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The Crystal Structure of Zinc-Containing Ferredoxin from a Thermoacidophilic Archaeon

Tomomi Fujii and Yasuo Hata

Ferredoxins (Fd) are electron transfer proteins which have iron-sulfur clusters as their active sites, and are distributed over a wide range of living organisms. Various kinds of Fds isolated from different organisms are classified by the geometry of the Fe-S cluster into several types. The dicluster-type Fds frequently isolated from bacteria are well known to share a common protein fold known as the (βαβ)2 fold ligating two cubane-like Fe-S clusters ([4Fe-4S] or [3Fe-4S][4Fe-4S]). This type of Fds are also isolated from Archaea.

Archaea (archaebacteria), which grow under extreme conditions such as high temperature, strong acidity, high salinity and anaerobicity, constitute a group of organisms which is distinct from Bacteria and Eucarya [1]. Sulfolobus sp. strain 7 is a thermoacidophilic archaeon which grows optimally at pH 2.5-3.0 and 75-80°C [2]. Ferredoxin from Sulfolobus sp. strain 7 is known to serve as an electron acceptor of a 2-oxoacid:Fd oxidoreductase. The Sulfolobus Fd molecule consists of a polypeptide of 103 amino acid residues, and two Fe-S clusters [3]. The primary structure of the Sulfolobus Fd is distinct from those of bacterial Fds in two regions; the Sulfolobus Fd has an N-terminal extension of about 40 residues and an insertion of about 10 residues in the middle of the polypeptide chain. Such a characteristic extension and insertion in sequence has also been found in ferredoxins from other thermoacidophilic archaea. Therefore, the additional regions are expected to adopt informative conformations characteristic to thermoacidophilic archaeal Fds. In order to elucidate the stabilization mechanism and the evolutionary status of archaeal proteins by investigating structural features of thermoacidophilic archaeal Fds, we have determined the crystal structure of ferredoxin from Sulfolobus sp. strain 7 by X-ray analysis.

The Sulfolobus ferredoxin was crystallized by a batch method using ammonium sulfate as a precipitant. The crystals belong to the tetragonal space group P4 3 2 1 2 with Tomomi Fujii and Yasuo Hata

Key words: X-ray analysis/ Zinc/ Iron-sulfur cluster/ Thermostability

MOLECULAR BIOLOGY AND INFORMATION – Biopolymer Structure –

Scope of research

Our research aims are to elucidate structure-function relationships of biological macromolecules, mainly proteins, by using physicochemical methods such as spectroscopic and X-ray diffraction methods. The following attempts have been made in our laboratory for that purpose. (1) Peptide secondary or supersecondary structures in aqueous or hydrophobic environments are studied to elucidate the stabilization mechanism and the evolutionary status of archaeal proteins by investigating structural features of thermoacidophilic archaeal Fds, we have determined the crystal structure of ferredoxin from Sulfolobus sp. strain 7 by X-ray analysis. Therefore, the additional regions are expected to adopt informative conformations characteristic to thermoacidophilic archaeal Fds. In order to elucidate the stabilization mechanism and the evolutionary status of archaeal proteins by investigating structural features of thermoacidophilic archaeal Fds, we have determined the crystal structure of ferredoxin from Sulfolobus sp. strain 7 by X-ray analysis.

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cell dimensions of \( a = b = 50.12 \, \text{Å} \) and \( c = 69.52 \, \text{Å} \). The structure was determined by the isomorphous replacement method for the uranium and platinum derivatives, supplemented with anomalous dispersion effects from the iron atoms of the Fe-S clusters as well as the uranium atoms in the derivative. In the course of the structural analysis, an uninterpreted high density peak in the derivative was identified as the Fe-S clusters and the residues which participate in interaction between \( \beta \)-sheets A and B are represented with ball-and-stick models. Fe-S cluster I and II are indicated as I and II, respectively.

Figure 1. Schematic drawing of the Sulfolobus Fd molecule. \( \beta \)-strands are shown as gray arrows and \( \alpha \)-helices are shown as gray spirals. The \([3\, \text{Fe}-4\, \text{S}] \) clusters, the seven cysteines, the zinc ion and the four zinc-ligand residues are represented as ball-and-stick models. Fe-S cluster I and II are indicated as I and II, respectively.

The overall structure of the Sulfolobus Fd molecule is depicted in Fig. 1. The protein folding of the Sulfolobus Fd can be divided into two parts by a structural comparison of the present archaeal Fd with other bacterial dicluster Fds (Fig. 2). One part is the core-fold part (residues 37-103), which binds two \([3\, \text{Fe}-4\, \text{S}] \) clusters and has a topologically conserved protein folding; a \((\beta\alpha\beta) \) fold, common to bacterial dicluster Fds, forms two antiparallel \( \beta \)-sheets, A (\( \beta 4 \) and \( \beta 7 \)) and B (\( \beta 5 \) and \( \beta 6 \)), and two \( \alpha \)-helices, \( \alpha 2 \) and \( \alpha 3 \). The other part is the N-terminal extended part (residues 1-36), which is mainly formed by one-turn \( \alpha \)-helix \( \alpha 1 \) and antiparallel \( \beta \)-sheet A’ of strands 1-3. \( \beta \)-Sheet A’ in the N-terminal part interacts with the terminal \( \beta \)-sheet A in the core-fold part through hydrogen bonds between strands \( \beta 3 \) and \( \beta 4 \) to form a larger five-stranded \( \beta \)-sheet, A’+A. As described above, the Sulfolobus Fd molecule contains a novel zinc-binding center, which had never been found in ferredoxins, at the interface between the core-fold part and the N-terminal extended part (Fig. 1). The zinc ion is tetrahedrally ligated by four amino acid residues, His 16, His 19 and His 34 from the N-terminal part, and Asp 76 from the core-fold part. Three ligand histidines, His 16, His 19 and His 34, to the zinc ion are located at the C-, N- and C-terminal ends of three \( \beta \)-strands, \( \beta 1 \)–\( \beta 3 \), respectively, which form \( \beta \)-sheet A’ in the N-terminal extended part. The zinc ion binds tightly through the Zn-His coordinate bonds to \( \beta \)-sheet A which interacts with \( \beta \)-sheet A through hydrogen bonds between \( \beta 3 \) and \( \beta 4 \) to form the larger sheet, A’+A. The last zinc ligand, Asp 76, is located at the C-terminal end of strand \( \beta 6 \) in \( \beta \)-sheet B. In this way, two \( \beta \)-sheets, A and B, in the core-fold part, are indirectly linked by both the zinc ligation between \( \beta \)-sheets B and A’ and the hydrogen bonds between \( \beta \)-sheets A’ and A (Fig. 2).

The core fold common to bacterial Fds adopts a quite simple \((\beta\alpha\beta) \) fold. In the core-fold part of bacterial dicluster Fds, \( \beta \)-sheets A and B are usually so apart from each other that they do not interact directly (Fig. 2). The unfolding of the core fold may begin with dissociation of the two \( \beta \)-sheets. If the interaction between the \( \beta \)-sheets is strong, the unfolding of the core fold would be unlikely to occur. Indeed, the Sulfolobus Fd seems to utilize the zinc ion, the N-terminal extension and the insertion in order to enhance the stability of the core fold through the indirect interaction between the two \( \beta \)-sheets. Therefore, thermoacidophilic archaeal Fds may acquire thermostability primarily by inserting the zinc ion in the interface between the extended N-terminal and the corefold parts, as observed in the Sulfolobus Fd. It is expected that biochemical and biophysical studies on the roles of the zinc ion in thermoacidophilic archaeal Fds might lead to elucidation of the role of metal ions in protein thermostability.

References