

Structural basis for donor sugar specificity in a plant galactolipid synthase

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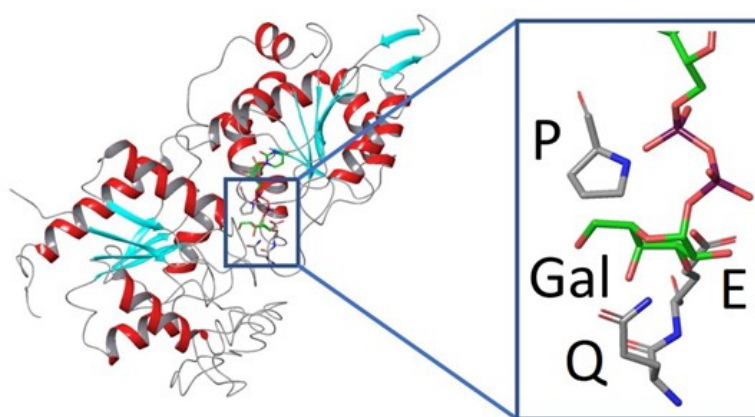
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Monogalactosyldiacylglycerol (MGDG) and digalactosyldiacylglycerol (DGDG) are essential galactolipids for the biogenesis of plastids and the functioning of the photosynthetic apparatus, and they comprise around 80% of the lipid content of photosynthetic membranes. In Arabidopsis, MGD1 is the major enzyme that initiates galactolipid synthesis. MGD1 is a monotopic membrane protein located in the inner envelope membrane of chloroplasts, which catalyzes the transfer of galactose from UDP-Galactose to diacylglycerol (DAG) to form MGDG.

It remains unclear why galactose (and not the more abundant glucose) was selected and conserved during the evolution of photosynthetic organisms, from cyanobacteria to plants. It was, therefore tempting to modify the substrate specificity of MGD1 so that it could use UDP-glucose (present in the cytosol but also in the stroma of chloroplasts) and to evaluate its impact on the different cellular functions of galactolipids in plants.

The crystal structure of MGD1 was previously solved [1], identifying three key residues that determine donor specificity: P433, Q455 and E456, also named the PQE motif. Several mutants were designed based on rational protein design and comparison of the equivalent 'PQE' motif in closely related glucosyltransferase. The P433 residue and its environment were key for donor specificity. The presence of a GPG motif seems to be a signature of a galactosyltransferase activity, whereas a GGX (X being an aliphatic residue) is indicative of a glucosyltransferase activity.



PQE motif of MGD1

BM and DJ: equal contributors

Bibliographic references:

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