Geophysical Research Abstracts, Vol. 9, 04818, 2007
SRef-ID: 1607-7962/gra/EGU2007-A-04818

The adaptation of the purple bacterium *Rhodopseudomonas palustris* to varying environmental conditions by means of malate dehydrogenase

M. Klimova, A. Eprintsev

Voronezh State University, Voronezh, Russia (mary_klimova@mail.ru / Phone: +74732-20-88-77)

Rhodopseudomonas palustris is one of the most metabolically versatile bacteria ever described. It has the potential to be very useful because it can degrade and recycle several different aromatic compounds that make up lignin, the main constituent of wood and the second most abundant polymer on earth.

R. palustris is a model organism to probe how the web of metabolic reactions that operates within the confines of a single cell adjusts and reweaves itself in response to changes in light, carbon, nitrogen and electron sources that are easily manipulated experimentally.

This bacterium prefers to generate all its energy from light by photosynthesis using carbon dioxide or some organic compounds like acetate or succinate. When oxygen is present, *R. palustris* generates energy by degrading a variety of carbon containing compounds and by carrying out respiration.

It's well known that organic acids are preferably metabolized through the tricarboxylic acid cycle (TAC) and the glyoxylate bypass where malate dehydrogenase (MDH) is one of the key enzymes. MDH in plants and animals plays an important role in adaptation to different stress conditions by means of synthesis of additional isoenzymes having different molecular weight and other distinctions. The adaptative mechanisms of microorganisms to varying conditions on the level of the MDH-system is not elucidated enough. Therefore, our work was designed to study a quaternary structure of MDH purified from *R. palustris* growing under different nutritional conditions.

It was shown that the changeover from one nutrition type to another is associated with

a change in the relative roles of the TAC and glyoxylate cycle in the bacterial cells. In cultures on acetate containing media, the glyoxylate cycle is induced in the bacterium, whereas growth on succinate is associated with induction of the TAC independently of energy source. Using then gel-chromatography, PAGE and SDS-PAGE it was determined that MDH in the first case was of 90 kD molecular weight, while in the second case it had molecular mass twofold more – 181 kD. SDS-PAGE of the protein revealed molecular weight of the subunit to be 47 kD in both cases. Under growth on acetate and succinate at once MDH from *R. palustris* was presented in two isoforms, dimer and tetramer. By means of selective inhibitory analyses it was demonstrated that the MDH-dimer is working in TAC while the MDH-tetramer is active in the glyoxylate bypass. In addition, catalytic properties of homogeneous preparations of the MDH-dimer and MDH-tetramer were significantly different. This fact is in concordance with the different functions of these isoforms in different metabolic processes.

Thus, it was determined that in the metabolically versatile bacterium *R. palustris* the quaternary structure transformation of the MDH plays an important role in adaptation to different nutritional conditions. Namely, the MDH-dimer is involved in the TAC functioning, whereas the MDH-tetramer provides for the functioning of the glyoxylate cycle.