

Expression and role of *hox* genes in the regeneration of internal organs in the sea cucumber *Eupentacta fraudatrix*

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Motivation and Aim: One of the most important adaptations for the survival of the organism is such a biological phenomenon as the ability to regenerate. Regeneration is widespread among animals and can be found in almost every large taxon. However, the potential for regeneration is different for everyone. Representatives of the Echinodermata type are distinguished by pronounced regenerative possibilities [1]. The sea cucumber *Eupentacta fraudatrix* was selected as the object of study because it is an excellent model for studying the mechanisms of regeneration. Many developmental genes play an important role in regeneration. Thus, the *hox* genes play a fundamental role in the correct formation of organs along the anteroposterior axis of multicellular bodies, such as worms, insects, vertebrates and echinoderms [2]. The participation of *hox* genes in the Holothuroidea class during regeneration is poorly understood. In this regard, the purpose of this work is to study the expression of *hox* genes in the process of regeneration of the internal organs of the sea cucumber *E. fraudatrix*.

Methods and Algorithms: A gene expression was estimated with qPCR, using *ef1a* and *tubulin* as reference genes. Gene identification was carried out using the construction of a phylogenetic tree. In order to construct RNA probes for *in situ* hybridization, the necessary sequences were produced. Hybridization was performed using antisense and sense (as control) RNA probes. AK and intestine, as well as AK rudiments, intestines, and body wall were subjected to hybridization at different stages of *E. fraudatrix* regeneration.

Results: We determined of 8 complete *hox* gene transcripts. Of them, two are anterior genes (*hox1*, *hox3*), three medial (*hox5*, *hox7*, *hox8*) and three back genes (*hox9/10*, *hox11/13a*, *hox11/13c*). With the regeneration of internal organs, the greatest change in activity is observed for the *hox5*, *hox7*, *hox9/10* and *hox11/13a* genes. The expression of the *hox5* and *hox9/10* genes was maintained above the level of the norm at all investigated stages of regeneration, *hox11/13a* had the highest level of activity on the 5th and 7th day after evisceration. The activity of the *hox7* and *hox9/10* genes is most pronounced in the structures of the ambulacral AK system. At the same time, these genes show spatial collinearity of expression. Observed expression of the studied genes of the Hox family in the sea cucumber *E. fraudatrix* shows their participation in the regulation of regenerative processes.

References

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