Evidence of Balansing Selection in Parallel Evolution of Closely Related Gammarus Species Genomes

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We compared the rate of parallel synonymous and nonsynonymous molecular evolution in different systematic groups. Orthologous group alignments of closely related Gammaridae species were used for this issue, and vertebrates exon alignments were added as a reference dataset. Where the same nucleotide substitutions had occurred in more than one lineage, nonsynonymous substitutions were found to be more frequent than synonymous ones. The overrepresentence of nonsynonymous parallel substitutions indicates of prevalent positive selection at sites of parallel evolution in closely related species. However, very high amount of heterozygous sites was found among these parallel substitutions. We suppose that combination of these factors might be a marker of high amount of balancing selection in early sympatric divergence.