



PENNISETUM GLAUCUM: A QUICK TO RECOVER CROP FOR DESERTS ENVIRONMENTS

Dr. Kumar Amit

Ph.D. (Science). PG Dept. of Botany, Maharaja College. VKSU. Ara. Bihar.

ABSTRACT:

Pearl millet [Pennisetum glaucum (L.) R. Br.; Syn. Cenchrus americanus (L.) Morrone] is the sixth most important cereal in the world. Today, pearl millet is grown on more than 30 million ha mainly in West and Central Africa and the Indian sub-continent as a staple food for more than 90 million people in agriculturally marginal areas. It is rich in proteins and minerals and has numerous health benefits such as being gluten-free and having slow-digesting starch. It is grown as a forage crop in temperate areas. It is drought and heat tolerant, and a climate-smart crop that can withstand unpredictable variability in climate. However, research on pearl millet improvement is lagging behind other major cereals mainly due to limited investment in terms of man and money power. So far breeding achievements include the development of cytoplasmic male sterility (CMS), resequencing a large number of germplasm lines and several population genomic studies provided valuable insight into the population structure, genetic diversity, and domestication history of the crop. The successful improvement in combination with modern genomic/genetic resources, tools, and technologies and the adoption of pearl millet will not only improve the resilience of the global food system through on-farm diversification but also dietary intake which depends on diminishingly fewer crops. Keywords Biofortification Climate Resilient Cytoplasmic male sterility Dwarfing gene pool Genomic-assisted breeding Pennisetum glaucum.

INTRODUCTION:

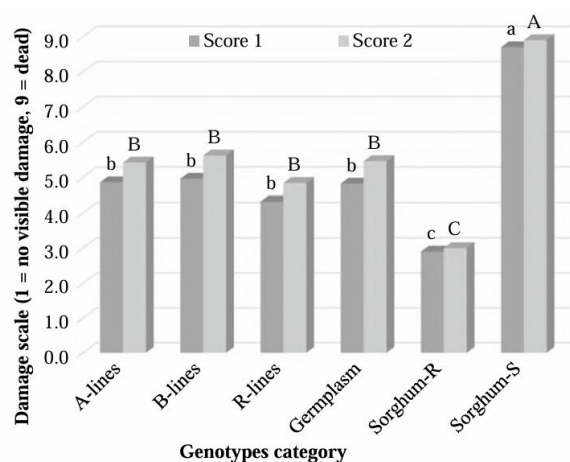
Good to Grow:

“Compared to the more commonly known cereals such as wheat, rice or corn, millets are capable of growing under drought conditions, under non-irrigated conditions even in very low rainfall regimes, having a low water

footprint”, explained Dr. Aburto, deputy director in the nutrition and food systems division of the UN Food and Agriculture Organization. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) based in Hyderabad, India, is a non-profit organization that conducts agricultural research for development. ICRISAT works closely with farmer communities and its partners, including the International Fund for Agriculture Development (IFAD), focusing on millets, among other crops. ICRISAT Assistant Director General for External Relations, Joanna Kane-Potaka, described millets as a smart food – good for people, the planet, and farmers. “Millets can help contribute to some of the biggest global challenges in unison - nutrition and health needs, mitigation and adaptation to climate change, poverty of smallholder and marginalized farmers in the dry zones - some of the toughest areas that will take longer to reach the sustainable development goals.”

MATERIALS AND METHODS:

The genetic improvement program progressed effectively initiating from the selection of local and traditional germplasm to the development of high-yielding hybrids possessing inbuilt tolerance and resistance to climatic stresses such as drought and heat along with different diseases. These hybrids were grown on 70% of the total pearl millet area, resulting in a 124% enhancement in productivity since 1986–1990. ICAR-All India Coordinated Research Project on Pearl Millet has developed several precise production and protection technologies for different agroecological regions of different states since its beginning in 1965. Till now, a total of 180 hybrids and 62 varieties have been identified and released for growing in different agroecological regions of India through ICAR-All India Coordinated Research Project on Pearl millet (Satyavathi et al., 2020).



DISCUSSION:

Photoperiodism Days to flowering is one of the most important plant characteristics that influence the cropping pattern of the natural environment (Takei and Sakamoto 1987). Besides being an adaptive trait, flowering time and photoperiodic sensitivity are influencing the yield and yield stability of pearl millet in arid and semi-arid regions of West and Central Africa (WCA). Pearl millet is generally a photoperiod-sensitive crop and almost all landraces flower in short-day conditions (Dave 1987).

As **photoperiodism** affects growth and development, it allows for flexible sowing dates by maintaining flowering and grain maturity at the end of the growing season. For instance, pearl millet varieties grown in the Sahel can mature in less than 90 days. Due to the short duration of the rainy season in the Sahel, photoperiodism has an advantage in such hot and dry conditions where the onset of rain varies from year to year. In temperate regions, the minimum temperature during the light period of 12 h and less is mostly below optimum for pearl millet growth and development. This low suboptimal temperature for the crop can potentially extend the number of days from floral initiation to anthesis and slow down grain maturity (Burton 1965) which exposes the crop to likely frost in the autumn. Therefore, pearl millet breeders are intended to develop early maturing day-neutral varieties. So, the day-neutral cultivars can flower in the long-day condition of the summer by accumulating growing degree days and mature earlier before the onset of frost. Selection in a flowering time pathway during domestication of pearl millet showed that genes for the trait underwent selection more frequently than expected (Cloutault et al. 2012). The maturity duration of the cultivars grown in WCA can broadly be classified into three groups:

- (1) early types (flower in 45 to 70 days) are mostly facultative short-day and grown in the northern dry regions of the Sahel;
- (2) intermediate types (flower in 70 to 100 days) and
- (3) late landraces (flower in 100 to 140 days)

Carbon Sequestration: Globally, under the terms of the Kyoto Agreement, several countries committed to reduce its greenhouse gas emissions in the first commitment period (2008–2012) below the 1990 baseline year levels. The agricultural sector is expected to help meet this target, by reducing their own GHG emissions, and increasing carbon sequestration.

Genome Plasticity: The adaptation of plants to a dynamic environment is defined by the controlled expression of genes both temporally in response to a

change in the environment and regularly for normal growth and development. To survive in a changing environment and reproduce, genome plasticity acquired through inheritance and mutation enables a plant to compete for the resources it needs to grow. Changes in nucleotide sequence that occur as a result of several forces, chemical and genetic, can alter the genetic content of a plant and genomic plasticity. Transposons, insertion sequence elements, DNA repetitions, introns, and DNA rearrangement are the reserves in the genome for changes in gene expression in response to external factors (Bennett 2004).

Cuticular Wax: Abiotic stress arises from exposure to climatic extremes such as drought, heat, cold, and frost. Plants have evolved to exist in conditions that are unideal for the maintenance of normal physiology and may be at the limit of survival. The above-ground surfaces of terrestrial plants are covered with cuticular wax (Jetter et al. 2007). Epicuticular waxes are complex mixtures of hydrophobic molecules that form the outermost layer of the hydrophobic cuticle, which is composed of a cutin polyester membrane and provides the last barrier to prevent uncontrolled water loss (Kosma and Jenks 2007). Cuticular wax plays a significant role in plant abiotic and biotic stress tolerance and has been implicated in defense mechanisms against excessive ultraviolet radiation, high temperature, bacterial and fungal pathogens, insects, high salinity, and low-temperature tolerance (Xue et al. 2017). Cuticular waxes consist of a homologous series of very long-chain fatty acids, alcohols, aldehydes, alkanes, esters, and cyclic organic compounds (Cameron et al. 2006). Primary plant surfaces are coated with hydrophobic cuticular waxes to minimize non-stomatal water loss. Wax compositions differ greatly between plant species, organs, tissues, and developmental stages (Guo et al. 2017).

Purple Foliage: Another notable trait in pearl millet is purple foliage. It is known to be controlled by three plant pigments: anthocyanidins-cyanidin, delphinidin, and pelargonidin (Raju et al. 1985). A genetic study revealed that the purple colour is determined by three alleles at a single locus: Rp2 (red), Rp1 (purple), and rp (green) (Hanna and Burton 1992). Red is dominant over the purple and normal green, whereas purple is dominant over normal green (Rp2 > Rp1 > rp). Red plant can be distinguished at 5 days, whereas, purple can be distinguishable two weeks after emergence. The Rp1-Rp2 locus was independent of the trichome less (tr), yellow (yn1), female sterile (fs), and light green (lgn1) loci but linked to the dwarf (d2) locus (about 28% recombination). The D2/d2 plant eight locus and the P/p foliage color locus are linked and mapped to pearl millet linkage group 4 (Azhaguvel et al. 2003).

Bristle Panicle: Bristliness in pearl millet is another important trait. The inflorescence consists of a central rachis covered with short hairs and bears fascicles on the rachilla. Each fascicle contains spikelet's surrounded by a wall of bristles (i.e., involucre). The extent of prolongation of the fascicle axis limits the length of the bristles. Long bristles have an advantage in deterring birds from feeding on the grain.

Genetic Resources: Genetic Resources of Climate-Smart Genes The genus *Pennisetum* consists of approximately 140 highly diverse species (Brunken 1977). The genus is a heterogeneous assemblage of species with four different basic chromosome numbers ($n = 5, 7, 8,$ and 9) (Jauhar 1981); ploidy levels ranging from diploid to octoploid, both sexual and apomictic reproductive behaviors, and annual, biennial or perennial life cycles (Martel et al. 1997). Cantered on morphological differences the genus is divided into five sections, namely *Gymnothrix* (P. Beauv.) Benth. & Hook. f., *Brevivalvula* Doll, *Heterostachya* Stapf & C. E. Hubb., *Eupennisetum* Stapf, and *Penicillaria* (Willd.) Benth. & Hook. f. (= *Pennisetum*) (Stapf and Hubbard 1934).

Gene pool Genetic diversity studies in *Pennisetum* recognized three gene pools and delineated them as primary, secondary, and tertiary gene pools. These gene pools were first proposed based on genetic relationships among the species (Harlan and De-Wet 1971). Later, these gene pools were identified based on Cross ability and cross-fertility of the wild species with the domesticated diploid cultivated *P. glaucum* and gene transfer complexity between gene pools. Some of the sections classified under secondary and tertiary gene pools have different life cycles, modes of reproduction, and/or basic chromosome numbers.

RESULTS:

Population challenges the world's need to produce more food to feed a rapidly growing global population, which is projected to reach 8.5 billion by 2030, and a staggering 9.7 billion by 2050. With a deepening climate crisis and aggravating environmental stresses, there is a heightened need for crop diversification by promoting crops suitable for cultivation in the toughest of environments. Acknowledging the role of millets in responding to nutritional, agrarian, and climate challenges, the UN resolution considers the “urgent need to raise awareness of the climate-resilient and nutritional benefits of millets and to advocate for diversified, balanced and healthy diets through the increased sustainable production and consumption of millets.” They are rich in vitamins and minerals, including iron and calcium; are high in protein, fiber, resistant

starch, and have a low glycemic index, which can help prevent or manage diabetes.

CONCLUSION:

Genetic Diversity: Genetic diversity is a reflection of a variety of genes in a given species which are important for survival of natural selection, for tailoring adaptation to a changing environment, and conservation of desired traits. Genetic diversity occurs as an outcome of mutations, recombination, genetic drift, migration, and selection. Natural and human selection processes over thousands of years have generated diverse cultivars of pearl millet adapted to different biophysical conditions, suited to various production systems and socio-economic conditions, and well-matched to various consumer preferences (Brunken 1977).

Phenotypic Diversity: Different phenotypic traits such as flowering time, panicle length, grain and stover characteristics, grain nutritional composition, and tolerance to biotic and abiotic stresses in cultivated pearl millet (Bhattacharjee et al. 2007; Amadou et al. 2013) have been used to study the genetic diversity at different times. A study conducted in Nigeria on 25 pearl millet genotypes collected for diverse morphological variation showed that farmers' husbandry practice resulted in the isolation of ideotypes, making landrace names a trade-off for genetic diversity (Danjuma and Mohammed 2014).

Genotypic Diversity: Analysis of molecular variation within and between Indian landraces (Bhattacharjee et al. 2002) and among inbred lines derived from WCA landraces (Stich et al. 2010) revealed more than two-fold variation between than within landraces. Population structure analysis among the latter categorized the landraces into five subgroups depicting the diversity of West African germplasm.

The potential of Association Studies for Germplasm Enhancement Diversity in Plant Genetic Resources (PGR) provides an opportunity for plant breeders to develop new and improved cultivars with desirable traits such as genetic yield potential, biotic stress tolerance, environmental adaptation, and quality attributes. Genetic diversity within and between plant populations is usually assessed using morphological, biochemical (allozyme), and molecular marker (DNA) analysis. In this postgenomic era, abundant single nucleotide polymorphism (SNPs) and the affordability of genotyping stimulated the application of genomic-assisted breeding and efficient utilization of genetic

diversity for crop improvement. Association mapping, also known as linkage disequilibrium (LD) mapping, utilizes ancestral recombination events in germplasm collections or natural populations to make marker-trait associations attributed to the strength of linkage disequilibrium between markers and functional polymorphisms across a set of diverse germplasm (Zhu et al. 2008). It also offers an alternative means of allele mining by enabling to survey of a much larger and diverse gene pool having thousands of recombination events, lending high mapping resolution, and the potential to identify the causal polymorphism within a gene and/or QTL.

Role of Bioinformatics: To conduct integrated genomics research on pearl millet, the utilization of a common communication tool among different centres is crucial. Having a common tool facilitates the efficient use of resources that are generated at different centres, such as genome information and the sharing of research results. In this regard, bioinformatics plays a vital role not only in boiling down the vast NGS data and generating useful information but also in communication. The availability of genome, comparative, gene expression, and protein databases provide useful information about the crop.

FUTURE PERSPECTIVES:

Today, fewer crop species are feeding the world than several decades ago. This scenario raises a serious concern about the resilience of the global food system in the wake of global climate change. With a lack of on-farm species diversity and dietary intake, more and more people are now exposed to harvest and health failures than ever. Many people are affected by gluten allergy. Gluten-free, protein and micronutrient-rich crops that can withstand climatic variability would have a great chance of coming to mainstream production in certain parts of the world where the consequence of climate change would be impactful.

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