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Perspective

Reaction Sequences of Cytochrome bc1 Complex in Mitochondrial Proteins

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DESCRIPTION

The bc1 complexes are intrinsic membrane proteins that catalyse the reduction of cytochrome c and the oxidation of ubihydroquinone in bacterial photosynthetic and respiratory chains as well as mitochondrial respiratory chains. The bc1 complex functions such as Q-cycle mechanism, which connects electron transfer to the production of the proton gradient that powers ATP synthesis. Mitochondrial myopathies are caused by genetic flaws that result in mutations in proteins of the respiratory chain, including the bc1 complex's subunits. Many of these myopathies are a direct result of malfunction at catalytic sites. Some myopathies, notably those that affect the cytochrome b subunit, make more superoxide at the site of ubihydroquinone oxidation, which worsens free-radical damage. It appears that the bypass reaction is an inherent part of the response process.

Reactive oxygen species from superoxide cause DNA and protein damage, which causes cellular ageing and is a major contributor to many age-related disorders. Bc1 structural studies have been incredibly, producing atomic-resolution structures of the protein from different animals and locked in distinct chemical intermediates. These structures have helped to our understanding of the mechanism underlying bc1 activities as well as its deactivation by respiratory inhibitors.

Pumping protons

The main pump in this procedure is cytochrome bc1. It attaches to the mitochondrial membrane's ubiquinol, a hydrogen atom transporter, and expels two protons and two electrons. For usage by ATP synthase, the protons are released on the exterior of the membrane. The electrons move in two different directions: one electron moves in a direction that is extremely favorable and leads to cytochrome c, while the other moves in a direction that is less favorable and leads to the inner side of the membrane.

Complex cofactors

The protein cytochrome bc1 is dimeric. One heme and an iron-sulfur cluster are among the several cofactors that make up each half, which is made up of 11 protein chains. Different forms of structures have been identified. The cofactor locations and the two pathways that electrons take were made clear by the structure.

Chromosome bc1

The cytochrome bc1 revealed the ubiquinol binding sites and the course of the electrons, as well as a surprise. An iron-sulfur cluster and a heme are both on the way to cytochrome c, which receives the electron from the cluster. Higher organisms cyt bc1 complexes also have Mitochondrial Processing Peptidase (MPP) activity. MPP activity is easily detectable in the purified bc1 complex from plant mitochondria, such as spinach, it is inactive in the bc1 complex from bovine mitochondria.

CONCLUSION

Since the beginning of the era of bc1 crystal structure determination fifteen years ago, structural features of the protein that were previously inaccessible using various experimental methods have surprised us and shed new light on the mechanisms underlying bc1 function and its inhibition. These structural features are not only beautifully illustrated the architecture of this integral membrane protein and confirmed the essence of the Q-cycle. Reconstructing the reaction sequence of bc1 function required the use of atomic resolution snapshots of bc1 trapped as different reaction intermediates, which were necessary for reconstructing the reaction sequence of bc1 function.

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