1SC-02

Characterization and regulation of aerobic and anaerobic respiratory enzymes of Pseudomonas aeruginosa

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Pseudomonas aeruginosa, a ubiquitously distributed opportunistic pathogen, has a highly branched respiratory chain terminated by multiple terminal oxidases and denitrification enzymes. At least five terminal oxidases for aerobic respiration have been identified in the P. aeruginosa cells. Three of them, the cbb1 oxidase, the cbb2 oxidase, and the aox oxidase, are cytochrome c oxidases and the other two, the box oxidase and the cyanide-insensitive oxidase, are quinol oxidases. Each oxidase has a specific affinity for oxygen, efficiency of energy coupling, and tolerance to various stresses. These terminal oxidases are used differentially according to the environmental conditions. P. aeruginosa also has a set of the denitrification enzymes that reduce nitrate to molecular nitrogen via nitrite, nitric oxide, and nitrous oxide. These nitrogen oxides function as alternative electron acceptors and enable P. aeruginosa to grow under anaerobic conditions. The control of the expression of these aerobic and anaerobic respiratory enzymes contributes to the adaptation of P. aeruginosa to a wide range of environmental conditions. Enzymatic characteristics and evolutionary implications of these respiratory enzymes and the regulatory system that controls the expression of the respiratory genes in the P. aeruginosa cells are overviewed in this presentation.

1SC-03

Crystal structure of nitric oxide reductase, a key enzyme in the molecular evolution of respiratory complex


Respiratory function is a fundamental process in which electrons generated by glycolysis and other energy metabolic pathways are utilized for the reduction of terminal electron acceptors. In aerobic respiratory chain, cytochrome c oxidases (COX) catalyzes the reduction of O2 molecule as a terminal electron acceptor, whereas, in anaerobic respiration, several kinds of metalloproteins reduce inorganic molecules like oxoyns of nitrogen or sulfur compounds as final electron acceptors. Denitrification, a representative anaerobic respiratory chain of facultative microbes, is composed of four reductases, each of which utilizes nitrogen oxides as terminal electron acceptor. Of these, nitric oxide reductase (NOR) catalyzes the reduction of NO with one equivalent of electron to form N2O. Interestingly, because catalytic subunit of NOR (NorB) shares characteristic features with subunit I of COXs, NOR has been thought to be an ancestor of the same progenitor with COXs in the molecular evolution of anaerobic to aerobic respiration.

We solved the crystal structure of c-type NOR (cNOR) from a denitrifying bacterium Pseudomonas aeruginosa at 2.7 Å resolution. From the structural comparisons between cNOR and COXs, we will discuss the molecular evolutionary history of terminal respiratory enzymes, that could be important for the adaptation to the drastic environmental changes occurred during the emergence of oxygenic photosynthesis.

1SC-04

Diversity in proton pumping mechanisms of the terminal oxidases

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D-pathway of cytochrome oxidase has been proposed to transfer both protons for pumping and water formation. One of the experimental supports for the proposal is that D-pathway is well conserved from mammalian to bacteria. However, recently it has been found that the D-pathway is not conserved in certain bacterial terminal oxidases. The conserved structures across all families of the heme-copper oxidoreductases include the heme a3cCoQ dinuclear site, the four histidine imidazole groups that coordinate the metals and the covalently linked His-Tyr moiety. It has been proposed that the O2 reduction site and proton pumping site are restricted to the conserved structure, based on the proposition that the structures of the proton-pumping system and the O2 reduction site are conserved completely among the terminal oxidases of cell respiration. An alternative interpretation is as follows: the O2 reduction reaction without release of reactive oxygen species is a set of well organized complex chemical reactions. No structure for the O2 reduction site better than the Fe/Cu system has been found in the history of evolution of all life. Therefore the structure of the O2 reduction site is conserved completely among the terminal oxidases. On the other hand, proton-pumping involves a set of chemically simple processes, protonation/deprotonation of polar functional groups. Many amino acid residues are expected to be involved in this process. Diversity among the proton pumping system is therefore not surprising.