Physiological and molecular mechanism of combined heat and drought stress tolerance in major millets

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Abstract: Millets can be used as food, forage and as a source of bio-energy. As most of the millets are considered to be stress tolerant they are ideal to study the stress tolerance mechanism. Drought and heat stress resistance in plants is regulated by hundreds of genes that control various morphological and physiological responses to these stresses. The elucidation of the complex mechanisms underlying combined drought and heat resistance in millets will shed light into the various players involved. Also identifying key causal candidate genes or linked molecular markers can facilitate the fast development of drought and heat tolerant varieties. With the recent advances in NGS technologies it has become quite affordable and easy to sequence the genome and transcriptomes of any plant species to identify and isolate candidate genes involved in the stress tolerance mechanism. Studying the interactive effects of drought and heat stresses on different morpho-physiological attributes and yield parameters is important. The concurrent occurrence of drought and heat is more severe for any crop growth than the single stress and it is most common in natural field conditions. There may be a conserved defence mechanism that exists among different plant species to deal with a combination of heat and drought stress. As millets are considered as stress tolerant in general, studying the stress response mechanism in millets is important. The functionally validated genes could be used as promising candidates in backcross breeding, genomic selection, and gene-editing schemes in pearl millet and other millet crops to increase the yield in droughtprone arid and semi-arid ecologies.

INTRODUCTION

Agriculture is severely affected by multiple environmental stresses due to changing climatic conditions. It is believed that the changing climate will have significant effects on the types of crops cultivated in the next century. In this context, millets are a good alternative for providing food and nutritional security to the ever increasing population. India produces >170 lakh ton 80% of Asia's and 20% of global production (FAO STAT 2021). Millets are having many nutraceutical and health promoting properties. Millets are nutritionally comparable to major cereals and serve as good source of protein, micronutrients and phyto chemicals. Today millet ranks as the

sixth most important grain in the world, sustains 1/3 of the world's population and is a significant part of the diet in northern China, Japan and various areas of the former Soviet Union, Africa, India, and Egypt. Millets are important as they can grow under a wide variety of agro ecological and harsh conditions. Millets are known for their climate-resilient characteristics, such as their ability to adapt to a wide range of ecological conditions, reduced irrigation requirements, improved growth and productivity under low nutrient input conditions and low vulnerability to environmental stresses. To cope with various environmental challenges, plants have evolved various morphological, biochemical,

physiological, and molecular systems. Plant cells detect stress events through a variety of sensors, which activate a variety of signalling pathways. Increasing abiotic stresses and interactive effect of temperature and drought at different phonological stages plays an important role on the physiological, biochemical parameters of millets and need to be simulated through modern drought FATE technology for observing clear understanding and selecting appropriate varieties for future changed climatic conditions. Hence studying the Morphological, physiological and biochemical adaptations to stress in millets is important. Also the plant response to combined stress at molecular level is also important. Screening germplasm for multiple stress tolerance and detailed study of response of millets will shed light into the potential characters leading to stress tolerance. An integrated analysis consisting of transcriptome and proteome analysis of combined heat and drought tolerance would reveal the coordination of differentially expressed genes and proteins for enhanced drought and heat tolerance in millets.

Jiguang Li et al., (2021) carried out and integrated approach to analyze the transcriptome and proteome of finger millet in response to drought stress. Sun et al., (2020) analyzed the transcriptome of heat and drought stress in pearl millet by transcriptome sequencing. Ambika et al., (2018) studied the transcriptome under drought stress in pearl millet and identified the differentially expressed genes and pathways involved in drought tolerance. Anitha et al., (2019) has analyzed balanced amino acid and higher micronutrients in millets and concluded that millets complement legumes for improved human dietary nutrition. Their study revealed the presence of significant levels of proteins, essential amino acids and micronutrients in the analyzed varieties of millets. Guo et al., (2018) studied brewing antioxidant wine from millet bran, as well as the nutritional evaluation. This study not only provides evidence for MBW as a nutraceutical with antioxidant activity, but also opens new avenues in the area of making comprehensive utilization of agricultural by-products. Wafula et al.,(2017) investigate the influence of phosphorus fertilizers on the concentrations of nutrients,

particularly calcium, protein, zinc, and iron in finger millet grains grown in different agroecologies in Kenya.Vischi *et al.*,(2021) evaluated proso millet for yield components and a range of morpho-physiological characters were recorded in two locations (Italy and Austria). In parallel, 85 SSR markers were tested on DNA samples extracted from randomly chosen plants of each variety and the 12 responsive markers used to genotype the whole variety set.

Animikha Chakraborty et al., (2022) identified candidate genes regulating drought tolerance in Pearl millet. In this they studied the drought response of 48 inbreds representing four different maturity groups at the flowering stage. Bonthala et al., (2022) carried out a de novo transcriptome analysis to identify key genes involved in dehydration stress response in kodo millet. A comparative study on comprehensive nutritional profiling of indigenous non-bio-fortified and bio-fortified varieties and bio-fortified hybrids of pearl millets was carried out by Mrinal et al., (2022). Biochemical indicators and metabolites linked with rancidity and browning of pearl millet flour during storage was characterized using four diverse pearl millet genotypes (Tara Satyavathi et al., (2023). Another study by Ali et al., 2023 revealed the effect of thermal treatments on the glycemic potential, and bioaccessibility of phenolics and micronutrients in pearl millet rotis. A comparative transcriptomic analysis was carried out to identify and validate candidate genes governing grain iron and zinc content in pearl millet Tara Satyavathi et al., (2022). Molecular characterization of 24 drought tolerant Genotypes of Pearl Millet carried out using 15 drought specific SSR primers Ambawat et al., (2021). Screening of Pearl Millet genotypes suitable for drought tolerance at early seedling stage was also carried out using various physiological parameters. Screening of Pearl millet genotypes for high temperature and drought tolerance based on morphophysiological characters was carried out using 15genotypes Meena et al., (2021).

CONCLUSION

High temperature and drought stress either alone or in combined form is a major environmental

stress that limits plant growth, metabolism, and productivity worldwide. It is a major concern for crop production and adopting different approaches for sustaining high yields of crops under combined heat and drought tolerance is an important goal. Stress induced gene expression and metabolite synthesis helps the plants to tolerate stress. Most of the millets are known for their heat and drought tolerance. Hence millets are ideal material to study and understand the drought and heat tolerance mechanism. Different studies at molecular level helps to identify important candidate genes for stress tolerance which can be deployed in crop improvement programmes.

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