FILOGENEZA BAKTERII
Z RODZAJU ACINETOBACTER

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Phylogeny of Acinetobacter genus

Abstract: The genomic species is one of the major concepts of a bacterial species and is based on quantitative similarities between chromosomal DNAs of bacteria (DNA reassociation values) as determined by DNA-DNA hybridization. This method is one of the recommended standards for delineating bacterial species and a genomic species is defined as a group of bacterial strains that have DNA-DNA reassociation values of approximately 70% or more. The similarity of small subunit rRNA (16S rRNA) sequences is increasingly being used for the classification of bacteria. However, the resolution of 16S rRNA sequence analysis is insufficient to distinguish closely related genomic species because of the extremely slow rate of base substitution in 16S rDNAs. On the other hand, phylogenetic analysis based on protein-encoding genes provides a greater degree of resolution than that based on 16S rRNA genes since the former genes evolve faster than the latter. Various protein-encoding genes such as recA, groEL, hsp75, rpoB, rpoD and gyrB have been used for the classification of bacteria at the intragenic level. It has been reported that the grouping of Acinetobacter strains based on 16S rRNA sequence analysis, DNA-DNA hybridization analysis and phenotypic methods is inconsistent and therefore the establishment of reliable methods for unambiguous identification of these strains is quite urgent. We are interested in examining the possibility that phylogenetic analysis using protein-encoding recA genes could be used for the
identification of *Acinetobacter* strains and to provide information equivalent to that of DNA-DNA hybridization analysis.