Proteomics technology has revealed a great number of proteins which play roles in plant growth, and adaptation to environmental stresses. Functional analysis of those proteins will contribute to develop regulating basic life phenomenon or assessing stress tolerance of plant. Our goals are (1) to elucidate the molecular basis for the adaptive traits of plant, and (2) to contribute of improvement the tolerance of plant to environmental stresses, which are the limitations for agricultural productivity worldwide. Here, the example of crop, especially soybean proteomics, is introduced. Flooding injury is one of the major constraints for cultivation of soybean, and improvement of flooding tolerance in soybean is important for increase in yield. To understand the response mechanism of soybean under flooding stress, proteomics technique was carried out. In the beginning, the Soybean Proteome Database was constructed to be data repository for functional analyses of soybean responses to flooding injury. Flooding injury was one of the major constraints for cultivation of soybean, and improvement of flooding tolerance in soybean is important for increase in yield. To understand the response mechanism of soybean under flooding stress, proteomics technique was carried out. In the beginning, the Soybean Proteome Database was constructed to be data repository for functional analyses of soybean responses to flooding injury. The Soybean Proteome Database integrates multiple “omes”. A unified temporal-profile tag attached to the mRNAs, proteins and metabolites facilitates retrieval of the data based on the temporal expression profiles. Results from the temporal expression profiles confirmed that proteins related to glycolysis and alcohol fermentation were significantly upregulated under flooding stress. Next, flooding-stress responding organelle proteins were identified using gel-based and gel-free proteomics techniques. Finally, these proteins were characterized using molecular biological and biochemical techniques. From these results, we will discuss functional roles of flooding-stress responding proteins identified using proteomics technique.

References

Keywords : Proteome, Soybean, functional analysis, flooding