

Reconstruction of paleo genomic information of metazoan based on a microsynteny analysis

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Since a variety of metazoan genome decoding, the conservation of gene order on the DNA (synteny) is recognized as a common event in the metazoan. For example, Putnam reported the some amounts of signatures of macrosynteny between human and sea anemone (*Nematostella vectensis*) (Putnam et al 2007). Subsequently, Irimia reported their hypothesis that two adjacent genes that shared their 5' cis region (head to head) may restraint their translocation. Because of this situation, I'm trying to use these syntenic constraint for reconstructing the ancient genome. To the start of such reconstruction analyses, I'm compared among the genome of Hemichordate, Sea urchin and Amphioxus. These analyses revealed their possible common developmental mechanisms kept since their common ancestor.

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