



Reviving Foxtail Millet in Uttarakhand Himalayas: Opportunities for Climate-Resilient Improvement using CRISPR-Cas Genome Editing

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Abstract

Millet has historically been central to the agricultural systems and food culture of Uttarakhand. The Himalayan region is characterized by steep slopes, fragmented landholdings, limited irrigation facilities, and high climatic uncertainty, which restrict the cultivation of major cereals such as rice and wheat. Under these conditions, millets have functioned as resilient crops capable of sustaining traditional hill farming systems (Dwivedi *et al.*, 2012; Yang *et al.*, 2012). Among these, foxtail millet (*Setaria italica*) has made a significant contribution to household food security, nutrition, and livelihoods.

Despite its adaptability and nutritional value, foxtail millet cultivation has declined markedly in recent decades due to the replacement of traditional crops with high-yielding cereals, changing food preferences, rural migration, and weak market linkages (Dwivedi *et al.*, 2012; FAO, 2018). Recent advances in plant genomics, including quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), and CRISPR–Cas–based genome editing, provide powerful tools to improve yield, stress tolerance, and adaptability in foxtail millet. The integration of these modern approaches with conventional breeding strategies offers significant potential to revive millet cultivation and enhance food and nutritional security in fragile Himalayan agroecosystems.

Keywords: Foxtail millet; *Setaria italica*; QTL mapping; GWAS; CRISPR–Cas; climate resilience

Introduction

Foxtail Millet: An Underutilized Crop of the Himalayan Region

Foxtail millet (*Setaria italica*), commonly known as kauni or kangni, belongs to the family Poaceae and is among the earliest domesticated cereal crops. Evidence from archaeological and genomic studies indicates that the crop was domesticated independently in East Asia and the Indian subcontinent more than 5,000 years ago (Yang *et al.*, 2012; Jia

et al., 2013). The species is well-adapted to rainfed and marginal environments due to its efficient C4 photosynthetic pathway, short life cycle, and tolerance to drought and high-temperature stress.

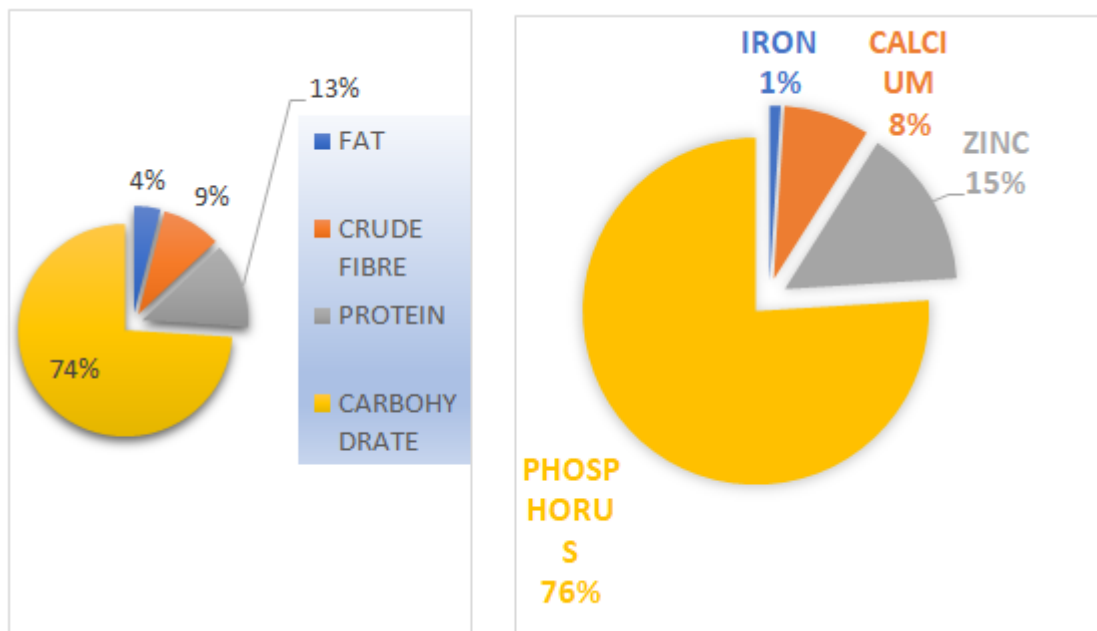
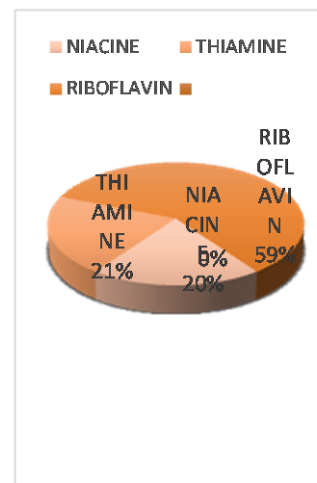


Fig.1- Diagrammatic representation of the nutritive value in Foxtail Millet. (Neeraja *et al.* 2017; Kumar *et al.* 2018)

In Uttarakhand, foxtail millet was traditionally cultivated in mid- and high-altitude districts such as Almora, Champawat, and Pithoragarh, where soil fertility is low, and rainfall is erratic (Dwivedi *et al.*, 2012). The crop grows to a height of 60–120 cm and produces compact panicles bearing small, oval grains that are nutritionally rich in carbohydrates, protein, dietary fiber, and essential micronutrients, including iron, calcium, and zinc (Yang *et al.*, 2012). In recent years, foxtail millet has gained global recognition as a **model C4 crop** due to its relatively small genome, short generation time, and high tolerance to abiotic stresses. These features make it an ideal system for studying stress physiology, grass genome evolution, and functional genomics (Yang *et al.*, 2012; Jia *et al.*, 2013). However, despite these advantages, the cultivation of foxtail millet in Uttarakhand has declined sharply. The erosion of traditional landraces, limited availability of improved varieties, and inadequate research investment have constrained its wider adoption. Indigenous landraces maintained by hill farmers represent valuable genetic resources for stress tolerance and nutrient-use efficiency, but these resources remain underexplored and are increasingly threatened.

Genetic mapping and qtl analysis in foxtail millet

Elucidating the genetic basis of agronomic traits is a prerequisite for systematic crop improvement. Early genetic studies in foxtail millet focused on the development of linkage maps and the identification of quantitative trait loci (qtls) governing plant height, tillering, flowering time, and inflorescence architecture (Doust *et al.*, 2004). These studies demonstrated that most agronomic traits are polygenic and distributed across the nine chromosomes of foxtail millet (Mauro-Herrera & Doust, 2016). Subsequent research utilizing F₂ and recombinant inbred line (RIL) populations, particularly those derived from crosses between *S. Italica* and its wild progenitor *S. Viridis*, enabled the detection of numerous qtls associated with yield-related traits, shattering resistance, and phenological development (Doust *et al.*, 2004; Mauro-Herrera & Doust, 2016). The construction of high-density genetic linkage maps using next-generation sequencing has further improved mapping resolution, allowing the identification of stable and major-effect qtls controlling plant height, panicle traits, heading date, and grain yield (Gao *et al.*, 2025). These qtls provide a valuable foundation for marker-assisted selection in breeding programs targeting stress-prone environments.



Genome-wide association studies and functional genomics

The availability of a high-quality reference genome and advances in sequencing technologies have facilitated genome-wide association studies (GWAS) in foxtail millet using diverse germplasm collections. GWAS analyses have identified numerous marker–trait associations linked to flowering behavior, plant architecture, and yield components (Jia *et al.*, 2013; He *et al.*, 2021). In addition to trait mapping, transcriptomic and genomic studies have revealed stress-responsive gene networks involved in abscisic acid signaling, reactive oxygen species detoxification, and osmotic stress regulation. These molecular pathways provide insights into the exceptional drought and heat tolerance exhibited by foxtail millet under marginal growing conditions (Yang *et al.*, 2012; He *et al.*, 2021).

Several genes controlling key agronomic traits have been cloned and functionally characterized. For instance, *siphyc* and *siprr37* regulate photoperiod sensitivity and flowering time, contributing to environmental adaptation (Li *et al.*, 2019). *Simads34* plays a critical role in inflorescence development and grain yield determination, while genes such as *sigw3* and *SGD1* influence grain size and weight (Peng *et al.*, 2018; Dai *et al.*, 2020). Genomic studies have also identified loci associated with grain nutritional quality, highlighting the potential of foxtail millet for nutritional enhancement and biofortification (Dwivedi *et al.*, 2012; Dai *et al.*, 2020).

Potential of crispr-cas-mediated genetic improvement

The identification of trait-associated loci through QTL mapping and GWAS has opened new avenues for precision breeding in foxtail millet. CRISPR-Cas-based genome editing has emerged as a powerful tool for targeted modification of genes controlling plant architecture, flowering time, grain size, yield, and stress tolerance (Chen *et al.*, 2019; Gao, 2021). Genome editing enables precise manipulation of candidate genes without altering the overall genetic background, thereby accelerating the development of improved cultivars. In addition to improving elite varieties, CRISPR-Cas technology enables the concept of **de novo domestication**, whereby favorable traits from wild relatives or traditional landraces can be rapidly incorporated by editing domestication-related genes (Chen *et al.*, 2019; Gao, 2021). This approach is particularly relevant for foxtail millet, where Himalayan landraces possess valuable adaptive traits that can be combined with improved agronomic performance. The integration of genome editing with conventional breeding and marker-assisted selection is expected to enhance breeding efficiency and facilitate the development of climate-resilient foxtail millet cultivars adapted to diverse agroecological conditions.

Research gap

Foxtail millet (*Setaria italica*) is a nutritious and climate-resilient crop, yet its cultivation in Uttarakhand remains limited. Key traits of indigenous landraces under marginal Himalayan conditions are poorly characterized, and integration of modern genomics tools with local breeding strategies is largely unexplored. Additionally, socio-economic constraints such as farmer adoption and market access hinder the crop's revival and wider utilization.

Conclusion

Foxtail millet (*Setaria italica*) is a nutritionally rich, climate-resilient, and underutilized cereal crop with considerable potential for sustainable agriculture in Uttarakhand. Although its cultivation has declined, recent advances in genetic mapping, genome-wide association studies, and CRISPR-Cas-mediated genome editing have substantially improved our understanding of the genetic architecture of key agronomic and stress-related traits. Future breeding strategies should prioritize the development of region-specific ideotypes that integrate yield stability, early maturity, lodging resistance, and abiotic stress tolerance. The strategic integration of modern genomic tools with traditional knowledge and landrace diversity can contribute to the revival of millet cultivation, conservation of agrobiodiversity, and strengthening of food and nutritional security in fragile Himalayan ecosystems.

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Biofortified foxtail millet: towards a more nourishing future - Scientific Figure on ResearchGate. Available from: https://www.researchgate.net/figure/Diagrammatic-representation-of-the-nutritive-value-of-foxtail-millet-This-is-an_fig2_363728395

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