unexpected structural change presented here provides a cautionary note about interpreting functional data derived from a mutated protein in the absence of its exact structure.

A new method for mapping interactions in the plant-type [2Fe-2S] ferredoxin

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Mapping of protein-protein interaction sites in the plant-type [2Fe-2S] ferredoxin


Iron-sulfur (Fe-S) clusters act as cofactors of various Fe-S proteins that are widely distributed in nature and required to maintain fundamental life processes. Recent studies revealed that the assembly of Fe-S clusters in several bacteria as well as eukaryotic mitochondria is achieved by a multicomponent system, called ISC machinery. This machinery is generally encoded by the iscSUA-hscB-fdx operon, and consists of six ISC proteins. Among them, the components playing central roles in de novo Fe-S cluster biogenesis are IscS and IscU. IscS is a cysteine desulfurase that catalyses the sulfur atom abstraction from cysteine substrate and provides the sulfur atom for the biosynthesis. IscU serves as a scaffold for assembly of a nascent Fe-S cluster, prior to its delivery to target Fe-S protein, in which directly accepts the sulfur atoms from the IscS.

We have refined the crystal structure of a recombinant plant-type [2Fe-2S] Fd I from the blue green alga Aphanothece sacrum (AsFd-I) at 1.46 Å resolution on the basis of the synchrotron radiation data. Incorporating the revised amino-acid sequence, our analysis corrects the 3D structure previously reported; we identified the short a-helix (67-71) near the active center, which is conserved in other plant-type [2Fe-2S] Fds. Although the 3D structures of the four molecules in the asymmetric unit are similar to each other, detailed comparison of the four structures revealed the segments whose conformations are variable. Structural comparison between the Fds from different sources showed that the distribution of the variable segments in AsFd-I is highly conserved in other Fds, suggesting the presence of intrinsically flexible regions in the plant-type [2Fe-2S] Fd. A few structures of the complexes with Fd-dependent enzymes clearly demonstrate that the protein-protein interactions are achieved through these variable regions in Fd. The results described here will provide a guide for interpreting the biochemical and mutational studies that aim at the manner of interactions with Fd-dependent enzymes.

Keywords: ferredoxin, iron-sulfur cluster protein, protein-protein interactions

Crystallographic analyses of the ISC proteins involved in de novo Fe-S cluster biogenesis

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Iron-sulfur (Fe-S) clusters act as cofactors of various Fe-S proteins that are widely distributed in nature and required to maintain fundamental life processes. Recent studies revealed that the assembly of Fe-S clusters in several bacteria as well as eukaryotic mitochondria is achieved by a multicomponent system, called ISC machinery. This machinery is generally encoded by the iscSUA-hscB-fdx operon, and consists of six ISC proteins. Among them, the components playing central roles in de novo Fe-S cluster biogenesis are IscS and IscU. IscS is a cysteine desulfurase that catalyses the sulfur atom abstraction from cysteine substrate and provides the sulfur atom for the biosynthesis. IscU serves as a scaffold for assembly of a nascent Fe-S cluster, prior to its delivery to target Fe-S protein, in which directly accepts the sulfur atoms from the IscS.

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Keywords: ferredoxin, iron-sulfur cluster protein, protein-protein interactions

Iron-sulfur cluster, cysteine desulfurase, protein-protein interactions


pH-dependent substrate recognition in human MTH1

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