Review

Cotton proteomics for deciphering the mechanism of environment stress response and fiber development☆

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ARTICLE INFO

ABSTRACT

Cotton fiber is considered as the backbone of the textile industry. The productivity of cotton crop is severely hampered by the occurrence of pathogens, pests, and various environmental factors. Nevertheless, cotton plant has developed sophisticated mechanisms to respond to environment stresses to avoid detrimental effects on its growth and development. Therefore, understanding the mechanisms of cotton fiber development and environment stress response is of considerable interest for designing agriculture breeding strategies to ensure sustainable productivity. The application of proteomics technologies to advance our knowledge in cotton fiber development and abiotic/biotic stress tolerance has increased dramatically in the last 5 years as evidenced by the large amount of publications in this area. This review summarizes the work which has been reported for cotton proteomics and evaluates the findings in context of the approaches that are widely employed with the aim to generate novel insight useful for cotton improvement.

Biological significance
Cotton (*Gossypium* spp.) is considered as the foremost commercially important fiber crop grown all over the world and is deemed as the backbone of the textile industry. Cotton is also an important source of edible oil seed and a nutrient-rich food crop as cottonseed contains high-quality protein and oil. The growth and productivity of cotton crop are often hampered by various biotic stress factors, such as insect pests and pathogens. In addition, cotton plants are frequently subjected to unavoidable environmental factors that cause abiotic stress, such as salt, heat and drought. Proteomic techniques provide one of the best options for understanding the gene function and phenotypic changes during cotton fiber development and stress response. This review first summarizes the work which has been reported for cotton proteomics about cotton fiber development and abiotic/biotic stress tolerance, and also evaluates the findings in

context of the approaches that are widely employed during last 5 years, with the aim to generate novel insight useful for cotton improvement.

This article is part of a Special Issue entitled: Proteomics of non-model organisms.

Contents

1. Introduction

Cotton (*Gossypium* spp.) is considered as the foremost commercially important fiber crop grown all over the world and is deemed as the backbone of the textile industry. Cotton is also an important source of edible oil seed and a nutrient-rich food crop as cottonseed contains high-quality protein and oil [1,2]. The growth and productivity of cotton crop are often hampered by various biotic stress factors, such as insect pests and pathogens. In addition, cotton plants are frequently subjected to unavoidable environmental factors that cause abiotic stress, such as salt, heat and drought (Fig. 1). Thus, cotton plants have developed sophisticated defense mechanisms to respond to various biotic and abiotic stresses so that they can cope with the harsh environmental conditions. Though the complete genome sequences of cotton are available [3], they do not address the main aspects of cotton stress response and development. To elucidate the molecular mechanism of these stress responses, the slightest changes of gene, protein and metabolite levels need to be observed with precision. It has been reported that transcriptomics has been used extensively to dissect the mechanism of plant growth and development. However, expression patterns at the protein and mRNA levels do not always correlate due to the effects of posttranslational regulatory mechanisms [4]. Thus, genome and transcriptome data alone is insufficient to reveal the facts concerning gene function, developmental/regulatory biology and the bio-chemical kinetics of the plants under stress conditions. Additionally, plants build up fast and highly adapted responses to diverse environmental stresses are directly related to protein abundance [5]. Therefore, proteomic techniques provide one of the best options for understanding the gene function and phenotypic changes during plant stress adaptation processes.

The applications of proteomic techniques in dissecting molecular mechanism have been validated at both cellular and subcellular levels against various environmental stresses in model plants *Arabidopsis* and rice [6]. During the last 5 years, in order to analyze the protein expression patterns, several studies have been carried out on different cotton tissues under different extreme environmental conditions such as salinity, drought and pathogens. These studies have produced good amount of data to implicate various proteins during a particular or integrative stress and also their impacts on cellular and subcellular metabolism. Here we review our current knowledge of translational proteomics from the crop plant cotton. The review focuses on the proteins and their modifications that have been identified and characterized as relevant for the cotton tolerance strategy and fiber development, aiming to identify the major breakthroughs in the use of proteomics to improve cotton tolerance to environment stress and fiber quality. Furthermore, strengths and weaknesses of different protein extraction technologies and future prospects of cotton proteome study both at organ and whole plant levels are discussed in detail to comprehend the underlying mechanism of environment stress acclimation and fiber growth.

2. Methodologies for the extraction of cotton proteins

A successful extraction method would be capable of reproducibly capturing and solubilizing the full complement of proteins. Cotton protein extraction and sample preparation, particularly from recalcitrant tissues such as fiber which contains relatively high endogenous levels of interfering substances such as cell walls, polysaccharides, phenolic compounds, pectin, lipids, and waxes [7] are the most challenging and critical aspects of proteomic analyses. The different protocols of protein extraction from diverse cotton tissues highlighted in this review mostly used trichloroacetic acid (TCA)/acetone or phenol extraction methanol/ammonium acetate precipitation methods (Table 1). In fact, large scale protein purification from cotton fiber began in 1996 [8]. The presence in cotton fiber of cell wall as well as large amounts of interfering compounds not only hampers high-quality protein extraction, but also impedes separation in high-resolution two-dimensional (2-DE) gels, resulting in streaking, smearing, and a significant reduction