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Polymorphism and molecular anatomy of ribosomes in extremely halophilic archaeon

- Evolution of ribosomes based on the study of halophilic microorganisms -

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Summary

In virtually all species, the sequences of multicopy of rRNA genes (rDNA) are identical or nearly identical. The molecular mechanism responsible for maintaining the sequence homogeneity has not yet been elaborated, although the necessity for such a mechanism seems obvious. The halophilic archaeon, *Haloarcula marismortui*, contains two different *rrn* operons in its genome. These two operons, designated as *rrnA* and *rrnB*, were previously cloned on separate genomic restriction fragments. The extremely halophilic triangular archaeon, *Haloarcula japonica* strain TR-1 is originally isolated from a Japanese saltern soil. Until now, however sequence determination of 16S rDNA in *H. japonica* is incomplete. In addition, copy number of the gene has not yet been estimated. To construct precise phylogenetic tree suggesting evolutionary position of the species in genus *Haloarcula*, the copy number and heterogeneity of 16S rDNA in *H. japonica* are essential.

In this study, the complete 16S rDNA sequences of the extremely halophilic triangular archaeon, *H. japonica* strain TR-1, were determined and then designated as 16S-A (*rrnA*) and 16S-B (*rrnB*). The substitutions are not uniformly distributed but rather are localized within three domains of 16S rRNA. Comparison of these two the strain TR-1 sequences to the 16S gene sequences from related halophilic genera suggests that (i) in diverging genera, mutational differences in 16S rDNA sequences are not clustered but rather are more generally distributed throughout the length of the 16S sequence and (ii) the 16SB rDNA sequence, particularly within the 508-823 domain, is more different from the out group sequences than is the 16SA rDNA sequence. Several possible explanations for the evolutionary origin and maintenance of this sequence heterogeneity within 16S rRNA of *H. japonica* will be discussed.