

Postgenomic tools for *Lotus japonicus*: Application to abiotic stress research

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Lotus japonicus is an ideal model species for legume genetics, genomics, and functional genomics research. Large-scale EST and genome sequencing has facilitated rapid progress in the areas of transcriptomics and proteomics, which together with tools for metabolomics are transforming the way experimental biology is performed. To illustrate this transformation, we present the results of a recent study of plant responses to non-lethal long-term salinity. Ionic profiling by inductively coupled plasma-atomic emission spectrometry (ICP-AES) revealed salt stress-induced reductions in potassium, phosphorus, sulphur, zinc and molybdenum. Microarray profiling using the Lotus Genechip® allowed the identification of 912 genes differentially expressed during salt acclimation. Gas chromatography-mass spectrometry (GC/EI-TOF-MS)-based metabolite profiling identified 147 differentially accumulated soluble metabolites, indicating a change of metabolic phenotype upon salt acclimation. Metabolic changes were characterised by a general increase in the steady-state levels of many amino acids, sugars and polyols with a concurrent decrease in most organic acids. Transcript and metabolite changes exhibited a stress-dose dependent response within the covered range of NaCl concentrations, although threshold and plateau behaviors were observed. The combined observations suggest a successive and increasingly global requirement for the reprogramming of gene expression and metabolic pathways to maintain ionic and osmotic homeostasis during salt stress.