Ribosomal Regulation of Mitochondrial Gene Expression

Several mitochondrial protein complexes contain subunits encoded in the nucleus as well as those encoded in mitochondria. Despite the essential nature of the few proteins encoded in mitochondria, surprisingly little is known about plant mitochondrial gene expression and its regulation (Millar et al., 2008). It has been proposed that post-translational regulation plays a major role, including at the level of protein complex assembly (Giege´ et al., 2005). New work from Kwasniak et al. (pages 1855–1867) provides strong support for this and shows that translation of mitochondrial transcripts can be differentially affected by alterations in mitochondrial ribosomes (mitoribosomes).

Kwasniak et al. characterized Arabidopsis thaliana lines silenced for nuclear RPS10, which encodes the S10 protein of the small subunit of the mitoribosome. Unexpectedly, although RPS10 transcript abundance was reduced, S10 protein levels were similar in wild-type and hemizygous silenced lines. Furthermore, the silenced lines contained increased amounts of both subunits of the mitoribosome, with the large subunit about twofold more abundant than the small subunit, and some small subunit complexes apparently lacked S10. These results suggest that the decreased RPS10 transcript abundance induced a feedback mechanism to maintain S10 levels and led to increased production of both mitoribosome subunits.

In contrast to the upregulation of the mitoribosome, all oxidative phosphorylation (OXPHOS) complexes were less abundant in the RPS10-silenced lines, but to different degrees, an effect that seemed to correspond with the number of mitochondrial– vs. nuclear-encoded subunits in the complex. The decrease in OXPHOS protein levels could not be attributed to mitochondrial transcriptional regulation; the silenced lines actually had more transcript for mitochondrially encoded components, which could be traced to increased mitochondrial genome copy number in the silenced lines, rather than transcriptional regulation per se.

The paradoxically decreased OXPHOS complex abundance despite increased transcription of the mitochondrially encoded components points to the importance of post-transcriptional regulation.

When the authors examined mitochondrial translation activity in the RPS10-silenced lines, they found that OXPHOS components generally had fewer ribosomes per transcript and a lower proportion of transcript with ribosomes. By contrast, most mitoribosome components were more translationally active. Nuclear-encoded subunits of both were generally unchanged. Together with the findings that certain proteases were upregulated in the silenced lines, these data suggest that coordination of components for bigenomic complexes in mitochondria occurs at the level of complex assembly – in this case, with excess nuclear-genome products being degraded.

The altered mitoribosomes had differential effects on mitochondrially produced proteins (see figure), suggesting that translation of individual mitochondrial proteins can be regulated by ribosome composition. Altogether, this report provides important evidence for the predominance of post-transcriptional regulation in plant mitochondrial gene expression and for coordination of nuclear and mitochondrial genomes at the level of complex assembly.


REFERENCES
Ribosomal Regulation of Mitochondrial Gene Expression
Nancy R. Hofmann

Plant Cell 2013;25;1487; originally published online May 30, 2013;
DOI 10.1105/tpc.113.250514

This information is current as of July 9, 2017

References
This article cites 3 articles, 2 of which can be accessed free at:
/content/25/5/1487.full.html#ref-list-1

Permissions

eTOCs
Sign up for eTOCs at:
http://www.plantcell.org/cgi/alerts/ctmain

CiteTrack Alerts
Sign up for CiteTrack Alerts at:
http://www.plantcell.org/cgi/alerts/ctmain

Subscription Information
Subscription Information for The Plant Cell and Plant Physiology is available at:
http://www.aspb.org/publications/subscriptions.cfm