Comparison of the feature in genome rearrangement of *Paramecium* with that of the other organisms

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The intergenic region between the hemoglobin (*hb*) and nucleosome assembly protein-1 (*nap-1*) genes in the *Paramecium caudatum* macronuclear genome was previously found to be heterogeneously composed. Cloning of this intergenic region from the macronuclear genomic DNA identified four unique DNA fragments of different sizes. Sequencing of the cloned fragments revealed extreme heterogeneity and characteristics of both internal eliminated sequence (IES) and imprecise internal deletion sequences (IIDSs) in the intergenic region. Southern blotting of the total genomic DNA and polymerase chain reaction (PCR) of the total genomic DNAs indicated that there exist a dozen DNA fragments of different sizes in this intergenic region. It is likely that the heterogeneity found in the *P. caudatum* macronuclear genome results from the variable removal of an intergenic region. Furthermore, we detected a chimeric DNA structure that may be generated by the tail-to-tail fusing of the 5' region of the *hb* gene to most of the *nap-1* gene. Short tandem repeats exist at the putative cleavage sites in the *hb* and *nap-1* genes, respectively. This suggested that the chimeric DNA may be generated by a novel mechanism distinct from those of TA-IES elimination, homologous recombination at hotspots, gene conversion or other transpositions by transposable elements.