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DISSERTATION SUMMARY

Studies on the signal transduction cascades responsible for the control of the expression of NiFe hydrogenases and photosynthetic apparatus in purple sulfur photosynthetic bacteria

Ákos T. Kovács

Department of Biotechnology, Faculty of Sciences, University of Szeged, Szeged, Hungary and Institute of Biophysics, Biological Research Center, Hungarian Academy of Sciences, Szeged, Hungary

The photosynthesis and hydrogen metabolism play important role in the energy metabolism of photosynthetic bacteria. If they are energetically linked, the expression of their components should be regulated by common factors. A pigment mutant strain of the purple sulfur photosynthetic bacterium, *Thiocapsa roseopersicina* BBS was isolated by plasposon mutagenesis. About 19 *orf*-s, most of which are thought to be genes involved in the biosynthesis of carotenoids, bacteriochlorophyll and photosynthetic reaction centre were identified surrounding the plasposon in a 22 kb long chromosomal locus. The carotenoid biosynthetic genes, *crtDC* and *crtE* genes were shown to be regulated by oxygen, and the role of CrtJ in aerobic repression was suggested (Kovács et al. 2003).

T. roseopersicina harbors two membrane bound [NiFe] hydrogenases (HupSL, HydSL). The two enzymes differ in their stability in the presence of oxygen, heat and proteases (Kovács et al. 2002). The organization of the *hyn* operon is extraordinary, since two additional *orf*-s (*isp1* and *isp2*) separates the structural genes: *hynS* and *hynL* (Dahl et al. 1999). The maturation of these enzymes requires several accessory proteins, which are involved in e.g. metal incorporation, formation of the active centre, the proteolytic cleavage of the large subunit (Fodor et al. 2001; Maróti et al. 2003).

Generally the expression of HupSL type regulation is controlled via a H_2 sensing system. We identified genes coding for the hydrogen sensor (HupUV) and the sensory kinase (HupT) of this signal transduction cascade. In spite of the presence of these genes, the expression of *hupSL* was apparently not effected by H_2, as indicated by hydrogenase activity measurements and *lacZ* fusion constructs, but repressed by traces of oxygen. The expression of the *hydSL* was also shown to be enhanced in the absence of oxygen. Upstream from the determined promoters a region was identified as an essential *cis* element for this anaerobic activation. The regulation of the *hyd* operon by O_2 could be observed in *Escherichia coli* and *Rhodobacter capsultus*, as well. The role of the FNR, but not the ArcAB or RegAB systems in the anaerob activation was demonstrated in *E. coli*, and in *R. capsulatus*. The comparison of these regulation styles will be discussed.

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Supervisors: Gábor Rákhely, Kornél L. Kovács
E-mail: kovacsa@nucleus.szbk.u-szeged.hu