



# Nutraceuticals of Foxtail Millet (*Setaria italica* L.): Insights

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## Abstract

*Setaria italica* (L.), commonly known as foxtail millet, is a C<sub>4</sub> model cereal with a genome sequence that is compact and completely annotated. In many parts of Asia and Africa, it serves as a primary food and feed source. In the present world, where urbanization and farmland scarcity is drastically increasing, there is an urgent need to switch to cereal crops that can be grown with less inputs, consume limited resources, withstand adverse weather conditions, and provide the majority of the human diet's essential nutrients. Under these conditions, foxtail millet is an ideal cereal crop that has the potential to significantly contribute to international efforts to improve food and nutrition security. Foxtail millet grains, which are gluten-free, are an excellent dietary staple because of their high protein, fiber, carbohydrate, calcium, zinc, iron, vitamin, and lipid content. The therapeutic

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benefits of foxtail millet include antihyperglycemic, antioxidative, anti-hyperlipidemic, anti-inflammatory, and antihypertensive activities and hence are strongly recommended that this grass family member be incorporated into a person's diet on a regular basis. The purpose of this chapter is to provide an overview of the nutraceutomics of the foxtail millet and the molecular efforts employed to improve the nutritional quality along with the traditional culinary applications of foxtail millet.

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**Keywords**

Foxtail millet · Nutraceutomics · Nutrients · Omics · *Setaria* · Traditional food

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## 1 Introduction

Millets are Poaceae family grass crops that have been cultivated for centuries. The Poaceae family consists of grasses and domesticated cereals including rice, maize, wheat, barley, millets, etc. “Millet” refers to cereal plants that produce numerous, minute seeds. Millet grains are a primary food source for many people worldwide, especially in the dry and semidry parts of Africa and Asia. Many economically relevant millets are used to produce biofuels and bioenergy products. Millets are particularly significant due to their high nutritional value and agro-industrial significance (Yousaf et al. 2021). After wheat, maize, sorghum, rice, and barley, millets are the world's sixth most important cereal grain crop. According to FAOSTAT 2020, between 2003 and 2018, nearly equal amounts of millets were produced in Asia and Africa, accounting for 96% of worldwide millet production, with the remaining 4% coming from the rest of the world (Yousaf et al. 2021). *Setaria italica* (L.) P. Beauv, commonly known as foxtail millet, is the world's second most extensively cultivated millet crop after pearl millet. Over 8000 years ago, in northern China, foxtail millet was said to have been domesticated from a wild species of green foxtail. Foxtail millet is a member of the *Setaria* genus, which consists of over 125 species predominantly spread in warm and temperate parts of the world (Lata et al. 2013). A typical foxtail millet plant attains a height of 120–200 centimeters and produces up to 13,000 seeds per plant. A thin stem terminates in a panicle of reddish or purple-hued bristles of around 5–30 cm in length. The characteristic shape of the panicle resembles a fox's tail, hence the common name “foxtail” for most cultivated *Setaria* species. *Setaria* genus members (foxtail millet [*S. italica*] and green foxtail [*S. viridis*]) are closely related to several millets, cereals, and biofuel grasses. Foxtail millet possesses a variety of beneficial characteristics, such as high photosynthetic efficiency, effective use of water and nitrogen even under unfavorable conditions, a high yield and productivity even with limited input resources, etc. In addition, foxtail millet grains are an excellent dietary staple because of their gluten-free, high protein, fiber, carbohydrate, calcium, zinc, iron, vitamin, and lipid content. The 2012 release of the *S. italica* genome sequence has substantially aided the development of large-

scale genomic resources (Bennetzen et al. 2012; Wang et al. 2012). Foxtail millet is a promising model for functional genomic studies in millets, cereals, and bioenergy grasses due to its small diploid genome (515 Mb), self-fertilization, and short cycle lengths (Lata et al. 2013; Lata and Shivhare 2017). Furthermore, because it is capable of NADP malic enzyme-type  $C_4$  photosynthesis, it has become a model crop plant for genetic studies.

According to traditional Chinese medicine, consuming foods with pharmacological properties, such as foxtail millet, can reduce the chance of developing chronic diseases or even heal them. Foxtail millet is particularly well known in China for its beneficial effects on the digestive tract of humans. Recent research studies on foxtail millet have highlighted the anti-inflammatory, hyperglycemic, antihypertensive, and antihyperlipidemic potential (Akoh and Min 2007; Chow 2008; Hou et al. 2018; Jali et al. 2012; Li et al. 2022). Selection and, to a lesser extent, recombination breeding have primarily been used to improve foxtail millet crops (Hariprasanna et al. 2017). This crop's unique floral morphology and flowering behavior make it challenging to pursue crosses between the ideal parents. Therefore, foxtail millet has a limited potential for conventional breeding. Molecular marker-based, population studies and multi-omics approaches are needed to improve the breeding of foxtail millet.

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## 2 Nutritional Composition and Therapeutic Values of Foxtail Millet

### 2.1 Nutritional Composition

The foxtail millet has more nutrients than other cereals like wheat and rice (Bandyopadhyay et al. 2017). Millet grains are a good source of nutrients, have a low glycemic index, are low in phytic acid, and do not contribute to stomach acid production. Millet is often referred to as “nutricereal” because it contains more nutrients per gram than other cereals. These include phytochemicals, micronutrients, antioxidants, and essential amino acids (except lysine and methionine) (Jali et al. 2012; Singh and Raghuvanshi 2012). According to some sources, foxtail millet (cultivar ‘RAU-8’) possesses the highest level of seed proteins among all millets (Chandel et al. 2014). In addition, foxtail millet ranks among the millets with the highest contents of protein, fat, ash, crude fiber, thiamine, and riboflavin (Bandyopadhyay et al. 2017).

Amino acids, both common and essential, have their foundation in proteins. Seed storage proteins (SSPs) found in millet grains are vital in facilitating seed germination after embryo development is complete. However, sulfur-containing amino acids like methionine and cysteine are more abundant in millets. All primary essential amino acids are present in foxtail millet except tyrosine (Table 1). The predominant amino acid found in foxtail millet is leucine (1040 mg/g of protein) followed by isoleucine (480 mg/g of protein) and valine (430 mg/g of protein). Foxtail millet also has the highest concentration of leucine and isoleucine of any millets (Bandyopadhyay et al. 2017). The foxtail millet has more elevated amounts of

**Table 1** Nutrient composition of foxtail millet (Saleh et al. 2013; Bandyopadhyay et al. 2017)

Nutritional composition (per 100 g)	
<b>Protein (g)</b>	12.3
Fat (g)	4.3
CHO(g)	60.9
Crude fiber (g)	8
Energy (KJ)	331
<b>Vitamin profile (mg)</b>	
Thiamin	0.59
Riboflavin	0.11
Niacin	3.2
Folic acid	15
Vit A	32
Vit E	31
Vit B6	–
Vit B5	0.82
<b>Essential amino acid profile (mg/g of N)</b>	
Arginine	220
Histidine	130
Lysine	140
Valine	430
Tryptophan	60
Phenylalanine	420
Methionine	180
Threonine	190
Leucine	1040
Cysteine	100
Isoleucine	480
Tyrosine	–
<b>Minerals profile (mg/100 g)</b>	
Calcium	31
Iron	2.8
Magnesium	81
Potassium	250
Sodium	4.6
Sulfur	171
Copper	1.4
Molybdenum	0.07
Manganese	0.6
Zinc	2.4
Chlorine	37
Chromium	0.03
<b>Fatty acid composition</b>	
Palmitoleic	–
Palmitic	6.4
Oleic	13
Linolenic	–
Linoleic	66.5
Stearic	6.3

almost all essential amino acids than rice and wheat. Vitamins, an externally supplied dietary requirement, play a crucial role in maintaining human physiological homeostasis. Foxtail millet grains, like other types of millets, are an excellent source of a wide variety of vitamins (Table 1). The crop has more significant amounts of all vitamins except vitamin B6. It has the most significant concentrations of thiamine and vitamin E among millets as well as rice and wheat (Bandyopadhyay et al. 2017). The vitamin profiling of foxtail millet revealed that it is a good source of vitamins A and E and folic acid. In addition, foxtail millet is a good source of calcium, iron, magnesium, potassium, etc. Analysis of the mineral composition of foxtail millet revealed an abundance of potassium, followed by sulfur, magnesium, chlorine, and calcium (Table 1). According to the reports, foxtail millet is one of the richer sources of zinc and iron, with levels of 2.4 and 2.8 mg/100 g of grain, respectively. Foxtail millet generally has consistently higher contents of significant minerals and can serve as an effective supplement to our conventional dietary practices. Moreover, foxtail millet is an excellent source of fatty acids such as stearic and linoleic acids, both found in relatively low concentrations in other millet varieties and in cereals that are not classified as millet.

## 2.2 Biochemical Pathways Highlighted in Foxtail Millet

It was shown that the foxtail millet cultivated in various locales had significantly variable metabolites, likely due to the weather conditions in those areas (Yang et al. 2021a, b). Foxtail millet's secondary metabolite profile revealed an excess of flavonoids, especially in their glycosylated forms (Li et al. 2018). This indicates the enrichment of the flavonoid biosynthetic pathway in foxtail millet. Flavonoids have a multitude of beneficial medical effects, including anti-inflammatory, antiviral, and anticancer activities. Moreover, they shield the brain and heart from damage (Ullah et al. 2020). In contrast to other cereals, foxtail millet has been shown to have a significantly higher concentration of flavone O-aglycones, which may be the product of an enriched gene duplication event. A similar accumulation of phenolamides, which are 100 times more abundant in foxtail millet than in rice, has been documented. Phenolamides have long been crucial in various biological functions, such as plant growth and development, resistance to pathogens, and protection from abiotic stressors (Li et al. 2018). Phenolamides have been found to have beneficial benefits against metabolic syndrome and neurological illnesses, in addition to their antioxidant, anti-inflammatory, anticancer, and antibacterial capabilities (Roumani et al. 2020).

## 2.3 Therapeutic Uses

Localized inflammation is a defensive reaction involving several cells and chemicals. It is often associated with excessive secretion of pro-inflammatory cytokines, such as IL-1b, IL-6, or TNF-a, which can cause harm to the immune

system and hamper organ function, in addition to inducing or aggravating several disorders (Favalli 2020; Guo et al. 2020; Navarro-González and Mora-Fernández 2008). Anti-inflammatory testing using grain extracts from several foxtail millet accessions showed that most foxtail millet grain extracts inhibit the generation of pro-inflammatory mediators of macrophage response (Li et al. 2022). This highlights the possibility of using foxtail millet as an anti-inflammatory agent. It is well documented that millets are an excellent source of carbohydrates, which are needed for the health and operation of the digestive tract (Flight and Clifton 2006). They give the body the fuel to function and aid in delivering vital micronutrients (Eastwood 2003). Millets, particularly foxtail millet, are low in saturated fat; nonetheless, they are an excellent source of polyunsaturated fats, which help in reducing low-density lipoprotein (LDL) cholesterol (Akoh and Min 2007). As a result, having low levels of LDL cholesterol lowers the chance of developing heart disease; hence, consuming low-LDL foods like foxtail millet is essential for ensuring adequate nutrition (Chow 2008).

Nutritional stability relies on a steady intake of essential amino acids. Lysine is a necessary amino acid for humans and animals (Tomé and Bos 2007). Therefore, the latent genetic variety of foxtail millet, which has a wide range of lysine content, may be helpful for human nutrition and animal feed. Thiamine, or vitamin B1, is essential for proper energy metabolism (Bettendorff et al. 2014). However, in economically developed countries, thiamine deficiency, which can lead to the potentially fatal disease beriberi, is uncommon due to dietary diversification and thiamine fortification of grains (Dwyer et al. 2015; Nathoo et al. 2005). However, in locations where nutritional sources of thiamine are restricted, such as Southeast Asia, thiamine deficiency does occur (Coats et al. 2012; Khounnorath et al. 2011). There is significant variation in the amount of thiamine found in foxtail millet germplasm, which suggests that it may have potential application in breeding. Increased popularity and production of foxtail millet, considered suitable food for diabetics, could contribute to reducing the worldwide prevalence of diabetes (Kam et al. 2016). In contrast to other cereal foods like rice and wheat, foxtail millet provides a steady stream of glucose without disrupting the body's metabolism (Jali et al. 2012). It is documented that incorporating foxtail millet into the diet has an antihypertensive effect (Hou et al. 2018). According to clinical trials, consuming 50 g of foxtail millet daily can reduce blood pressure, body mass index, body fat percentage, and fat mass. Additionally, this improved blood glucose levels.

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### 3 Genetic Resources of Foxtail Millet

About 125 species make up the genus *Setaria*, which is found all over the world in warm and temperate climates (Dwivedi et al. 2012). Various phenotypic features within and across species, as well as a wide range of life cycles, ploidy levels, and breeding strategies at the genus level, suggest a highly complicated taxonomy for the *Setaria* genus, which includes both cultivated and wild species. Three separate gene

pools for the *Setaria* species have been found due to variations in genome structure. The AA genome, annotated with the genetic parameters  $2n = 2x = 18$ , represents the primary gene pool of foxtail millet (Benabdelmouna et al. 2001a). Probably evolved from a natural cross between the diploid species *S. viridis* (green foxtail) and *S. adhaerens* (bristly grass), the weedy tetraploid species *S. faberi* (giant foxtail) and *S. verticillata* (bristly grass) both carry an AABB genome (Benabdelmouna et al. 2001b). The remaining landraces of *Setaria*, including *grisebachii*, *queenslandica*, *pumila*, and *pallide-fusca*, make up the tertiary gene pool. A diploid species known as *S. grisebachii* with a CC genome is also reported from Mexico (Wang et al. 2009). While *S. pumila* (yellow foxtail) and *S. pallide-fusca* are likewise polyploidy *Setaria* species, they lack the AA genome and are therefore not autotetraploid like *S. queenslandica* (Benabdelmouna et al. 2001a, b; Benabdelmouna and Darmency 2003). However, *S. pumila* and *S. italica* have been recognized as separate species of *Setaria* based on the appearance of their inflorescence. Both the *viridis* and the *italica* subspecies belong to the species *S. italica*. Once again, the *italica* subspecies have been classified into three races and ten subraces (Upadhyaya et al. 2011).

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#### 4 Molecular Marker Studies and QTLs Associated with Nutritional Value

The development of DNA-based molecular markers has aided in mapping genes and quantitative trait loci (QTLs) for use in plant breeding and producing genetic maps. In foxtail millet, substantial work has been conducted on developing large-scale genome-wide markers, generating maps, and tagging agronomically important genes and QTLs (Muthamilarasan et al. 2015). Intron-length polymorphisms, transposable-elements-based markers, microRNA (miRNA)-based markers, and expressed sequence tag (EST)-derived simple sequence repeats (SSRs) have all been developed due to the availability of the foxtail millet genome sequence (Kumari et al. 2013; Muthamilarasan et al. 2014; Pandey et al. 2013; Yadav et al. 2014; Zhang et al. 2014). A gene that is responsible for the “spikelet-tipped bristles” (*stb*) trait in foxtail millet was mapped by Sato et al. in 2013. This trait is essential in determining grain yield (grain number per panicle) in foxtail millet. By utilizing two F<sub>2</sub> populations, as well as transposon display (TD) markers and SSR markers, the location of the *stb1* gene on chromosome 2 was determined (Sato et al. 2013). Using information from the foxtail millet genome sequence, they also produced unique SSR markers, formed nine linkage groups with a total length of 1287.5 cM, and mapped *stb1* more precisely on chromosome 2. Earlier, Fang et al. (2016), by employing a Longgu7 x Yugu1 F<sub>2</sub> intraspecific population, detected 29 QTLs for 11 agronomic traits. In order to create a high-density genetic map, 167 members of a Yugu1 Longgu7 F<sub>2</sub> population were genotyped using 1013 SSR markers demonstrating polymorphism between Yugu1 and Longgu7 (Fang et al. 2016). There were 1035 loci on the genetic map, which covered a distance of 1318.8 cM at an average marker separation of 1.27 cM. In a natural population of 184 foxtail millet accessions from various regions, Gupta et al. (2014) found eight SSR markers on distinct chromosomes

that showed significant relationships with nine agronomic traits (Gupta et al. 2014). In order to investigate, extract, retain, and examine the untrodden genetic diversity of foxtail millet at the molecular level and discover the variability of its nutritional traits, Trivedi et al. (2018) analyzed 30 accessions from the Central Himalayan Region that possessed unique characteristics of agronomic significance. There was a wide variety in the nutritional aspects of husked grains, including dietary fiber, carbohydrate, protein, lysine, and thiamine content (Trivedi et al. 2018). The assembled germplasm repository might be used to generate nutritionally rich and agronomically favorable varieties of foxtail millet and to build strategies for harnessing utilizing unexploited genetic variety for food and nutrition security in agro-ecological regions. There have been many reports of molecular marker research on foxtail millet, but only a small number of these have focused on the nutritional characteristics of the crop.

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## 5 Genomics-Aided Breeding for Nutritional Traits

### 5.1 Functional Genomic Studies

During the past decade, numerous studies and attempts have been made by the scientific community at large using various molecular genetic tools to investigate and enhance crop plants' nutrient use efficiency. Among these are the implementation of genome-wide association studies (GWAS), functional genomic approach, molecular marker-assisted breeding (MAB), and characterization of nutrient transporter genes. Functional genomic research on nutrient transporters is a crucial aspect of the various strategies implied. Crop plant yield, quality, and the plant's ability to overcome unfavorable conditions of low nutrient soils are all affected by nutrient use efficiency, which refers to the nutrient acquisition and utilization efficiency (Nieves-Cordones et al. 2020). The mechanism of nutrient transport in plants has been studied using foxtail millet as a model system. In addition, the recent research has opened up new possibilities for using foxtail millet as a C<sub>4</sub> model system to understand better and improve nutrient use efficiency (Ceasar 2022). To date, foxtail millet transporters for a variety of nutrients, including phosphate, potassium, boron, nitrogen, iron, zinc, ammonium, amino acid, and sugar, have been identified (Alagarasan et al. 2017; Ceasar et al. 2017; Liu et al. 2022; Nadeem et al. 2018; Wang et al. 2022; Yang et al. 2021a, b; Zhang et al. 2018). Uptake and redistribution of inorganic phosphate (Pi) have been linked to the phosphate transporter 1 (*PHT1*) family of candidate genes, and the expression patterns of these genes in foxtail millet have been studied (Ceasar et al. 2014; Nadeem et al. 2020). Twelve different *PHT1* family members were discovered in foxtail millet (*SiPHT1;1-1;12*). Of these 12, downregulation of the *PHT1;2* genes significantly affected yeast growth, foxtail millet phenotype, and Pi transport, suggesting that this transporter is crucial for Pi uptake and export (Ceasar et al. 2017). Similarly, nitrate transporters involved in nitrate uptake in foxtail millet have been identified (Nadeem et al. 2018). Using forward and reverse genetic methods, a boron (B) transporter gene (*SiBOR1*) was



recently characterized in the cultivar Yugu 1 (Wang et al. 2022). This gene is an ortholog of the rice B transporter OsBOR1. Panicles showed prominent expression of *SiBOR1*. Overall, it appears that *SiBOR1* is required for the development of the panicle to keep the grain yield in the foxtail millet stable.

Amino acid transporters (AATs) are essential for plant growth and development because they control the transmembrane transfer of amino acids. Long-distance amino acid transport, seed germination, quality development, sensitivity to pathogenic microbes, and abiotic stress are all examples (Yang et al. 2021a, b). Scientists have identified 94 AAT genes in foxtail millet, dividing them into 12 distinct subfamilies. A subclass of amino acid transporters, amino acid permeases (AAP) genes are closely associated with grain development and quality formation in numerous species. The amino acid contents of lysine, phenylalanine, leucine, and aspartic acid were found to be lower in an *Arabidopsis* AAP mutant (AtAAP6). The differential expression of *SiAAP20*, a homologous gene of AtAAP6, is proposed to explain the observed variation in leucine content between foxtail millet and other species. In a comparison of the two C4 plants, maize and foxtail millet, the expression of the sugar transporter, SWEET proteins, was found to be significantly higher in maize leaves (Liu et al. 2022). Higher sugar transport capacity from leaves to seeds in maize can be attributed to the higher expression of SWEET proteins in maize than in foxtail millet. It is possible that this is what keeps the carbohydrate content of foxtail millet so low compared to rice, wheat, and maize. Recent years have seen the isolation of candidate genes and gene families from foxtail millet, including resistance gene analogs, *SiNAC*, and the calcium sensor CaM gene. These have opened the door to developing functional markers for MAS and breeding for nutritional quality improvement and blast disease resistance (Puranik et al. 2011; Weng et al. 2009).

## 5.2 Genome-Wide Association Studies (GWAS)

Genome-wide association studies (GWAS) are essential to examine complex trait genetics. This method is preferable to interval mapping since it provides a higher resolution, uses past recombinations, allows mining a large number of alleles, and requires less time and effort. A recent report by Jaiswal et al. (2019) detailed for the first time the genetic determinants of ten nutritional elements in foxtail millet, including potassium, nickel, calcium, boron, magnesium, phosphorus, sulfur, zinc, manganese, and iron. A genome-wide association study (GWAS) was performed using 93 diverse accessions and 10,000 SNPs. Seventy-four marker-trait associations (MTAs) were connected with the ten elements listed above, with ten MTAs displaying high confidence (those associated with B, Mg, Zn, and Fe). In addition, a sizeable pyramiding effect demonstrated that connected elements might be substantially enhanced by merging numerous MTAs (Jaiswal et al. 2019). High-throughput multi-omics techniques and platforms are being developed, which will aid in metabolically deciphering the mysteries of domestication (Zhan et al. 2022). Li et al. (2022) attempted to establish a relationship between the transcriptome, metabolome, and anti-inflammatory properties of foxtail millet through a multi-omics

investigation. In order to gain a better understanding of the genetic and metabolomic variations among foxtail millet accessions, the research team conducted a high-throughput and comprehensive study on a diverse collection of foxtail millet germplasms (398 geographically diverse accessions) from China. Profiling these accessions' metabolomes revealed a significant difference in metabolites between foxtail millet and its wild relative *S. viridis*. Compared to foxtail millet, *S. viridis* displayed more fluctuation and lower overall levels of 1104 metabolites. These metabolites included serotonin, N-acetylserotonin, N-(p-coumaroyl) serotonin, trimethoprim, etc. Researchers also performed a metabolite genome-wide association study (mGWAS) to understand the genetic basis for the observed diversity in metabolic characteristics among millets. Possible causes of variance in metabolic characteristics were narrowed down to 511 genes, which were linked to 692 lead SNPs (Li et al. 2022). Li et al. (2022) used mGWAS data along with genetic and biochemical evidence to show that the foxtail millet gene *SiPSY1* encodes a limiting enzyme in the carotenoid biosynthesis pathway, thereby contributing to the millet's yellow color and the production of carotenes.

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## 6 Traditional Practices and the Necessity of Protecting Them

Genetic resources, especially Plant Genetic Resources for Food and Agriculture (PGRFA), are essential and significant in ensuring food security. These are vital to sustainable agriculture. In addition, climate change impacts like drought, global warming, salt, temperature, and sporadic floods are the primary challenges to dependable crop production. In this way, plant genetic resources (PGR) and traditional knowledge (TK) contribute to the resilience of food crop production in the face of climate change. Despite widespread knowledge of the health benefits of millet, it is generally only consumed by indigenous peoples. This is because there are not enough convenient, accessible, or ready-to-eat alternatives to staples like rice and wheat. There have been recent efforts to make millets more accessible to consumers in more accessible forms, primarily due to their high fiber content (Deshpande and Poshadri 2011). Bread (fermented or unfermented), porridges, and snack foods are just some of the many traditional foods that can be made from millet in many parts of Africa and Asia, especially among the less privileged members of those regions' societies (Chandrasekara et al. 2012).

As a precaution against drought during sowing, Chinese farmers traditionally keep a variety of landraces that mature at different rates or are resistant to heat (Li and Wu 1996). In addition, a traditional practice of keeping specific cultivars with a short life span is also practiced in China as a precaution against drought and other natural disasters like frost and pests. Since plant thinning by hand is so time-consuming and labor-intensive, using landraces with varying growth rates could facilitate more efficient scheduling of sowing, management, and harvest. Over many years of farming, farmers developed methods for choosing the best seeds for the following year's planting. Farmers choose the best panicles in the field according to their favored ideotypes (Li and Wu 1996). The chosen panicles were allowed to dry in the open air.

As a result of the spikelets in the middle of the panicle beginning to blossom and produce grains earlier than the rest, these spikelets can obtain more nutrients that have been translocated from other organs. Each end of the panicle was removed, and the remaining parts were combined and threshed. Farmers also placed a premium on seed purity, focusing extensively on eliminating genetically diverse seed samples through a process known as “seed picking.” Sun-drying, drought hardening (soaking and drying two or three times), and fumigation by burning toxic plants were common pre-sowing seed treatments used in China to improve germination vigor, drought resistance, and disease prevention, respectively (Li and Wu 1996).

Foxtail millet is also known as *tarreang* in Indonesia. This region is home to a number of local cultivars of foxtail millet, many of which are cultivated and processed by the local people into a wide range of traditional foods (Ramlah and Daryono 2020). During the festival season, the foxtail millet porridge known as *ule-uleq* is usually prepared. In addition to being processed into porridge, *tarreang* can also be processed into various other forms of local food that are processed using coconut milk. Some examples of these forms include *Sokkoltarreang*, *Jelly tarreang*, *Buras tarreang*, *Jepagollamamea*, *Jepaanjoroi*, and *Dodoltarreang* (Ramlah and Daryono 2020). Foxtail millet is the primary ingredient in Nigeria’s national dish, *tuwanaduwa*, which is prepared using traditional methods (Issoufou et al. 2017). *Korramurukulu* is the name given to a beverage made from foxtail millet that does not contain any alcohol (Ramashia et al. 2021). Foxtail millet and Bengal gram flour are the two primary ingredients in the preparation of *korramurukulu*.

PGR and TK are being utilized commercially by stakeholders in developed nations due to the rapid development of technology in various domains (Salgotra and Gupta 2016). Both developing and developed countries can benefit from indigenous peoples’ wisdom. However, the rewards accruing from TK use are not being distributed fairly. Developed country’s stakeholders have granted IPRs on the vast majority of PGR and related sources, with benefits being shared with local and indigenous communities. However, most nations’ intellectual property laws are not robust enough to safeguard their PGR and TK. The debate over IP protection for the TK of indigenous farming communities has opened a new line of inquiry into moral concerns. Due to the unawareness of TK and IP laws protecting them, most of these issues’ international disputes remained contentious and unresolved. It is imperative that these issues be discussed at the international level with world organizations, stakeholders, and NGOs to find solutions to these complex problems. Indigenous peoples should be provided with up-to-date information through IPR-related awareness programs (Salgotra and Gupta 2016).

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## 7 Conclusion and Future Prospects

Foxtail millet, one of the world’s oldest and most widely grown crops, has a high tolerance for soils with low fertility. It serves as an excellent experimental platform for researching the genetics of  $C_4$  plants. Functional genomic investigations were

hastened by the availability of the genome sequence, leading to the characterization of various dietary features. Foxtail millet's anti-diabetic, antihypertensive, anti-hyperlipidemic, and antioxidative potential makes it a vital part of any healthy diet in a society where lifestyle disorders are so prevalent. Foxtail millet, formerly an overlooked and understudied crop, is now recognized as a high-quality genetic resource with many practical applications. Although various functional genomics, proteomics, metabolomics, and population studies have been reported on foxtail millet, the number of studies concentrating on the millet's nutritional properties is minimal. Applying omics or multi-omics techniques to enhance the nutritional quality of foxtail millet could potentially open up new avenues for plant breeding initiatives using this ancient grass crop. The substantial diversity of molecular clustering and nutritional features and the correlation between the two can be utilized to build further techniques tailored to produce nutritionally dense variations.

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