

18S-28S rRNA スペーサー領域の塩基配列 による *Saccharomyces* 種の系統解析

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A phylogenetic Analysis of *Saccharomyces* Species by the Sequence of 18S-28S rRNA Spacer Regions

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ABSTRACT Sequences of two internally transcribed spacer regions between 18S and 28S rRNA genes were determined to assess the phylogenetic relationship in the strains belonging to the genus *Saccharomyces*. The sequences of *S. bayanus* and *S. pastorianus* were quite similar, but not identical. Two phylogenetic trees constructed by the neighbor-joining method showed that all the species examined were distinguished from one another. The *Saccharomyces sensu strict* species: *S. cerevisiae*, *S. bayanus*, *S. paradoxus* and *S. pastorianus*, were closely related and far from the *Saccharomyces sensu lato* species including *S. barnetti*, *S. castellii*, *S. dairensis*, *S. exiguus*, *S. servazzii*, *S. spencerorum* and *S. unisporus*, and an outlying species, *S. kluyveri*.

抄録 *Saccharomyces* に属する菌株の 18S-28S rRNA 遺伝子スペーサー領域の塩基配列を決定し、系統学的な関連性を評価した。*Saccharomyces sensu strict* に属する種は互いに近縁であるが、*Saccharomyces sensu lato* に属する種および *S. kluyveri* とは遺伝的な隔たりが大きいことが示された。