

Poster Presentation

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A novel six-coordinated ferric ion binding mode of TtFbpA

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Iron is an essential element for the growth and survival of nearly all living organisms. However, it is difficult for most organisms to get enough iron from the environment, because of the extremely low solubility of ferric ion. One of the strategies for iron acquisition is to use the ATP-binding cassette (ABC) transport system. In Gram-negative bacteria, a typical iron uptake ABC transporter consists of a ferric ion-binding protein (Fbp) located in periplasm (FbpA), two transmembrane proteins that form a pathway for ferric ions (FbpB), and two peripheral ATP-binding proteins located at the cytoplasm side of the inner membrane (FbpC). TtFbpA is a ferric ion-binding protein of a putative iron uptake ABC transporter from *Thermus thermophilus* HB8. Here we report the crystal structures of the apo-form and ferric ion-bound form of TtFbpA at 1.8-Å and 1.7-Å resolutions, respectively [1]. The crystal structure of the ferric ion-bound TtFbpA shows that a ferric ion binds to a specific site of TtFbpA to form a six-coordinated complex by three tyrosine residues, two bicarbonates and a water molecule, revealing a novel mode of coordination to a ferric ion. Another crystal structure of ferric ion-bound TtFbpA reported earlier showed the bound ferric ion is five-coordinated by three tyrosine residues and a carbonate bound in the bidentate manner [2]. The different modes of the coordination would probably result from the different pHs used for crystallization: pH 5.5 (six-coordinated) vs. pH 7.5 (five-coordinated). The Gram negative bacterium *T. thermophilus* HB8 can live in a wide pH range of 3.4–9.6. We propose that TtFbpA, a periplasmic protein of *T. thermophilus* HB8, can act as a ferric ion-binding protein over the wide pH range by taking at least two different coordination manners to a ferric ion depending on pH. This is the first example of a periplasmic ferric iron-binding protein that can coordinate a ferric ion via multiple types of coordination complex formation.

[1] S. Wang, M. Ogata, S. Horita et al., *Acta Cryst*, 2014, D70, 196-202, [2] Q. Wang, Q. Lu, Q. Zhou et al., *Biochem. Biophys. Res. Commun.*, 2013, 434, 48-53

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