Note

Evolutionary Position of N-Alkane-Assimilating Yeast Candida maltosa Shown by Nucleotide Sequence of Small-subunit Ribosomal RNA Gene

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Received April 5, 1993

We clarified the evolutionary position of Candida maltosa, an n-alkane-assimilating yeast, by sequencing the nucleotides of the small-subunit ribosomal RNA gene. Phylogenetic analyses showed the close evolutionary relationships of C. maltosa with C. tropicalis, C. viswanathii, C. albicans, C. parapsilosis, and C. guilliermondii, forming a sub-group within this genus.

Growth of Candida maltosa on highly hydrophobic compounds like n-alkane and fatty acids leads to the induction of various enzymes, such as cytochrome P-450 (P-450alk), and to the proliferation of the endoplasmic reticulum and the peroxisomes in which these enzymes are located. Genetic approaches to investigate the molecular mechanisms underlying the regulation of gene expression and organelle proliferation by these highly hydrophobic compounds have been frustrated by the fact that C. maltosa has an almost diploid genome and lacks a sexual life-cycle. To overcome this problem, we have developed and used the genetic engineering systems of C. maltosa strain IAM 12247.

The genus Candida is a heterogeneous assemblage unified mainly by the absence of any sexual state (teleomorph). The phenotypic character-based classification has created a confusing taxonomy and a great heterogeneity within the genus. The evolutionary relationships among several Candida species and their relatives have been described on the basis of small-subunit ribosomal RNA (srRNA) sequences.9,10 The srRNA sequences are commonly used for phylogenetic analysis of yeasts.11

During the course of isolating n-alkane-inducible genes (induced by n-alkane but not by glucose) from a genomic library by differential screening, we had isolated a highly expressed clone (TIG2) which had homology to the genomic DNA of Saccharomyces cerevisiae.8 The nucleotides of this clone were sequenced (Fig. 1) and disclosed high homology to other organisms. We aligned the srRNA sequences from Candida yeasts and relatives using "Clustal V" programs,12 and constructed the phylogenetic tree shown in Fig. 2 by the neighbor-joining method.13 The srRNA sequences used for comparison were derived from the DDBJ, EMBL, and GenBank Nucleotide Sequence Databases, and their accession numbers are shown in the legend of Fig. 2.

The topology of the tree is largely compatible with those of the recently published srRNA trees for several members of the genus Candida and its relatives.9,10 Candida maltosa formed a sub-group lineage with C. tropicalis, C. viswanathii, C. albicans, C. parapsilosis and C. guilliermondii in this genus. The bootstrap analysis indicated 99.2% support for this lineage monophyly. Saccharomyces cerevisiae, C. kefyr, Kluyveromyces lactis, C. glabrata, Hansenula polymorpha and C. krusei, form another sub-group. Candida lusitaniae and Yarrowia lipolytica are excluded from these two sub-groups.

C. maltosa was originally identified as a species closely related to C. parapsilosis, showing the same morphological characteristics and sharing many biochemical properties.13 The close relationship between C. maltosa and members of this sub-group is also supported by the comparison of other macromolecular sequence data. A comparison of the sequences of L41 ribosomal protein shows an amino acid identity of 99.1% between C. maltosa and

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Fig. 1. The Nucleotide Sequence of the srRNA Gene of Candida maltosa.

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Abbreviations: srRNA, small-subunit ribosomal RNA; P-450alk, n-alkane-inducible cytochrome P-450.
by the phylogenetic analysis based on the 5S rRNA sequences. Only four of the 14 yeasts shown in Fig. 2 were confirmed in their assignment of the CUG codon. Candida albicans and C. parapsilosis assigned it to serine, but S. cerevisiae and Y. lipolytica have CUG as the universal leucine codon. Considering the close evolutionary relationships of C. maltosa with C. albicans and C. parapsilosis, it is speculated that the amino acid assignment of the CUG codon is serine in C. maltosa and other members of this sub-family. In vitro and in vivo experiments to determine the amino acid assignment of the CUG codon in C. maltosa are in progress.

Acknowledgments. We thank Dr. T. Ueda of the Department of Industrial Chemistry, the University of Tokyo for providing his data before publication. We also thank Dr. N. Najimuddin of the University of Science Malaysia for critical reading of the manuscript.

References