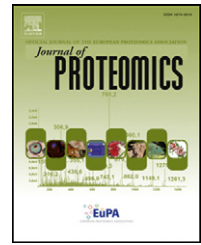


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Review

'Omics' techniques for identifying flooding–response mechanisms in soybean☆

Setsuko Komatsu^{a,*}, Naoki Shirasaka^b, Katsumi Sakata^b^aNational Institute of Crop Science, Tsukuba 305–8518, Japan^bMaebashi Institute of Technology, Maebashi 371–0816, Japan

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ABSTRACT

Plant growth and productivity are adversely influenced by various environmental stresses, which often lead to reduced seedling growth and decreased crop yields. Plants respond to stressful conditions through changes in 'omics' profiles, including transcriptomics, proteomics, and metabolomics. Linking plant phenotype to gene expression patterns, protein abundance, and metabolite accumulation is one of the main challenges for improving agricultural production. 'Omics' approaches may shed insight into the mechanisms that function in soybean in response to environmental stresses, particularly flooding by frequent rain, which occurs worldwide due to changes in global climate. Flooding causes significant reductions in the growth and yield of several crops, especially soybean. The application of 'omics' techniques may facilitate the development of flood-tolerant cultivars of soybean. In this review, the use of 'omics' techniques towards understanding the flooding-responsive mechanisms of soybeans is discussed, as the findings from these studies are expected to have applications in both breeding and agronomy.

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Abbreviations: 2-DE, Two-dimensional polyacrylamide gel electrophoresis; CE, Capillary electrophoresis; GABA, Gamma-aminobutyric acid; MS, Mass spectrometry; TCA, Tricarboxylic acid.

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* Corresponding author at: National Institute of Crop Science, Kannondai 2-1-18, Tsukuba 305–8518, Japan. Tel.: +81 29 838 8693; fax: +81 29 838 8694.

E-mail address: skomatsu@affrc.go.jp (S. Komatsu).

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1. Introduction

Among functional genomics tools, 'omics' techniques are the most commonly used for the quantitative and qualitative analysis of biological samples [1]. The 'omics' techniques, which include genomics (DNA), transcriptomics (RNA), proteomics (protein), and metabolomics (metabolites), have been extensively developed and utilized to obtain an overview of the response of plants to environmental conditions. Transcriptomics, proteomics, and metabolomics approaches have been used as functional genomics tools for the high-throughput phenotyping necessary for large-scale physiological, molecular, and genetic studies aimed at identifying the function of genes and protein-protein interactions involved in the control of stress response [1] and plant development. In addition to providing a static picture of the physiological status of a target organ, tissue, or cellular compartment at a particular stage of plant development [2], 'omics' data also provide information on concentration changes of the complete set of cellular metabolites, proteins, and genes [3,4]. Plants respond to environmental stresses through differential expression of a subset of genes, which changes the 'omics' profile. Linking gene expression, protein abundance, and metabolite accumulation to the phenotype of plants is one of the main challenges for improving agricultural production.

Holistic approach in 'omics' fits together well with the systems biology approach which is an inter-disciplinary field of study that focuses on complex interactions within biological systems [5]. One of the major objectives of the systems biology is to model properties of cells, tissues and organisms functioning as a system based on a number of quantitative data with numerical and computational techniques. Recent high-throughput transcriptomics, proteomics and metabolomics techniques can be used to collect the quantitative data to generate the models [6–8]. A quantitative model is based on enzyme kinetics. We will introduce an omics approach to map multiple omics data on a metabolic network in the chapter 5. The approach will be effective to elucidate the stress response mechanism of soybean based on the enzyme kinetics.

Climate change involves significant changes in the variability or average state of the atmosphere, such as related to temperature, precipitation and/or wind patterns. In particular, various environmental stresses such as high/low temperature, flooding, drought, salt, and ozone, often lead to reduced seedling growth and decreased crop yields. 'Omics' techniques are ideal for studying the effects of environmental stress on crops and have been used to obtain insight into mechanistic cellular responses to drought [9], salt [10], ozone [11], and flooding stresses [1].

Flooding caused by heavy or continuous rainfall in areas with poorly drained soil is one of the most damaging environmental stresses affecting plants, which are particularly sensitive at early growth stages. The flooding tolerant species have both constitutive and inducible mechanisms for morphological and physiological adaptation to aqueous habitats. Rice is the best-characterized flooding-tolerant crop. Rice seeds are capable of germinating in water, and the submerged seedlings can elongate to escape the oxygen-deficient flooded environment. However, many kinds of crop including soybean, wheat and maize are categorized as flooding sensitive [1]. However, most studies on flooding stress have focused on relatively flood-tolerant species from genera. Among crops, soybean is particularly susceptible to flooding stress [1]. Soybean at early stages of growth shows differential regulation of genes involved in signal transduction and hormonal signaling [6], transcriptional control [6], glucose degradation and sucrose accumulation [7], alcohol fermentation [12], gamma-aminobutyric acid (GABA) shunt [8], suppression of the active oxygen scavenging system [13], mitochondrial impairment [14], ubiquitin/proteasome-mediated proteolysis [15] and cell wall loosening [16] under flooding conditions. Together, these factors and pathways retard the growth of soybean under flooding.

At early stage of the growth, soybean is influenced by the flooding stress in a widespread area of the biological systems. The metabolism was observed to be significantly affected, and citrate, isocitric acid, fumaric acid, GABA, and alanine were perturbed [8]. Structural proteins of the root, cell membrane proteins and cell wall proteins, were also significantly influenced at an early stage by submersion under water. Especially, the protein group participating in lignin synthesis and lignifications were suppressed under the flooding stress [6]. The 'omics' approach can cover such multilayered data across 'omes'. Furthermore multiple omics data can be used to compensate lacking data on each biological layer and validate mutually the results from the layers.

The ability of crops to cope with environmental stress depends on rapid changes in cellular protein levels, which may be increased or decreased as a result of altered gene expression [17]. The alteration of protein levels also affects the accumulation of cellular metabolites that play essential functions in the regulation of stress responses or adaptation processes, allowing plants to survive and recover from stress [16,18]. In the present review, 'omics' data from transcriptomics, proteomics, and metabolomics studies of soybean under flooding stress are presented, and approaches for using 'omics' techniques to help elucidate the critical mechanisms functioning in soybean in response to flooding stress are discussed.

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