

The 18S ribosomal RNA gene of an anthozoan *Anthopleura kurogane*: a comparison with *Anemonia sulcata*

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Received July 26, 1993; Accepted July 30, 1993

EMBL accession no. Z21671

As a part of a study to understand the sequence variability of 18S rRNA gene among anthozoans (phylum Cnidaria), we have determined the complete 18S rDNA sequences of a coral species, *Anthopleura kurogane*, by means of PCR cloning and Taq sequencing as in (1). There is only one species in anthozoans, *Anemonia sulcata*, in which the complete nucleotide sequences of 18S rRNA gene were known. We compared the nucleotide sequences of *A.kurogane* [Family Actiniidae, from the present study] with those of *A.sulcata* [Family Actiniidae, from Hendricks *et al.* (2)]. Therefore the present study shows the sequence variability between different genera within same family in anthozoans. We aligned the sequences of two species using FASTA program (3). The numbering system of nucleotide position found in the following is that of *A.sulcata* without considering the insertion and/or deletion resulting from the alignment.

The total length of the 18S rDNA of *A.kurogane* is 1796 bp, which is shorter than that of *A.sulcata* by 3 bases. The G + C content is about 47% in each of two species. This value is lower than those of crustaceans and vertebrates (4, 5). The total numbers of different, identical, and null (insertion and/or deletion site) nucleotides between two species are 39, 1752, and 13 respectively from alignment. The similarity between two species is 97.8% when the null sites were excluded. If we include the null sites and consider these sites as the unweighted nucleotide differences between two species, the similarity is 97.1%. No big insertion is found between two species. There are 6 insertion sites (8 nucleotides) in *A.sulcata* and 5 (5 nucleotides) in *A.kurogane*,

and the number of nucleotide in each insertion site is one or two. Among 39 different nucleotides between two species, 29 nucleotides are located at the variable regions [6 in V2, 1 in V3, 11 in V4, 6 in V7, 2 in V8, 3 in V9; variable regions are according to Neef *et al.* (6)]. Of the rest 10 nucleotides, one nucleotide is found in the region between 5' end and V1, 3 in V2-V3, 1 in V4-V5, 4 in V5-V7, 1 in V7-V8, and altogether, 7 nucleotides are found in the single stranded area and 3 in helices.

ACKNOWLEDGEMENTS

This work was supported by research grants from the Ministry of Education of Korea (Institute for Molecular Biology and Genetics) and Korea Science and Engineering Foundation through the Research Center for Cell Differentiation (92-4-3).

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