

## **DYNAMIC CHANGES IN ARABIDOPSIS TRANSCRIPTOME DURING SHADE AVOIDANCE RESPONSE**

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The success of competitive interactions between plants determines the chance of survival of individuals and eventually of whole plant species. Shade-tolerant plants have adapted their photosynthesis to function optimally under low-light conditions. These plants are therefore capable of long-term survival under a canopy shade. In contrast, shade-avoiding plants adapt their growth to perceive maximum sunlight and therefore rapidly dominate gaps in a canopy. Daylight contains roughly equal proportions of red (R) and far-red (FR) light, but within vegetation that ratio is lowered as a result of the R absorption by photosynthetic pigments. This light quality change is perceived through the phytochrome system as an unambiguous signal of the proximity of neighbours resulting in the shade avoidance response. This adaptive reaction is achieved by a set of responses including enhanced internode and petiole extension growth, increased apical dominance, retarded leaf development, and an acceleration of flowering. However, if a plant succeeds in the attempt to overgrow its neighbours and the photosynthetic organs perceive daylight again, the shade avoidance response is rapidly switched off through phytochrome photoconversion. The adaptive responses result in changes in the distribution of assimilates between leaves, stems, and roots.

Genomic and genetic analyses by our and other laboratories have identified several low R/FR-regulated genes and key regulators involved in the shade avoidance response. However, very little is known about the cascade of events triggered by low R/FR that give rise to the full activation of the response and, later on, to the adaptation process when a plant does not succeed to overgrow its neighbours. Therefore, shade avoidance response was examined by genome wide expression profiling in wild type and genetically altered plants exposed to low R/FR light for different times. To identify gene networks, both computational and experimental approaches are being pursued. Informatic analyses provided insights into functional clusters and their dynamics, predictions of cis-regulatory elements for genes temporally regulated during shade avoidance response, inference of gene regulatory interactions. Together, these analyses uncovered novel aspects of shade avoidance, and generated testable hypotheses on gene regulatory circuitry underlying plant responses to light quality changes.

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