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Editorial

Phylogenetics of Molecular Regulators Contributing to Plant Stress Tolerance

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Abstract: Genetic studies on model plants and crops in the last few decades have uncovered numerous genes that play vital roles in plant tolerance to adverse environments. These genes could be used as targets for genetic engineering to improve plant tolerance to abiotic and biotic stresses. Recent advances in CRISPR-based genome editing have accelerated modern plant breeding and wild-species domestication. However, the stress regulators in many crops and horticultural cultivars and their wild species remain largely unexplored. Thus, transferring the accumulated knowledge of these molecular regulators from model plants to a wider range of other species is critical for modern plant breeding. Phylogenetic analysis is one of the powerful strategies for studying the functional conservation and diversity of homologous gene families among different species with complete genome sequences available. In addition, many transcriptome datasets of plants under stress conditions have been publicly released, providing a useful resource for addressing the stress response of given gene families. This Special Issue aims to illustrate the phylogenetics of molecular regulators with potential in contributing to plant stress tolerance and their stress response diversity in multiple non-model plants.

Keywords: phylogenetics; stress response; plant stress tolerance; genetic diversity; genome editing

Plants encounter numerous environmental stresses throughout their lives because of their immobile nature. Unfavorable environments include abiotic stresses such as aberrant temperatures (cold or heat), drought and hypertonic stress, and biotic ones such as infections by viruses, bacteria and fungi. Although plants have evolved a variety of strategies to adapt to their growth environments, these stresses have led to massive yield losses, and global climate change is expected to limit crop production further. Thus, breeding stress-resistant crops to maintain or increase yields under challenging environments is essential for feeding a growing population. To date, numerous genes that contribute to plant stress tolerance and defense have been revealed in model plants and a few crops through genetic studies. The discovery of these molecular regulators opens a window for molecular breeding to improve plant resilience to stresses. As the most powerful genome editing tool, the CRISPR (clustered regularly interspaced short palindromic repeats)-Cas (CRISPR-associated protein) system has accelerated modern plant breeding and wild-species domestication [1,2]. However, the majority of these important gene families have not yet been investigated in a large range of crops and horticultural plants including vegetables, flowers and trees.

Phylogenetic analysis is a powerful method for translating the accumulated knowledge of molecular stress regulators in model plants to other plant species. Additionally, with the advances in high-throughput sequencing, the genome assembly of many plants has been completed, and subsequent transcriptome profiles under different environmental stresses are publicly available, providing an important data resource for illustrating phylogenetic trees and exploring the expression patterns of given gene families. These include transcriptional regulators such as transcription factors that regulate the expression of hundreds and thousands of downstream genes, playing a critical role in plant responses to stress signals. More specifically, heat shock factors (HSFs) are well known to promote plant tolerance to extremely high temperatures [3], while WRKY transcription factors function in diverse stress responses including abiotic and plant immunity responses [4,5]. Correspondingly, the phylogenetic analysis of *HSFs* and their expression profiling under heat stress have been performed in tomatoes [6], and the phylogenetic tree of the *WRKY* gene family and the responses to multiple stresses have also been demonstrated in non-model plants such as the wild potato [4,7]. Besides, some transcription factors are critical in plant development, but the same family members are also responsive to specific stresses, indicating a key role in balancing plant development and stress responses. For example, previous studies of TCP transcription factors were more focused on their function in controlling plant development [8], but expression pattern analysis showed that the transcription of *TCP* genes was induced or repressed by drought and cold in cassava [9]. Given the progresses achieved, there is still much left to learn about the functional conservation and genetic diversity of transcription factors among different plant species.

In addition to transcriptional regulators, many post-transcriptional regulators contribute to plant stress tolerance as well. For instance, the post-transcriptional gene silence (PTGS) system plays a vital role in plant defenses against viral infections [10], and many small RNAs function in plant stress tolerance through PTGS [11]. Therefore, the key components of small RNA biogenesis pathways provide potential targets for genome editing. Regarding this, the essential small RNA biogenesis genes Dicer-like proteins (*DCLs*), Argonautes (*AGOs*) and RNA-dependent RNA polymerases (*RDRs*) were identified genome-wide in three legume crops, and their roles in biotic stress responses were uncovered [12]. Recent findings have evidenced that several RNA modifications, such as N6-methyladenosine (m^6A) and 5-methylcytosine (m^5C), can influence plant responses to salt, high temperatures and virus infections [13–15]. Thus, the key components and complexes known as writers, readers and erasers of these RNA modifications are also potential editing loci for improving plant yields for confronting environmental stresses. Given their importance, a phylogenetic tree of 278 YTH domain-containing proteins (m^6A readers) from 22 plant species was constructed [16], while the expression pattern of these genes under stressful conditions in these species remains unclear. Overall, more post-transcriptional regulators need to be characterized genome-wide in non-model plants and to be studied extensively for their response to stresses.

The molecular regulators contributing to stress tolerance also include post-translational regulators such as autophagy pathway players [17], metabolic enzymes [18] and genes involved in phytohormone signaling pathways. For instance, as a plant stress hormone, abscisic acid (ABA), plays a critical role in plant responses to multiple abiotic stresses [19]. Therefore, the genome-wide characterization of the ABA receptor *PYL* gene families and their stress responses in rice provides useful information for the further application of *PYL* gene editing in crops [20]. Furthermore, this study also identified single amino acid polymorphisms of these *OsPYLs* across different rice genotypes [20], which could be used as base editing targets. Therefore, detailed information of genetic variations within the same species and among different species will provide potential precise editing loci for breeding stress-resistant crops. Still, there are many stress regulators left to be uncovered in depth through phylogenetic studies in non-model plant species.

Taken together, this Special Issue aims to collect a vast set of work by providing insights into the phylogenetics and stress-response diversities of molecular regulators, which could be potentially applied in genetic engineering to improve plant stress tolerance.

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