

MS08-P04 | STRUCTURAL BASIS OF ASCORBATE-DEPENDENT IRON REDUCTION BY HUMAN DCYTB INVOLVED IN INTESTINAL IRON ABSORPTION

Sugimoto, Hiroshi (RIKEN SPring-8 Center, Hyogo, JPN); Ganasen, Menega (University of Hyogo, Hyogo, JPN); Togashi, Hiromi (RIKEN SPring-8 Center, Hyogo, JPN); Takeda, Hanae (University of Hyogo, Hyogo, JPN); Shiro, Yoshitsugu (University of Hyogo, Hyogo, JPN); Mauk, Grant (University of British Columbia, Vancouver, CAN); Sawai, Hitomi (University of Hyogo, Hyogo, JPN)

Duodenal cytochrome *b* (Dcytb) is a Fe³⁺ reductase that was identified in the duodenal brush border. Since DMT-1 favors the absorption of divalent metal including Fe²⁺, the reduction of Fe³⁺ to Fe²⁺ by Dcytb in the duodenum is essential for effective intestinal iron absorption. Dcytb is an integral membrane protein that catalyzes reduction of nonheme Fe³⁺ by electron transfer from ascorbate across the membrane. Here we report the crystallographic structures of human Dcytb and its complex with ascorbate and Zn²⁺ [1]. Each monomer of the homodimeric protein possesses six transmembrane helices and cytoplasmic and apical heme groups, as well as cytoplasmic and apical ascorbate-binding sites located adjacent to each heme. Zn²⁺ coordinates to two hydroxyl groups of the apical ascorbate and to a histidine residue. Biochemical analysis indicates that Fe³⁺ competes with Zn²⁺ for this binding site. These results provide a structural basis for the mechanism by which Fe³⁺ uptake is promoted by reducing agents and should facilitate structure-based development of improved agents for absorption of iron.

[1] Ganasen et al. *Commun. Biol.* 1,120 (2018)