

Phylogenetic Diversity of Light Dependent Phosphorylation of Thr78 in Rubisco Activase

Background/Objective

Rubisco activase is an ATP-dependent chaperone that facilitates dissociation of inhibitory sugar phosphates from the catalytic sites of Rubisco during photosynthesis. In Arabidopsis, Rubisco activase is negatively regulated by dark-dependent phosphorylation of Thr78. However, it is not clear whether this proposed mechanism is relevant outside of Arabidopsis. To address this issue, we sought to define the prevalence of this post-translational modification in photosynthetic organisms.

Approach

This was achieved by considering the following: (i) At what stage of flowering plant evolution did Thr78 emerge? (ii) How conserved is Thr78 among photosynthetic angiosperms? (iii) To what extent is Thr78 phosphorylated in different species? (iv) Is light-dependent de-phosphorylation of Thr78 a general mechanism of controlling of RCA activity? To study the impact of phosphorylation in C4 grass plants, we analyzed Rca phosphorylation in four species of C4 grass: *Sorghum bicolor* (Sb), *Miscanthus* (Ms), *Saccharum officinarum* (Su), and *S. viridis* (Sv).

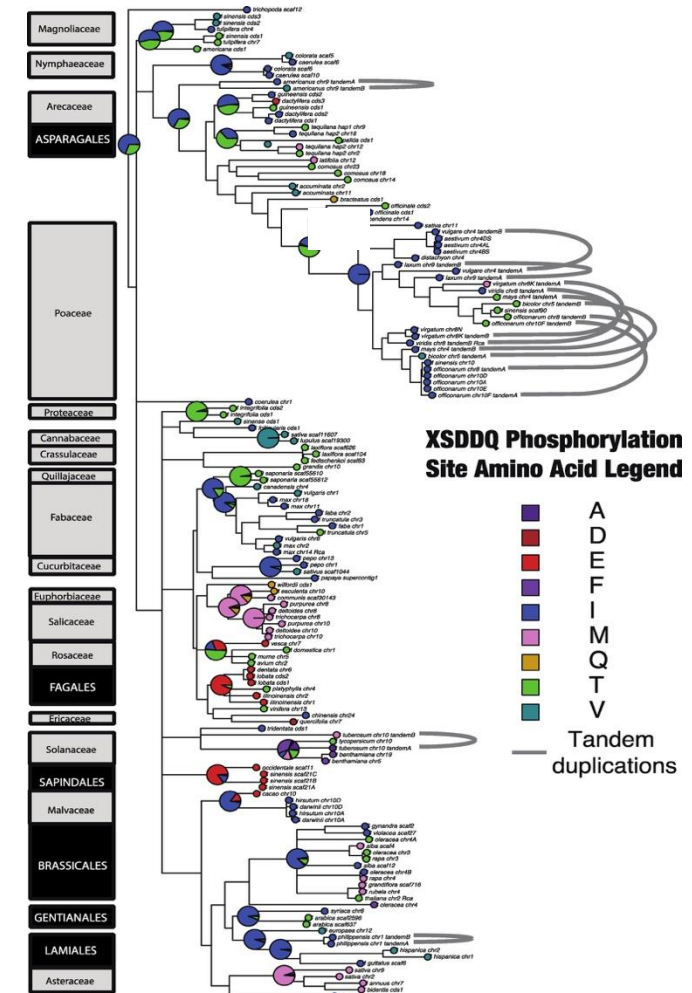
Results

The prevalence of Thr78 in Rubisco activase was investigated across sequences from 91 plant species, finding that 29 (~32%) species shared a threonine in the same position. Analysis of seven C3 species with an antibody raised against a Thr78 phospho-peptide demonstrated that this position is phosphorylated in multiple genera. However, light-dependent dephosphorylation of Thr78 was observed only in Arabidopsis. Further, phosphorylation of Thr78 could not be detected in any of the four C4 grass species examined.

Significance/Impacts

The results suggest that despite conservation of Thr78 in Rubisco activase from a wide range of species, a regulatory role for phosphorylation at this site is more limited. This provides a case study for how variation in post-translational regulation can amplify functional divergence across the phylogeny of plants beyond what is explained by sequence variation in a metabolically important protein.

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Phylogenetic representation of the amino acid present at the phosphorylation site (peptide position 78) within extant Rca gene models.