Structural Diversity of Plant Glutathione S-Transferases,

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Glutathione S-Transferases (GSTs) are a diverse family of catalytic and binding proteins. In plants five main classes of GSTs have been identified. The two main classes are the plant specific Phi and Tau classes. The three smaller classes are Zeta, Theta and Lambda. A sixth class of GST-like proteins with dehydroascorbate reductase (DHAR) activity has also been identified in *Arabidopsis*, soybean and rice [1]. Although GSTs have low sequence identity (40% within class and less than 25% between classes) their structure is well conserved. The well conserved N-terminal domain has a thioredoxin like fold and contains the glutathione (γ-glutamyl-cysteinyl-glycine, GSH) binding site. The C-terminal domain is helical, less well conserved and is responsible for substrate specificity. GSTs are active as homo- or hetero-dimers.

Crystals of a rice Tau class GST *Os*GSTU4 were grown and diffracted to 2.3Å at Daresbury SRS station 14.1. The space group was $P4_122$ and unit cell dimensions $\alpha = \beta = 56.09$Å, $\gamma = 157.15$Å. The structure was solved by molecular replacement using the wheat protein *Ta*GST4-4 (PDB id 1GWC) [2] as a search model. The structure has been refined to an R_{work} of 18.2% and an R_{free} of 25.4%. The structure of *Os*GSTU1 has been compared to the Tau class GSTs *Ta*GST4-4 and *Os*GSTU1 (PDB id 1OYJ) as well as to GSTs of other solved plant classes.

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