

Genetic Dissection of UVB Signaling Pathways in *Arabidopsis thaliana*

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Ultraviolet B (UVB), an integral part of sunlight, affects all sun-exposed organisms. Typically high fluence-rate (HF) UVB ($> 1.0 \text{ mole m}^{-2} \text{ s}^{-1}$) causes cellular damage in plants, whereas low fluence-rate (LF) UVB ($< 1.0 \text{ mole m}^{-2} \text{ s}^{-1}$) may provide important environmental cues for plant growth and development. The damaging effects of HF UVB have been extensively studied, but little is known about the molecular mechanism of how LF UVB serves as a signal to regulate plant growth and development. Understanding the molecular mechanisms of how UVB regulates growth and development is fundamentally important to agriculture and human health. An *Arabidopsis* root UVB sensitive (*rus1*) mutant has been identified. *rus1* mutants are hypersensitive to very low fluence-rate (VLF) UVB and show developmental arrest when exposed to light that contains as little as $2 \text{ nmol m}^{-2} \text{ s}^{-1}$ UVB. More recently, a *rus2* mutant that shows identical phenotypes to that of *rus1* has also been identified. Our studies showed that RUS1 together with RUS2 function as key regulatory components in UVB responses. The striking phenotypes and extreme UVB sensitivities of *rus1/rus2* provide a uniquely feasible platform to identify genetic suppressors that can be good candidates for UVB-specific receptors and signaling components. *rus1* seeds were mutagenized and suppressor screens have been carried to identify suppressors of *rus* (*sor*) in M2 seedlings. More than 70 *sor* individuals have been identified so far. We are currently in the process of mapping and cloning these identified *sor* mutations. Our goal is to fully characterize the functional roles of SORs in UVB responses via various genetic and biochemical approaches. Experiments are currently underway to analyze how *sor* mutations interact with *rus1/rus2* and whether/how SOR proteins physically interact with RUS1/RUS2 proteins.