levels of the hormone. Our observations, however, indicated BR effects are also influenced by differential hormone responsiveness.

The aim of our studies was to characterize the expression of BRI1 and find out if it can influence developmental and organ-specific changes in BR sensitivity. In order to determine the transcriptional activity, we generated transgenic plants carrying *BRI1* promoter-reporter gene fusions. In *BRI1* prom-*GUS* plants histochemical analysis of glucuronidase activity revealed close correlation between BR-dependent elongation and transgene activity. On the other hand, time-course measurements with *BRI1* prom-*LUC* lines showed strong induction of *BRI1* activity upon germination, and that the expression level was increased by dark, whereas decreased by light treatments. To test how differential BRI1 accumulation can influence morphogenic events, we prepared transgenic lines that express in bri1 mutant background BRI1::LUC fusions, with full receptor activity, under the control of various organ-specific promoters. We found that *BRI1::LUC* expression via the photosynthesis-associated *CAB3*, vascular *SUC2*, and procambial *ATHB8* promoters resulted in different types of partial complementation, which all resulted in disproportionate organ development. The observed expression patterns and morphogenic effects of *BRI1* expression strongly suggest a role for the receptor abundance in determining the intensities of local BR responses.

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Identification of Novel Regulatory Factors of Plant Stress Responses Using New Genetic Approaches

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Plants frequently encounter abiotic stress conditions, such as drought, soil salinity, unfavorable temperature, submergence or high light. These conditions severely limit plant growth, development and productivity; plants have developed various defense mechanisms to increase stress adaptation. Drought and salinity are regarded as the major environmental stresses primarily impose osmotic stress on plants. Still poorly understood how plant defense mechanisms is actually performed against salt and osmotic stresses. To dissect plant signaling pathways *Arabidopsis thaliana* is the supreme genetic model, however as a glycophyte its tolerance to salt stress is limited.

Thellungiella salsuginea (*halophila*) is a close halophyte relative of Arabidopsis, tolerates drought and salinity as well as extreme cold, accordingly has turned to be a model system in salt tolerance research (Bressan 2001). Thellungiella possesses many prosperous attributes of Arabidopsis, like short life cycle, self-pollination, small genome size (about 2X of Arabidopsis), and even its genetic transformation can be accomplished by simple floral dipping. In addition Thellungiella genes show 90-95% sequence identity to Arabidopsis.

We have developed new genetic technologies to identify novel regulatory factors controlling salt tolerance. Random cDNA libraries of Arabidopsis and Thellungiella have been cloned into the estradiol inducible pER8 plant expression vector (Zuo et al. 2001) The transformation competent cDNA library of Thellungiella has been introduced randomly into Arabidopsis plants, and 20,000 transformant seedlings have been screened for salt tolerance in the presence of estradiol. Fourteen estradiol dependent salt tolerant lines have been isolated, and the inserted cDNA clones of these lines have been cloned and sequenced, the corresponding Thellungiella genes were identified by Arabidopsis sequence homology search. Salt tolerance was confirmed by repeated germination and growth assays in 10 lines, and 2 lines have been selected for further characterization. The line TL1-2 expressed the cDNA of a Thellungiella putative translational initiation factor, the insertion of TL1-26 line contained the cDNA of a putative RNA-binding aminopeptidase.

Another approach has been devised to identify salt stress regulatory factors at cellular level. Arabidopsis cell culture has been transformed with the Arabidopsis cDNA library and the transformed cells have been selected on plant culture media supplemented with salt and estradiol. Four cell colonies have been selected with superior growth on selective medium. cDNA inserts of these calli have been cloned and identified by sequencing. One of these cDNA inserts encoded a novel heat shock factor, its overexpression could improve various abiotic stress tolerance of transgenic Arabidopsis plants.

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