6A, 18B/1999G106

CRYSTAL STRUCTURE OF A NOVEL-TYPE ARCHAEAL RUBISCO WITH PENTAGONAL SYMMETRY

Ken Kitano,* Norihiro Maeda,[1] Toshiaki Fukui,[1] Haruyuki Atomi,[1] Tadayuki Imanaka,[1] and Kunio Miki*[2]

* Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan,
[1] Graduate School of Engineering, Kyoto University, Sakyo-ku, Kyoto 606-8501, Japan,
[2] RIKEN Harima Institute / SPring-8, Koto 1-1-1, Mikazukicho, Sayo-gun, Hyogo 679-5148, Japan.

Ribulose 1,5-bisphosphate carboxylase/ oxygenase (Rubisco) is the key enzyme of the Calvin-Benson cycle and catalyzes the primary reaction of CO_2 fixation in plants, algae, and bacteria. Rubisco's have been so far classified into two types. Type I is composed of eight large subunits (L-subunits) and eight small subunits (S-subunits) with tetragonal symmetry (L_8S_8), but type II is usually composed only of two L-subunits (L_2). Recently, some genuinely active Rubisco's with unknown physiological function have been found from archaea [1].

The crystal structure of Rubisco from the hyperthermophilic archaeon *Thermococcus kodakaraensis* KOD1 (*Tk*-Rubisco) was determined at 2.8 Å resolution. The enzyme is composed only of L-subunits and showed a novel $(L_2)_5$ decameric structure (Fig. 1) [2]. Compared to previously known type I enzymes, each L_2 dimer is inclined approximately 16 û to form a toroid-shaped decamer with its unique L_2-L_2 interfaces. Differential scanning calorimetry (DSC), circular dichroism (CD), and gel permeation chromatography (GPC) showed that *Tk*-Rubisco maintains its secondary structure and decameric assembly even at high temperatures.

The present study provides the first structure of an archaeal Rubisco, an unprecedented $(L_2)_5$ decamer. Biochemical studies indicate that *Tk*-Rubisco maintains its decameric structure at high temperatures. The structure is distinct from type I and type II Rubisco's, and strongly supports that *Tk*-Rubisco should be classified into a novel type III Rubisco.

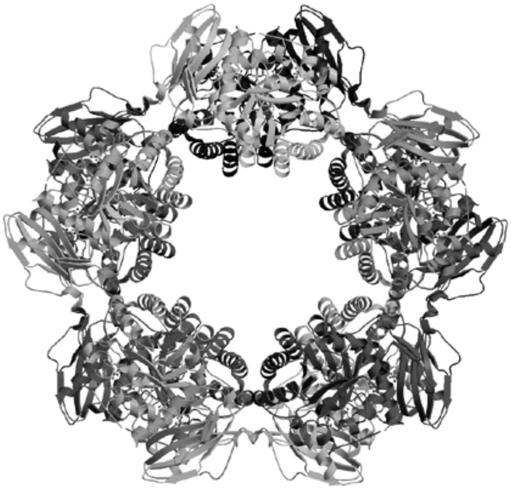

Fig. 1. Crystal structure of *T*k-Rubisco decamer

References

[1] N. Maeda, K. Kitano, T. Fukui, S. Ezaki, H. Atomi, K. Miki, and T. Imanaka, *J. Mol. Biol.* 1999; 293: 57-66.

[2] K. Kitano, N. Maeda, T. Fukui, H. Atomi, T. Imanaka, and K. Miki, *Structure*, 2001; 9: 473-481.