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Structural analysis of a 4414-bp element in *Drosophila melanogaster*

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ABSTRACT. We cloned a 4414-bp element from a mutant of *Drosophila melanogaster*. Its insertion site was 18,929,626 bp. Analysis of the nucleotide and amino acid sequences demonstrated that the element is homologous to Pifo_I, first obtained from *D. yabuka*, which belongs to the *gypsy*/*Ty3* subfamily. We also obtained a 3754-bp length element from a wild-type fly by PCR, with a pair of primers designed from the conserved region of the 4414-bp length element. The two elements included a pair of long terminal repeats and part of the GAG and ENV proteins, but the POL protein was completely lost. This element is found in the subgenus of *D. melanogaster*, but it is a degenerate type of Pifo_I and is not infective. Also, a 714-bp region structured in 5.0 tandem repeats of 143 bp each was found in the 5'UTR of the degenerate element; these could interact with transcription factor CF2. Phylogenetic analysis and alignment of amino acids indicated that the Pifo_I element was closer to the *ZAM* retrotransposon, which gave us some clues to their functional similarity. Based on these data, we propose that there is a relationship between the degenerate element

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and the mutant phenotype, which would provide a foundation for further research.

Key words: *gypsy*/*Ty3*; 4414-bp element; 3754-bp element; Pifo_I; *ZAM*