FILOGENEZA BAKTERII
Z RODZAJU *ACINETOBACTER*

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1. Molekularne systemy odtwarzania drzew filogenetycznych. 2. Drzewo filogenetyczne odtwarzane w oparciu o sekwencję nukleotydową genu kodującego 16S rRNA. 3. Drzewo filogenetyczne odtwarzane w oparciu o sekwencję nukleotydową genu *gyrB*. 4. Gen recA w badaniach filogenetycznych bakterii. 5. Amplifikacja fragmentu genu recA *Acinetobacter* sp. i sekwencjonowanie. 6. Molekularne drzewo filogenetyczne rodzaju *Acinetobacter* w oparciu o sekwencję nukleotydową fragmentu genu recA. 7. Podsumowanie

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 1 6S 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.

1. Molecular systems for reproducing phylogenetic trees. 2. Phylogenetic tree reproduced based on nucleotide sequence of 16S rRNA gene. 3. Phylogenetic tree reproduced based on nucleotide sequence of *gyrB* gene. 4. *recA* gene in phylogenetic studies of bacteria. 5. Amplification of *Acinetobacter* sp. *recA* gene fragment and sequencing. 6. Molecular phylogenetic tree of *Acinetobacter* genus based on nucleotide sequences of *recA* gene fragment. 7. Summary