster. The ParaHox gene is composed of Gsx related to anterior group (PG1-2), Xlox to central group (PG3), and Cdx to posterior group (PG 9+).

In the presented study, we isolated three different ParaHox genes (named Pex-Gsx, Pex-Xlox and Pex-Cdx) through PCR based approaches from the earthworm *Perionyx excavatus*. To identify all three ParaHox gene sequences, we performed comparative and phylogenetic analyses with the homeodomain residues of other organisms.

Furthermore, we used whole-mount in situ hybridization to confirm developmental expression pattern of the three ParaHox genes. Pex-Xlox of the three ParaHox is expressed all over in the gut at early developmental stage. Spatial expression pattern of Xlox in gastrula embryos was quite broad and ubiquitous. Such an expression pattern differs from those reported for other vertebrate and invertebrate organisms

As development proceeds, Pex-Xlox-expressing cells become far anterior to the posterior.

Expression of Xlox in central regions of the presumptive gut has been already reported in *Amphioxus*, leeches and vertebrates and Xlox homeobox genes have been implicated in the function of endodermal differentiation in both vertebrate and invertebrate organisms, we think that Xlox homologues in earthworm embryos may play important roles in their development.

This is the first report for identification and expression of all three ParaHox genes in annelids.