Recently, a new mechanism for energy coupling called Flavin-Based Electron Bifurcation (FBE) was proposed to explain energy conservation in anaerobic organisms [1]. This mechanism, which allows the thermodynamically unfavorable reduction of ferredoxin with NADH by coupling it to a favorable reduction, was most likely present in the early life forms on Earth. Here we describe a new NAD(P)H dehydrogenase (FloxABCD) likely to be involved in FBE, which was identified in sulfate reducing organisms [2,3]. The floxABCD genes are usually found next to hdrABC genes that code for a heterodisulfide reductase [3]. The flox-hdr cluster is found in a large number of bacteria belonging to Chlorobi, Proteobacteria, Firmicutes, Bacteroidetes, Spirochaetes and Acidobacteria phyla, pointing for a general and important role in the energy metabolism of these organisms. Here, we present results on the function of the FloxABCD-HdrABC in Desulfovibrio vulgaris Hildenborough that indicate its involvement in ethanol oxidation and a possible link to sulfite reduction.

References

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S8.P22

Divide to conquer: From the study of the individual subunits to the understanding of the whole alternative complex III
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In Rhodothermus marinus membranes, the quinol:electron acceptor oxidoreductase activity is performed by the alternative complex III (ACIII) [1–4]. This seven subunit complex is a member of a recently identified family of enzymes, which catalyzes an equivalent reaction to the bc1 complex, but is structurally unrelated to it. The available information on the structure and operating mechanisms on ACIII is still scarce. Therefore, the aim of this work was to characterize the ACIII subunits as individual proteins. For that, the genes coding for the subunits, namely those coding for the two cytochromes, were cloned and expressed in Escherichia coli. The biochemical characterization of the proteins was carried out and their function within the complex was explored. This knowledge provides new insights into the ACIII structure and function.

References

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S8.P23

Factors in culture medium enhancing amino acid production and switching branches of the respiratory chain of Corynebacterium glutamicum
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Corynebacterium glutamicum is an aerobic Gram-positive bacterium of industrial importance, in the production of amino acids, e.g. glutamate and lysine, used as nutritious additives in food and feed. In a series of our early studies to understand its aerobic energy metabolism, we have identified three enzyme complexes in the respiratory chain and their gene clusters: cytochrome bc1-type menaquinol oxidase [1], cytochrome “bcc”-type quinol:cytochrome c oxidoreductase (Complex III) [2], and cytochrome aa3-type cytochrome c oxidase (Complex IV) [3]. These enzymes compose two electron-transferring routes, bd route and bc-c-aa3 route, which have different ratios of proton translocated/electron transferred [4]. These routes are selectively operated depending on subspecies of the organism and environmental or growth conditions such as the extent of aeration, and this switching can be monitored precisely by a newly developed assay system using the green fluorescent protein (GFP) as a reporter [5]. Recently, we also found that the selection of the respiration routes was dependent on the concentration of yeast extract contained in the growth medium. Proteomic analyses indicated that several soluble enzymes in the central metabolism, various oxidoreductases, and some transcription factors were either increased or decreased by adding yeast extract to the medium. In addition, this ingredient also markedly enhanced glutamate production by partial puriﬁcation with hydrophobic and ion-exchange chromatographies, mass analyses and so on.

References

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