

P012 A proteomics approach to elucidate the proteolysis of a floral repressor

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Regulator of CONSTANS (CO) expression (rce) is a novel flowering time mutant of *Arabidopsis* that has been positioned on the long day (LD) photoperiodic promotion pathway. The response to photoperiod is determined by a complex set of interactions involving specific photoreceptors and the circadian clock. *Rce* flowers at the same time as WT plants in short day (SD) conditions due to the induction of flowering through the gibberellin pathway. However the late flowering phenotype of *rce* in LDs suggests that it is defective in a photoperiodic inductive signal normally seen in LDs. Real-time quantitative PCR has shown that levels of the *CO* transcript are 10 fold lower in *rce* compared to WT. Sequence analysis has revealed that *RCE* encodes a novel RING-finger protein. RING-finger proteins act as components of the ubiquitin proteasome pathway which targets specific proteins for degradation via the 26S proteasome. It is hypothesised that *RCE* targets a repressor of flowering for degradation in inducing LD conditions. We will present an approach to identify the putative repressor of flowering by epitope tagging *RCE* and performing pull down experiments *in planta* followed by mass spectrometry to identify purified proteins.