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DROUGHT DEPENDENT MODULATION OF PHOTOPERIODIC SIGNALLING VIA HORMONAL INPUTS

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The transition to flowering marks the initiation of reproductive competence in plants. Because of this, the timing of this transition needs to be precisely aligned with the most favourable environmental conditions. Several environmental signals contribute to accelerate flowering, including drought stress. The role of drought cues in modulating the transition to flowering is adaptively significant whereby a shortening of the plant life cycle can lead to drought escape, defined as the ability of plants to anticipate potentially severe stress conditions.

The drought escape syndrome is tightly related to seasonal cues in *Arabidopsis thaliana* as long day photoperiods (typical of summer) promote drought escape whereas no drought escape takes place under short days. Data from our group have uncovered the basic genetic structure of the drought escape response; these are the photoperiodic gene *GIGANTEA* (*GI*), and the drought–related phytohormone abscisic acid (ABA). GI and ABA signalling converge upon the transcriptional activation of the florigen genes *FT* and *TSF*.

Our recent molecular genetics studies led us into defining how ABA signals might affect the transcriptional activation of *FT*; first, we demonstrate a requirement of the *CONSTANS* (*CO*) gene (an *FT* upstream regulator). Secondly, we reveal a molecular interaction between GI and CO proteins, possibly mediated by ABA. Indeed, transgenic approaches coupled with the study of the nuclear distribution of CO and GI proteins *in vivo* indicate that ABA and GI promote *FT* upregulation via modifying CO protein function, and not its transcriptional activation. Interestingly, our genome-wide expression analyses further indicate that GI is required for the proper activation of ABA/drought transcriptional responses, thus revealing a novel link between light signalling and water status information mediated by GI. The role of ABA in stimulating GI protein function underscores the contribution of quantitative changes in *FT* accumulation in conferring plasticity in flowering in the face of varying water availability. It also provides insights into how plants can respond to dry environments by coupling drought stress–related gene expression with proper photoperiodic cues.