Commentary on Plastid Transformation

A Major Advance in Plastid Transformation

In this issue of Plant Physiology, Pal Maliga’s laboratory reported a major advance in plastid transformation. Stable manipulation of the plastid genome of flowering plants was first reported nearly 30 years ago (Svab et al., 1990). The approach was to select transplastomic plants using spectinomycin, which blocks translation by the prokaryotic-type 70S ribosomes found in plastids. Thus, in the presence of spectinomycin, development is inhibited because plastid-dependent processes as diverse as assembly of the photosynthetic apparatus and fatty acid metabolism are compromised. In the case of fatty acid metabolism, inhibition is due to the fact that the acetyl-Coenzyme A carboxylase complex that synthesizes long-chain fatty acids is composed of one subunit encoded by the plastome. Stable transformation of tobacco plastids was achieved by introducing the aadA gene encoding aminoglycoside-3'-adenylyltransferase, which modifies spectinomycin so that it no longer binds the 16S rRNA, and inhibition of 70S plastid ribosomes is relieved. Although the number of species in which aadA has been used to generate transplastomic plants has increased (Ruf et al., 2001; Kanamoto et al., 2006), for key species including cereal crops and the widely used model Arabidopsis (Arabidopsis thaliana), this spectinomycin-based approach has proved ineffective.

Relatively recently, it was shown that ecotypes of Arabidopsis vary in their sensitivity to spectinomycin (Parker et al., 2014). Careful analysis of a mapping population showed that highly sensitive ecotypes contained a mutant allele of the nuclear gene ACC2, which encodes an acetyl-Coenzyme A carboxylase that functions in fatty acid metabolism. The ACC2 gene product is targeted to plastids and so provides an alternate to the partially plastid-encoded acetyl-Coenzyme A carboxylase that is inactivated by spectinomycin. Parker et al. (2016) proposed that their findings may provide a route to increase efficiency of chloroplast transformation in the Brassicaceae.

Yu et al. (2017; this issue) now provide strong support for this conjecture. Using the acc2-1 mutant allele of Columbia-0 and the hypersensitive Slavice-0 ecotype, they report that by removing redundancy afforded by ACC2, efficient selection for transplastomic events can be achieved in Arabidopsis. However, as the authors point out, plastid transformation requires efficient regeneration of shoot material from callus, a characteristic not readily associated with many accessions of Arabidopsis. The next challenge is therefore to identify procedures and ecotypes that facilitate this conversion of transplastomic callus of Arabidopsis into stable and heritable plant material.

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