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Site-specific large-deletions in yeast *Saccharomyces cerevisiae* mitochondrial *oxi3* gene

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It was already shown that site-specific large-deletions are exceptionally frequent in the oxi3 gene encoding the subunit I of the cytochrome c oxidase in yeast Saccharomyces cerevisiae mitochondrial genome. Most of deletions fall into only two classes, A and B. A-deletion extend between two GC clusters that constitute perfect direct repeats of 31 bp. One end is lying in the 5'-untranslated leader, the other end about 11.3 kb downstream in the fifth intron open reading frame. In the case of B-deletion, interestingly, left end coincides with the 3'-slice site(intron/exon junction) of first intron, right end 8,222 bp downstream in the fifth intron open reading frame as in A-deletion. The possible deletion mechanisms and the role of the enzymes possibly involved in this kind of frequent,site-specific deletions in yeast Saccharomyces cerevisiae mitochondrial oxi3 gene will be discussed.

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Genetic Instability of Coliphages Revealed by Random Amplified Polymorphic DNA(RAPD) Analysis

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Genetic analysis was conducted on newly isolated coliphages from wet soil. Since we reported general characteristics of the coliphages with conventional methods, here we concentrated on the genetic variation of coliphage genomes by using RAPD analysis. From the initial results with various random primers, strong genetic variation was found among coliphages C2 and C3, which implied genetic instability of the coliphages within two or three generation passages. In addition, phylogenetic relationship was also determined, and we confirmed that coliphage C1 was mostly unrelated to other coliphages such as C2, C3 and C4.