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EXISTENCE OF A NOVEL PERIPLASMIC MOLECULAR CHAPERONE-LIKE PROTEIN OF A PHOTOTROPH

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We have isolated DppA as a molecular chaperone-like protein from the periplasm of *Rhodobacter sphaeroides* f. sp. *denitrificans* using the in vitro refolding system of acid unfolded dimethyl sulfoxide reductase (DMSOR). DppA has also an activity to prevent aggregation of the unfolded rhodanese. DppA was suggested to function as a molecular chaperone in the periplasm. The *dppA*-disrupted mutants, however, synthesized the folded DMSOR protein. It suggested that other proteins exist which complement the function of DppA as a molecular chaperone. Then, we investigated the periplasm of the *dppA*-disrupted mutant whether there exist proteins preventing aggregation of the unfolded DMSOR in the periplasmic fraction of the *dppA*-disrupted strain.

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MULTIPLICITY AND EXPRESSION OF GENES CODING FOR THE CORE LIGHT HARVESTING COMPLEX 1 (LH1) IN THE PURPLE BACTERIUM *Allochromatium vinosum*

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The complete nucleotide sequence of *puf* operon from the purple sulfur bacterium, *Allochromatium vinosum*, was determined. The operon contained genes coding for the α and β subunits of the LH1 core complex and for L, M and cytochrome subunits of the reaction center as in other purple bacteria. However, *A. vinosum* contained the second and third sets of genes homologus to *pufB* and *pufA* at the downstream region of *pufBALMC* (*pufBA2* and *pufBA3*, respectively). The amino acid sequences of the *pufB1*, *pufA2* and *pufB3* predicted from the nucleotide sequences were identical to those directly determined from the purified LH1 polypeptides. The northern hybridization analysis clarified that these two additional *pufBA* genes are co-transcribed with the upstream *pufBALMC* genes as a 5.3 kb mRNA. Moreover, the two downstream *pufBA* genes had their own mRNA. Correlation between expression of the unique *puf* operon and the conformation of the LH1 core complex in *A. vinosum* will be discussed.

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EXPRESSION OF PHOTOSYNTHETIC APPARATUS IN PURPLE BACTERIA *Roseateles depolymerans* AND *Rubrivivax gelatinosus*

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Roseateles depolymerans is a BChl *a*-containing obligate aerobe phylogenetically neighboring upon *Rubrivivax gelatinosus*. These two bacteria have structurally similar *puf* operons coding for photosynthetic apparatus(1). However, the latter is a genuine phototroph which grows anaerobically under the light, while the former has characteristics resembling to aerobic photosynthetic bacteria. In the present study the accumulations of photosynthetic pigments and the *puf* mRNA in the two bacteria were determined in the dark under different nutrient- and oxygen-conditions. *Rvi. gelatinosus* was pigmented under all conditions determined so far, and the pigmentation was greater in anaerobic and nutrient poor conditions. On the other side, *Rat. depolymerans* was pigmented under aerobic and nutrient poor conditions, but did not show any accumulations of photosynthetic pigments and *puf* mRNA under anaerobic and nutrient rich conditions. The regulatory behavior responding to oxygen in these two species seemed different. Furthermore, *Rat. depolymerans puf* operon was considered to be regulated more strictly by nutritional conditions.

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AEROBIC EXPRESSION OF PHOTOSYNTHESIS GENES IN THE PURPLE BACTERIUM, *RHODOVULUM SULFIDOPHILUM*

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The purple photosynthetic bacterium *Rhodovulum sulfidophilum* synthesizes photosynthetic apparatus even under highly aerated conditions. To understand the oxygen-independent expression of photosynthetic genes, the expression of *puf* operon coding for the light-harvesting-1 and reaction center proteins was analyzed. The *puf* mRNA synthesis was not significantly repressed by oxygen in this bacterium. There are three *puf* operon promoters, two of which have a high degree of sequence similarity with those of *Rhodobacter capsulatus*, which shows a high-level of oxygen repression on the photosystem synthesis. Deletion analysis showed that the third promoter is oxygen-independent. The post-transcriptional *puf* mRNA degradation is not significantly influenced by oxygen in *R. sulfidophilum*. From these results, we conclude that the *puf* operon expression in *R. sulfidophilum* is weakly repressed by oxygen, perhaps as a result of the following: 1) there are three promoters for *puf* operon transcription, one of which, at least, is oxygen-independent; 2) readthrough transcripts which may not be affected by oxygen may be significant to maintain the *puf* mRNA levels; and 3) the *puf* mRNA is rather stable even under aerobic conditions.