The Plant Cell, Vol. 19: 1139, April 2007, www.plantcell.org

IN BRIEF

Mitochondrial Recombination Surveillance

The plant mitochondrial genome is highly recombinogenic, and rearrangements often occur in tissue culture conditions, during wide hybridization events, or as spontaneous events. Mitochondrial genomic rearrangement is often detected as the induction or loss of cytoplasmic male sterility (CMS). A number of substoichiometric DNA intermediates are retained over multiple generations within the mitochondrial population, and a phenomenon called substoichiometric shifting (SSS) has been observed, which is characterized by the amplification or suppression of specific subgenomic molecules under certain conditions. SSS is influenced by nuclear gene expression and alters the expression of genes (including CMS mutations) encoded in the subgenomic intermediates. **Shedge et al. (pages 1251–1264)** investigate two genes associated with SSS in *Arabidopsis*. *MSH1* and *RECA3* encode homologs of *E. coli* MutS mismatch repair component and RecA protein, respectively, and mutations at either locus result in SSS. The authors find that *RECA3* and *MSH1* are uniquely adapted in plants to control mitochondrial genome maintenance. The expression of both genes is low in most plant tissues but enhanced during flower development, when SSS likely occurs. The SSS process appears to be associated with nuclear regulation of de novo mitochondrial nonhomologous recombination initiated by double-strand breaks. *RECA3* and *MSH1* are postulated to be part of a surveillance mechanism that directs conversion events between short repeats while allowing recombination-dependent replication to be initiated at long repeats. *recA3* or *msh1* mutations render the recombination surveillance system nonfunctional, shifting the stoichiometry of various segments of the genome, and these events in the mutants resemble low-frequency, sporadic events that result in SSS and CMS in wild populations.

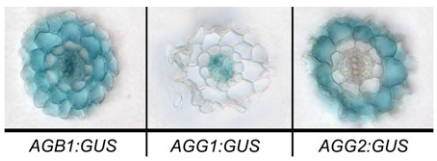
Abnormal flower morphology of *recA3 msh1* double mutant plants in which the stigma matures before the pollen, and fewer pollen grains are present than in the wild type.

www.plantcell.org/cgi/doi/10.1105/tpc.107.190410

G Protein γ Subunits Provide Functional Selectivity

Heterotrimeric G protein signaling mediated by transmembrane G protein–coupled receptors (GPCRs) is ubiquitous among eukaryotes. The G protein heterotrimer consists of α, β, and γ subunits bound to specific GPCRs. Ligand binding to the GPCR induces a change in Gα and the exchange of bound GDP for GTP, which turns the Gα subunit and the Gβγ dimer into two functional signaling units. Intrinsic GTPase activity of Gα returns the heterotrimer back to the inactive form. Diversity and selectivity in G protein signaling in mammals is provided by the existence of gene families for each of the G protein subunits. Humans contain at least 23 Gα subunits, 6 Gβ subunits, and 12 Gγ subunits, which show selectivity in their interactions and differences in tissue specificity. By contrast, *Arabidopsis* and a number of other plants contain one Gα subunit, one Gβ subunit, and two Gγ subunits (some legumes have two Gα subunits). Evidence is emerging that Gα and Gβγ are involved in signaling in specific and independent pathways in plants. **Trusov et al. (pages 1235–1250)** show that the two Gγ subunits in *Arabidopsis* provide functional selectivity to Gβγ signaling. Genetic analyses reveal that the two Gγ subunits provide specificity to the Gβγ dimer action in at least three different signaling pathways: fungal resistance, glucose sensing, and auxin-mediated lateral root development.

www.plantcell.org/cgi/doi/10.1105/tpc.107.190411



Distinct patterns of expression of the two Gγ genes, *AGG1* and *AGG2*, in root tissue, relative to expression of *AGB1*, which encodes the Gβ subunit.

Nancy A. Eckardt
News and Reviews Editor
neckardt@aspb.org

G Protein γ Subunits Provide Functional Selectivity

Nancy A. Eckardt

Plant Cell 2007;19;1139a
DOI 10.1105/tpc.107.190411