IN BRIEF

Sugar Signaling between Plastids and the Plasma Membrane

Heterotrimeric G-protein signaling is involved in numerous processes in plants, including germination, cell division, and stress responses, yet few specific downstream targets have been identified. Huang et al. (pages 1226–1238) show that the plastid protein THYLAKOID FORMATION1 (THF1) interacts with GPA1, the Gα subunit of the heterotrimeric G-protein complex in Arabidopsis, as part of a sugar signaling mechanism between plastids and the plasma membrane that influences root growth.

THF1 and GPA1 were found to interact in yeast two-hybrid tests and in vitro and in vivo coimmunoprecipitation experiments. Using Förster resonance energy transfer (FRET) analysis, the authors show that the interaction between THF1, which is localized to the stroma, outer plastid membrane, and plastid stromules, and GPA1, which is localized at the plasma membrane, occurs at sites where the plastid membrane abuts the plasma membrane.

This work is significant because it uncovers a mechanism for communication between plastids and the plasma membrane, identifies a previously undiscovered role for G-proteins in sugar signaling, and provides support for the hypothesis that stromules (tubular extensions of plastids that have an undetermined function) play a role in signaling. In addition, it is an excellent example of the use of FRET to investigate in vivo protein–protein interactions in plants.

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Ancient Polyploidy in the Sister Families Brassicaceae and Cleomaceae

Recent studies suggest that Arabidopsis thaliana (Brassicaceae) experienced at least one genome duplication event between 15 and 86 million years ago, possibly near the divergence of the Brassicaceae from its sister family Cleomaceae. Schranz and Mitchell-Olids (pages 1152–1165) used a comparative genomics approach to examine whether this polyploidy event was unique to the Brassicaceae, shared with the Cleomaceae, or whether there were independent polyploidy events in each lineage. The Cleome spinosa (Cleomaceae) genome is just 1.9 times the size of A. thaliana, facilitating comparative genome analysis. The authors sequenced three genomic regions from diploid C. spinosa, each of which is homeologous to a duplicated region shared between the At5 and At3 chromosomes. Phylogenetic reconstructions and synonymous substitution rates support the hypothesis that a genomic triplication in C. spinosa occurred independently of and more recently than the duplication event in the Arabidopsis lineage. Interestingly, a strong correlation was found in the copy number (single versus duplicate) of individual genes between the two lineages, suggesting that similar evolutionary constraints have influenced gene copy in these two independently evolving lineages.

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Nancy A. Eckardt
News and Reviews Editor
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Nancy A. Eckardt

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