560 Genetic and Spectroscopic Analysis of Marine Photosynthetic Bacteria

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Despite the biotechnological importance of marine photosynthetic bacteria, relatively little is known about them, in comparison to freshwater photosynthetic bacteria. The purpose of this present work is to characterize further marine purple nonsulphur photosynthetic bacteria isolated in this laboratory from Japanese coastal waters. We have purified chromatophore membranes from a number of strains and carried out spectroscopic analysis of photosynthetic pigment protein complexes. Careful study of this data and the absorption peaks attributed to intra cellular carotenoids has shown that the biodiversity of marine photosynthetic complexes is far greater than previously expected. One strain showed near infrared absorption peaks at 800, 830 and 870 nm. This pattern has not been found in freshwater photosynthetic bacteria and may represent a new type of photosynthetic complex. SDS-PAGE analysis of chromatophore membranes also revealed different sized reaction centre polypeptides of one marine strain which is spectroscopically similar to Rb.sphaeroides. We also present here homology analysis of genes encoding the reaction centre and light harvesting polypeptides between freshwater and marine photosynthetic bacteria using standard hybridization techniques and also using polymerase chain reaction (PCR) technology. Sequencing of the 16s rRNA genes of several marine strains is being carried out to improve classification of these organisms and to shed light on the molecular evolution of photosynthesis.

561 Nucleotide sequences of two genomic DNAs encoding peroxidase of Arabidopsis thaliana

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Peroxidase is an important enzyme that oxidize several compounds (hydrogen donors) in the presence of H_2O_2, and is found widely in animals, plants and microbes. It is suggested that the biological functions of peroxidase in plants include the formation of lignin polymer and rigid cross-links between lignin, cellulose, and extensin in the secondary plant cell wall. Now it is believed to be involved in auxin catabolism and defense against pathogen attack.

The peroxidase gene of Arabidopsis thaliana was screened from a genomic library using a cDNA encoding a neutral isozyme of horseradish (belonging to the same family, Brassicaceae, as Arabidopsis) peroxidase (HRP) as a probe, and two positive clones were isolated. From the comparison of the sequences of the HRP genes, we concluded that two clones contained peroxidase genes, and they were named prxCa and prxEa. Both genes consisted of 4 exons and 3 introns, and introns had consensus nucleotides, GT and AG, at the 5' and 3' ends, respectively. The lengths of each putative exon of prxEa gene were the same as those of the HRP basic isozyme gene, prxC3, and coded for 349 amino acid residues with a sequence homology of 89% to that coded on prxC3. The prxCa gene was very close to the HRP neutral isozyme gene, prxC1b, and coded for 354 amino acid residues with 91% homology to that on prxC1b. The amino acid sequence homology was 64% between the peroxidases encoded on prxCa and prxEa. Sequences in proximal and distal His regions concerning heme-binding and 8 Cys residues for S-S cross-linking were well conserved in horseradish and Arabidopsis peroxidases.

prxCa and prxEa genes had a putative promoter sequence, TATA box and CAAT box, in the 5' upstream region and a poly A signal, AATAAA, in the 3' noncoding region. prxCa and prxEa were mainly expressed in root, and the transcription start points were -53 and -63 from the translation start point, respectively.

In Southern blot analysis, Arabidopsis genome seemed to contain one copy of prxCa and prxEa gene, respectively.