



Genetic and genomic research in foxtail millet: preface

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Foxtail millet (*Setaria italica*) is a C4 model cereal crop which was domesticated from green foxtail (*Setaria viridis*) in northern China (He et al. 2015). For over 11,000 years, this crop has been widely cultured in Asia's semi-arid regions for human and animal consumption. Compared to other crops, foxtail millet has high drought resistance, tolerance to low soil nutrient availability, and good yield stability. A decade ago, the genome sequences of two cultivars, Yugu 1 and Zhanggu, were released (Bennetzen et al. 2012; Zhang et al. 2012), which laid the foundation for functional genomics studies. Recently, an efficient transformation method and new CRISPR/Cas9 genome-editing tools for foxtail millet have been established (Yang et al. 2020; Liang et al. 2022). Such developments promote foxtail millet as a novel model plant to understand the special developmental mechanism of C4 plants and the mechanism of plant stress tolerance.

This special issue provides cutting-edge research in understanding the growth, development, and stress response-related functional genomics of foxtail millet. Three review and perspective papers are included in the special issue. Panchal et al. presented an excellent review of the origin, evolution, genomic diversity, genetics and genomics resources, database resources, and recent advancements in functional genomics, proteomics, and metabolomics analysis in foxtail millet. The characterized abiotic stress-responsive genes and genome editing tools used to identify these genes in foxtail millet were also summarized (<https://doi.org/10.1007/s10725-022-00858-1>). Ingle et al. reviewed the nutritional value of foxtail millet and the technology used to increase

the nutrients' availability. Their investigation focused on genes involved in nutrient biosynthesis, transport, and metabolism in foxtail millet, which will help to overcome global nutrient deficiency (<https://doi.org/10.1007/s10725-022-00900-2>). Foxtail millet has a high tolerance to the soil with low nutrient availability (He et al. 2015). Ceasar's review focused on the membrane-bound nutrient transporters and their regulation mechanism in foxtail millet. Many transporters have been identified in foxtail millet and are under regulation in a similar process to other crops, proposing foxtail millet as an ideal model plant for comparative studies on nutrient transport (<https://doi.org/10.1007/s10725-022-00878-x>). In this special issue, the role of high-affinity K⁺ transporters in K⁺/Na⁺ balance under stress has been reported, suggesting multiple functions of these transporters in foxtail millet (<https://doi.org/10.1007/s10725-022-00903-z>). Recently, the potassium channels in foxtail millet have also been analyzed (Zhang et al. 2022). These investigations will help us understand the high nutrient use-efficiency of foxtail millet and improve the yields of other cereals on low-nutrient soils.

This special issue includes nine papers focused on the functional characterization of genes and stress resistance-related mechanisms. Liang et al. identified the *SiMAPK* and *SiMKK* gene families in foxtail millet and analyzed their transcription patterns under different abiotic stresses or phytohormone treatments (<https://doi.org/10.1007/s10725-022-00877-y>). Yang et al. analyzed the high-affinity K⁺ transporters *SiHKT* genes in foxtail millet and reported the role of *SiHKTs* in preventing sodium toxicity under salt stress (<https://doi.org/10.1007/s10725-022-00903-z>). Su et al. identified the *Si-miR156* family genes and analyzed their role in response to environmental stress response in foxtail millet (<https://doi.org/10.1007/s10725-022-00919-5>). Guo et al. compared the transcriptomic change among three cultivars under drought stress and identified 46 genes whose trends of transcription change were consistent with the drought resistance trends among different cultivars (<https://doi.org/10.1007/s10725-022-00875-0>). Zhang et al. found that expressing *SiWRKY89* could bind to the W-box elements

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of AtNCED3 in Arabidopsis, activate the ROS scavenging system, and improve plant drought tolerance (<https://doi.org/10.1007/s10725-022-00916-8>). Hou et al. reported that spraying exogenous salicylic acid enhanced the resistance in foxtail millet against the biotrophic pathogen *Sclerospora graminicola* (<https://doi.org/10.1007/s10725-022-00854-5>). Shah et al. analyzed the response of decarboxylation mechanisms in foxtail millet under salt stress. They also reported that lower doses of selenium enhance the mixed mode of decarboxylation, alleviating salt stress's effects (<https://doi.org/10.1007/s10725-022-00888-9>). Zhang et al. investigated the function of *SiFPGS2*, which increased folate content and promoted root growth by inducing cell division in the root apical meristem zone (<https://doi.org/10.1007/s10725-022-00904-y>). Xu et al. compared the bacterial and fungal populations between the foxtail millet continuous cropping system and the foxtail millet-soybean-potato rotational cropping system. They found higher beneficial microorganism diversity in the rotational cropping system, leading to higher millet yield and lower disease incidence (<https://doi.org/10.1007/s10725-022-00936-4>).

This special issue also contains one paper focusing on genotype analysis in the field. Zhang et al. assess genotypes by environment interaction using the AMMI model and GGE Biplot. They found that three foxtail millet cultivars, Yugu35, Zhangzagu21, and Datong29, had the most stable and high yield (<https://doi.org/10.1007/s10725-022-00885-y>).

Foxtail millet is a fantastic C4 model plant to study response mechanisms to combat abiotic stresses. Based on the genetic and genomics data in foxtail millet, further research is needed to validate putative stress-related gene function. It will significantly contribute to revealing novel stress-responsive mechanisms for crop improvement. Introducing these stress-related genes into major crops like rice and wheat will help sustainable crop production.

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Declarations

Competing interests The authors have not disclosed any competing interests.

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