Crystal Structure of ACC Synthase and Evidence for Divergent Evolution of Vitamin B6-Dependent Enzymes

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Beamline(s): **X12C**

Introduction: ACC synthase (ACS) catalyzes the conversion of S-adenosylmethionine (SAM) to 1-aminocyclopropane-1-carboxylic acid (ACC), a rate-determining step in ethylene biosynthesis (Yang & Hoffman, 1984). Ethylene, a plant hormone, profoundly influences the growth and development of plants at various stages such as seed germination, fruit ripening, root initiation, and flower senescence (Kenda, 1993). The ACS catalysis requires pyridoxal-5'-phosphate (PLP) as the cofactor, thus classifying ACS as a member of large family of vitamin B6 dependent enzymes (Jansonius, 1998).

Methods: Diffraction data were collected from a crystal of ACS complexed with PLP and inhibitor aminoethoxyvinylglycine (AVG) on beamline X12C. The crystal structure has been determined by molecular replacement and is currently refined to R-factor of 0.23 and R-free of 0.29 at 2.5 Å resolution.

Result and Discussion: The structure of the ACS-PLP-AVG complex contains a large α/β domain and a small domain, and has type I fold, the same as the AAT family of PLP-enzymes. However, our careful comparison showed that residues 135-270 of ACS are super imposable with fragment 149-280 of mouse ornithine decarboxylase in the fold type III family, thus suggesting a divergent evolution of the PLP-dependent enzymes. In addition, conservation of key residues for the PLP binding across all the families of PLP-enzymes implies that PLP-enzymes share a common pathway of the catalysis. Comparison of our structure with biochemical data suggests that inhibitor AVG simulates the binding of substrate. Modeling of substrate SAM into the active site showed that Tyr152 might form a covalent intermediate with sulfur of SAM for the elimination of the adenosine moiety of SAM. Thus, the ACS-PLP-AVG structure provided an insight into the mechanism of ethylene biosynthesis.

References:

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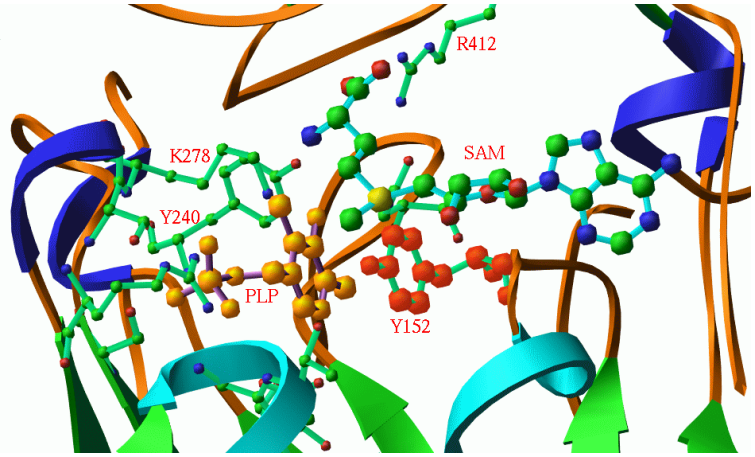

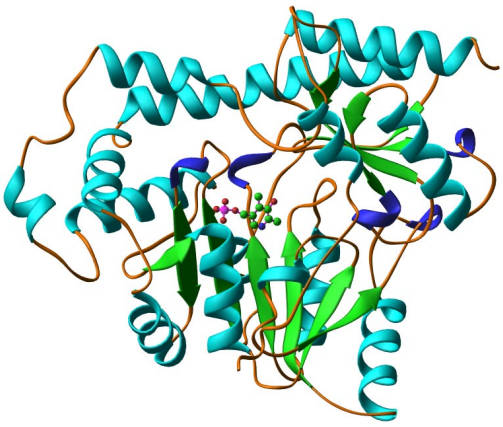

Tomato ACC synthase