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Evo-Devo and Genomics of Vertebrate Hox Gene Cluster

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Gene duplication and subsequent genetic divergence are considered as a mechanism by which we can explain complexity of the vertebrate body plan. This pattern is widely exemplified by the Hox gene clusters. It has been proposed that new body plans may arise through alterations in the temporal and spatial expressions of Hox genes, which may be mediated by modifications in control regions and occurrences of new regulatory domains of the Hox genes.

To reconstruct the evolutionary history of Hox cluster origins, genomic organizations of vertebrate Hox clusters have been investigated by means of genomic PCR survey, contig map, large scale sequencing and sequence analysis. By comparative structural examinations between and within the major vertebrate lineages we understand whether independent cluster duplications and gene loss events have occurred. The current data support that the duplications of vertebrate Hox gene clusters in major lineages were followed by duplications and gene loss events have occurred independently in individual clades. It is presumed that independent cluster duplicaitons and gene drop-out events may contributed to generate somewhat different developmental control systems to some degree.

In the other hand, in our investigations of the developmental and evolutionary roles of the Hoxc8 enhancer, we found modifications on enhancer motifs that are candidates for binding sites of transcription factors can be correlated with body plan changes by report gene analyses in the mouse system. We also suggest that potential variations in regulatory domains may provide evolutionary modifications unique to corresponding clades. Based on pairwise and multiple sequence comparisons we are getting understood evolutionary origins of separate regulatory regions which may responsible for different body plans of corresponding vertebrate lineages.

In addition to a comparative genomic approach for cluster duplications, we are doing functional analyses by making large constructs maintained in pClasper, a yeast-bacteria shuttle vector, and using transgenic systems to know relations between the modification and different origin of each regulatory domain and corresponding body plan change.