MS07-05 | Arabidopsis and Chlamydomonas Phosphoribulokinase Crystal Structures Complete the Redox Structural Proteome of the Calvin-Benson Cycle

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Photosynthetic CO_2 fixation is a fundamental source of food, fuels and chemicals for human society. In land plants and algae, carbon fixation is operated by the Calvin-Benson cycle (CBC), a pathway of 13 distinct reactions catalyzed by 11 enzymes that takes place in the chloroplast, a specialized organelle operating the photosynthetic process. Thioredoxins (TRXs) are small ubiquitous proteins that coordinate the two stages of photosynthesis through a thiol-based mechanism. Among the CBC enzymes, the TRX target phosphoribulokinase (PRK) has yet to be characterized at the atomic scale. To fill this gap, the crystal structures of PRK were determined from two model species: the green alga *Chlamydomonas reinhardtii* (*Cr*PRK) and the land plant *Arabidopsis thaliana* (*At*PRK). PRK is an elongated homodimer characterized by a large central β-sheet of 18 strands, extending between two catalytic sites positioned at its edges. The electrostatic surface potential of the catalytic cavity shows a positive region suitable for binding the substrate phosphate groups and an exposed negative region to attract positively charged TRX-f. In the catalytic cavity, the regulatory cysteines are 13 Å apart and connected by a flexible region (clamp-loop) exclusive to photosynthetic eukaryotes which is believed to be essential for structural rearrangements required by the oxidation. Structural comparisons with prokaryotic and evolutionarily older PRKs revealed that both *At*PRK and *Cr*PRK have a strongly reduced dimer interface and increased number of random coiled regions, suggesting that a general loss in structural rigidity correlates with TRX sensitivity acquisition during the molecular evolution of PRKs in eukaryotes.