

Homeobox genes are generally known as key factors directing processes during the morphogenesis of organ systems. Recently, research of homeobox genes evolution has focused on evolutionary old groups of species, such as Cnidarians. In Cnidarians, there are more homeobox genes compared with more complex organism, such as fruit flies. Several homeobox genes have also been described in plants and fungi. General opinion is that homeobox genes are a very old group of genes, originating even before the main kingdoms of multicellular organisms.

Six homeobox genes that have been identified as homologues of *Drosophila sine oculis*, an important factor for compound-eye formation, take part in numerous developmental processes directed by the PAX-SIX-EYA signal pathway. In Vertebratae, as representatives of Deuterostomes, there are six genes in three sub groups, whereas in *Drosophila melanogaster*, as a representative of Protostomes, three homologues have been described, always one for each subgroup. The ancestral six genes diverged even before the divergence of groups Bilateralia and Cnidaria. In freshwater jellyfish *Craspedacusta sowerbyi* we distinguished both HD and SD regions for five SIX proteins. Four of these six genes of *Craspedacusta sowerbyi* belong to the established Six groups (Six1/2, Six3/6 and Six4/5), where in the sub group Six3/6, the ancestral six3/6 gene have been duplicated. In *Craspedacusta sowerbyi* there are two six3/6 genes, the same as has been described by Deuterostomes. It is possible, that in Cnidarians the six genes may divide into four subgroups. Moreover, we described one protein very similar to IRX group of homeobox proteins.