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PEARL MILLET: A CLIMATE-RESILIENT NUTRITIONAL CEREAL FOR MITIGATING HIDDEN HUNGER AND PROVIDE NUTRITIONAL SECURITY

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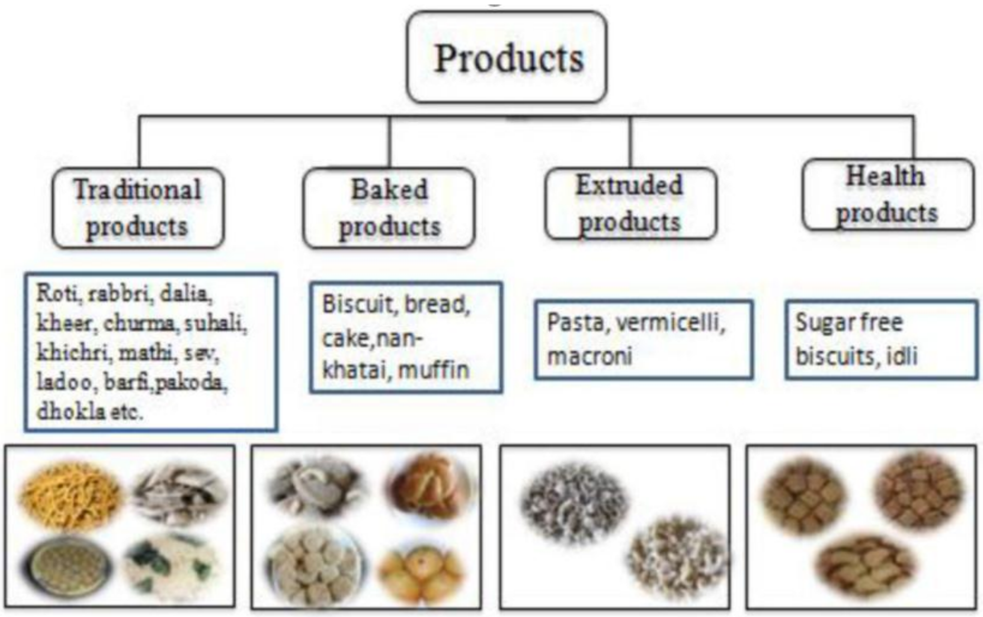
ABSTRACT:

Pearl millet being a climate-resilient crop is important to minimize the adverse effects of climate change and has the potential to increase income and food security of farming communities in arid regions. Pearl millet has a deep root system and can survive in a wide range of ecological conditions under water scarcity. It has high photosynthetic efficiency with an excellent productivity and growth in low nutrient soil conditions and is less reliant on chemical fertilizers. These attributes have made it a crop of choice for cultivation in arid and semi-arid regions of the world; however, fewer efforts have been made to study the climate-resilient features of pearl millet in comparison to the other major cereals. Several hybrids and varieties of pearl millet were developed during the past 50 years in India by both the public and private sectors. Pearl millet is also nutritionally superior and rich in micronutrients such as iron and zinc and can mitigate malnutrition and hidden hunger. Inclusion of minimum standards for micronutrients-grain iron and zinc content in the cultivar release policy-is the first of its kind step taken in pearl millet anywhere in the world, which can lead toward enhanced food and nutritional security. The availability of high-quality whole-genome sequencing and re-sequencing information of several lines may aid genomic dissection of stress tolerance and provide a good opportunity to further exploit the nutritional and climate-resilient attributes of pearl millet. Hence, more efforts should be put into its genetic enhancement and improvement in inheritance to exploit it in a better way. Thus, pearl millet is the next-generation crop holding the potential of nutritional richness and the climate resilience and efforts must be targeted to develop nutritionally dense

hybrids/varieties tolerant to drought using different omics approaches.

Products of the Pearl Millet:



INTRODUCTION:

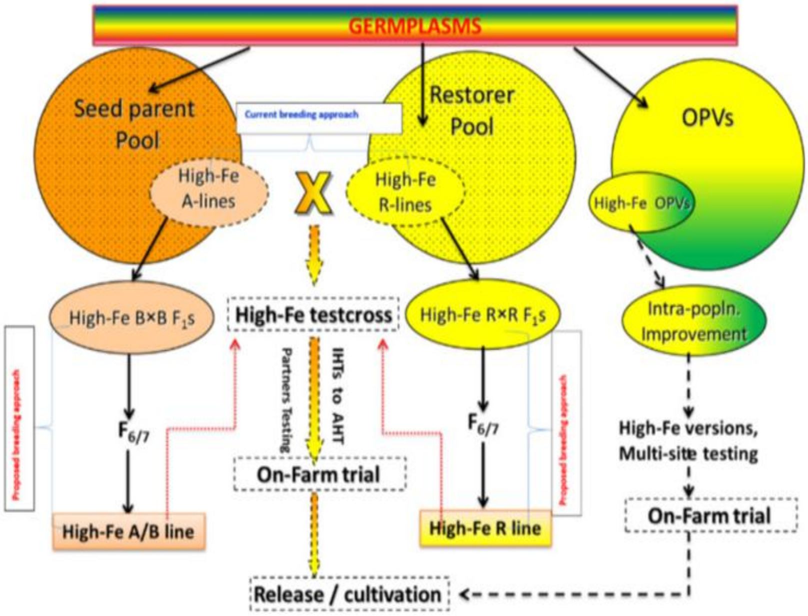
Identification of Stable Resistance to Smut in Pearl Millet. R. P. Thakur, Pearl Millet Improvement Program, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru P.O., Andhra Pradesh, India. K. V. Subba Rao, and R. J. Williams, Pearl Millet Improvement Program, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru P.O., Andhra Pradesh,India; S. C. Gupta, ICRISAT-CNRA, Bambey, Senegal; D. P. Thakur, Haryana Agricultural University, Hisar, India; S. D. Nafade, Millet Research Station, Gujarat Agricultural University, Jamnagar, India; N. V. Sundaram, ICRISAT, Institute of Agricultural Research, ABU, Zaria, Nigeria; J. A. Frowd, ICRISAT, Ouagadougou, Burkina Faso; and J. E. Guthrie, ICRISAT Sahelian Center, Niamey, Niger. Plant Dis. 70:38-41. Accepted for publication 6 June 1985. Copyright 1986 The American Phytopathological Society. DOI: 10.1094/PD-70-38.

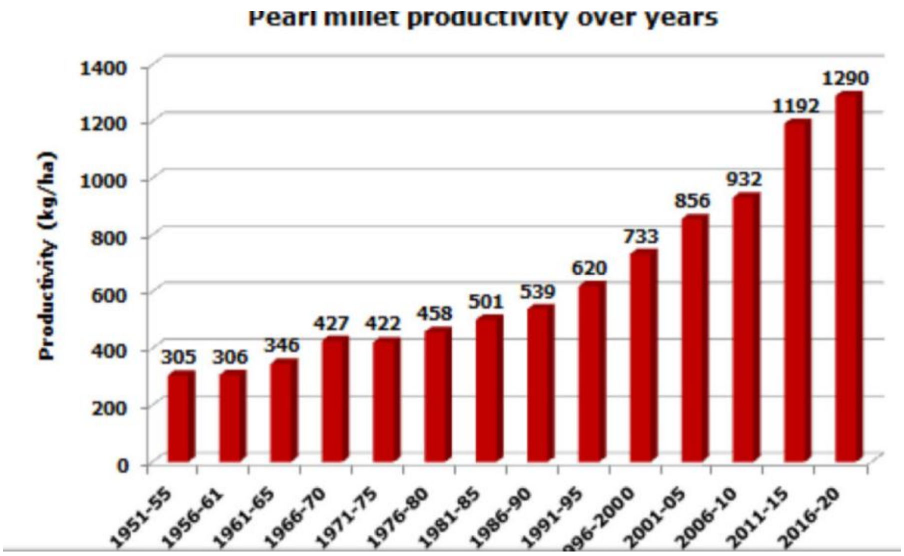
More than 1,500 accessions from a germ plasm working collection and 6,200 advanced breeding lines were screened to identify resistance to smut in pearl millet. All advanced breeding lines were susceptible, but resistance was detected in several germ plasm accessions originating from Nigeria, Senegal, Mali, Cameroon, Uganda, Lebanon, and India. To combine resistance with agronomic eliteness, crosses were made between smut-resistant lines and agronomically elite inbred lines, and pedigree selection was carried out in the segregating generations up to the F6 generation under high disease pressure. Stability of resistance was tested through a multilocational testing program, the International Pearl Millet Smut Nursery (IPMSN). Selections from six germ plasm accessions (SSC FS 252-S-4, ICI 7517-S-1, ExB 132-2-S-5-2-DM-1, ExB 46-1-2-S-2, ExB 112-1-S-1-1, and P-489-S-3) and four, newly developed, smut-resistant, agronomically elite lines (ICMPS 100-5-1, 900-9-3, 1600-2-4, and 2000-5-2) showed consistently high levels of smut resistance for 1–6 yr at six or seven locations in India and West Africa. These lines had across-location mean smut severities of less than 5% compared with 35% or more in the susceptible checks. These lines were also resistant to downy mildew in India.

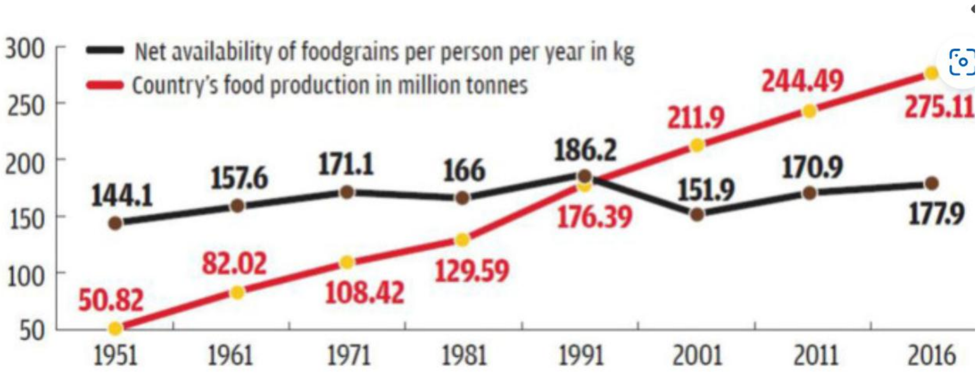
RESULTS:

Area, production and productivity of Pearl millet in India since 2000.

Current breeding approaches followed for developing biofortified cultivars in pearl millet (Adapted from: Govindaraj et al., 2019).


GERMPLASMS
Seed parent Pool
Current breeding approach
Restorer Pool
OPVs
High-Fe A-lines
X
High-Fe R-lines
High-Fe OPVs
High-Fe B×B F₁s
High-Fe testcross
High-Fe R×R F₁s
Intra-popln. Improvement
Proposed breeding approach
Partners Testing
IHTs to AHT
F6/7
F6/7
Proposed breeding approach
High-Fe versions, Multi-site testing
On-Farm trial
High-Fe A/B line
High-Fe R line
On-Farm trial
Release / cultivation

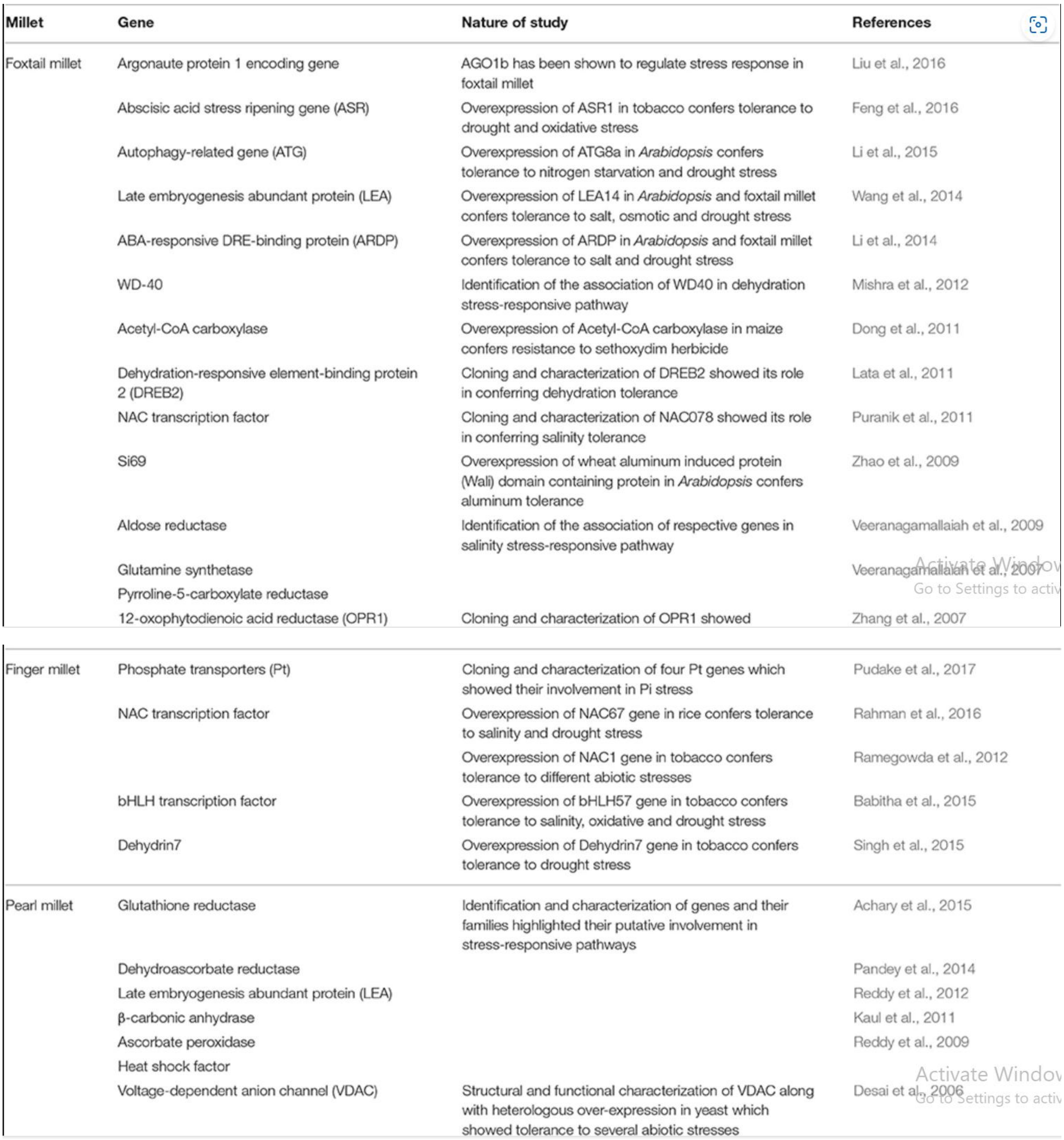

Pearl millet productivity over years
Productivity (kg/ha)
0
200
400
600
800
1000
1200
1400
305
306
346
427
422
458
501
539
620
733
856
932
1192
1290
1951-55
1956-61
1961-65
1966-70
1971-75
1976-80
1981-85
1986-90
1991-95
996-2000
2001-05
2006-10
2011-15
2016-20


Net availability of foodgrains per person per year in kg
Country's food production in million tonnes
300
250
200
150
100
50
144.1
157.6
171.1
166
186.2
151.9
170.9
177.9
50.82
82.02
108.42
129.59
176.39
211.9
244.49
275.11
1951
1961
1971
1981
1991
2001
2011
2016

DISCUSSION:

Recently, GAB has gained momentum in the arena of crop improvement as it implicates the next-generation genome analysis platforms and conventional as well as molecular breeding strategies for crop improvement. The scope for development of genomic resources for GAB in foxtail millet is relatively higher than other millets owing to the availability of genome sequence information. Moreover, the advent of next-generation genome sequencing (NGS) has enabled the development of high-throughput molecular markers in other millet crops. In finger millet, the transcriptome of high and low seed calcium genotypes was sequenced, and thousands of simple sequence repeat (SSR) containing microsatellite markers were identified (Kumar et al., 2015). Similarly, novel SSR markers were developed through sequencing the genome of allotetraploid tef (Eragrostis tef) (Cannarozzi et al., 2014). This information on the genome as well as genome-wide markers coupled high-throughput approaches including genotyping-by-sequencing (GBS) and genome-wide association mapping studies (GWAS) potentiate the discovery of novel genes/alleles or QTLs responsible for nutritional traits (Varshney et al., 2014; Muthamilarasan et al., 2016). Considering the importance of whole-genome sequence information, genome sequencing of few other millets including pearl millet and finger millet is underway.

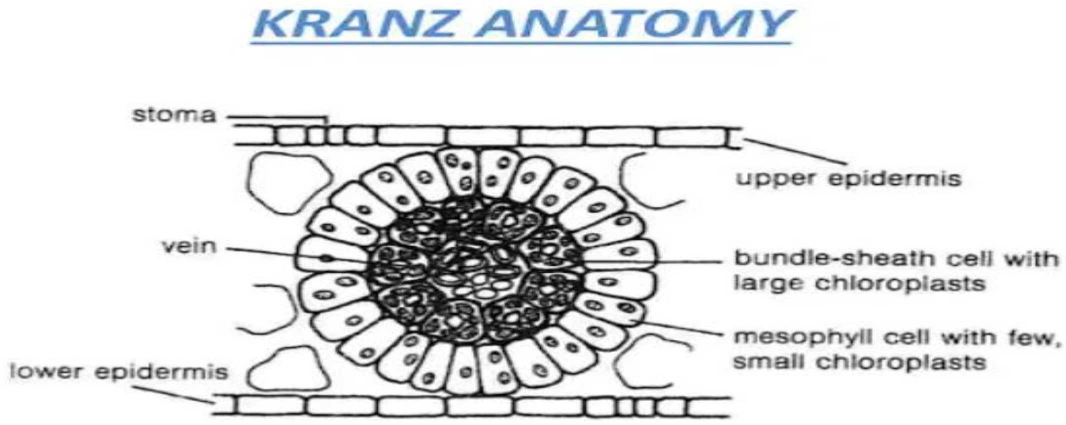
Below Table Summary of genes identified and characterized in different millets for their roles in conferring tolerance to abiotic stresses.

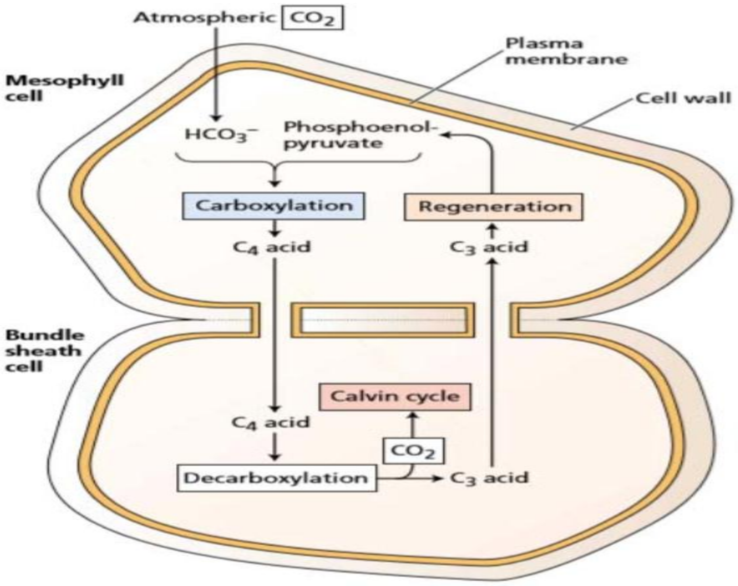


Millet	Gene	Nature of study	References
Foxtail millet	Argonaute protein 1 encoding gene	AGO1b has been shown to regulate stress response in foxtail millet	Liu et al., 2016
	Abscisic acid stress ripening gene (ASR)	Overexpression of ASR1 in tobacco confers tolerance to drought and oxidative stress	Feng et al., 2016
	Autophagy-related gene (ATG)	Overexpression of ATG8a in *Arabidopsis* confers tolerance to nitrogen starvation and drought stress	Li et al., 2015
	Late embryogenesis abundant protein (LEA)	Overexpression of LEA14 in *Arabidopsis* and foxtail millet confers tolerance to salt, osmotic and drought stress	Wang et al., 2014
	ABA-responsive DRE-binding protein (ARDP)	Overexpression of ARDP in *Arabidopsis* and foxtail millet confers tolerance to salt and drought stress	Li et al., 2014
	WD-40	Identification of the association of WD40 in dehydration stress-responsive pathway	Mishra et al., 2012
	Acetyl-CoA carboxylase	Overexpression of Acetyl-CoA carboxylase in maize confers resistance to sethoxydim herbicide	Dong et al., 2011
	Dehydration-responsive element-binding protein 2 (DREB2)	Cloning and characterization of DREB2 showed its role in conferring dehydration tolerance	Lata et al., 2011
	NAC transcription factor	Cloning and characterization of NAC078 showed its role in conferring salinity tolerance	Puranik et al., 2011
	Si69	Overexpression of wheat aluminum induced protein (Wali) domain containing protein in *Arabidopsis* confers aluminum tolerance	Zhao et al., 2009
	Aldose reductase	Identification of the association of respective genes in salinity stress-responsive pathway	Veeranagamallaiah et al., 2009
	Glutamine synthetase		Veeranagamallaiah et al., 2007
	Pyrroline-5-carboxylate reductase		
	12-oxophytodienoic acid reductase (OPR1)	Cloning and characterization of OPR1 showed	Zhang et al., 2007
Finger millet	Phosphate transporters (Pt)	Cloning and characterization of four Pt genes which showed their involvement in Pi stress	Pudake et al., 2017
	NAC transcription factor	Overexpression of NAC67 gene in rice confers tolerance to salinity and drought stress	Rahman et al., 2016
		Overexpression of NAC1 gene in tobacco confers tolerance to different abiotic stresses	Ramegowda et al., 2012
	bHLH transcription factor	Overexpression of bHLH57 gene in tobacco confers tolerance to salinity, oxidative and drought stress	Babitha et al., 2015
	Dehydrin7	Overexpression of Dehydrin7 gene in tobacco confers tolerance to drought stress	Singh et al., 2015
Pearl millet	Glutathione reductase	Identification and characterization of genes and their families highlighted their putative involvement in stress-responsive pathways	Achary et al., 2015
	Dehydroascorbate reductase		Pandey et al., 2014
	Late embryogenesis abundant protein (LEA)		Reddy et al., 2012
	β-carbonic anhydrase		Kaul et al., 2011
	Ascorbate peroxidase		Reddy et al., 2009
	Heat shock factor		
	Voltage-dependent anion channel (VDAC)	Structural and functional characterization of VDAC along with heterologous over-expression in yeast which showed tolerance to several abiotic stresses	Desai et al., 2006

MILLETS AS THE MODEL FOR STRESS BIOLOGY:

The exceptional tolerance of millets toward diverse abiotic stresses including drought, salinity, light and heat makes them a tractable system to study their stress-responsive traits at the cellular, molecular and physiological levels. Several morpho-physiological and biochemical studies in millets have shown their stress adaptation strategies. For example, Bidinger et al. (2007) have shown that pearl millet adjusts flowering phenology according to the pattern of rainfall. Balsamo et al. (2006) observed an increase in leaf tensile strength in teff during drought, and in little millet, an increase in root length was reported by Ajithkumar and Panneerselvam (2014). Similarly, increase in biochemical activities such as enhanced levels of antioxidants, reactive oxygen species and their scavenging enzymes, enzyme activity of catalase and superoxide, and synthesis of osmolytes and other stress-related proteins has been reported in response to abiotic stresses in foxtail millet (Lata et al., 2011), little millet (Ajithkumar and Panneerselvam, 2014) and teff (Smirnoff and Colombe, 1988). van der Weerd et al. (2001) showed the dynamics of membrane permeability for water in pearl millet in comparison to maize for achieving better water status during osmotic stress. In addition, several novel genes, alleles and QTLs have been identified in millets whose functional characterization has revealed their roles in conferring stress tolerance. Compared to other millets, foxtail millet has been studied extensively, and several genetic and genomic resources have been developed (Muthamilarasan and Prasad, 2015). Whole genome sequencing of foxtail millet and comparison of gene families among 15 sequenced plant genomes showed that 1517 genes were specific only to foxtail millet (Zhang et al., 2012). Among this, 586 genes were annotated as “response to water,” which could be playing significant roles in conferring drought and dehydration stresses, thus facilitating the adaptation of this crop to arid and semi-arid zones. The genes involved in C4 pathway namely, carbonic anhydrase (CAH), malate dehydrogenase (MDH), malic enzyme (ME), phosphoenolpyruvate carboxylase (PEPC), phosphoenolpyruvate carboxylase kinase (PPCK) and pyruvate orthophosphate dikinase (PPDK) were also identified and compared to that of sorghum, maize, rice and Brachypodium. The study showed that foxtail millet has a higher number of MDH (7 genes) and PPDK (3 genes) than other crops. Zhang et al. (2012) have also performed phylogenetic and evolutionary analysis of CAH homologs among all the five grass genomes, which showed that Ft_CA1 was highly expressed in the mesophyll, and this could be a potential candidate for studying C4 pathway in foxtail millet. Despite this progress, studies providing insights into the molecular machinery underlying stress tolerance is largely lacking in millets. In addition, knowledge on the genetic determinants of stress tolerance identified through association mapping and biparental mapping is limited. In this context, extensive phenotypic screening to observe the natural genetic variations in stress tolerance across diverse millet germplasms is greatly needed to fully harness the underlying genetic potential through conventional/molecular breeding approaches and transgenic technologies. This is required to facilitate crop improvements in millets and non-millet crops in the wake of increased desertification and salinity of the farmlands due to climate change.





C4 cycle

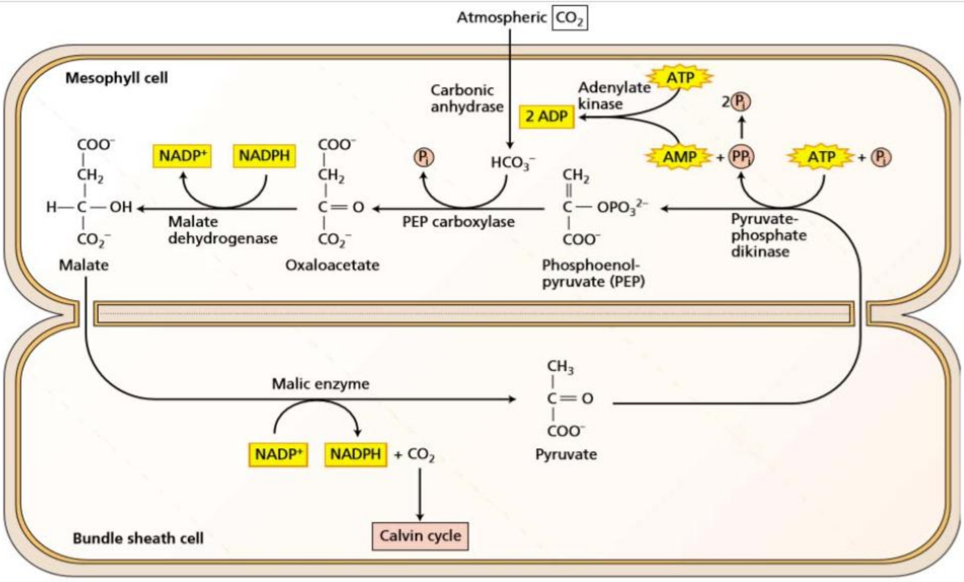


Fig: Explanation of C4 cycle

CONCLUSION:

It is realized that millets hold great promise for food security and nutrition amid ever-increasing agricultural costs, climate change and burgeoning mouths to feed worldwide. They are nutritious, possess additional health benefits, requires significantly fewer input costs for cultivation and are naturally tolerant to most biotic and abiotic stresses. These features accentuate millets as crops of choice for the world population amid growing concerns about climate change. Given the same, there is a growing need to investigate the natural genetic variation across their diverse germplasms to exploit them for crop improvement with regard to many agronomically and nutritionally important traits. With the advent of NGS technologies and high-throughput GWAS platforms, identification of candidate genes/alleles/QTLs regulating such traits is possible at a pace and precision not contemplated before, which in turn would facilitate the development of breeding lines for crop improvement. Moreover, a renewed focus on millets has important implications for the improvement of cereals and bioenergy grasses given their common ancestry from poaceae family and the presence of significant synteny between the genomes.

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