
Preface

Foxtail millet [*Setaria italica* (L.) P. Beauv.] is one of the world's oldest domesticated crops, and it has become a major crop adapted to tropical, sub-tropical, and temperate regions of India, China, and other parts of Asia, North Africa, and the Americas. It has a small diploid genome (~515 Mb), short growing cycle 0–80 days), self-fertilization, and small morphological stature. Its prolific seed production per plant has made this crop a novel model for grass research. Belonging to the tribe Paniceae in the subfamily Panicoideae, foxtail millet is evolutionarily close to major cereals including sorghum (*Sorghum bicolor*), maize (*Zea mays*), rice (*Oryza sativa*), and candidate biofuel crops such as switchgrass (*Panicum virgatum*), napiergrass (*Pennisetum purpureum*), and pearl millet (*Pennisetum glaucum*). These biofuel crops possess polyploid genomes, long generation times, and large statures, and hence are difficult to study. Therefore, foxtail millet serves as an excellent surrogate genome for studying the genetics and genomics of bioenergy grasses. Efficient biomass productivity and improved water- and nitrogen-use efficiencies are attributable to C₄ photosynthesis, which is assumed to be a prime constituent of exceptional productivity among cereals including maize and sorghum, and bioenergy grasses such as pearl millet and switchgrass. C₄ photosynthesis has evolved as a result of 66 independent plant lineages, and therefore their study is important for understanding the biochemistry, physiology, and molecular biology of C₄ photosynthesis, which could be useful in transferring this system to C₃ species.

Extensive research has been carried out on maize and sugarcane to elucidate the C₄ biology; however, the genome complexity of these crops has resulted in little success. With the availability of reference genomes, haplotype maps, and small genome size, foxtail millet is accentuated as a model system for molecular characterization of C₄ genetics and physiology. In addition, being a staple crop of arid and semi-arid regions of the world, foxtail millet is well known for its tolerance to several abiotic stresses, particularly drought and salinity. This characteristic feature is more important in studying the genetics and genomics of stress tolerance and, therefore, foxtail millet is also considered as a model crop for abiotic stress biology. Recently, the health-benefiting properties of millets have gained importance in nutritional research and, importantly, grains of foxtail millet are reported to be rich in protein, dietary fiber, and energy content, which are three- to fivefold higher than major cereals such as rice, wheat, and maize. Altogether,

foxtail millet holds the thrust for establishing climate-resilient agriculture in order to serve nutrient-rich food and fodder to the ever-growing global population.

India tops the list in global millet production; however, pearl millet and finger millet are the top two varieties extensively cultivated in India. Despite the prominent attributes encompassed by foxtail millet, breeding technologies used in this crop are far behind those of pearl millet and finger millet, and other major cereals such as rice and wheat. Foxtail millet has also received very little research attention worldwide, and less effort has been invested towards dissecting the genetic determinants of the prominent traits which are important for improvement of this model species as well as other millets, cereals, and biofuel crops. In this context, the book enumerates the national and international efforts invested in delineating structural, functional, and nutritional genomics of this important crop. The book has 11 chapters describing the general introduction to foxtail millet followed by sequencing efforts, and structural and functional genomics. Chapter 1 provides a general introduction to the crop by outlining its agro-economic importance, origin, distribution, taxonomy, and cytology. Chapter 2 summarizes the sequencing efforts, the outcomes, and the application of sequence information in expediting genomics studies in foxtail millet. Chapter 3 provides interesting information on the impact of transposable elements on distribution pattern and evolution of foxtail millet and its wild progenitor, green foxtail. Chapter 4 summarizes the genetic and genomic resources available in this crop for use in the improvement of foxtail millet per se as well as other related millets, biofuel crops, and cereals. Chapter 5 describes the breeding strategies implemented in foxtail millet and gives an elaborate picture of how the same is being performed in India. Chapters 6 and 7 discuss the association mapping studies and genetic structure analysis of foxtail millet performed using high-throughput molecular markers. Following this, Chap. 8 covers the genetic determinants of abiotic stress tolerance, Chap. 9 the genetic transformation system available in both foxtail millet and green foxtail, Chap. 10 the nutritional potential of this crop and the relevance of nutritional genomics in delineating the health benefiting traits, and Chap. 11 the small RNA biology of foxtail millet. Altogether, the book serves as a primary resource material for researchers, breeders, and students working on millet genomics.

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