

The Genomics of Chloroplast Biogenesis

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Plastids are highly derived descendants of an endosymbiotic event, and are widely distributed in plants, algae and apicomplexans. In plants the basal form is the proplastid, which is small, colorless, and found in tissues such as roots and meristems. Upon illumination of dark-grown seedlings, or in an acropetal gradient in leaves of monocots such as maize, the etioplast or proplastid differentiates into a chloroplast. Greening of developing seedlings is a rapid, intricate process, and the elaboration of photosynthetic capacity, or chloroplast biogenesis, involves a large number of genes, either as measured by array studies focused on light-induced gene expression, or by the fact that genetic screens have revealed hundreds or even thousands of nuclear loci whose products are required for or related to photomorphogenesis. In addition, proteomic studies have led to estimates that chloroplasts contain as many as 4,000 proteins. Because plastid genomes generally do not exceed about 120 genes in coding capacity, the vast majority of organelle-localized proteins are nucleus-encoded. However, plastid-encoded functions are essential and can be divided into photosynthesis and gene expression, with the latter specifying components of the transcription/ translational apparatus. These genes are regulated by nuclear factors, which act on transcriptional, RNA processing/stability, and translation/post-translational levels. A broad understanding of chloroplast biogenesis requires extensive use of genetics to isolate relevant mutants, including those that affect chloroplast gene expression, genomics resources to functionally analyze these nuclear factors, and finally detailed biochemical analyses. These in turn will facilitate the manipulation of chloroplast-localized traits, including already successful efforts to create chloroplast transgenics. My laboratory uses three model systems: the eukaryotic green alga *Chlamydomonas reinhardtii*, maize, and *Arabidopsis*, to study chloroplast biogenesis, focusing on nuclear proteins that regulate chloroplast gene expression. In this seminar, I will spend some time describing the attributes of *Chlamydomonas* for understanding chloroplast functions in higher plants, including newly-available genomics resources and how they may be applied, with special emphasis on abiotic stress responses. In a second part, I will describe analogous resources for maize, including a large collection of chloroplast biogenesis mutants that is being exploited in a collaborative effort. These programs have yielded fundamental biological insights, and also generated resources that are freely available to other researchers.