

Unraveling ancient segmental duplication events in human genome by phylogenetic analysis of multigene families residing on HOX cluster paralogs

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Abstract

Background

Vertebrate genomes contain extensive intra-genomic conserved synteny, which is the presence of similar set of genes on two or more chromosomes (paralogs). The existence of these paralogs has led to the proposal that vertebrate genome was structured by one or more rounds of ancient whole genome duplications (2R hypothesis).

Results

The 2R hypothesis was tested by phylogenetic analysis of gene families residing on human HOX bearing chromosomes (HOX cluster paralogs). These results revealed that, based on their duplication history, 23 gene families with representation on three or four of the human HOX bearing chromosomes can be partitioned into four discrete co-duplicated groups. The distinct genes within each co-duplicated group share the same evolutionary history and are duplicated in concert with each other, while the constituent