

F823 An Evidence for the presence of an hAT Transposable element in the Earthworm, *Eisenia andrei*

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Transposable elements are ubiquitous mobile genetic elements found in all organisms. The first transposable element, the maize *Activator* element, is an *hAT* family that has a broad host range, including plants, fungi, animals and even man. Several DNA sequences similar to the *hobo* element of *Drosophila melanogaster* were isolated and characterized in the earthworm, *Eisenia andrei*. The basic structure and functional features of this mobile genetic element are discussed. In addition, phylogenetic analysis was performed with deduced amino acid sequence, which is a part of the conserved region of transposase. Emphasis is given to the use of *hAT* transposons as tool for gene tagging and genetic transformation.

F824 The distribution screening of Transposable elements in Natural populations of *Drosophila melanogaster* by PCR approach.

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Transposable elements, pieces of selfish DNA present in the genomes of most organisms, have been divided into two major classes according to their mode of transposition. Class I elements transpose via RNA intermediates, whereas class II elements transpose by means of a DNA intermediates encoding transposase in *D. melanogaster*. The elements of *P*, *hobo*, *I* elements and *mariner*-like elements contain several functional ORFs, which putatively

encodes a endonuclease. Here we report that the distribution and functional analysis of transposable elements containing integrase-transposase domain in Korean local population. Practical approach was directed to analyze the distribution of variable transposable elements using modified nested PCR. Autonomous element containing functional ORF was detected in several lines of local population and most of strains tested appeared to be intermediate strain type in dysgenic system. This fact would suggest that detected elements potentially have repression activity.

F825 Spatial and temporal expression of the Alpha-amylase during developmental stage in *Drosophila melanogaster*

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We report the structure and expression patterns of alpha-amylase genes during development of *D. melanogaster*. These -amylases are related to digest the carbon sources during development. These -amylase genes, encoding digestive amylases, are expressed in all developmental stages without embryonic stage tested with similar size of PCR products. However, -amylase appeared to be expressed in all stages except embryonic stages, suggesting that -amylase genes are not functional in embryonic stage. The putative -amylase of *Drosophila* do not seem to be similar to the digestive protein reported as egg specific or yolk protein. The results reported here are discussed in relation to the evolution and function of amylase.