FINAL REPORT

Sunlight, in the form of photosynthetically-active radiation (PAR) is life for plants. Unsurprisingly, therefore, they have evolved intricate photosensory systems to track this ultimate energy source. These systems constantly monitor the ambient environment for the presence, absence, duration, quantity and quality of impinging light, and pleiotropically induce growth and developmental responses to the prevailing conditions, that maximize (or optimize) the capacity for interception of PAR and conduction of CO_2 to photosynthetically-active tissues and cells. Morphogenically, these responses include the well-known “foraging for light” behavior of plants through aggressive vegetative axis growth (to compete with neighbors for unimpeded PAR access), and adaptive leaf positioning and/or orientation within the canopy to maximize (or optimize) light exposure. At the cellular level, these include initiation and dynamic control of chloroplast development (through induction and regulation of the estimated 3,000 nuclear-encoded chloroplast-protein genes), intracellular chloroplast movement to maximize (or optimize) photon capture, and regulation of stomatal density, to maximize CO_2 diffusion and carbon capture. Once captured, the partitioning of carbon within the plant is also regulated by the photosensory signaling systems. Most notably, from a biofuel perspective, photosensory detection of competing neighbors triggers increased partitioning of carbon to the cellulose of the vegetative axes (stems, tillers, etc) at the expense of the deposition of sugars, starch and oils in reproductive and storage organs (seeds, fruit, tubers, roots, etc). The predominant light signal regulating these responses is the ratio of red/far-red wavelengths (R/FR ratio). Radiation enriched in FR, generated by chlorophyll-imposed depletion of R photons in light reflected or transmitted by neighboring vegetation, is perceived by the phytochrome (phy) system. This system provides the plant with an exquisitely-sensitive ‘color vision’ mechanism for detecting and responding to the threat of decreased PAR accessibility. This is defined as the Shade AvoidanceResponse (SAR). Studies on seedling deetiolation have advanced our understanding considerably, of the mechanism by which the photoactivated phy molecule transduces its signal into cellular growth responses. The data show that a subfamily of phy-interacting bHLH transcription factors (PIFs) promote skotomorphogenic seedling development in post-germinative darkness, but that the phy Pfr conformer reverses this activity upon initial light exposure, inducing the switch to photomorphogenic development. Mechanistically, this reversal involves light-triggered translocation of the activated phy molecule into the nucleus where it binds to and induces the degradation of PIF-family members, rapidly altering target-gene expression.

This project has made considerable progress in defining phy-PIF signaling activity in controlling the SAR. The biological functions of the multiple PIF-family members in controlling the SAR, including dissection of the relative contributions of the individual PIFs to this process, as well as to diurnal growth-control oscillations, have been investigated using higher-order *pif*-mutant combinations. Using microarray analysis of a quadruple *pif* mutant we have defined the shade-induced, PIF-regulated transcriptional network genome-wide. This has revealed that a dynamic antagonism between the phys and PIFs generates selective reciprocal responses during deetiolation and the SAR in a rapidly light-responsive transcriptional network. Using integrated RNA-seq and ChIP-seq analysis of higher order *pif*-mutant combinations, we have defined the direct gene-targets of PIF transcriptional regulation, and have obtained evidence that this regulation involves differential direct targeting of rapidly light-responsive genes by the individual PIF-family members.

This project has provided significant advances in our understanding of the molecular mechanisms by which the phy-PIF photosensory signaling pathway regulates an important bioenergy-related plant response to the light environment. The identification of molecular targets in the primary transcriptional-regulatory circuitry of this pathway has the potential to enable genetic or reverse-genetic manipulation of the partitioning of carbon between reproductive and vegetative (cellulose-accumulating) tissue, toward enhanced bioenergy yield.

List of Publications Attributable to DOE Funding

1. Franklin, K. and Quail, P. H. 2010. Phytochrome functions in Arabidopsis development. J. Exp. Bot., 61:11-14. PMCID: PMC2800801. (Previously cited as “in press”, now published).

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3. Leivar, P. and Quail, P. H. 2011. PIFs: Pivotal components in a cellular signaling hub. Trends in Plant Science. 16: 19-28. PubMed PMID: 20833098.

4. Leivar, P., Tepperman, J. M., Cohn, M. M., Monte, E., Al-Sady, B., Erickson, E., and Quail P. H. 2012a. Dynamic Antagonism between Phytochromes and PIF Family Basic Helix-Loop Helix Factors Induces Selective Reciprocal Responses to Light and Shade in a Rapidly Responsive Transcriptional Network in Arabidopsis. Plant Cell, 24: 1398-1419. PMCID: PMC3398554.

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