Recent Trends in Breeding of Tropical Grass and Forage Species

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ABSTRACT

Germplasm enrichment in major tropical grasses and their characterization for emerging environmental challenges have been major focussed area in the recent past. Breeding efforts in tropical grasses are still limited to few selected species viz. *Panicum* spp, *Cenchrus* spp, *Pennisetum* spp and *Bracharia* spp and all other grasses use of land races for varietal development through selection have been major source of improvement. The pace of breeding efforts in the tropical grasses have been slowed because of many inherent characteristics viz. apomixis, poor seed set, high photo and thermo sensitivity often creating problem in designing and implementing an effective breeding programme. Identification of sexual lines using the modern tools of biotechnology have given new ways for the improvement in these group of crops. This paper provides overview of the recent development that has taken place in the germplasm collection, utilization and significant achievement made through genomic and biotechnological research.

Keywords: Genetics, Germplasm, Improvement, Tropical grasses, Variety

Introduction

Grasses belong to a wide range of genera and over 600 species are currently used for grazing and livestock feeds. Grasses for tropical environments are primarily from the warm-season tribes Andropogoneae, Paniceae, Chlorideae, and Eragrosteae. Most of the tropical grass species originated in Africa while two important genera, *Paspalum* and *Axonopus*, are native to tropical and subtropical America. Indian sub-continent is one of the world's mega centres of crop origin and crop plant diversity, as it presents a wide spectrum of eco-climate ranging from humid tropical to semi-arid, temperate to alpine. Indian sub-continent has grass diversity for 245 genera and1,256 species. One-third of Indian grasses are considered to have fodder value. Few Examples are *Bothriochloa, Dichanthium, Cynodon, Panicum, Pennisetum, Cenchrus, Lasiurus,* etc. The main centres of genetic diversity are peninsular India (for tropical types) and North-Eastern Region (for sub-tropical types) besides some micro-centres for certain species.

The breeding system in tropical perennial forage grasses is quite different than the cultivated cereals. The temperate grasses represent all three types of mode of reproduction i.e. sexual, asexual and clonal. About 60% of the tropical grasses are apomictic- in which identical true to types plants of mother are produced. The advantage of this system is that hybrid vigour can be fixed if the phenomenon of apomixis is properly understood. Choice of the vigorous plants and percentage of selection intensity has contributed astoundingly to genetic advance. Improvement of forage yield, quality and adaptation has given primacies traditionally by phenotypic breeding. Direct selection of plants from populations has been resulted in the cultivar development which assured 80 to 130 % more productive in leaf, 26 % increase in digestibility. Producing the higher dry matter yield and with nutritious quality both objective might be negatively correlated, but the primary need is to maximum yield of metabolizable energy.

Important tropical grasses

Dry (<600mm rainfall):

Grasses

Cenchrus setigerus, *Cenchrus ciliaris*, *Bothriochloa pertusa*, *Astrebla lappacea*, *Setaria incrassate*, *Andropogon gayanus*, *Digitaria milanjiana*, *Urochloa mosambicensis*

Medium (600-1000 mm rainfall)

Grasses

Dichanthium annualatum, Cenchrus ciliaris, Cynodon dactylon, Bothriochloa pertusa, Bothriochloa insculpta, Pennisetum purpureum, Panicum maximum, Brachiaria humidicola, Panicum antidotale, Paspalum plicatulum, Setaria incrassate, Brachiaria decumbens, Andropogon gayanus, Urochloa mosambicensis, Melinis minutiflora

Wet (>1000 mm rainfall)

Grasses

Cynodon dactylon, Bothriochloa pertusa, Pennisetum purpureum, Panicum maximum, Brachiaria humidicola, Digitaria eriantha subsp. Eriantha, Brachiaria mutica, Paspalum plicatulum, Brachiaria decumbens, Andropogon gayanus, Digitaria milanjiana, Axonopus affinis and A. compressus, Urochloa mosambicensis, Melinis minutiflora

Genetic resources of tropical grass

Tropical grasses collection and conservation

World-wide 1500 genebanks are registered in the WIEWS (World Information and Early Warning System on PGR) database (http://apps3.fao.org/wiews/) and conserve a total of 7.1 million accessions belonging to 53109 species, including major, minor and neglected crop species, trees and wild plants. Out of total germplasm conserved, 651024 accessions belonging to forage crops (FAO 2010).

The number of grass species and total accessions (about 17,000) of selected genera conserved in gene banks of the world show that most accessions are in the *Brachiaria*, *Cenchrus*, *Digitaria*, *Panicum*, *Paspalum* and *Pennisetum* genera. Important genebanks that conserved forage species are CIAT Columbia, ICARDA Syria, ILRI Nairobi, CSIRO-Australia, IGER-UK, USDA-Fort Collins and EMBRAPA-Brazil. ILRI, CIAT and CSIRO are the most important genebanks conserving forage grass germplasm (Table1). The ILRI Gene bank conserves more than 18 thousand accessions of forages from over 1000 species. This is one of the most diverse collections of forage grasses, legumes and fodder tree species held in any gene bank in the world. Out of 18 thousand accessions of forage crops, 1,820 accessions belong to forage grasses germplasm (www.ilri.org). CIAT genebank keeps 23,139 forage crops accessions out of these 668 are of different species of grasses and legumes from 72 countries, that have been collected over the past 30 years (www.ciat.cgiar.org).

Table 1 : Forage grass germplasm conserved in different gene banks

Institute	Number of spp.	Number of acc.
CIAT	105	1880
CSIRO	252	2670
ILRI	139	1820
NBPGR	63	1116

In India National Bureau of Plant Genetic Resources (NBPGR), New Delhi is the nodal organization for exchange, quarantine and other activities like collection, conservation, evaluation and the systematic documentation

of plant genetic resources as National Gene Bank (NGB). The present base collection holdings in NGB are about 0.4 million accessions belonging to 1812 species (http://www.nbpgr.ernet.in/). NBPGR has introduced > 13,000 forage germplasm during last three decades. NBPGR has 56 National Active Germplasm Sites (NAGS). Responsibility of NAGS is crop specific collection, multiplication, evaluation, maintenance and conservation of active collections and their distribution to users at a national level. Indian Grassland and Fodder Research Institute (IGFRI) is the NAGS for forage crops. IGFRI conserved >8500 germplasm accessions of forage crops (cereals, grasses, legumes and trees) including 2815 accessions of tropical grasses (Table 2).

Table 2 : Forage grass germplasm conserved in IGFRI gene bank

Tropical grass	Botanical name	Number of accessions
Buffel grass	*Cenchrus spp*	585
Heteropogon	*Heteropogon spp*	371
Marvel grass	*Dichanthium annulatum*	529
Chrysopogon	*Chrysopogon fulvus*	135
Rhodes grass	*Chloris gayana*	47
Guinea grass	*Panicum maximum*	704
Sehima	*Sehima nervosum*	237
Pennisetum	*Pennisetum spp*	207

Characterization and evaluation

Although there are huge number of germplasm accessions maintained in genebanks, there is no corresponding utilization in the crop improvement programme, indicating that the collections were not being used to their full potential. Thus, a very large gap exists between availability and actual utilization of the materials.

The accessibility of collections depends largely on the information available on them. Accurate passport and characterization data are the first requirements for users of plant genetic resources, particularly plant breeders, have also emphasised the need for improved evaluation of accessions. It is worth emphasising that both characterization and evaluation data provide an effective source of information for genetic diversity studies. The results can be used to help understand patterns of variation in crop species and to identify groups of accessions with high diversity or with shared characteristics.

To enhance the utilization through greater access to information of the germplasm conserved in Indian National Genebank, NBPGR developed PGR Portal which is accessible to researchers, farmers, students and policy makers. Users of PGR portal can search passport, characterization and evaluation data of each conserved accession (www.nbpgr.ernet.in). IGFRI forage germplasm collections have largely been evaluated for their descriptive morphological traits with biomass yield. These were published in the form of grass species specific catalogues viz., Deenanath, Guinea grass, *Cenchrus*, Napier. Descriptors were also developed in *Dichanthium Bothriochloa* Complex. A total 14 novel cytotype/trait specific germplasm lines have been registered at NBPGR for utilization by different researchers (Table 3). Developing a representative core and mini core collections to overcome the size related problems of collections also enhance the utilization of germplasm in breeding programme. Over 60 core collections were identified in a wide range of different crops and wild relatives. In forage crops, core collection has been developed in Burmudagrass, annual medics, cowpea etc.. Further core collections developed by different institutes for specific crop may be merged to develop composite collection.

Table 3 : Grass germplasm lines registered for specific trait at NBPGR, New Delhi

Tropical grass species	Trait	Year	INGR
Pennisetum pedicellatum	Octoploid (2n = 8x = 72)	2006	INGR 06018
Pennisetum squamulatum	New cytotype (2n = 56)	2006	INGR 06017
Panicum maximum	Triploid cytotype (2n=3x=24)	2009	INGR 09039
Panicum maximum	Tetraploidcytotype (2n=4x=32)	2009	INGR 09040
Panicum maximum	Pentaploidcytotype (2n=5x=40)	2009	INGR 09041
Panicum maximum	Hexaploidcytotype (2n=6x=48)	2009	INGR 09042
Panicum maximum	Octoploidcytotype (2n=8x=64)	2009	INGR 09043
Panicum maximum	Nonoploidcytotype (2n=9x=72)	2009	INGR 09044
Cenchrus ciliaris	Sexual plant of *C. ciliaris* (IGFRI-CcSx-08/1)	2011	INGR 11062
Pennisetum	Inter-specific hybrid	2013	INGR13036
Pennisetum	Inter-specific hybrid	2013	INGR13037
Pennisetum	Inter-specific hybrid	2013	INGR13038
Pennisetum	Inter-specific hybrid	2013	INGR13039
Pennisetum	Tri-species hybrid	2013	INGR13040

Breeding methodologies and priorities

Breeding is the key for the future development of superior forages varieties. Selection of plants has involved vigorous nature, and contributed greatly to genetic advance (Busey, 1989). In all important tropical grasses concentrated efforts has been world wide develop varieties for different growing conditions including cut and carry and for pasture and grassland purpose.

i. Selection

Direct selection based on phenotypic traits in large germplasm and identification of superior accessions has given importance and assured 80 to 130 % more productive in leaf, 26 % increase in digestibility (Burton, 1989; Burton *et al.*, 1993). Most cultivars of tropical grasses available commercially are wild ecotypes selected from natural diversity (Hacker & Jank, 1998). In India many wide

Table 4 : Direct utilization of grass biodiversity in varietal development programme

Tropical grass species	Varieties developed
Pennisetum pedicellatum	Bundel-2, Jawahar Pennisetum-12, Pusadeenanath grass, Bundel-1
Panicum maximum	Bundel Guinea-1, Bundel Guinea-2, Punjab Guinea grass-1, Harithasree
Cenchrus ciliaris	Bundel Anjan-1, Bundel Anjan-3 , Marwar Anjan 1, CO-1
Cenchrus setigerus	CAZRI-76, Marwar Dhaman
Sehima nervosum	Bundel Sen Ghas-1
Heteropogon contortus	Bundel Lampa Ghas-1
Chrysopogon fulvus	Bundel Dhawalu Ghas-1

(Source: modified from Singh and Joshi, 2012)

adaptable and farmers preferred varieties in grasses have developed through utilization of natural variability available in germplasm collection (Table 4).

The simplest breeding procedure for improvement of forage species is mass selection, harvesting and bulking seed without progeny evaluation. Along with this several breeding ethos has also been employed in development of varieties and superior cultivars. Resistance to many disease and insect pests is based on additive genes, dominant gene or some degree of dominance.

ii. Hybridization

Biggest bottleneck in recombination breeding in tropical grasses are apomictic reproduction behavior thus the identification and generation of sexual lines in apomictic grasses may prove to be new era of research direction. On availability of appropriate sexual lines the benefits of hybrid vigour can be fixed taking the advantage of apomixis. Hybrid breeding has been utilized in some species viz. guinea grass, buffel grass and Bracharia where either obligate or facultative sexual lines are available. In *P. maximum* increased foliage percentage, seed production, rapid re-growth (Jank *et al*., 2001, 2004; Muir & Jank, 2004; Resende *et al*., 2004) has been observed in F_1 compared to parents. Many wide adaptable varieties in guinea grass (PGG 9, PGG 14, PGG 19, PGG 518 and CO 2) have been developed and released from PAU, Ludiana and TNAU, Coimbatore. The high forage quality and determined flowering cycle of *B. ruziziensis*, the yield and resistance to spittlebug of *B. brizantha* and the vigour and adaptation to acid, infertile soils of *B. decumbens* (Valle *et al*., 2000; Peters & Lascano, 2003) have been observed. A generalized scheme breeding for apomictic grasses (Hanna 1999) give in fig 1.

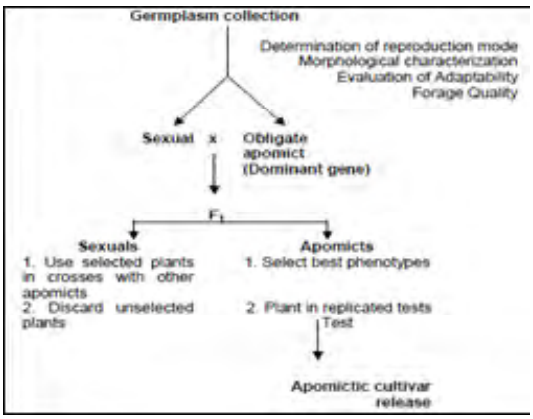

Fig 1 : General scheme for hybridization in apomictic grasses

iii. Interspecific and polyploidy breeding

Crossing between sexual and apomictic plants of *B. ruziziensis* directly or by chromosomal doubling with colchicine to make cross compatible and to induce variability along with quality traits has been attempted in grasses (Lutts *et al*. 1994). The ploidy level resulted in the discovery of a sexual accession, which was artificially doubled to make crosses with tetraploid accessions feasible (Pinheiro et al. 2000). High seed producing cultivars of *P. purpureum* obtained by crossing *P. purpureum* and *P. glaucum* (L.). The progenies from this cross are triploid and sterile, but once doubled by colchicine become hexaploid and fertile (Pereira and Lédo 2008). Ploidy series of grasses has been developed at ICAR-IGFRI, Jhansi, India made to decode the genome complexity a native stage of most of the grass species. ICAR-IGFRI has developed world largest ploidy series of *Panicum maximum* to under the ploidy regulated phenomenon at genetic level (Table 3). Better fodder plant types in pearl millet generated through interspecific hybridization *P. glaucum* x *P. squamulatum*; *P. glaucum* x *P. orientale* at IGFRI, Jhansi. The resultant plant

have shown higher biomass, better adaptability, better tolerance for moisture deficit and improved forage attributes compared to other tropical grasses (IGFRI, Annual Report 2014-15).

In India and world wide Bajra × Napier hybrids have been recognized as revolution due its wide adaptation, wide biomass yield, better forage attributes, tolerance to abiotic stresses and perennial nature. The interspecific cross between annual *P. glaucum* with perennial *P. purpureum* was used to produce this species. The details of cross is given below:

P. glaucum Diploid (2n = 14) × *P. purpureum* *Tetraploid (2n = 28)*

↓

Triploid (2n = 21) Sterile

Combines high quality and faster growth of bajra with the deep root system and multicient habit of napier grass

Varieties- CO-1,2,3, IGFRI-5,6,10, PBN -83, 233, Suguna, Supriya, Sampoorna

Breeding efforts in the cool season grasses also have focused on the introgression of drought tolerance from the fescues into the ryegrasses (Humphreys and Thomas 1993). The "stay green" gene has successfully been transferred from *F. pratensis* into *L. perenne* amenity types (Thorogood 1996). Crown rust resistance has been transferred from *F. pratensis* to *L. multiflorum* (Oertel and Matzk 1999) were some of the major achievements. Allopolyploid hybrids between important forage grasses (*L. multiflorum* × *Dactilys glomerata*; *F. pratensis* × *D. glomerata*; and *F. rubra* × *L. perenne*), hybrid ryegrass from crosses between perennial× Italian ryegrass, and Festulolium from crosses between *Lolium* spp. × *Festuca* spp. has also been attempted to generate variability and introgression of the desirable traits.

Problems in forage crop breeding

Breeding in forage crops involves the same principles of breeding for self or cross pollinated crop in sexually propagated crops. Dealing breeding with apomictic grasses should be taken into consideration while choosing the breeding methods. Some grasses are difficult to propagate as individual lines from seed, creating problem to maintain their identity due to cross pollination nature. Species with small floral parts, making tough in artificial hybridization and pollination control. Diversity in pollination of the different species, irregularities in fertilization, seed setting, and perennial habit of crops in important forage species etc. limiting the extent to which they may be self-pollinated / cross pollinated. This restrict the attempt for recombination breeding in the apomixis species causing problems in crossing and obtaining gene recombination. Similarly, low viability and seed setting in forages species is another important points that restrict the variability generated through seeds. Breeding lines may perform differently with different environment and systems of grazing management. Along with, taking log years to evaluate the perennials grasses for persistence and productiveness. 70% of the species in the grass family and 23% of the species in the legume family are polyploids causing genome complexity (Poehlman, 1987). The primary information on breeding behavior, methods of breeding and evaluation procedure has been developed for many forage species. The large number of forage species increases the problem of assembling and maintaining adequate germplasm collections of each species.

Understanding apomixis

Understanding the apomixis component and development of marker system for

identification of genomic region govern by apomixis mechanism. In this context, some recent studies to understand the phenomenon of apomixes has been carried out in different species viz. *Paspalum notatum, Cenchrus ciliaris, Panicum maximum, Pennisetum clandestinum, etc.*

In buffel grass, an apomictic species, it has been shown that the apomictic reproductive process is genetically controlled with progenies segregating plants that reproduce apomictically and plants that have normal sexual reproduction. With apomixis, genetic segregation is prevented and superior heterozygous plants may be uniformly propagated, as with vegetative propagation or cloning. Apomictic species, irregular chromosome numbers may be propagated in the progeny, giving rise to aneuploids and polyploids. Failure of apomictic plants to undergo gene recombination and segregation reduces the capability of an apomictic forage species to adapt to changing environments and restricts ecotype formation. However, once a desirable apomictic genotype is produced, it may have greater persistence and vigor than sexual plants of the same species because all of the plants will have the superior genotype. Understanding the apomixis and its utilizing two different aspects: Apomixis component were partitioned into apomixes component to understand genetic and molecular biology and multigene theory. Understanding may involve methods of polyploidy, interspecific hybridization and evaluation. The approach involve is identification of sexual lines and generated sexual lines, segregating population; Identification of marker and molecular mapping of the region for mode of reproduction. The techniques HAPA, generated ploidy series to understand ploidy regulated gene expression in the apomictic crop has given platform to scientist to way forward. The elite technique in utilizing partitioned aposporosis for gene transfer in apomictic crops through (2n + n) hybridization: way to generate variability and generate gene transfer in the apomictic grasses. Recently development involved, identification of sexual lines in apomictic grasses at ICAR-IGFRI, Jhansi, India and other institute of world has given a major breakthrough to understand the apomixis.

Breeding efforts in some important grasses

***Cenchrus*:** *Cenchrus*, a member of the tribe paniceae of the Poaceae family, is also one of the important components of major grass cover of the world. It is distributed throughout the arid and semiarid tropical regions of the world. Considering the diversity and present-day distribution, *Cenchrus* probably originated in the eastern tropical Africa and tropical Asia and is widely naturalized in new world countries. *Cenchrus ciliaris* and two closely related species, *C. setigerus* and *C. pennisetiformis*, are three main species of *Cenchrus* having the potential for forage production across the world. They are well adapted to harsh climatic conditions and flourish vigorously with the availability of soil moisture. *C. ciliaris* is more widespread and more valued as forage grass for dry areas because of its high biomass production and tolerance to low rainfall conditions.

In addition to *C. ciliaris*, other two closely related species, *C. pennisetiformis* and *C. setigerus* (birdwood grass), are also potential grass for pasture plantation, but they are less common than *C. ciliaris*. *C. setigerus* can adapt to more wide range of soil types as compared to *C. ciliaris*; however, it prefers light textured sandy soils. *C. Setigerus* shows more resistance to heat and frost compared to *C. ciliaris*; however, it has lower yield as compared to *C. ciliaris* and *C. pennisetiformis*. This species is

well adapted to arid and semiarid regions with a long dry season and is very effective in stabilizing the moving sand. These agronomic traits if incorporated in *C. ciliaris* can yield rich dividends. Importance of wild species in improvement of *C. ciliaris* can be realized with these two species (*C. pennisetiformis* and *C. setiger*), although more studies are warranted in wild species of the genus *Cenchrus*.

Conventional genetic improvement of *C. ciliaris* is met with reproductive and breeding barriers (i.e., its allopolyploid and apomictic nature), which limits the possibility of selecting and obtaining new promising cultivars. Hence, alternative means to increase genetic variability are desirable. One system of obtaining a novel germplasm is by using non-conventional methods, as induced mutations. In India varieties of *Cenchrus ciliaris* like Bundel Anjan-1, Bundel Anjan-3, Marwar Anjan, Co-1 released through clonal selection. In C. Setigerus varieties like Black Kolukattai, CAZRI-76 and CAZRI-175 released through clonal selection. GFRI have identified an obligate sexual C. ciliaris plant and have developed F2 mapping population segregating for the mode of reproduction between apomictic and sexual plants. DNA-based molecular markers (AFLPs and SCARs) linked to apomixis in C. ciliaris were developed using F2 mapping population and selected obligate apomictic plants of F2 population are under testing in station trial.

***Panicum*:** Description of over 460 species of grasses previously classified under *Panicum* genera are available in Royal Botanical Garden, Kew "GrassBase" database, which include 68 species of Panicum under revised taxonomic delimitation. *Panicum* species are adapted to tropical, subtropical, and warm temperate regions throughout the world. Some species are distributed more widely than others. For example, *P. miliaceum* and *P. capillare* of section *Panicum* are found adapted to tropical, subtropical and temperate regions of countries in all the continents, while *P. virgatum* is found primarily in the US, Mexico, and Brazil in addition to other countries of South America, regions of Mesoamerica, and the Caribbean. Three species, *P. coloratum, P. dichotomiflorum,* and *P. repens*, of section Dichotomiflora are distributed in tropical, subtropical, and temperate environments in countries in North America, South America, Africa, Europe, Asia, and Australasia. Interestingly, the adaptation of large number of *Panicum* species is restricted to countries in the western hemisphere; US, Mexico, the Caribbean, Mesoamericana, Brazil, and other countries in South America. Brazil and its neighboring regions possess diverse species of *Panicum*.

Panicum maximum Jacq. (guinea grass) is a very diverse, seed-producing species with about a dozen botanical varieties. It is native to fertile soils of Africa. Guinea grass is widely distributed in the tropics and subtropics with annual rainfall of about 900 mm or more. Guinea grass can survive long droughts and grows well when soil pH is above 5.0, even on soils high in Al and Mn. Guinea grass can be used for "cut and carry" feed and most cultivars can also be grazed successfully, if not overstocked. It is better adapted to fertile, non-waterlogged conditions. In India sexual line in *Panicum maximum* has been identified and obligate apomictic varieties like PGG 9, PGG 19, PGG 14, PGG 518 and CO 2 was developed by using sexual line. Varieties Haritha and Marathakam were developed through mutation breeding.

***Pennisetum*:** The genus *Pennisetum* belongs to the family Poaceae, group Paniceae of the subfamily Panicoideae and is closely related to the genera *Cenchrus* and *Setaria*. It includes approximately 140 species distributed in tropical and subtropical regions. The primary

gene pool consists of the domesticated form (*P. glaucum* ssp. *glaucum*), the wild annual and weedy forms (*P. glaucum* ssp. monodii represented by two ecotypes: *P. violaceum* and *P. mollissimum*). These wild forms cross easily with the cultivated form to produce viable seeds and fertile hybrids. The secondary gene pool includes a perennial fodder wild relative to *P. glaucum*, *P. purpureum*, named as Elephant or Napier grass. Recently, *P. squamulatum* was included in the secondary gene pool. These two species are easily crossable with pearl millet, but the hybrids are highly sterile. The tertiary gene pool includes true biological species compared to the primary and secondary gene pool species. Indeed, strong reproductive barriers impede natural gene flow and occurrence of hybrids between the members of the tertiary gene pool and the forms belonging to primary and secondary gene pools.

Pennisetum pedicellatum is distributed in tropical Africa, south Africa, Asia (India, Malaysia, Philippines, Thailand), Australia, Fiji, United States. Its habitat is drier sites, savannahs and woodland margins, a weed in croplands, grasslands, waste places. Varieties like Bundel-1, Bundel-2, Pusa Deenanath Grass and Jahawar Pennisetum-12 developed through selection. Variety COD-1 developed through gamma radiation (30 KR) mutation of Dinanath Pusa 3.

Pennisetum purpureum Schumach (elephant grass, napier grass) is a robust African grass that has been introduced to all tropical areas of the world. This grass probably has been the most important grass in small farm "cut-and-carry" management systems primarily for dairy cattle. Persistence is good under this system if annual rainfall is about 1000 mm or more (without a long dry season). This grass is difficult to manage under grazing. Napier grass is usually planted vegetatively because of low or no seed production. Because of its deep root system, grass vigour can be markedly reduced under prolonged waterlogging. Napier grass grows vigorously in the subtropics and tropics in high fertility soils. The quality of napier grass, regardless of fertilizer input, depends upon the leaf-to-stem ratio, which decreases as the regrowth interval increases. It is not uncommon to have 12 to 20% CP in leaves and a digestibility up to 70%, but digestibility of stems is low. A variety Pusa Giant Napier was developed by IARI.

NB hybrid is an inter-specific hybrid between bajra and napier grass and combines high quality and faster growth of bajra with the deep root system and multicut habit of napier grass. It is widely distributed in sub-tropical regions of Asia, Africa, Southern Europe and America. The hybrid once planted supplies fodder continuously and regularly for a period of three years. It grows fast and produces high herbage but the stems are hard and the plants less persistent. In India different institutions like IGFRI, TNAU, PAU etc developed many varieties of NB hybrid.

Genomic research in forage crops

New approaches based on biotechnology are becoming more accessible; including functional genomics leading to marker assisted introgression and selection. Tropical grasses are genetically diverse in comparison to other crops due to a polyploidy and apomictic nature and high opportunity for hybridisation between related species and the absence of genetic bottlenecks caused by domestication. Conservation of this biodiversity across a range of geographical and ecological niches provides a rich resource for allele mining to facilitate response to future challenges, such as changes in climate and land use. The genomic information on tropical grasses has been extensively generated in last few years. Trait-based forward genetic procedures such as

mapping and expression profiling have successfully provided new candidate genes or genome regions affecting forage quality. Respective information can easily be transferred across related forage species. Since several genes in major biochemical pathways related to forage traits have been isolated, gene-based reverse genetic approaches (transformation, association studies) are promising. Functional genomics will provide new candidate genes at high speed for several traits due to better understanding of their biochemical role. Genes of interest can, in principle, be identified for any forage crop by exploiting information based on sequence homology or conserved map position.

Breeding of tropical forages involves mainly evaluation and selection of natural ecotypes by exploiting the variability existing in the genetic resources. Genomics and biotechnology have become valuable tools in forage crop breeding approaches as they offer simple and robust means of assaying variation. Simple Sequence Repeats (SSR) based markers have demonstrated their applicability in assessing the genotypic variation and are effective for exploring genetic diversity and analyzing genetic value in selected candidates derived from intraspecific crosses and the performance of their hybrid progenies (Varshney et al. 2005, Ebina et al. 2007). In guinea grass, SSR markers developed using genomic libraries were able to estimate genetic relationships and differentiate inter specific hybrids showing their potential utility for genetic studies on population structure and molecular breeding in this species (Sousa et al, 2010; Chandra and Tiwari, 2010).

Grasses reproduce by apomixis, in which plants identical to mother plant are produced thereby maintaining genetic uniformity. Furthermore, the polyploidy of most apomicts hinders genetic mapping studies and the building up of populations for reverse genetics. However, few genotypes in natural populations exhibit sexual reproductive mode (Savidan et al 2000) and are important in promoting diversification. Understanding the apomixis phenomena through identification of the genes responsible for controlling this complex trait enables more rapid and efficient breeding by overcoming the reproductive barriers. Apomixis-specific gene-1 (ASG-1) expression was observed in different stages of aposporous embryo sac development, indicating this gene role in apomixis (Chen et al 2005), several transcripts specific to aposporous ovules from the Apospory-Specific Genomic Region (ASGR)-carrier chromosome in Pennisetum hybrids were detected using 454-FLX technology (Zeng et al 2011). High-throughput sequencing (RNA-seq) constitute a comprehensive genomic resource to assess gene expression and patterns of regulation in non-model organisms with large genome sizes and enable the rapid identification of genes that are involved in pathways important forage production. Transcriptome derived microsatellites and single nucleotide polymorphism (SNP) markers developed in guinea grass (Toledo-Silva et al 2013) and *Brachiaria humidicola* (Silva et al 2013) can be utilized for population genetics, linkage mapping and comparative genomics studies in forage grasses.

Conclusions

Exploitation of available variability through conventional plant breeding methods have been most important method for the improvement in tropical grasses. The germplasm exploration, characterization and utilization strategies needs to be strengthen and more emphasis is required to enhance the collection in gene banks. Applying precision

breeding for improvement and development of tropical forage varieties will continue and powered by developments in marker-assisted selection, genome mapping and introgression. Genetic manipulation through hybridization, poly-ploidization, mutation etc. remains a potentially useful approach to generate genetic variability. Along with accessing novel genetic must be identified. Constraints in breeding need to be answered through collaboration among the institutes. The limitation of resources under forage breeding system such availability of donor parents, characterization of forage resources need to be prioritised.

References

Abberton, M.T., T. P. T. Michaelson-Yeates and I. A. H. Marshal. 2000. Molecular marker analysis in white clover. In: Provorov NA, Tichonovich IA and Veronesi F (Eds.). New approaches and techniques in breeding sustainable fodder crops and amenity grasses. All-Russia Institute for Agricultural Microbiology, St Petersburg: 192-195.

Anonymous. 2012. Fifty years research of IGFRI. Indian Grassland and Fodder Research Institute, Jhansi

Burton, G. W. 1989. Registration of 'Tifton 9' Pensacola bahiagrass. *Crop Science*, 29:1326.

Burton, G. W., R. N. Gates and G. M. Hill. 1993. Registration of 'Tifton 85' bermudagrass. *Crop Science*, 33: 644.

Busey, P. 1989. Progress and benefits to humanity from breeding warm-season grasses for turf. In: Sleper DA, Asay KH and Pedersen JF (eds.).Contributions from breeding forage and turf grasses, CSSA Special Publication no. 15, Crop Science Society of America, Wisconsin: 49-70.

Cameron, D. F. 1983. To breed or not to breed. In: McIvor JG and Bray RA (Eds.). Genetic resources of forage plants, CSIRO, Melbourne: 237-337.

Chandra, A. and K. K. Tiwari. 2010. Isolation and characterization of microsatellite markers from guineagrass (Panicum maximum) for genetic diversity estimate and cross-species amplification. *Plant Breed* 129: 120–124.

Chen, L., L. Guan, M. Seo, F. Hoffmann and T. Adachi. 2005. Developmental expression of ASG-1 during gametogenesis in apomictic guinea grass (Panicum maximum). *J Plant Physiol* 162:1141–1148

Donnison I. S., P. Cisneros, T. Montoya, I. P. Armstead, B. J. Thomas, A. M. Thomas, R. N. Jones and P. Morris. 2002. The floral transition in model and forage grasses. *Flowering Newsletter* 32: 42-48.

Ebina, M., K. Kouki, S. I. Tsuruta, R. Akashi, T. Yamamoto, M. Takara, M. Takahara, M. Inafuku, K. Okumura, H. Nakagawa, and K. Nakajima. 2007: Genetic relationship estimation in guineagrass (*Panicum maximum* Jacq.) assessed on the basis of simple sequence repeat markers. *Japan Soc. Grassl. Sci.* 53: 155-164.

FAO, 2010. The Second Report on The State of the World's Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, Rome. Available online (accessed 29 September 2011): www.fao.org/docrep/013/i1500e/i1500e.pdf.

Hacker, J. B. and L. Jank. 1998. Breeding tropical and subtropical forage plants. In: Cherney JH and Cherney DJR (Eds.). Grass for dairy cattle, CABI Wallingford: 49-71.

Humphreys M. W. and H. Thomas. 1993. Improved drought resistance in introgression lines from *Lolium multiflorum* x *Festuca arundinacea* hybrids. *Plant Breed* 111:155–161.

Jank, L., C. B. Do Valle, J. De Carvalho and S. Calixto. 2001. Evaluation of guinea grass (*Panicum maximum*Jacq.) hybrids in Brazil. In: *Proceedings of the XIX International Grassland Congress*, Piracicaba, Brazil: 498-499.

Jank, L., R. M. S. Resende, S. Calixto, M. M. Gontijo Neto, V. A. Laura, M. C. M. Macedo and C. B. Do Valle. 2004. Preliminary performance of *Panicum maximum* accessions and hybrids in Brazil. In: In: *Proceedings of the XX International*

Grassland Congress, Dublin

Muir, J. and L. Jank. 2004. Guinea grass. In: Sollenberger LE, Moser L and Burson B (eds.) Warm-season (C4) grasses, *Agronomy monograph*, ASA-CSSA-SSSA, Madison, 45:589-621.

Oertel, C. and F. Matzk. 1999. Introgression of crown rust resistance from *Festuca* spp. into *Lolium multiflorum*. *Plant Breed*. 118:491-496.

Peters, M. and C. E. Lascano. 2003. Forage technology adoption: linking on-station research with participatory methods. *Tropical Grasslands* 37: 197-203.

Poehlman, J. M. 1987. Breeding Field Crops. 3rd Edi.Springer Science Business Media, LLC

Resende, R. M. S., L. Jank, C. B. Do Valle and A. L. V. Bonato. 2004. Biometrical analysis and selection of tetraploid progenies of *Panicum maximum* using mixed model method. *Pesquisa Agropecuária Brasileira* 39: 335-341.

Savidan, Y. 2000. Apomixis: genetics and breeding. In: Janick J, editor. Plant breeding reviews. Oxford: John Wiley & Sons, Vol. 18: 13–86

Silva, P. I. T., A. M. Martins, E. G. Gouvea, M. Pessoa-Filho and M. E. Ferreira. 2013. Development and validation of microsatellite markers for *Brachiaria ruziziensis* obtained by partial genome assembly of Illumina single-end reads. *BMC Genomics* 14: 17

Singh, T. and D. C. Joshi. 2012. Plant genetic resources of dual purpose forage crops. Compendium of lectures Model training course on Dual purpose fodder crops and trees for nutritional and food security. 19-26 Nov. 2012. pp 10-15.

Sousa, A. C. B., L. Jungmann, T. Campos, D. A. Sforça, L. R. Boaventura, *et al.* 2011. Development of microsatellite markers in Guineagrass (Panicum maximum Jacq.) and their transferability to other tropical forage grass species. *Plant Breed* 130: 104–108

Thorogood, D. 1996. Varietal colour of *Lolium perenne* L. turfgrass and its interaction with environmental conditions. *Plant Varieties and Seed* 9: 15–20.

Toledo-Silva, G., C. B. Cardoso-Silva, L. Jank and A. P. Souza. 2013. De Novo Transcriptome Assembly for the Tropical Grass *Panicum maximum* Jacq. *PLoS ONE* 8(7): e70781.

Varshney, R. K., A. Graner, M. E. Sorrells M. E. 2005. Genic microsatellite markers in plants: features and applications. *Trends Biotechnol*. 23(1):48–55.

Zeng, Y., J. Conner and P. Ozias-Akins. 2011. Identification of ovule transcripts from the Apospory-Specific Genomic Region (ASGR)-carrier chromosome. *BMC Genomics* 12(1):206

http://www.ciat.cgiar.org/Paginas/index.aspx

http://www.fao.org/docrep/013/i1500e/i1500e03.pdf

http://www.fao.org/docrep/013/i1500e/i1500e12.pdf

http://www.ilri.org/ForageDiversity

http://www.nbpgr.ernet.in/