Poster Presentation

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Structure & acceptor recognition of CLG1_GBSS, a cyanobacterial starch synthase.

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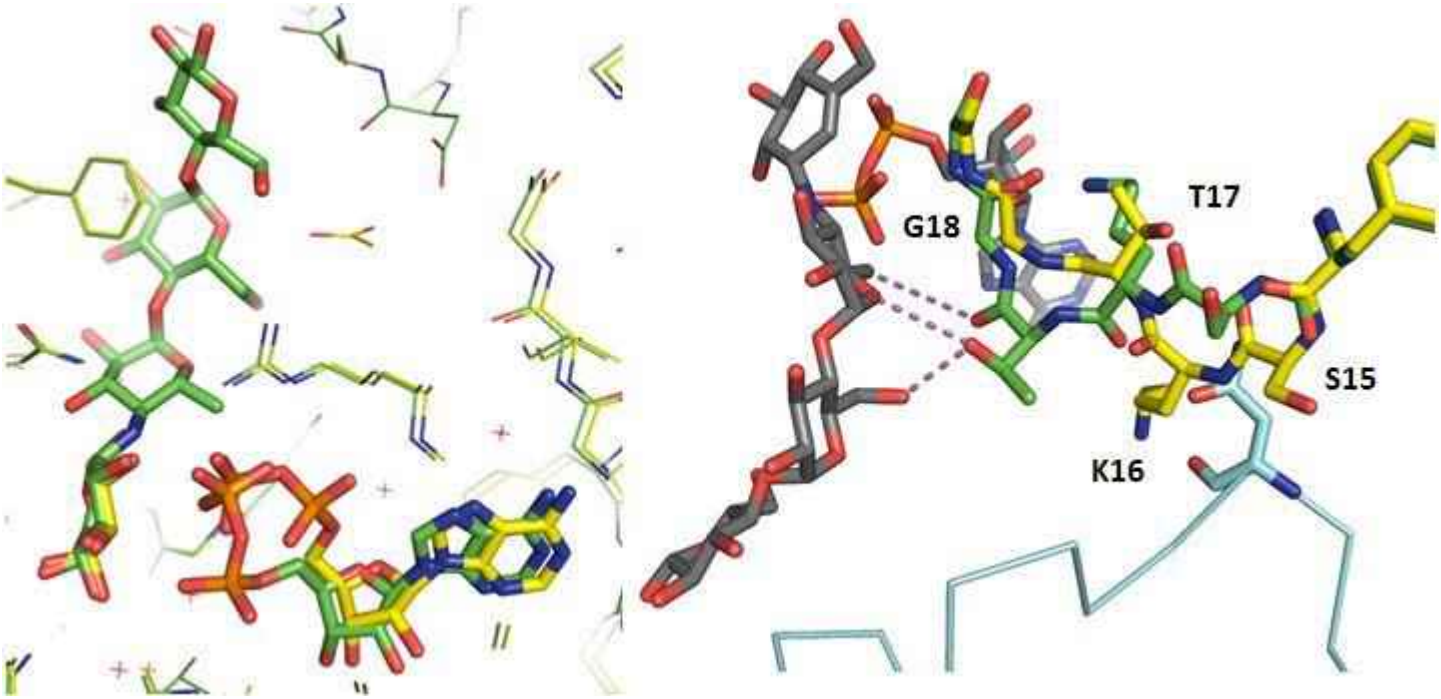
Starch synthesis was thought to occur exclusively in archaeplastida, which include green algae and land plants. Recently, amylopectin-like polymers have been identified in group V cyanobacteria[1]. In particular, a newly isolated cyanobacterium, CLG1, synthetizes granules containing both amylose and amylopectin essentially identical to plant starch[2]. These cyanobacteria are believed to have contributed some of the key starch synthesizing enzymes to plants. Starch synthases are the enzymes responsible for elongation of the maltooligosaccharide chains that compose the starch granule, working in concert with many other enzymes to create the complex structures of amylopectin and amylose. Here we report the crystal structure, refined to 2.2 Å, of GBSS, the granule bound starch synthase responsible for amylose synthesis in CLG1, in complex with ADP and either acarbose or glucose in the acceptor binding site. The structure reveals different conformational states of the ternary complex in three copies of GBSS in the asymmetric unit. The variations between monomers shed light on changes on the protein upon substrate recognition. In particular it clarifies the effect of acceptor binding in the conformation of the active site. This structure also illustrates the conformation of parts of the primary sequence that were absent from all plant starch synthase structures to date. Features in this structure are compared to both glycogen synthase and starch synthase structures. Both the similarities and the differences advance our knowledge on the necessary components of a starch synthase and point the way to their targeted structural and functional modification. The world-wide demand of cereals is expected to double from its current values by 2050 (FAO). Modification of proteins involved in starch synthesis, be it via traditional breeding or via genetic engineering, will likely be crucial to meeting the caloric intake needs of the human population in the coming decades.

[1] *P. Deschamps, C. Colleoni, Y. Nakamura et al., Molecular Biology and Evolution, 2008, 25(3), 536-548,* ***[2]*** *E. Suzuki, M. Onoda, C. Colleoni et al., Plant & Cell Physiology, 2013, 54(4), 465-473*



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