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Genetic improvement of dominant tropical Indian range grasses

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Abstract

Grassland and rangeland ecosystems play a major role in livestock productivity, livelihood and rural economics in India. These grasslands are under heavy grazing pressures and have deteriorated to a large extent and needs rejuvenation. India holds rich diversity of native grasses. Various problems encountered especially in rangeland grasses genetic improvement with multiple objectives including breeding for yield, quality, anti-nutritional factors, abiotic stress etc. have been elaborated. Problems of polyploidy and apomictic breeding nature of most of the perennial grasses of high forage value were also presented with possible advancement through biotechnological approach, search for sexual lines etc. The recent advances in apomixis have offered unlimited potential in developing superior varieties where heterosis and heterozygosity can be fixed leading to next generation revolution. The article provides the advances made in a few selected important grasses of arid and semi-arid regions including a list of cultivars of the grass varieties released in India.

Keywords: Apomixis, Biotechnological approach, Genetic improvement, Range grasses

Introduction

The world grasslands and rangeland ecosystems comprising 26% of earth's surface or 70% of the world agricultural area (Zhaoli, 2004) contribute to the livelihoods of more than 800 million people, of which 100 million is in arid zone only. Of these total grasslands, 45% is in arid and semiarid grassland ecosystems (Huntsinger and Hopkinson, 1996; Reid *et al*., 2008, Branson *et al.,* 1981; Malaviya *et al.,* 2018). More than one third of the world poorest population lives in grasslands (Nalule, 2010). However, it is decreasing fast in many tropical countries, India being the worst hit, owing to several socio-political changes as well as climate change.

Animal products are an integral and important component of the food supply chain across the globe. With increasing awareness about health and increasing purchasing power and urbanisation, the demand of dairy products and meat is gradually increasing. Livestock and grazing based livestock husbandry have important role to play in increasing demand in near and distant future.

India possesses unique integration of agriculture and animal industry in diversified rich cultural environment. Greater part of rural economy in the country relies upon mixed farming system and the grazing-based livestock husbandry plays an important role in the rural economy. Nearly 30 pastoral communities in hilly or arid/semi-arid regions in northern and western parts of India, depend on grazing-based livestock production. Nomadic pastoralism, a traditional form of human-livestock-grassland interaction, is still predominant in the dry lands of western India, the Deccan Plateau, and in the mountainous reaches of the Himalayas (Roy and Singh, 2013).

Most of the rangeland and grassland resources in India are natural and are fast degrading due to overgrazing and conversion to other purposes. These grasslands in addition to being major source of forage for the livestock are also habitat to a large variety of wild animals and birds. Approximately, 12.15 million ha of land in the country is classified as permanent pastures; however animals graze on about 40% of the land area. Temperate region has up to 70% area under pasture as compared to quite less area in tropical region.

Members of grass family Poaceae (Gramineae), the most prominent taxa in the grasslands, are most useful plant family and base to evolving civilization as it is said that 'Grasses feed the world'. The cereal grasses, rice, wheat, maize, barley, oats, sorghum, and millet coupled with sugarcane meets more than half of human energy and protein. Forage grasses provide supplementation of human food in form of meat, milk, eggs etc through intermediaries of animal kingdom. Grasses are cosmopolitan from the equator to the arctic circle. Grasses and herbivores evolved about the same time. Hyams (1971) believes that "It is possible to argue that the astounding success of *Homo sapiens* as a species is ultimately due to the power possessed by grass to grow again after being eaten down by animals."

Indian gene centers hold rich diversity of native grasses and legumes which are conserved due to diverse eco-climatic conditions and variety of habitats and niches. These include both cultivated and rangeland species comprising of grasses, trees, browse species and shrubs. There are reports of 263 genera and 1,291 species of Poaceae of which about 21 genera and 139 species are endemic. Most of the forage grasses belong to the tribes Andropogoneae (30%), Paniceae (15%), and Eragrosteae (9%). The main centers of genetic diversity are peninsular India (for tropical types) and North-Eastern Region (for sub-tropical types) besides some micro-centres for certain species spread over the subcontinent. Major forage grass genera with biodiversity include *Bothriochloa, Dichanthium, Cynodon, Panicum, Pennisetum, Cenchrus, Lasiurus, etc*.

Grasses are important constituents of these grasslands. As per survey done during 1954 and 1962, the grass cover of India was classified into a few distinct but overlapping major types (Dabadghao and Shankarnarayan, 1973). This includes *Sehima-Dichanthium* type (spread over whole of Peninsular India including central India Plateau, Aravali ranges and Coastal region), *Dichanthium-Cenchrus-Lasiurus* type (spread over sub-tropical and semi-arid regions of Gujarat, Rajasthan except–Aravali ranges, Western U.P , Delhi, Punjab and Haryana), *Phragmites–Saccharum-Imperata* type [spread over Gangetic plain (U.P., Haryana, Bihar & West Bengal) and Brahamaputra valley in N.E states], Themeda-Arundinella type (spread over entire sub-mountain tract of northern- western part of U.P., Punjab, H.P., J&K and Haryana. Principal species), *Temperate Alpine Type* (spread over The Hindu Kush Himalayan (HKH) region and dominated by *Themeda, Arunidnella, Hamertheria, Heteropogon*) and arid and semi-arid grasslands (spread in Rajasthan and Gujarat and dominated by *Cenchrus, Lasiurus* and *Chloris*). India proudly conserves some ethnic grasslands such as Banni Grasslands (dominated by *Dichanthium-annulatum, Sporobolus helvolus, Chloris barbate, Cenchrus biflorus, Eleusine bianata, Elysecarpus rugosus, Digitarea sanguinalis, Indigofera spp. Cenchrus setigerus, Aristida, Setaria rhachitricho, Eragrostis* and *Cyperus),* Shola grassland of the Western Ghats, Thar Deserts or famous Sewan grasslands, Terai Grasslands and the Kangeyam grassland dominated by *Cenchrus* species.

The Indian grassland ecosystems are under heavy grazing pressures. The semi-arid and arid grasslands are most affected. For example, the carrying capacity of semi-arid grasslands is reported to reduced to 1 Adult Cattle Unit (ACU) per ha (Shankar and Gupta, 1992) and that of arid grasslands it is 0.2-0.5 ACU per ha (Raheja, 1966). After these studies the productivity has further declined. Thus, the present day rangelands/grasslands are no longer providing needed forage for the livestock. Hence, it is right time to rejuvenate these grasslands.

There have been several factors for degradation of theses grasslands including grazing pressure, social factors, policy issues, climate change and dominance of invasive species. Such degradation is leading to serious concern such as low fodder availability, soil erosion, increased water runoff and poor carbon sequestration. Hence, multi-pronged approach is needed for their rejuvenation. However, here we discuss only about addressing the problem through genetic improvement of the important tropical grasses and cultivars of the grass species developed is also listed (Table 1).

Genetic improvement of the tropical grasses– common issues

Domestication of desired plant species have helped in identification of useful plant species and exploited as per human need. Pasture plant breeding in the temperate grasses has significant achievements, whereas it was not so successful in tropical grasses. The valuable tropical grasses are the evolutionary result of the grass/large ruminant herbivore ecosystems, mostly in Africa (Clayton, 1983), and hence these grasses have acquired many attributes such as high growth rate, protected growing points, underground reserves. With their C_4 photosynthesis, they have an inherently higher growth rate than the C_3 legumes. Early researchers focused on the widely recognized species that farmers were actually using and had certain traditional knowledge about their cultivation, flowering, seeding and time of grazing or utilization etc. These valuable forage and pasture plants were already adopted by farmers and graziers. Clayton (1983) suggests that "it is likely that all useful species are already known to the herdsman".

Table 1. List of varieties of tropical range grasses developed in India

Variety	Year	Area of adoption	Parentage
Guinea grass (*Panicum maximum*)			
RSDGG-1(Dharwad guinea grass -1)	2016	All India	Selection from IC 558122
TNGG-062 (CO (GG) 3)	2014	All India	Clonal selection from Mumbasa
CO-1	1993	Tamil Nadu	Clonal selection from Coimbatore local
CO-2	2000	Tamil Nadu	Derivative of the cross CO-1 x Centenario
PGG-9	1987	Temperate and Northwest zones	Sexual clone (CPI 63450) x Apomictic clone (CPI 60013)
PGG-101	1996	Punjab	Cross between sexual clone – 82059 x obligate clone – 80013
Hamil	1963	Kerala	Introduced material
Makueni	1963	Kerala	Introduced material
Riversdale	1964	Kerala, TN, Andhra Pradesh	Introduced material
Marathakam	1993	Kerala	Mutation breeding on clone F.R. 600
Haritha	1990	Kerala	Mutation breeding on clone F.R. 600
Harithasree	2006	Kerala	Selection from JHGG-96-4
PGG-14	1989	UP, MP, Gujarat, Punjab, Haryana, HP, Maharashtra	Sexual clone (CPI 63450) x Apomictic clone (CPI 60013)
PGG-19	1988	Punjab, Rajasthan, U.P.	CPI – 63450 (Sexual line) x CPI – 60013 (Apomictic line)
PGG-518	1999	Punjab	Sexual clone P-5 x apomictic clone (male) PGG-9
PGG-616	2001	Punjab, Haryana, Rajasthan, western UP and Plains of Uttrakhand	Cross P-5 (sexual clone) x PGG-101 (apomictic clone -male) Selection from Australian material
PGG-1	1982	Punjab, Haryana and Delhi	COI- 59985
Bundel Guinea-1 (JHGG-96-5)	2005	All India	Selection from germplasm TGPM-19 (IG 01-80)
Bundel Guinea-2 (JHGG-04-1)	2009	All India	Selection from exotic germplasm, EC-400533 (IG 97-3)
JHGG 08-1 (Bundel Guinea -4)	2012	All India	Selection
Anjan grass / Buffel grass (*Cenchrus ciliaris*)			
Marwar Anjan (CAZRI-75)	1985	Rajasthan, Punjab, Haryana, UP, Andhra Pradesh, TN, Karnataka	EC-14369 (Exotic material from Australia)
Bundel Anjan-1	1989	All India	IGFRI S-3108 (An indigenous material)
GAAG-1	2012	Gujarat	Selected from Kutchh district
Bikaneri Dhaman (RCCB -2)	2016	Rajasthan	Collections from western Rajasthan
Bundel Anjan -3 (IGFRI-727)	2006	Rajasthan, Punjab, Haryana, UP, Andhra Pradesh, TN, Kerala, Karnataka	Selection from an exotic material EC – 397692 from Tanzania
Phule Madras Anjan-1 (RCC-10-6)		Punjab, Rajasthan, Gujarat, UP, Maharashtra	Selection from local germplasm RCC-06

Genetic improvement of range grasses

Variety	Year	Area of adoption	Parentage
CAZRI Anjan-358(CAZRI 358)	2018	Rajasthan	Germplasm from Gadra Raod area of Barmer
CAZRI Anjan 2178 (CAZRI 2178)	2018	Rajasthan	Selection from western Rajasthan (IC no. 198632)
Gujarat Anand Anjan Grass-2 (GAAG-2)	2011	Gujarat	Selection from Kutchh district
Dhaman grass/ bird wood grass (*Cenchrus setigerus*)			
Marwar Dhaman (CAZRI-76)	1985	Rajasthan, Punjab, Haryana, Western U.P., Andhra Pradesh, TN, Karnataka	Exotic material (EC-17655), from Australia
Dharaf grass/ dhawalu grass (*Chrysopogon fulvus*)			
Bundel Dhawalu Grass	2007	All India	Selection from germplasm IG 2014 B from Western India
Dongari Gawat 2-4-11	1975	Maharashtra	-
GAU D-1	1985	Gujarat, Rajasthan, Maharashtra	Local collection from Dhari, Gujarat.
Dinanath grass (*Pennisetum pedicellatum*)			
Jawahar Pennisetum-12	1974	MP, UP, Chhattisgarh, Maharashtra	Derived from Pusa, Bihar P. No. 12
Pusa Dinanath Grass	1983	All India except hilly tracts	Mass selection from African material
COD-1 (TNDN-1)	1997	Tamil Nadu	Mutant of Dinanath Pusa-3 (Gamma rays-30 kR)
Bundel-1	1987	All India	Selection from germplasm No. IGFRI-43-1from MP
Bundel Dinanath-2	1989	All India	A mutant line from IGFRI 3808-4-2-1
Lampa ghas (*Heteropogon contortus*)			
Bundel Lampa Ghas-1 (IGHC 03-4)	2007	All India	Germplasm (IG 95-284) from Maharajpura, Datia
Sen grass (*Sehima nervosum*)			
Bundel sen Ghas-1 (IGS-9901)	2007	All India	Germplasm IG-2045 from western India
Marvel grass (*Dichanthium annulatum*)			
Marvel -7	1973	Maharashtra	Indigenous collection of Gujarat
Marvel -8	1962	Rajasthan and Gujarat	Clonal selection from Chharodi farm in Gujarat
Marvel-93	1973	Maharashtra	Indigenous collection of Gujarat state
Bundel Marvel 2013-2 (JHD 2013-2)	2018	Punjab and Rajasthan	Selection from local germplasm IG - 1978
Gujarat Marvel Grass-1 (GMG-1)	1980	Rajasthan and Gujarat	Clonal selection from Chharodi farm in Gujarat
Phule Marvel-06-40	2015	Maharashtra	-

Variety	Year	Area of adoption	Parentage
Marvel-09-4	2017	Gujarat, UP, MP, Maharastra	Selection from local Laling area, Dhule district
Phule Govardhan (Marvel 2008-1)	2017	Maharashtra	Clonal selection from germplasm collected from Junnar area
Phule Marvel-1 (Marvel 90-4)	-	Maharashtra, MP,UP, Gujarat	-
Sewan grass (*Lasiurus sindicus*)			
Jaisalmeri Sewan (RLSB-11-50)	2016	Rajasthan	Local collection from Jaiselmer
CAZRI Sewan-1 (CAZRI 30-5)	2018	Rajasthan	Local collection from CAZRI 317
Rhodes grass			
Rhodes-10	1974	Maharashtra	Indigenous collection of Gujarat
Signal grass (*Brachiaria ruziziensis* Jacq.)			
Dharwad *Brachiaira ruziziensis* Selection-1(DBRS-1)	2016	Karnataka	Selection from cv. Kennedy

Source : Pandey and Roy, 2010; Roy *et al.,* 2018; CVRC notifications https://seednet.gov.in

Forage breeding presents certain unique problems and difficulties not normally observed in the cultivated crops. Forage breeding, requires multidisciplinary approach involving several disciplines, *viz*., plant breeding, genetics, agronomy, pathology, nematology, entomology, physiology, biotechnology and animal nutrition *etc.* The grass breeding has its own limitations. Some of the problems include non-synchronous flowering/ anthesis and spikelet maturity, abscission of spikelets after maturity, self incompatibility, small floral parts, making artificial hybridization tedious, poor ovule to seed ratio, seed with low viability, poor seedling vigour and competitive ability, differential response to different systems of grazing management, persistence against grazing and the abiotic stresses, polyploidy coupled with apomictic nature and inadequate germplasm base. Furthermore very limited, almost negligible molecular and genetic studies have been done. The polyploidy nature coupled with interspecific hybrids in nature which survive through vegetative propagation makes even the species boundaries undefined.

The common breeding objectives include: high green fodder and dry matter yield; better quality components-crude protein content, *in-vitro* dry matter digestibility, free from anti-nutritional factors; ease and low cost of establishment; extreme drought tolerance, stand persistence, tolerance to pests, overgrazing and trampling by livestock; fast growth and competing ability. Development of varieties of forage crops depends on collection, evaluation of available array of natural variations from the center of origin and other places. The various biometric parameters like the plant character associations, heritability, genetic advance and cause-effect relationship between various traits; genetic divergence and clustering of genotypes have helped the breeders to develop suitable selection criteria based on agronomic traits. The varieties developed in the tropical grasses in India are mostly from introduction followed by selection for different agro-climatic zones. The fodder yield as well as fodder quality are complex characters and are multi-genic which are quantitatively inherited and significantly influenced by environment. The observed phenotypic variation does not reveal the potential genotypic variability.

Stress tolerance breeding: Abioitc stress tolerance is one of the most desirable traits required in any grass species to be grown in rangelands/grasslands. These conditions include stress for light, moisture, salt and nutrients. Abiotic stress is defined as environmental conditions that reduce growth and yield below optimum levels. Plant responses to abiotic stresses are dynamic and complex involving several major genes (Wang *et al.,* 2003). These genes include three major categories: are involved in signalling cascades and in transcriptional control, function directly in the protection of membranes and proteins, involved in water and ion uptake and transport (Wang *et al.,* 2003).

Abiotic stresses also play an important role in limiting the persistence of the species. Hence, breeding for complex traits through conventional breeding methods appears difficult particularly in situation when most of the tropical grasses have apomictic mode of reproduction. In the present state of knowledge the biggest strength is available germplasm variability created in nature in over a period of time. Variation in the apomictic guinea grass has been reported to be result of sexuality as well reproductive pathways of seed formation owing to partitioning of apomixes components (Kaushal *et al.,* 2008a). If such variability is subjected to evaluation in target environment, germplasm lines can be well identified for tolerance to various levels of stresses. For example germplasm of guinea grass with wide variation (Kaushal *et al.,* 1999; Malaviya, 1996) was evaluated under shade and lines were identified for shade tolerance (Kaushal e*t al.,* 2000) and sustained productivity (Malaviya, 1998).

Nevertheless, in the post-genomic era, comprehensive analyses using three systematic approaches or omics have increased our understanding of the complex molecular regulatory networks associated with stress adaptation and tolerance. It includes ‘transcriptomics’ (for the analysis of expression profiles of RNAs); ‘metabolomics’ (to analyze a large number of metabolites) and ‘proteomics’ (protein and protein modification profiles to understand regulatory networks (Cramer *et al*., 2011). Hence, these new tools can be utilized for target breeding. So far almost nil reports are available on tropical forage grasses using these techniques.

Quality improvement: Genetic improvement of forage crops for desirable quality traits is the most cost-effective mechanism for increasing the nutritional value. Even a small increase in digestibility results in appreciable improvements in animal performance and productivity. Improvement in IVDMD results from desired changes in chemical and morpho-anatomical traits. The positive correlation of quality traits with yield, biotic and abiotic stress tolerance should also be kept in mind while breeding with this objective. It is quite a tedious and nearly impossible job to get a cultivar with all the desired traits. However, accumulation of as much possible desired genes by suitable conventional and modern breeding tools will certainly result in a long lasting variety.

Breeding for anti-nutritional factors: Many types of plant compounds and structures can be detrimental to utilization of forage crops by livestock. These factors reduce palatability, digestibility, intake, ultimately affecting the health and productivity of livestock. These include toxins, estrogenic compounds, alkaloids, saponins, tannins, estrogens, etc. Genetic variability and relatively simple inheritance patterns have been demonstrated for many of these compounds, which are fairly amenable to selection.

Climate resilient grass breeding: Climate change is a complex interaction of several biotic and abiotic components. Agriculture and food security especially in the arid and semi-arid zone are most climate-sensitive economic sectors. Impact can be felt at the level of individual crop, whole farming system or natural resource base like water, soil, temperature etc. Major climate related factors which will affect agricultural productivity include changes in temperature, precipitation, carbon dioxide (CO_2), short-term weather variability. Fourth Assessment Report of the Intergovernmental Panel on Climate Change (IPCC AR4) has concluded warming of earth’s climate system. The temperature increase during 2090-2099 is expected in the range of 1.1 to 6.4°C in relation to 1980-99. The global CO_2 concentration has increased from a pre- industrial value of 280 ppm to 379 ppm in 2005.

With change in various components of climate, due to competition dynamics, the composition of mixed grasslands may be affected. For example, legume species will benefit from increases in CO_2 and in tropical grasslands, the mix between legumes and grasses could be altered. Increased temperatures increases lignification of plant tissues and thus reduces the digestibility and the rates of degradation of plant species. Climate change will have significant effect on Indian agriculture system. In India an increase of 0.4°C in surface air temperature has been observed over the past century. Vulnerability of the Himalayan eco-system is expected to increase on account of climate change. Effects on primary productivity of grassland and rangeland will depend significantly on location, system, and species. In C_4 species, temperature increases up to 30-35 °C may increase productivity of crops, fodders and pastures. In C_3 plants, temperature has a similar effect but increases in CO_2 levels will have a positive impact on the productivity of these crops.

***Biotechnological approach for grass improvement*:** Significant advances in biotechnological tools including transgenic and omics techniques have equipped the scientists to tailor the plants as per need. The improvement of forage crops through biotechnological approach has started in late eighties has made remarkable headway in temperate fodder crops. Biotechnological approach offers opportunities for creation of novel variations in forages, not possible through conventional methods. The various means of creating variation in forage grasses and achievement are somaclonal variation, somatic hybridization, genetic transformation etc. A number of techniques such as embryo rescue, micro-propagation, androgenic haploid plant production and creation of novel variations help the conventional breeding methods (Chandra *et al*., 2010).

In grasses, the success achieved so far has been limited and successful transformation has been reported only in a few perennial grasses, *viz*., *Lolium, Festuca, Agrostis, Dactylis, Paspalum* and *Dichanthium* species. Genetic diversity using molecular markers have been studied in *Dichanthium* (Chandra *et al.,* 2004; 2006). Characterization of germplasm is one of the most important aspects, especially in the context of the changing scenario with regard to IPR regime. It is desirable that all grass varieties are subjected to molecular characterization in order to avoid any dispute regarding use of germplasm in the coming years. The major problem encountered with these molecular markers of the grass species is that most of the cultivars are synthetic populations and variability exists within the population. However, the efforts have been made for characterizing the varieties based on RAPD, RFLP markers and discrimination between the varieties can be based on gene frequencies. Transferability of CISP markers of sugarcane in tropical grasses and *Avena sativa* genotypes, *Chrysopogon fulvus, Sehima nervosum, Heteropogon contortus* and *Dichanthium annulatum* were demonstrated (Chandra *et al*., 2013).

Genetic mapping and gene tagging in tropical forage species has not been attempted much. For single gene control traits, gene tagging is important but in case of grasses most of the desirable agronomic traits are multi-genic and are difficult to tag. Another important area needing attention of biotechnologist is the development of stress tolerance, both biotic and abiotic, in fodder crops and range species through gene pyramiding of identified QTLs. Paudel *et al.* (2018) surveyed the genome and constructed high density linkage map and reported that napier grass (*Cenchrus purpureus*) sequences displayed high synteny to the pearl millet genome along with genomic rearrangements between the two genomes. Yadav *et al.* (2019) conducted AFLP based analysis on apomictic and sexual species/accessions of *Cenchrus* and identified some of the AFLP markers to delineate the apomictically and sexually reproducing *Cenchrus* species. Kumar *et al.* (2017) reported SCAR markers to screen out apomictic plants from sexual ones, but failed to discriminate between facultative and sexual in *Cenchrus*.

Apomixis: Apomixis is a method of reproduction to generate clonal seeds and offers unlimited potential to fix heterozygosity and hybrid vigour (Sailer *et al.,* 2016) and is proposed as a “next generation breeding technology” (Hand and Koltunow, 2014). It comprises of three distinct components, viz., apomeiosis (leading to formation of unreduced egg cell), parthenogenesis (development of embryo without fertilization) and functional endosperm development. Various studies and reviews have given insights into the phenomenon including cyto-embryological and molecular processes in model aposporous (*e.g., Brachiaria, Pennisetum, Cenchrus, Hieracium*, *Paspalum, Poa, etc.)* (Pupilli and Barcaccia, 2012; Schmid *et al.,* 2015; Hojsgaard, 2018). Apomixis is a complex phenomenon, involving numerous major and minor factors, in addition to genotypic effects. Availability of recombination potential between its three components (apomeiosis, parthenogenesis and functional endosperm-development) offers advantages for understanding the origin, evolution, genetics and molecular biology of the phenomenon (Kaushal *et al.,* 2019).

Apomixis has been described as a nightmare for taxonomists mostly because it allows fixation of interspecific or even intergeneric hybrids that would have been eliminated if they were to have sexual reproduction because of their sterility (Savidan, 2001). Information on inheritance models, genetic recombination potentials, molecular markers and molecular mapping studies in gametophytic apomicts have been compiled in recent reviews (Hand and Koltunow, 2014; Brukhin, 2017; León-Martínez and Vielle-Calzada, 2019), which indicate that dominance, polyploidy, hybrid origin and suppressed recombination are common features related to apomixis. Apospory Specific Genomic Region (ASGR) in *Pennisetum* spp. and *Cenchrus ciliaris* (Akiyama *et al.,* 2005; Conner *et al.,* 2008), and Apospory (Apo) locus in *Panicum maximum* (Ebina *et al.,* 2005; Takahara *et al.,* 2014) have been reported. A few reports are available informing mutagenesis in natural apomictic plants converted them to sexual (Takahara *et al.,* 2014; 2016), or vice-versa single mutation converting a sexual plant to apomictic (Chen *et al.,* 2018; Gaafer *et al.,* 2018). Sahu *et al.* (2012) worked out transcriptome analysis of differentially expressed genes in interspecific hybrids of *Pennisetum* during embryo sac development.

In grass breeding, identification of genes controlling apomixis is an area that can pay good dividends. Identification and cloning of these genes can well be patented and can also be used in transferring in other cross pollinated crops for fixing heterosis and thus save on the cost on account of producing hybrid seeds every year. Identification of sexual lines in grasses is another aspect which can boost breeding efforts. There is need to develop reliable molecular techniques for screening of the grass species for the presence of sexuality as it would accelerate the breeding process. In the past, the identification of sexual lines has led to significant contributions in genetic improvement of various grasses such as *Panicum maximum* (Combes, 1975; Savidan, 1980) *Cenchrus ciliaris* (Taliaferrow and Bashaw, 1966). The plants with better agronomic traits and apomixis can be selected and advanced for developing better varieties.

Variability has been successfully generated through addition of genomes utilizing BIII hybridization in otherwise apomictic species, such as *Brachiaria decumbens, Panicum maximum, Poa pratensis, E. curvula, C. ciliaris, Pennisetum orientale etc* (Kaushal *et al.* 2015a; 2015b; 2019).

HAPA breeding: A recent concept of partitioning of apomixis components in *Panicum maximum* (Kaushal *et al.,* 2008a) and its further utilization in generating a ploidy series has opened up possibilities of introgressing genes into the otherwise apomictic grasses. In this process, plants expressing any single component of apomixis *i.e.* apomeiosis, parthenogenesis and endosperm development are identified. The plants expressing apomeiosis are used to develop BIII plants *i.e.* 2n+n whereas plant expressing parthenogenesis is used for M1 plant generation i.e. haploid of the mother plant. Thus, introgressing of genes can be achieved in BIII plant development and effect of half dose of chromosome can be seen in M1 plants.

Few tropical genera and species having forage potential with specific reference to India

Panicum

Panicum (tribe Paniceae; sub family Panicoideae) is one of the largest genera of Poaceae and comprises about 500 species (Hunt *et al.,* 2014). The genus shows a wide range of variation, Brown (1977), in a study based on anatomical and physiological data, postulated that a C_3 *Panicum* could be the ancestor of all remaining Paniceae. Clayton and Renvoize (1986), placed *Panicum* as the core genus of the tribe, from which all other genera were derived. The lack of an obvious synapomorphy, the broad range of morphological and physiological variation, and the suggestion of being a group, from which all others are derived, indicate the likely para- or polyphyletic nature of Panicum (Aliscioni *et al.,* 2003).

Basic chromosome numbers within *Panicum* is reported to vary in multiples of 8, 9, 10, 11, and 15 in a review by Aliscioni *et al.* (2003). However, the most common basic chromosome numbers are 9 and 10. The number 2n=32 appears to have been derived through the multiplication of a basic number of x=9 chromosomes, followed by the loss of 4 chromosomes during the course of evolution (Jauhar and Joshi 1969). The diploid number 2n=18 was encountered in *P. capillare*, *P. laevifolium*, *P. antidotale* and *P. coloratum* with 3B-chromosomes recorded in the later species. The tetraploid chromosome number 2n=36 was found in *P. miliaceum, P. miliare, P. coloratum* and ***P.*** *virgatum.* The hexaploid number 2n=54 was recorded in *P. bulbosum, P. dichotomiflorum* and *P. esculentum*. *Panicurn maximum* Jacq. constitutes a complex, heterogeneous assemblage (Jauhar and Joshi, 1966) comprising several forms with chromosome numbers as 2n=18, 36, 32, 44 and 48 (Carnahan and Hill, 1961; Jain *et al.,* 2003) which are poorly understood cytologically and phylogenetically. *Panicum maximum* agamic complex includes three species: *P. maximum, P. trichocladum,* and *P. infestum* (Combes, 1975).

P. maximum**:** *P. maximum* (Guinea grass) has its origin in East Africa. It is a native of Africa, particularly East Africa, Kenya and Tanzania, where wide genetic diversity is found. Because of its high yield, nutritious fodder and wide adaptability to diverse ecological niches it has been introduced and exploited widely in many countries. *P. maximum* is widely distributed and sexual diploid forms have been identified (Combes and Pemes, 1970), though they are very rare. The other forms are tetraploid and facultative apomicts. Occasionally, penta and hexaploid forms have been detected (Savidan *et al.,* 2001). Successful manipulation of ploidy in guinea grass was reported utilizing Hybridization-supplemented Apomixis-components Partitioning Approach (HAPA) (Kaushal *et al.,* 2008). Recently the largest ploidy series has been developed utilizing partitioning components of apomixis (Kaushal *et al.* 2008a; 2008b; 2008c; 2019). Presence of 2x, 5x and 6x clones in predominantly 4x population in Cote d'ivoire *P. maximum* collection was also reported by Combes (1975).

In first transcriptome profiling of the reproductive tissues in *P. maximum*, transcriptome data was generated from the spikes representing the pre-meiotic development stage of apomictic and sexual genotypes which resulted in identification of 57,647 transcripts in sexual and 49,093 transcripts in apomictic type (Radhakrishna *et al.,* 2018).

Guinea grass is widely adapted perennial grass for utilization as fodder because of its ease of propagation, fast re-growth and high nutritional quality. It is suitable for rangelands receiving 900 to 1500 mm annual rainfall with high biomass production. However, it can survive under less than 400 mm rainfall with production restricted to rainy season only. There are distinct annual as well as perennial types (Malaviya, 1996) which make the crop suitable for irrigated as well as rainfed conditions. The annual types show higher productivity in first year, but do not get eliminated in a season and continue with less productivity. Evaluation of global germplasm collection of guinea grass had shown existence of high degree of variation for yield and yield attributing traits (Malaviya, 1995; 1996; 1998; 2001; Malaviya *et al.,* 2006). Variability based on cytological and isozyme study has also been reported (Jain *et al.,* 2005). Such variability in *P. maximum* has been attributed to a continued contact between sexual and apomictic modes of reproduction through diploid-tetraploid-dihaploid cycles (Savidan and Pernes, 1982).

Guinea grass possesses shade tolerance nature also and is recommended for cultivation as under-storey crop in agroforestry /silvipasture and forestry systems. Genotypic variation in guinea grass for shade tolerance and increase in protein content under shade was observed by Kaushal *et al.* (2000). Morphological adaptation of genotypes under shade includes increase in plant height (Anita and Lakshmi, 2014) and linear increase in leaf area (Durr and Rangel, 2000).

P. maximum, being pre-dominantly C_4 species, possesses structurally a superior photosynthate translocation and water distribution system by developing denser networks of small longitudinal and transverse veins, while keeping a constant density of large longitudinal veins (Ueno *et al.,* 2006). Hence, it has more relevance in climate change scenario because with increasing temperature, reduced availability of water and increased temperature such grasses are expected to perform well. Four different genotypes of Guinea grass were sequenced, and the combined reads were assembled de novo into 38,192 unigenes and annotated; the unigenes are involved in a wide range of biological processes and metabolic pathways, including C4 photosynthesis and lignocellulose generation, which are important for cattle grazing and bioenergy production. A number of potential molecular markers, including 5,035 microsatellites (SSRs) and 346,456 single nucleotide polymorphisms (SNPs) were identified.

The germplasm is highly heterozygous and heterogeneous, suggesting the existence of a large amount of genetic variability within the species. Intervarietal hybridization, utilizing the sexual forms and selection from among the available natural genetic diversity has been the successful breeding strategy in the crop. Important varieties of guinea grass world-wide include Tobiatã, Tanzânia-1, Riversdale, Mombaça, Makueni, Hamil, Centenário, Atlas etc.

***Panicum coloratum*:** Coloured Guinea grass (*Panicum coloratum*) formerly known as *P. makarikariense* (Gooss.) Rensb. is commonly known as klein grass, small buffalo grass or blue panic grass. It's annual or sometimes perennial types are represented by small forms (var. *coloratum*) to large and robust forms (Kabulabula type). The glabrous leaves are generally bluish green with white powdered silica coating. The pyramidal panicle is characterized by seeds of shedding nature for which significant varietal differences have been reported (Young, 1986). It is a drought hardy species and provides a highly palatable pasture (*Cook et al.,* 2005). It was originated in Africa but domesticated in many tropical and subtropical regions of the world. It grows well in salinity up to EC of 16.4 dS/m (Anonymous, 2017). Saponin caused toxic effects have been reported in sheep, goats, cattle and horses grazing on pastures rich in *P. coloratum* component.

The species possesses high levels of seed dormancy that can last from 3-6 months in var. *coloratum* and up to 3 years in var. *makarikariense*. The species is represented in diploid as well as polyploid forms ($2n$=18, 36, 54) alongwith cytotypes (2n=32, 44, and 56). Polyploid forms (2n=36 or 45) represented by var. *makarikariense* are robust (Anonymous, 2017). Tetraploid form *Kabulabula* is erect and bright green in colour. Hexaploid (sometimes 2n=45 also) var. *coloratum* is with fine stems and green or blue-green leaves. Diploid forms are also small with very fine stems and leaves, small panicles.

The species is predominantly cross-pollinated and sexually propagated with some evidence of apomixis in some forms.

Some of the important cultivars of *Panicum coloratum* var. *coloratum include* 'Bushman Mine'; Nakuru, Solai; 'Selection 75', 'Verde'; 'Tamidori', Tayutaka and that of *Panicum coloratum* var. *makariariensis* 'Bambatsi' ; 'Burnett', 'Pollock' and 'Prinshof 11/12'.

***Panicum antidotale* Retz:** *Panicum antidotale* Retz. (blue panic grass) is a tall, coarse, woody perennial grass throughout the Himalaya and the Upper Gangetic Plain. The grass is native to Yemen in Arabian Peninsula; Afghanistan, Iran in Western Asia and India, Pakistan. It plays a role in sand dune stabilization in areas of low rainfall (Saini *et al.,* 2007). It has high tolerance against a multitude of stressful environments. It extensively occurs in arid and semi-arid region where plants usually experience drought stress (Cope, 1982). The species is highly drought tolerant owing to rhizomatous nature. Blue panic has ability to withstand a variety of climatic conditions including drought and salt stress up to 15,000 mg L-1 (Ahmad *et al.,* 2010). It is an ideal fodder grass because of its high protein content (15-18%) (Bokhari *et al.,*1988).

Pennisetum

Pennisetum (bristle grass) tribe Paniceae, subfamily Panicoideae is mainly characterized by its false spike with spikelet on contracted axes surrounded by involucres crowded with slender bristles (Watson and Dallwitz, 1992). It is a large genus divided into five sections: Gymnothrix, Eu-Pennisetum, Pennicillaria, Heterostachya, and Brevivalvula. The genus is represented by 80–140 species (Brunken, 1977; Clayton and Renvoize, 1986) and exhibit diversity in form of annual/perennial, asexual/apomictic. The somatic chromosome number also varies from 2n = 10 to78 (Jauhar, 1981a; 1981b) and ploidy levels from diploid to octoploid. Cultivated species *P. glaucum* is a diploid whereas *P. pedicellatum, P. subangustatum, P.atrichum, P. setosum, P. squamulatum and P. polystachyon* are polyploids (Robert *et al.,* 2011; Kaushal *et al.,* 2008a; 2008b; 2008c). The genus is closely related to the genus *Cenchrus* with unclear boundaries. The genus is represented in almost all continents. Some of the species with high forage value are discussed bolow-

***P. pupureum* Schumach. (Elephant grass):** Elephant grass (syn *P. benthamii* Steud. or *Cenchrus purpureus* (Schumach.) is one of the highest yielding tropical grass. It is a native to eastern and central Africa (Boonman, 1997). It is robust, rhizomatous, tufted and has a vigorous root system. It can grow from sea level up to altitude of 2000 m, however, growth at this altitude is slow (Francis, 2004). It is valuable forage in cut-and-carry systems (FAO, 2015). Elephant grass can be grazed, provided it can be kept at the lush vegetative stage as the livestock tend to feed only the younger leaves (FAO, 2015). It is an important source of forage for elephants in Africa (Cook *et al.,* 2005) and tropical and subtropical humid grasslands in India. The dwarf cultivars with relatively thin stems, narrow glabrous leaves and high yields identifies as "Merkeron" and "Mott" are leafy and exhibit high feed value (Cook *et al.,* 2005). It is cross compatible with pearl millet (*Pennisetum glaucum*) and the sterile hybrids developed from this cross are one of the most successful perennial forage which is benefited with desirable characteristics of pearl millet such as vigour, drought resistance, disease tolerance, forage quality and aggressiveness, perenniality, palatability and high DM yield from elephant grass (Timbo *et al.,* 2010).

Having origin in sub-Saharan tropical Africa (Clayton *et al.,* 2013), the grass is now introduced as forage into most tropical and subtropical regions worldwide owing to its drought hardy nature. Elephant grass is shy seeder and is propagated mostly through vegetative means. It's a good source of bio-fuel also (Woodart and Sollenberger, 2015). Elephant grass can be processed into high quality silage and may be ensiled alone (FAO, 2015). However, the high moisture when its nutritive value is highest is an obstacle for using it as silage (Manyawu *et al.,* 2003). In general, the grass is considered higher in nutritive value compared to *Brachiaria* sp and *Panicum* at early growth stage (Gomez *et al.,* 2011). Rusdy (2016) reported IVDMD and IVOMD to vary from 35 to 77.4% and attributed low IVDMD to maturity of the plant. With increasing harvest interval, NDF and ADF increases and digestibility decreases (Van Soest, 1994).

***Pennisetum pedicellatum*:** Dinanath grass (*Pennisetum pedicellatum* trin) is a cultivated annual warm season grass. It belongs to section Brevivalvula, tribe Paniceae. It is closely related to *P. atrichum, P. glaucum, P. hordeoides, P. pedicellatum, P. polystachion, P. setosum* (syn. *P. polystachion*) and *P. subangustum*, which together form a polyploid and agamic complex (Schmelzer, 1997). The species is thought to be native to tropical Africa (Schmelzer and Renno, 1997), however, widespread in West to East Africa, Asia, Africa, North America and

Oceania. In India and Nepal it is found on cultivated and pasture lands but it doesn't survives well under shade. It was introduced as a fodder crop to the Andaman Islands, India (Gangwar and Jayan, 1986; Krishna and Kumar, 1996). Two subspecies are accepted, subsp. pedicellatum and subsp. unispiculum. It is found growing in the natural grasslands on poor and marginal soils of Bihar, Odisha, West Bengal, Madhya Pradesh, and Uttar Pradesh. Ease in planting through seeds coupled with high initial growth vigour makes the grass popular. The mature plant can also be used as a nutritive dry fodder.

Regeneration after cutting is very poor, however with early stage harvesting, two harvests are possible. The young leafy plants are succulent, nutritious and palatable forage. It provides forage for longer duration than Jowar or Bajra. It can withstand drought, heat and heavy rains. Forage yield improvement through hybridization in this species is very difficult due to its apomictic nature. However, this species exhibits considerable morphological polymorphism as well as ploidy level differences. The annual form are tertaploid to hexaploid (2n=36, 54) whereas octaploid perennial forms have been reported to be segmental allopolyploid (Zadoo *et al.,* 1997). *P. pedicellatum* has apomictic reproductive behaviour (Chaix and Marchais, 1996). The species is an alternative host of downy mildew (*Sclerospora graminicola*), but shows resistant reaction which can be utilized in pearl millet (*Pennisetum glaucum*) breeding resistance (Singh and Navi, 2000).

P. squamulatum**:** *P. squamulatum* Fresen., a native of Kenya and Tanzania, is a tufted perennial grass with tolerance to biotic and abiotic stresses. Although the apomictic trait has not been introduced into major crops, it has been transferred from *P. squamulatum* into pearl millet (*Pennisetum glaucum*) (Dujardin and Hanna, 1989). Patil *et al.,* (1961) proposed that *P. squamulatum* was an autoallohexaploid species. Sindhe (1976) observed 2 extra chromosomes defined as B chromosomes. Dujardin and Hanna (1984) reported that *P. squamulatum* accession PS24 has 54 chromosomes and is hexaploid. The species was believed to be 2n=9x=54 (Raman *et al*., 1959; Patil *et al*., 1961), however, recent discovery of 2n=56 cytotypes (Roy *et al*., 2003, Goel *et al*. 2003), their hybrids with pearl millet (Kaushal *et al*., 2008a) and molecular cytogenetics studies (Akiyama *et al*., 2006) has suggested the species with 2n=8x=56 genomic status. Goel *et al.* (2003) observed that *P. squamulatum* accession PS26 has 56 chromosomes, and 8 chromosomes had 18S-5.8S-26S rDNA loci. *P. squamulatum* is one of the major plant species in which apomixis has been well studied (Ozias-Akins *et al.,* 2003). The trait has been transferred to a sexual relative, *P. glaucum* (pearl millet), by cross and backcross hybridization between *P. squamulatum* as the paternal and pearl millet as the maternal and recurrent parent (Dujardin and Hanna, 1989).

The hybrids (F_1s and advanced back-cross generations) between pearl millet and *P. squamulatum* (Dujardin and Hanna 1983a; 1983b; 1983c; 1985; Kaushal *et al*., 2007) have been produced in view to transfer apomixes genes in *P. glaucum* and to study inheritance of apomixis. Cytogenetic studies on interspecific hybrids revealed limited affinity of chromosomes of the species with pearl millet. *P. squamulatum* hybrids with pearl millet segregated for mode of reproduction (apomixis/sexuality) and were extensively utilized for characterization of a genomic region controlling apospory (Ozias-Akins *et al*., 1998; 2003; Conner *et al*., 2008; Huo *et al*., 2009).

Dichanthium- Bothriochloa complex

Dichanthium and *Bothriochloa* together with genus *Capillipedium* form an interrelated agamic complex. They are closely related members of the tribe Andropogoneae, of the family Poaceae. They are important constituents of Indian grasslands. Several species and races along with various intermediate introgressed derivatives are widely distributed throughout tropical and sub-tropical parts of the country and isoclimates over the world.

Dichanthium an important perennial range grass genus is one of the important constituents of the two major grass covers of India, *i.e. Dichanthium-Cenchrus-Lasiurus* and *Sehima-Dichanthium* (Dabadghao and Shankarnarayan, 1973). Eight species of the genus are distributed in various agro-ecological zones of India (Arora *et al.,* 1975), however only two species, viz. *D. annulatum* (Forsk.) stapf and *D. caricosum* (*L.*) A. camus, are important as forage because of high biomass production. Out of the eight species, four are endemic to India (Bor, 1960). Another genus *Bothriochloa* is represented by seventeen species, of which seven are endemic, in Indian grasslands (Bor, 1960). *B. pertusa* and *B. intermedia* have good fodder quality and are widespread in different parts of India (Dabadghao and Shankarnarayan, 1973). In *Bothriochloa* species, genetic variability has been reported for most of the forage yield related morphological traits (Andres and Cardero, 1995).

Marvel grass (*D. annulatum*) is indigenous to the Indian and African gene centers. Maximum genetic diversity is observed in India and South Africa (Mehra and Magoon, 1974). It is distributed from tropical Africa to South East Asia, New Guinea and northern Australia. It is common in tropical and subtropical India with rainfall range of 500-900 mm and from altitude up to approx. 1400 m. It can tolerate alkanine soil and is used for soil conservation also. Of the four distinct geographic races reported, the two races *i.e.*, the tropical morphotype in China, Myanmar, Indian sub continent and the Mediterranean morphotype in Morocco, Algeria, Tunisia, Egypt, Jordan, Iraq, Afghanistan are predominant (Mehra, 1966). Different ploidy levels and morphologically distinct types are reported in the *D. annulatum* complex (Mehra, 1961). In India, marvel grass is distributed from the hills to the low rainfall areas in Rajasthan and Gujarat to heavy rainfall areas of western and southern India (Kanodia, 1987).

Marvel grass is an excellent fodder grass liked by all ruminants. In mixed pastures, marvel grass is preferred to all other grasses (Cook *et al.,* 2005). Marvel grass can be grazed in pastures or can be used in cut-and-carry system for hay or silage making if harvested before flowering (FAO, 2010).

The grass is largely apomictic with some forms showing facultative apomictic behaviour. Despite its apomictic nature high level of polymorphism has been reported (Chandra *et al.,* 2003; 2004). Saxena and Chandra (2006) analyzed 30 genotypes of tetraploid *D. annulatum* and found that the accessions belonging to south India were more polymorphic than those of central plateau. The histological analysis indicated that central plateau's lines were better suited for drought stress.

Presence of considerable inherent genetic variability with respect to forage yield potential and its components as well as for forage quality makes the *Dichanthium-Bothriochloa* species adapted to different agro-ecological situations (Skerman and Riveros, 1990; Gupta *et al.,* 1994). Wide variation is reported among *Dichanthium* accessions collected from different agro-ecological zones (Agarwal *et al.,* 1998; Gupta *et al.*, 1996). In *D. annulatum,* high phenotypic and genotypic variations have been reported for the quantitative characters (Yadav *et al.*, 1976), and forage quality traits (Awasthi and Joshi, 1998). In *Dichanthium-Bothriochloa* complex, number of tillers, tiller height and leaf number are the important traits for the fodder yield (Gupta *et al.*, 1996; Awasthi and Joshi, 1998; Andres and Cardero, 1995). Yadav *et al.* (1976) reported high or moderate heritability accompanied with high genetic advance for leaf number, tiller number and fodder yield, indicating that selection for these traits is likely to accumulate more additive genes and these traits may be used as selection criteria. In *D.annulatum* out of the fifteen-character correlations studied at the genotypic level the leaf number, node number and culm girth were correlated significantly and positively with each other. The phenotypic correlation between the tiller number and fodder yield was significant and positive (Yadav *et al.*, 1976). Gore *et al.* (2016) evaluated 20 genotypes and observed wide variability and reported that plant height, number of tillers and leaf area is important for developing high yielding genotype.

In a study of *Bothriochloa sp.* made over eight grassland environments for a range of yield related morphological traits, differences for heritability for most of the traits between populations were recorded (Andres and Cardero, 1995). Broad sense heritability of the traits was low indicating that traits are highly influenced by environmental effects and selection would be ineffective.

In *D. annulatum*, accessions from different parts of the country representing varied agro-ecological situations have shown wide range of diversity for different characters (Agarwal *et al*., 1999). The accessions were classified into eight clusters using the Euclidian non-hierarchical cluster analysis technique. The clustering pattern of the accessions was independent of their geographical distribution, which indicated the presence of sufficient genetic diversity within a particular region. Studies on genetic variability for chemical composition of forage grasses indicates sufficient variability for N, P, Ca, K, Crude protein and Crude fiber content in marvel grass (Awasthi and Joshi, 1998).

Different ploidy levels and morphologically distinct types are reported in *D. annulatum* complex (Mehra, 1961). Fedorov (1974) has reported 2n=20, 40, 60 in *D. annulatum*. The diploids with regular meiotic behavior were observed in the tropical type whereas irregular meiotic behaviour was observed in hexaploids of the south-African type. The tetraploids found all over the Indo-Gangetic plains and central and southern Indian plateau show evidence of introgression from *Bothriochloa*, (Mehra, 1961). *D. annulatum* complex consists of a polyploid series with basic chromosome number as n=10 and frequent occurrence of diploids, tetraploids and hexaploids. In a study on 58 accessions only four were diploid (2n=20) and seven were hexaploids (2n=60) and forty-seven were tetraploids (Celarier *et al.,* 1958). The diploid forms occur in Bengal and Bihar and the tetraploid forms all over the Indo-Gangetic plains and central and southern Indian plateau (Mehra, 1961).

Active introgression was reported between *B. intermedia* and *D. annulatum in* Indo-Gangetic plains (Harlan *et al.,* 1958), and intermediate form have been described as new species i.e. *Bothriochloa grahamii* (Bor, 1960). Similarly, extensive introgression was observed between the Gangetic race of *B. intermedia* and *B. ischaemum* in the foothills of Himachal Pradesh (Harlan, 1963b). Tetraploids forms of *B. ischaemum* (*L.*) Keng, occur in Himachal Pradesh and Jammu & Kashmir (Celarier and Harlan, 1956). Diploids forms of *B. intermedia* complex have been reported from Nilgiris and Western Ghats whereas the tetraploids forms are reported from Indo-gangetic plains (Harlan, 1963a). In *B. pertusa* complex, the diploids and tetraploids are known from India, while tetraploids and hexaploids are reported from Africa (de Wet and Higgins, 1964). In agamic complex, cytological studies indicate that the diploid (2n=20) reproduces sexually whereas; tetraploids are facultative or obligate apomicts (Gupta *et al.,* 1969) and compulsive bivalent pairing in species and their hybrids was controlled by a single dominant gene (Chheda and Harlan, 1962). Analysis of pachytene and somatic chromosomes in *D. annulatum* has shows 10 homomorphic pairs of which only 2 are median and the rest sub-median (Roy *et al.,* 1965). In *Dichanthium* sexuality and apomixis were associated with ploidy level with apomictic line as auto-tetraploid, 2n=4x=40 (Cruz and Reddy, 1971).

D. papillosum and *D. fecumdum* that is isolated geographically but each overlap with *D. annulatum*. These two species are closely related to *D. annulatum* and may be classified as *D. annulatum* var. *papillosum* (2n=60) and *D. annulatum* var. *fecundum* (2n=40), respectively (Singh and Mehra, 1965). Apomictic *D. annulatum* formed multiple embryo sacs, of which majority were unreduced, four nucleate, *Oenothera* type. The diploid species *D. aristatum* and *D. caricosum* formed a single eight nucleate, polygonum type of embryo sac, which was characteristic of sexual reproduction observed in the grass species (Reddy, 1967; Reddy and Cruz, 1969). *D. aristatum* was also reported to be facultative apomicts.

The facultative apomictic tetraploid *D. annulatum* (2n=40) as female parent was crossed with the diploid sexual biotypes of *D. aristatum* (2n=20) and *D. caricosum* (2n=20). There were six pentaploid (2n=50), one tetraploid (2n=40), one triploid (2n=30) and three aneuploids (2n=31, 42 and 46). Embryological studies indicated that diploid were sexual, tetraploids were apomictic, triploids and aneuploids were sterile and pentaploids were partially sterile and partially apomictic (Cruz and Reddy, 1971). Hybridization studies exhibited preponderance of apomicts in F_1, F_2 and later generations suggesting that apomixis is inherited as a dominant character (Gupta, 1995). Srivastava and Purnima (1990) investigated apomixis in *D. annulatum*, *B. intermedia* and their natural hybrids. Agamospermy occurred as facultative aposporous apomixis with two types of embryo sacs, sexual and aposporic. Yu *et al*. (2000) have studied apomixis in *Dichanthium-Bothriochloa* complex and found that it is of the pseudogamous apospory and adventative embryony type. Higher ratio of embryo sac abortion is also an important factor causing sterility in *D. setosum*. A comparison between obligate sexual reproduction and facultative apomixis indicates that obligate sexual reproduction leads to high seed set. Ninety lines of *D. annulatum* were evaluated which indicated the presence of facultative apomixis in the complex (Pandey *et al*., 2002). Gupta *et al*. (1998) estimated frequency of apomixis in *D. annulatum* by auxin-induced parthenocarpy. The frequency of parthenogenetic and sexual caryopses was 65.44 and 34.56% in the parent, whereas among the somaclones they varied from 53.33 to 72.22% and 27.78 to 46.67% respectively indicating facultative apomixis.

Crop improvement programme in this complex is mostly dependent on germplasm collection and evaluation followed by selection for different agro-ecological zones. Apomixis phenomenon can also be exploited after careful screening for sexuality. A number of cultivars have been released and notified for different zones of the country. Active research work is going on at IGFRI, Jhansi; MPKV Rahuri; AAU, Anand etc. IGFRI Jhansi has collection of more than 500 accessions in IGFRI gene bank collected from all over India. A descriptor of *Dichanthium-Bothriochloa* complex and a minimal descriptor was also published (Roy *et al.,* 2009; 2017).

Cenchrus

Cenchrus is a genus of Panicoid grasses and comprises both annuals and perennial species. Many species of the genus *Cenchrus*, with different ploidy are important components of world grasslands. *C. ciliaris* and *C. setigerus* are the most commonly used for forage production.

Cenchrus ciliaris: *C. ciliaris commonly known as* buffel grass or African Foxtail or *Anjan* grass is a native of tropical and subtropical Africa, India and Indonesia. It is reported from the Hindustani and Indochina-Indonesia Centers of Diversity and is widespread in the arid hot, drier areas of the world and used as cultivated or rangeland pasture. It is widely naturalised in sub-humid and semi-arid tropics and subtropics.

In India, It is considered excellent for pasture as highly nutritious grass and is widely distributed in hotter and drier parts in grassland in its natural habitat in Rajasthan, Haryana, Punjab, Gujarat, western Uttar Pradesh and Tamil Nadu. It is found as a natural grass in the *Dichanthium*/ *Cenchrus*/ *Elyonurus* cover between 23°N and 32°N latitude and 60°E and 80°E longitude. It is distributed from sea level to 2000-m altitude. Anjan grass is largely apomictic with occasional facultative sexuality. Plants can be propagated vegetatively.

The species are drought resistant, a good soil binder and can also grow very well under irrigation. *C. ciliaris* utilizes the C_4 photosynthetic pathway, which provides an advantage under hot and dry growing conditions. It is polymorphic, perennial with extensive native range in the form of various ecotypes and cytotypes. Tremendous genetic variation has been found among *C. ciliaris* accessions, resulting in variable morphology and ecological tolerances (Hignight *et al.,* 1991).

In Buffel grass, GFY was reported to be highly correlated to plant height, tillers number/ plant, leaf number/ tiller and leaf length (Mishra *et al.,* 1999). Plant height was positively correlated with leaf weight, stem weight, GFY and DMY which indicated that plant height, tillering, leaf weight and stem weight are the important forage yield components (Jatsara and Thakral, 1986). Yadav *et al.* (1974) reported that plant height, leaf breadth; spike length and fodder yield were positively and significantly correlated with each other both genotypically and phenotypically. Tiller number was positively correlated with yield. In *C. ciliaris* maximum variability was recorded for GFY followed by DMY indicating that these characters are highly variable. Least variance was recorded for leaf width followed by spike width (Bhat *et al*., 2002). Major differences among accessions include days to 50% flowering, plant height, number of tillers per plant, leaf length and peduncle length thereby indicating that these characters are important for improvement in forage yield through selection (Rajora, 1998).

The species are protogynous with stigma emerging in basipetal succession. Self fertilization is common but cross fertilization also occurs frequently. *C. ciliaris* is apomictic, producing asexual seeds genetically identical to the mother plant; however, genetic markers study indicates occasional likely sexual reproduction also (Kharrat-Souissi *et al*., 2011; 2014). Facultative apomicts are also reported however most ecotypes are obligate apomicts. A unique sexual mutant from a US population has been used in plant breeding programs. One sexual plant of *C. ciliaris* (IGFRI-CcSx-08/1) has also been registered (INGR 11062) by IGFRI in 2011.

The basic group representing heterogenous assemblage consists of *C. ciliaris, C. setigerus, C. nultifflorus, C. prieurii, C. biflorus, C. mjosuroiles and C. caliculatus* having basic chromosome number x=9. These are restricted to Africa, India, Pakistan and southern East Asia. *C. ciliaris* and *C. setigerus* in their natural stands are generally tetraploid (2n=36) representing various cytotypes ranging from 2n=35 to 42. Hexploid (2n=56) are also reported occasionally. *Cenchrus ciliaris* has a basic chromosome number of x = 9 with polyploidy and aneuploidy common with varied levels of 2*n* = 32, 34, 36, 40, 44, 52, 54. Most common being 2n=4x=36 (Cook *et al.,* 2005) Das (1993) subjected 20 genotypes of 3 *Cenchrus sp*. to cytological analysis. Eleven genotypes had 2n=44, seven had 2n=36 and two had 2n=42. Among the thirteen *C. ciliaris* types, ten were aneuploid (2n=44) and three tetraploid (2n=36). Of the five *C. setigerus* types, four were tetraploid (2n=36) and one aneuploid (2n=42). Based on occurrence of quadrivalents, it was inferred that tetraploid forms of *C. ciliaris* were segmental allotetraploids, but in the aneuploid forms, both quadrivalents and hexavalents were observed.

Among 568 accessions screened, 54% were tetraploids with 36 chromosomes, 24% were pentaploids with 45 chromosomes, 4% were hexaploids with 54 chromosomes, >1% were septaploids with 63 chromosomes, and 17% were aneuploids (Burson *et al.,* 2012). Molecular cytogenetic study using double fluorescence *in situ* hybridization has shown that the two rDNA families, 5S and 18S-5.8S-26S (18S), displayed intraspecific variation in number of loci among different ploidy levels. Data of the FISH experiments show proportional increase of ribosomal loci number during polyploidization processes (Souissi *et al.,* 2012). Gustin *et al.* (1996) studied 22 isozyme systems for segregation for apospory in *C. ciliaris* and reported that 12 isozyme exhibit polymorphism but none co-segregated with apomixis. Chandra and Dubey (2009) studied eight *Cenchrus* species representing three ploidy (diploid, tetraploid, hexaploid) levels and two life spans (annual/ perennial). It indicated that perennial tetraploid and hexaploid are more suited to drought conditions in comparison to annual diploid.

Worldwide important varieties of *Cenchrus* grass include Zeerust, Nunbank, Tarewinnabar, Lawes, Viva, Frio, Mopani, Pecos, Berg buffel *etc.*

Cenchrus setigerus**:** *Cenchrus setigerus* Vahl commonly known as birdwood grass, motha dhaman, kala-dhaman is similar to *C. ciliaris*. It is native to east *Africa*, western *Asia* (Southern Iran, Yemen, India, and Pakistan) and occurs commonly in open dry bush and grassland. It is naturalized in dry tropics and subtropics and very tolerant to drought and heat and is adapted to arid and semi-arid zone with a long dry season and 200 mm rainfall (Tran, 2016). It is a pasture species with good nutritional qualities with 7-10% CP and up to 65% IVDMD at pre-flowering stage (Cook *et al*., 2005). It is apomictic species with occasionally facultative apomictic ecotypes also reported. The basic chromosome number is x=9 with most common ecotypes $2n = 4x = 36$. Occasionally 2n=54 has also been reported. It can hybridize with *C. ciliaris*. It is more drought hardy than *C. ciliaris.*

In India active research work is currently going on at IGFRI, Jhansi; CAZRI Jodhpur; TNAU, Coimbatore; SKRAU, Bikaner; MPKV, Rahuri and other SAUs. The strategies adopted are largely introduction and selection for agro-climatic zones. Several varieties have been identified / notified for this grass.

Sehima

Genus *Sehima* belongs to tribe Andropogoneae of family Poaceae. Nine species of *Sehima* have been recognized from different parts of the world, which includes *S. alpinii, S. cilirae* (Munro) Roberty, *S. ischaemoides*, *S. galpinii* Stent, *S. nervosa* (Rottler) Stapf, *S. nervosum* (Rottler ex Willd.) Stapf, *S. notatum* (Hackel) A. Camus, *S. sulcata* (Hackel) A. Camus, *S. sulcatum* (*www. ciencia.net*).

Sehima nervosum: *Sehima nervosum* (Rottler ex Willd.) Stapf commonly known as Rat's tail grass or white grass or *Sain Ghas* in Hindi is the most dominant species of this genus in India and other tropical countries. It is widely distributed in South East Asia, Australia and Eastern Africa. It is a perennial excellent fodder grass, with multi tillering behaviour. Rainfall requirement of the grass is 250-1375mm (optimum up to 1000mm). It is a good forage grass and is utilized for grazing and hay making (Bor, 1960). As it is highly palatable, it is first to disappear under impact of grazing (Dabadghao and Shankarnaryanan, 1973). The grass responds well to nitrogen fertigation and biomass yield get doubled with substantial increase in crude protein content (Kumar and Shankarnarayan, 1980).

Basic chromosome number seemed to be n=10 in *Sehima* with incidence of polyploidy ranging from diploid to tetraploid forms (Oke, 1970). Previous studies indicate variable chromosome numbers in different species. *Sehima nervosum* Stapf. [2n = 34 (Sampath and Ramanathan, 1949), 2n = 20, 40 (Mehra, 1955), n = 20, 2n = 40, (Celarier and Harlan, 1956); *S. spathiflorum* Blatt. et McCann. 2n = 20 (Joshi *et al.,* 1959); *S. sulcatum*, A. Camus 2n=20 (Joshi *et al.,* 1959)]. Fedorov (1974) has reported 2n= 20, 34, 40.

Sehima nervosum is a facultative apomictic species and coupled with polyploidy nature, is a difficult species for genetic manipulation as conventional breeding techniques such as hybridization, mutation *etc.* have little chances of success. Roy *et al.* (1999) evaluated *S. nervosum* genotypes for forage yield and its contributing traits and found maximum variability for plant weight and number of tillers which were also positively correlated with GFY. The study indicated that plant height, number of tillers and leaf length are important traits while constructing selections criterion for forage yield in *Sehima.* Direct effect of leaf length towards GFY was quite high, which suggested that a restrictive selection programme through this trait could be taken up, while keeping restriction on stem thickness and leaf width (Roy *et al.*, 1999). Chauhan *et al.* (2008) evaluated 97 accessions of *Sehima nervosum* collected from different parts of India for various morphological traits and observed wide variability. Obtaining good quality seed is a problem due to low seed setting, fluffy and chaffy seeds, seed shedding and dormancy. Studies carried by Kumar *et al.* (2007) revealed that entry IGS 9901 supplemented with 60kg N + 40kg P_2O_5/ha and cutting schedules of 30 days interval may provide higher biomass and crude protein for sustaining the livestock in arid region. Evaluation of forty two genotypes of *Sehima nervosum* collected from different parts of the country indicated the existence of considerable genetic diversity (Yadav *et al.,* 2010). Most of the traits displayed moderate to high broad sense heritability. The genotypes were divided into two major clusters *viz.* cluster-1 comprising 22 genotypes including two outliers and cluster-2 with 20 genotypes including two outliers. Most of traits showed significant positive correlation with GFY. Among the various yield related traits, longest leaf length, panicle length and plant height revealed significant direct effect on GFY in path analysis.

Heteropogon

Heteropogon contortus, a member of tribe Andropogoneae family Poaceae, is an important perennial fodder grass (Bor, 1960). It has wide adaptability being found in tropical, sub-tropical, arid, semi-arid and lower hills and tolerate various abiotic stress situations such as drought, salinity *etc.* It has good yield, palatability during vegetative phase, perenniality, and to grow on poor soils are its main attributes. However, production of numerous robust awns which shed easily and cause damage to animals are its main deficiencies. It can be made into hay as well as silage.

Heteropogon is an obligate aposporous apomict with 2n= 20, 40, 44, 60, 80 (Fedorov, 1974). The species is reported to be obligate apomicts with only aposporous embryo sacs (Srivastava and Purnima, 1990). *Heteropogon contortus* being largely apomictic in nature, the increased variability in sub-humid dry regions of south India might be due to the presence of natural crossing owing to residual sexuality in some plants.

Goergen and Daehler (2001) reported that *H. contortus* is drought-tolerant, perennial, C_4 bunchgrasses, apomictic with low germination rate (13%). Carino and Daehler (1999) used RAPD markers to assess genetic variation within and among Hawaiian populations of *H. contortus*. 56 individuals sampled from 6 populations on Oahu and Hawaii was studied and 55 unique genotypes were detected using 33 polymorphic markers. This lack of uniformity among individuals may indicate frequent sexual reproduction in these populations. Analysis of molecular variance revealed significant variation among populations (30.2%), but higher levels of variation within populations (68.1%). Cluster analysis revealed a high degree of clustering for most populations, but populations from different islands did not cluster together. Tewari and Roy (2005) worked out the various ways to overcome the exogenous dormancy in different accessions.

Roy (2004) evaluated 87 genotypes of *H. contortus* for 13 morphological traits and reported that for an effective selection more emphasis should be given to tiller number, high nodal number and longer leaf. Bhat and Roy (2014) evaluated 89 genotypes collected from different parts of India using four enzymes, *viz.* peroxidase, superoxidase dismutase (SOD), glutamate oxalo-acetate transaminase (GOT). Clustering reveals that genetic diversity could not be correlated to the geographical origin of the accessions. The study indicates that considerable genetic diversity exists in the species and collection from different geographical places will help in identifying suitable genotypes for various agro-ecological situations for rangeland conditions (Bhat and Roy, 2014). *H. contortus* growing wild in natural habitats exhibits large phenotypic variation. Even diverse forms have been reported from material collected at the same locations and the clustering patterns based on morphological attributes in *Heteropogon contortus* indicated independent groupings with their geographical distribution (Bhat and Roy, 2007).

Setaria

Setaria, family Poaceae is a large genus of 140 species and majority of species grow in moderately humid areas. A native of tropical and subtropical Africa, it is widely cultivated in Africa, Australia, Taiwan, New Guinea, Philippines, Israel, Madagascar, Fiji, Taiwan, Florida and Brazil. It was introduced into many countries where it became naturalized (Cook *et al.*, 2005). It is cultivated under irrigation in Morocco and Israel (Bogdan, 1977). Setaria was first introduced to India in 1950 and is now spread to medium rainfall areas of 500-800 mm rainfall. It is cold tolerant and during hot and dry weather remains dormant.

Boonman (1993) reported *Setaria sphacelata* as a polymorphous species and different names were used at times at the (sub) species level. However, reports indicated that inter-specific hybridization with other Setaria species was easy. Within *Setaria sphacelata* a whole range of ploidy levels can be found; diploid (Nandi) and tetraploid (Kazungula; Narok), but Hacker (1969) reported accessions also of 2n = 45, 54, 72, and 90 with chromosome pairing in most of the combinations that had even chromosome numbers. Between ploidy levels cross-fertilization commonly occurs (Boonman, 1993). Mostly diploids (2*n*=18) and tetraploids (2*n*=36), although hexaploids, octoploids and rarely decaploids have also been identified.

Clayton (1979) re-examined morphological relationships of tropical African specimens assignable to the four commonest traditional species. He reported that *S. sphacelata, S. anceps* and *S. splendida* represent segments of a continuous gradient of plant size. It is evident that, both in the cytogenetic and morphological sense, these entities form a continuum, and that there is no case for recognizing more than one species (Clayton, 1979). In this article we are treating *Setaria sphacelata* and *S. anceps* as synonyms.

Setaria anceps Stapf (commonly known as golden timothy, golden bristle grass and golden millet) is a palatable, drought resistant grass having seasonal water logging tolerance and suited to the low rainfall situations. It can grow at high altitudes pasture grass as it survives freezing temperatures (Hacker, 1992). It does better when temperatures are between 18-22°C but can still grow during winter if frost is not too heavy (FAO, 2017). The plants can be easily established by seed and can persist under moderate level of ruminant grazing. Gildenhuys (1950) estimated fertility of several morphologically distinct ecotypes of *S. sphacelata* and concluded that this species is normally cross pollinated; the small amount of segregation in the progeny of the highly self fertile type indicates the occurrence of a certain degree of natural self pollination.

It is good quality forage for ruminants and can be fed fresh and ensiled form. The crude protein and crude fibre content of the grass range from 7.0 to 12.0 and 24 to 34%, respectively. Due its good digestibility, the cattle accept its stubble grazing. *Setaria* grass is also known to have variable levels of oxalates.

The popular cultivars released abroad are *Nandi Setaria, Nandi Mark 2, Kazungula, Narok Setaria,* Solander, and Splenda. Popular Indian varieties PSS-1, S-92, S-20 are good performers in the Himalayan region with good nutritive value and low oxalate contents. The future research work should concentrate on prolonging the vegetative growth period, frost tolerant perennial cultivars suitable for sub-tropics, shade tolerant lines suitable for horti-silvipasture.

Lasiurus

Lasiurus, a genus of Asian and African origin, is found primarily in arid regions. *Lasiurus scindicus* Henr., is native to dry areas of North Africa, Sudanese and Sahelian regions, East Africa, and Asia. It is found between 25 and 27°N latitude in dry open plains, rocky ground and gravelly soils (Quattrocchi, 2006; Clayton *et al.,* 2002). It is distributed in North Africa, Mali, Niger, Ethiopia, Iraq, Southern Pakistan and northwest India (Skermon and Riveros, 1990).

Sewan grass is most common and endemic perennial grass of western Rajasthan and parts of Pakistan and considered as the King of desert grasses. An extremely drought resistant grass, it survives hot arid zone with harsh climate like -1 to 48°C and <150 mm rainfall. In India, sewan grass covers 0.1million hectares of area (Bhagmal *et al.,* 2011).

Sewan grass is one of the dominant grass species of *Dichanthium-Cenchrus-Lasiurus* type grass cover. It has a high nutritive value and is preferentially consumed by cattle in the desert. It is a vital component of western Rajasthan rangeland, can live up to 20 years and is also important in stabilizing the sand dunes and desert (Khan and Frost, 2001). It is a bushy, multi-branched desert grass with ascending to erect wiry stems, up to a height of 1-1.6 m, and a stout woody rhizome (FAO, 2010; Ecocrop, 2010).

Grasslands with Sewan grass as dominant species in general are able to sustain high carrying capacity (Das, 1973). The grass is widely grazed and has CP rangeing from 12-14% in early stage up to 15 days of crop to around 4-5% when the crop is 4 months old. Similarly IVDMD ranges from 60-70% in young stage up to 45 days old plant which decreases up to 53% when 120 days old. (Gupta, 1987). The breeding effort in the grass is limited to variability analysis, collection of germplasm and selection using biometrical parameters. Sharma *et al.* (2017) studied 27 genotypes of *L. sindicus* using 18 RAPD and 14 ISSR markers and observed wide genetic variability among the accessions. Paul Chowdhury *et al.* (2009) analyzed the rhizosphere related population of this grass and they identified eight major bacterial taxa in a total of 121 16S-rRNA gene clones. It indicated that *L. sindicus* harbours a diversity of bacteria with potential for nitrogen fixation. Sanadya *et al.* (2018) studied 273 accessions for 11 agro-morphological traits and found that two characters *viz.*, number of tillers per plant and dry matter yield per plant have high phenotypic coefficient of variation, respectively.

References

Agarwal, D. K., S. Gupta, A. K. Roy, S.R. Gupta and S. Gupta. 1999. Study on agro morphological variation *vis-à-vis* geographical distribution in marvel grass (*Dichanthium annulatum* L. Stapf.). *Plant Genetic Resources Newsletter* 118: 27-29.

Agarwal, D.K. A. K. Roy and S. Gupta. 1998. Forage genetic resources for improving quality and productivity in Indian rangelands. *In: Proceedings of International Conferene on 'Security and Crop Science' (Nov 3-6, 1998)*, CCSHAU, Hissar.

Ahmad, M.S.A., M. Ashraf and Q. Ali. 2010. Soil salinity as a selection pressure is a key determinant for the evolution of salt tolerance in Blue Panicgrass (*Panicum antidotale* Retz.). *Flora* 205: 37-45.

Akiyama, Y., S. Goel, Z. Chen, W.W. Hanna and P. Ozias-Akins. 2006. *Pennisetum squamulatum*: Is the predominant cytotype hexaploid or octaploid. *Journal of Heredity* 97: 521–524.

Akiyama, Y., W. W. Hanna and P. Ozias-Akins. 2005. High-resolution physical mapping reveals that the apospory-specific genomic region (ASGR) in *Cenchrus ciliaris* is located on a heterochromatic and hemizygous region of a single chromosome. *Theoretical and Applied Genetics* 111: 1042–1051.

Aliscioni, S. S., L. M. Giussani, F.O. Zuloaga and E. A. Kellogg. 2003. A molecular phylogeny of *Panicum* (Poaceae: Paniceae): Tests of monophyly and phylogenetic placement within the Panicoideae. *American Journal of Botany* 90: 796–821.

Andres, A.N. and J. Cordero. 1995. Genetical and ecological aspects of *Bothriochloa longuoides* (D.C.) Pilg. I. Genetic variability. *Informe-Tecnico-Estacion-Experimental-Agropecuaria-Pergamino* No. 301. pp.16.

Anita, M. R. and S. Lakshmi 2014. Growth characters of guinea grass (*Panicum maximum* Jacq.) under varying light intensity and potassium. *In: e-Proceedings of International Conference on 'Green India: Strategic Knowledge for Combating Climate Change: Prospects & Challenges'*. Pondicherry University, Excel India Publications, India.

Anonymous. 2017. Panicum coloratum. http://www.tropicalforages.info/key/forages/Media/Html/entities/panicum_coloratum.htm

Arora, R. K., K. L. Mehra and M. W. Hardas. 1975. The Indian gene centre, prospects of exploration and collection of herbage grasses. *Forage Research* 1: 11-12.

Awasthi, A. and S.P. Joshi. 1998. Nutritive value of some plant species of Doon valley in different phonological stages. *Annals of Forestry* 6: 232-238.

Bhagmal, K. A. Singh, A. K. Roy, S. Ahmed and D. R. Malviya. 2011: Forage crops and grasses. In: *Handbook of Agriculture*. ICAR (6th revised edition), New Delhi, pp. 1353-1417.

Bhat, B.A. and A.K. Roy. 2007. Genetic diversity in *Heteropogon contortus*. *Range Management and Agroforestry* 28: 300-301.

Bhat, B.A. and A.K. Roy. 2014. Genetic diversity based on isozymic banding pattern in *Heteropogon contortus*- A perennial tropical forage grass. *Indian Journal of Agricultural Sciences* 84: 1464-1469

Bhat, V., U.S. Mishra and D.S. Katiyar. 2002. Studies of genetic variability in *Cenchrus ciliaris*. *In: Proceedings of National Symposium on 'Grassland and Fodder Research in the New Millennium.* RMSI, Jhansi. pp. 48.

Bogdan, A.B. 1977. *Tropical Pastures and Fodder Plants.* Longman: London and New York.

Bokhari, U.G., F. Alyaeesh and M. AL- Noori. 1988. Potentials of forage crops. *Saudi Arabian Journal of Scientific Research* 6: 359-367.

Boonman, J. G. 1993. *East Africa's Grasses and Fodders: their Ecology and Husbandry.* Kluwer Academic Publishers, Dordrecht, The Netherlands.

Bor, N. L. 1960. *The Grasses of Burma, Ceylon, India and Pakistan*. Pergamon Press. London.

Branson, F. A., G. F. Gifford, K. G. Renard and R. F. Hadley. 1981. Rangeland Hydrology. Society for Range Management, Range Science Series No.1, Second Edition. pp. 1-339.

Brown, W.V. 1977. The Kranz syndrome and its types in grass systematics. *Memoirs of the Torrey Botanical Club* 23: 1–97.

Brukhin, V. 2017. Molecular and genetic regulation of apomixis. *Russian Journal of Genetics* 53: 943-964.

Brunken, J.N. 1977. A systematic study of *Pennisetum* sect. Pennisetum (Gramineae). *American Journal of Botany* 64: 161–176.

Burson, B. L., J. M. Actkinson, M. A. Hussey and R. W. Jessup. 2012. Ploidy determination of buffel grass accessions in the USDA national plant germplasm system collection by flow cytometry. *South African Journal of Botany* 79: 91–95.

Carino, D.A. and C.C. Daehler. 1999. Genetic variation in an apomictic grass, *Heteropogon contortus*, in the Hawaiian Islands. *Molecular Ecology* 8: 2127-2132.

Carnahan, H. L. and H. D. Hill. 1961. Cytology and genetics of forage grasses. *Botanical Review* 27: 1-162.

Celarier, R.P. and J.R Harlan. 1956. Old world Blue Stems. *Oklahoma Agricultural Experiment Station Annual Report of Progress in Forage Crops Research in Oklahoma.*

Celarier, R.P., K.L. Mehra and M.L.Wulf. 1958. Cytogeography of *Dichanthium annulatum* complex. *Britonia* 10: 59-72.

Chaix, G. and L. Marchais 1996. Diversity of penicillariam millets (*Pennisetum glaucum* and *Pennisetum purpureum*) as for the compatibility between their gynoecia and pollens from some other Poaceae. *Euphytica* 88: 97-106.

Chandra, A, R. Saxena, A.K. Roy and P.S. Pathak. 2004. Estimation and genetic variation in *Dichanthium annulatum* genotypes by RAPD technique. *Tropical Grasslands* 38: 245-252.

Chandra, A. and A. Dubey 2009. Assessment of ploidy level on stress tolerance of Cenchrus species based on leaf photosynthetic characteristics. *Acta Physiologie Plantarum.* DOI 10.1007/s11738-009-0317-0

Chandra, A., A.K. Roy and S. Kumar. 2010. Molecular techniques for improvement of forage crops. *Range Management and Agroforestry* 31: 87-96.

Chandra, A., A.K. Roy, R. Saxena and A. Dubey. 2003. Identification of suitable primers to develop DNA fingerprints of marvel grass. *Indian Journal of Agricultural Biochemistry* 16: 23-27.

Chandra, A., R. Jain, S. Solomon, S. Shrivastava and A. K. Roy. 2013. Exploiting EST databases for the development and characterisation of 3425 gene-tagged CISP markers in biofuel crop sugarcane and their transferability in cereals and orphan tropical grasses. *BMC Research Notes* 6: 47.

Chandra, A., R. Saxena and A. K. Roy. 2006. Polymorphism and genotypic-specific markers for *Dichanthium* identified by random amplified polymorphic DNA. *Genetic Resources and Crop Evolution* 53: 1521-1529.

Chauhan,0 R., R. Tewari, A. K. Roy, D. R. Malaviya, P. Kaushal and A. Chandra. 2008. Genetic variability for morphological traits in *Sehima nervosum,* an important perennial range grass. In: *Proceedings of National Symposium (Dec 15-17, 2008)*. National Research Centre for Agroforestry, Jhansi.

Chedda, H.R. and J.R. Harlan. 1962. Mode of chromosome association in *Bothriochloa* hybrids. *Caryologia* 15: 461-476.

Chen, X., H. G. Lai, Q. Sun, J. P. Liu, S. B. Chen and W. L. Zhu. 2018. Induction of apomixis by dimethyl sulfoxide (DMSO) and genetic identification of apomictic plants in cassava. *Breeding Science* 68: 227–232.

Clayton, W. D. and S A. Renvoize. 1986. Genera Graminum- Grasses of the world. *Kew Bulletin, Additional Series* 13: 1–389.

Clayton, W. D., R. Govaerts, K. T. Harman, H. Williamson and M. Vorontsova. 2013. *World Checklist of Poaceae*. Richmond, UK: Royal Botanic Gardens, Kew.

Clayton, W.D. 1979. Notes on Setaria (Gramineae). *Kew Bulletin* 33: 501-509.

Clayton, W.D. 1983. Tropical grasses. In: J.G. McIvor and R.A, Bray (eds). *Genetic Resources of Forage Plants*. East Melbourne, Australia: Commonwealth Scientific and Industrial Research Organization (CSIRO). pp. 39-46.

Clayton, W.D., M.S. Vorontsova, K.T. Harman and H. Williamson. 2002. W*orld Grass Species: Descriptions, Identification, and Information Retrieval*. http://www.kew.org/data/grasses-db.html.

Combes, D. 1975. Po~morphisme el modes de reproduction dons 10 section des *Moximae du* genre *Ponicum* (Graminees) en Afrique. Memoires ORSTOM (Paris) #77.

Combes, D. and J. Pernès**.**1970. Variations dans le nombres chromosomiques du *Panicum maximum* Jacq. en relation avec le mode de reproduction. *Comptes Rendues Academie des Sciences Paris*, Séries D.0 270: 782-785.

Conner, J. A., S. Goel, G. Gunawan, M. M. Cordonnier-Pratt, V. E. Johnson and C. Liang. 2008. Sequence analysis of bacterial artificial chromosome clones from the apospory-specific genomic region of *Pennisetum* and *Cenchrus. Plant Physiology* 147: 1396–1411.

Cook, B. G., B. C. Pengelly, S. D. Brown, J. L. Donnelly, D. A. Eagles, M. A. Franco, J.Hanson, B. F. Mullen, I. J. Partridge, M. Peters and R. Schultze-Kraft. 2005. *Tropical Forages.* CSIRO, DPI&F (Qld), CIAT and ILRI, Brisbane, Australia.

Cope, T.A. 1982. Flora of Pakistan. In: E. Nasir and S.L. Ali. (ed.). *Family Poaceae*. Department of Botany, University of Karachi, Karachi. 143: 678-682.

Cramer, G.R., Kaoru Urano, Serge Delrot, Mario Pezzotti and Kazuo Shinozaki. 2011. Effects of abiotic stress on plants: a systems biology perspective. *BMC Plant Biology* 11:163.

Cruz, R.D. and P.S. Reddy. 1971. Inheritance of apomixis in *Dichanthium. Indian Journal of Genetics* 31: 451-460.

Dabadghao, P.M. and K.A. Shankarnarayan. 1973. *The Grass Covers of India*. Indian Council of Agricultural Research, New Delhi. pp 1-713.

Das, L.D.V. 1993. Cytology of some *Cenchrus* grasses. *Nucleus* 36: 68-72.

Das, R. B. 1973. Managing pastures in arid areas. *Indian Farming* 23: 30-31.

De Wet, J.M.J. and M.L. Higgins. 1964. Cytology of the *Bothriochloa pertusa* complex. *Cytologia* 29: 103-108.

Dujardin, M. and W.W. Hanna.1984a. Microsporogenesis, reproductive behaviour, and fertility in five P*ennisetum* species. *Theoretical and Applied Genetics* 67: 197-201.

Dujardin, M. and Hanna, W. W. 1984c. Inducing male fertility in crosses between pearl millet and *Pennisetum orientale* Rich. *Crop Science* 27: 65-68.

Dujardin, M. and W. W. Hanna 1983a. Meiotic and reproductive behaviour of facultative apomictic BC_1 offspring derived from *Pennisetum americanum-P. orientale* interspecific hybrids. *Crop Science* 23: 156-170.

Dujardin, M. and W. W. Hanna 1984b. Pseudogamous parthenogenesis and fertilization of a pearl millet x *Pennisetum orientale* derivative. *Journal of Heredity* 75: 503-504.

Dujardin, M. and W. W. Hanna. 1989. Developing apomictic pearl millet—characterization of a BC 3 plant. *Journal of Genetics and Breeding* 43: 145-151.

Dujardin, M. and W.W. Hanna. 1983b. Apomictic and sexual pearlmillet x *Pennisetum squamulatum* hybrids. *Journal of Heredity* 74: 277–279.

Dujardin, M. and W.W. Hanna. 1985. Cytology and reproduction of reciprocal backcrosses between pearl millet and sexual and apomictic hybrids of pearl millet and *Pennisetum squamulatum. Crop Science* 25: 59–62.

Durr, P. and J. Rangel. 2000. The response of *Panicum maximum* to a simulated subcanopy environment. 1. Soil x shade interaction. *Tropical Grasslands* 34: 110-117.

Ebina, M., H. Nakagawa, T. Yamamoto, H. Araya, S. Tsuruta and M. Takahara. 2005. Co-segregation of AFLP and RAPD markers to apospory in guinea grass (*Panicum maximum* Jacq.). *Grassland Science* 51: 71–78.

Ecocrop. 2010. *Ecocrop database.* FAO.

FAO. 2010. *Grassland Index. A searchable catalogue of grass and forage legumes.* FAO, Rome, Italy.

FAO. 2015. *Grassland Index. A searchable catalogue of grass and forage legumes*. FAO, Rome, Italy.

FAO. 2017. *Grassland Index.* A searchable catalogue of grass and forage legumes. FAO, Rome, Italy.

Fedorov, A. 1974. *Chromosome Numbers of Flowering Plants*. Otto Koeltz Science Publishers, D-624, Koenigstein, West Germany.

Francis, J. K. 2004. *Pennisetum purpureum* Schumacher. In: J.K. Francis (ed.). *Wildland Shrub of the United States and its Territories: Thamnic Descriptions*: Volume 1. General Technical Report, IITF-GTR-26. USDA Forest Service, International Institute of Tropical Forestry. pp. 1-830.

Gaafer, R. M., A. R. El Shanshoury, A. A. El Hisseiwy, M. A. AbdAlhak, A. F. Omar and M. M. A. El Wahab. 2018. Induction of apomixis and fixation of heterosis in Egyptian rice Hybrid line using colchicine mutagenesis. *Annals of Agricultural Science* 62: 51–60.

Gangwar, B. and P. K. Jayan. 1986. New crop introductions in Andamans. *Indian-Farming* 35: 18-21.

Gildenhuys, P. J. 1950. Fertility studies in *Setaria sphacelata* (Schum) Stapf and Hubbard. *Science Bulletin No. 314*. Department of Agriculture and Forestry, Union of South Africa.

Goel, S., Z. B. Chen, J.A. Conner, Y. Akiyama, W.W. Hanna and P. Ozias-Akins. 2003. Delineation by FISH of a single hemizygous chromosomal region responsible for aposporous embryo sac formation in *Pennisetum squamulatum* and *Cenchrus ciliaris. Genetics* 163: 1069–1082.

Goergen, E. and C.C. Daehler. 2001. Reproductive ecology of a native Hawaian grass (*Heteropogon contortus*; Poaceae) versus its invasive alien competitor (*Pennisetum setaceum*; Poaceae). *International Journal of Plant-Sciences* 162: 317-326.

Gomez, R. O., E. C. Gallegos, J. J. Rodriguez, R. E. Hernandes, E. O. Zavaleta and B. V. de la Mora. 2011. Nutritive quality of grasses during the rainy season in a hot-humid climate and ultisol soil. *Tropical and Subtropical Ecosystem* 13: 481-489.

Gore, V. R., P. P. Surana and G. C. Shinde. 2016. Genetic variability studies for forage yield and associated traits in marvel grass (*Dichanthium* spp.). *Forage Research* 42: 172-175.

Gupta, A. K. 1987. Effect of growth and development on the qualitative attributes of Lasiurus sindicus Hner. *Annal of Arid Zone* 26: 17-24.

Gupta, M.G., S. Gupta, B.V. Bhat, V. Bhat, S.T. Ahmad, S. Gupta and V. Bhat. 1998. Estimation of frequency of apomixis by auxin induced parthenocarpy technique in *Dichanthium annulatum* (Forsk.) Stapf. *Range Management and Agroforestry* 19: 149-153.

Gupta, P.K. 1995. *Cytogenetics*. Rastogi Publications, Meerut.

Gupta, P.K., R.P. Roy and A.P. Singh. 1969. Aposporous apomixis: Seasonal variation in tetraploid *Dichanthium annulatum* (Forsk.) Stapf. *Portugaliae Acta Biologica* 11: 253-260.

Gupta, S.R., A.K. Roy and J.N. Gupta. 1996. Ecological diversity and tiller dynamics in *Dichanthium annulatum* (Forsk.) Stapf. *In: Proceedings of National Symposium on 'Agriculture and Environment'* (March 6-8, 1996), Jhansi, India.

Gupta, S.R., Sanjeev Gupta and U.P. Singh. 1994. Rangelands genetic resources management in India. *In:* P. Singh, P.S. Pathak and M.M. Roy (eds.). *Agroforestry of Degraded Lands.* Vol. 2. Pp. 543-550. Oxford and IBH Publishing Co., New Delhi.

Gustin, D. L., R.T. Sherwood, Y. Gounaris and D. Huff. 1996. Isozyme, protein and RAPD markers within a half-sib family of buffelgrass segregating for apospory. *Crop Sci*ence 36: 723-727.

Hacker, J. B. 1992. *Setaria sphacelata* (Schumach.) Stapf & Hubbard ex M.B. Moss. In: L.T. Mannetje and R.M. Jones (eds). *Record from Proseabase*. PROSEA (Plant Resources of South-East Asia) Foundation, Bogor, Indonesia.

Hacker, J. B. and R. J. Jones.1969. The Setaria sphacelata complex - a review. *Tropical Grassland* 3: 13-34.

Hand, M. L. and A. M. G. Koltunow. 2014. The genetic control of apomixis: asexual seed formation. *Genetics* 197: 441-450.

Harlan, J.R. 1963a. Two kinds of gene centers in *Bothriochloininae*. *American National* 97: 91-98.

Harlan, J.R. 1963b. Natural introgression between *Bothriochloa ischaemum* and *B. intermedia* in West Pakistan. *Botanical Gazette* 124: 294-303.

Harlan, J.R., R.P. Celarier, W.L. Richardson, M.H. Brooks and K.L. Mehra. 1958. Studies on old world bluestems II. *Oklahoma Agricultural Experiment Station Technical Bulletin.* pp. 1-72.

Hignight, K.W., E.C. Bashaw and M.A. Hussey. 1991. Cytological and morphological diversity of native apomictic buffel grass *Pennisetum ciliare* (L.) Link. *Botanical Gazette* 152: 214-218.

Hojsgaard, D. 2018. Transient activation of apomixis in sexual neotriploids may retain genomically altered states and enhance polyploid establishment. *Frontiers in Plant Science* 9: 230.

Huntsinger, L and P. Hopkinson. 1996. Viewpoint: Sustaining Rangeland Landscapes: A Social and Ecological Process. *Journal of Range Management* 49:167-173.

Huo, H., J. A. Conner and P. Ozias-Akins. 2009. Genetic mapping of the apospory-specific genomic region in *Pennisetum squamulatum* using retrotransposon-based molecular markers. *Theoretical and Applied Genetics* 119: 199-212.

Hyams, E. 1971. *Plants in Service to Man.* J.B. Lippincott, Philadelphia and New York.

Jain, A., A.K. Roy, P. Kaushal, D.R. Malaviya and S.N. Zadoo. 2005. Isozyme banding pattern and estimation of genetic diversity among Guinea grass germplasm. *Genetic Resources and Crop Evolution* 53: 339-347.

Jain, A., S.N. Zadoo, A.K. Roy, P. Kaushal, D.R. Malaviya. 2003. Meiotic system and probable basic chromosome number of *Panicum maximum* Jacq. accessions. *Cytologia* 68: 7-13.

Jatasra, D.S. and N.K. Thakral. 1986. Components of forage productivity in Buffel grass. *Forage Research* 12: 59-62.

Jauhar, P.P. 1981a. *Cytogenetics and Breeding of Pearl Millet and Related Species*. Alan R.Liss, New York. pp. 1-91.

Jauhar, P.P. 1981b. Cytogenetics of pearl millet. *Advances in Agronomy* 34: 407–470.

Jauhar, P.P. and A. B. Joshi. 1966. Cytotaxonomic investigations in the *Panicum maximum* complex-I. Morphological studies. *Bulletin of the Botanical* Survey *of* India 8: 287-295.

Jauhar, P.P. and A. B. Joshi. 1969. Cytotaxonomic Investigations in the *Panicum maximum* Complex III. Cytological features, chromosome diminution and evolution of the karyotype. *Cytologia* 34: 222-233.

Joshi, A. B., B. D. Patil and P. L. Manchanda.1959. Chromosome numbers in some grasses. *Current Science* 28: 54-55.

Kanodia, K.C. 1987. Forage resources of heavy rain fall areas in western India with special reference to grassland amelioration. In: P. Singh (ed). *Forage Production in India*. Range Management Society of India, Jhansi. pp.153-163.

Kaushal, P, K.K. Dwivedi, A. Radhakrishna, M. K. Srivastava, V. Kumar, A. K.Roy and D. R. Malaviya. 2019. Partitioning apomixis components to understand and utilize gametophytic apomixis *Frontiers in Plant Science* 10: 256.

Kaushal, P, A. Agarwal, D.R. Malaviya, S.A. Siddique and A.K. Roy. 2008a. Ploidy manipulation in Guinea grass (*Panicum maximum* Jacq., Poaceae) utilizing a hybridization-supplemented apomixis-component partitioning approach (HAPA) *Plant Breeding* 128: 295-303.

Kaushal, P., A. Khare, S.N. Zadoo, A.K. Roy, D.R. Malaviya and A. Agrawal. 2008b. Sequential reduction of *Pennisetum squamulatum* genome complement in *P. glaucum* (2n = 28) × *P. squamulatum* (2n = 56) hybrids and their progenies revealed its octoploid status. *Cytologia* 73: 151–158.

Kaushal, P., A.K. Roy, A. Khare, D.R. Malaviya, S.N. Zadoo and R.N. Choubey. 2007. Crossability and characterization of interspecific hybrids between sexual *Pennisetum glaucum* (pearl millet) and a new cytotype (2n=56) of apomictic *P. squamulatum. Cytologia* 72:111–118.

Kaushal, P., D. R. Malaviya and K. K. Singh. 1999. Evaluation of exotic accessions of guinea grass (*Panicum maximum* Jacq.). *Indian Journal of Plant Genetic Resources* 12: 215–218.

Kaushal, P., D. R. Malaviya and K. K. Singh. 2000. Identification of shade tolerant genotypes and alterations in nutrient contents under shade in guinea grass. *Range Management and Agroforestry* 21: 74-78.

Kaushal, P., D.R. Malaviya, A.K. Roy, S. Pathak, A. Agrawal, A. Khare, S.A. Siddiqui. 2008c. Reproductive pathways of seed development in apomictic guinea grass (*Panicum maximum* Jacq.) reveal uncoupling of apomixis components. *Euphytica* 164: 81-92.

Kaushal, P., K. K. Dwivedi, A. Radhakrishna, M. K. Srivastava, D. R. Malaviya and A. K. Roy. 2015a. Development and characterization of a hexaploid *Pennisetum orientale* (2n = 6x = 54) cytotype recovered through BIII hybridization. *Cytologia* 80: 37-43.

Kaushal, P., S. Paul, S. Saxena, K. K. Dwivedi, M. Chakraborti and A. Radhakrishna. 2015b. Generating higher ploidies (7x and 11x) in guinea grass (*Panicum maximum* Jacq.) utilizing reproductive diversity and uncoupled apomixis components. *Current Science* 109: 1392–1395.

Khan, T. I. and S. Frost. 2001. Floral biodiversity: a question of survival in the Indian Thar desert, *Environmentalist* 21: 231–236.

Kharrat-Souissi, A., A. Baumel, F. Torre, M. Juin, S. Siljak-Yakovlev, A. Roig and M. Chaieb.2011. New insights into the polyploid complex *Cenchrus ciliaris* L. (Poaceae) show its capacity for gene flow and recombination processes despite its apomictic nature. *Australian Journal of Botany* 59: 543–553.

Kharrat-Souissi, A., S. Siljak-Yakovlev, S. C. Brown, A. Baumel, F. Torre and M. Chaieb. 2014. The polyploid nature of *Cenchrus ciliaris* L. (*Poaceae*) has been overlooked: new insights for the conservation and invasion biology of this species – a review. *The Rangeland Journal* 36: 11-23.

Krishna, K. and K. Kumar. 1996. Some new records of angiosperms for Andaman Islands. *Journal of Economic and Taxonomic Botany* 20: 27-29.

Kumar, R. and K. A. Shankarnarayanan. 1980. Response of fertilizers in natural grassland of *Sehima nervosum* (Rottl.) Staff. *Forage Research* 6: 15-20.

Kumar, S., A.K. Roy and S.A. Faruqui. 2007. Performance of *Sehima nervosum* genotypes under different fertility levels and cutting intervals in semiarid region. *Range Management and Agroforestry* 28: 375-376.

Kumar, S., S. Saxenan and M. G. Gupta. 2017. Marker-assisted screening of breeding populations of an apomictic grass *Cenchrus ciliaris* L. segregating for the mode of reproduction. *Crop Breed. Appl. Biotechnol.* .17(1). http://dx.doi.org/10.1590/1984-70332017v17n1a2.

León-Martínez, G. and J. P. Vielle-Calzada. 2019. Apomixis in flowering plants: developmental and evolutionary considerations. *Current Topics in Developmental Biology* 131: 565–604.

Malaviya, D.R., A.K. Roy and P. Kaushal. 2018. Rangelands/grasslands of India- current status and future prospects. In: V.R. Squires, J. Dengler, H. Febg and L. Hua (eds). *Grasslands of the World Diversity, Management and Conservation*. CRC Press. pp. 223-240.

Malaviya, D.R. 1995. Components of green fodder yield in *Panicum maximum* Jacq. *Indian Journal of Genetics* 59: 83-86.

Malaviya, D.R. 1996. Distribution of morphological diversity among germplasm lines of *Panicum maximum. Indian Journal of Plant Genetic Resources* 9: 193-196.

Malaviya, D.R. 1998. Evaluation of *Panicum maximum* lines for sustained productivity. *Range Management and Agroforestry* 19: 126-132.

Malaviya, D.R. 2001. Breeding for quality characters in *Panicum maximum* Jacq. *Indian Journal of Genetics* 61:169.

Malaviya, D.R., P. Kaushal and B. Kumar. 2006. Differential response of guinea grass (*Panicum maximum)* morphotypes to shade under rainfed condition. *Range Management and Agroforestry* 27: 70-76.

Manyawu, G. J., S.Sibanda, I. C. Chakoma, C. Mutisi and P. Ndiweni. 2003. The intake and palatability of four different types of Napier grass (*Pennisetum purpureum*) silage fed to sheep. *Asian-Australasian Journal of Animal Sciences* 16: 823-829.

Mehra, K. L. 1955. Chromosome number in the tribe Andropogoneae Gramineae. *Indian Journal of Genetics* 15: 144.

Mehra, K. L. and M. L. Magoon. 1974. Collection, conservation and exchange of gene pools of forage grasses. *Indian Journal of Genetics* 34: 26–32.

Mehra, K.L. 1961. Chromosome number, geographical distribution and taxonomy of the *Dichanthium annulatum* complex. *Phyton* 17: 157-166.

Mehra, K.L. 1966. The *Dichanthium annulatum* complex 4. Study of natural hybridization from herbarium specimen. *Revista de Biologia* 5: 295-302.

Mishra, U.S., D.S. Katiyar and Ashok Kumar. 1999. Character association and path analysis in Buffel grass. *Range Management and Agroforestry* 20: 136-139.

Nalule, A. S. 2010. *Social Management of Rangelands and Settlement in Karamoja Subregion.* European Commission, Humanitarian Aid and FAO.

Oke, J. G. 1970. Chromosome numbers in some species of *Ischaemum* linn and *Sehima* forsk. In parts of western India. *Proceedings of the Indian Academy of Sciences,* B, Vol. LXXIII, Pl. VIII: 285-289.

Ozias-Akins, P., D. Roche and W.W. Hanna. 1998. Tight clustering and hemizygosity of apomixis-linked molecular markers in *Pennisetum squamulatum* implies genetic control of apospory by a divergent locus that may have no allelic form in sexual genotypes. *Proceedings of National Academy of Sviences USA* 95: 5127–5132.

Ozias-Akins, P., Y. Akiyama and W.W. Hanna. 2003. Molecular characterization of the genomic region linked with apomixis in *Pennisetum, Cenchrus*. *Functional and Integrative Genomics* 3: 94-104.

Pandey, A.K., A. Jain, A.K. Roy and S.N. Zadoo. 2002. Morphological variation in relation to sexuality in *Dichanthium-Bothriochloa* complex. In: Proceedings of *National Symposium on 'Grassland and Fodder Research in the New Millennium.* Indian Grassland and Fodder Resaerch Institute, Jhansi. India.

Pandey, K.C. and A. K. Roy**.** 2010. *Forage Crop Varieties*. Indian Grassland and Fodder Resaerch Institute, Jhansi. India.

Patil, B. D., M.W. Hardas and A.B. Joshi. 1961. Auto-alloploid nature of *Pennisetum squamulatum* Fresen. *Nature* 189: 419-420.

Paudel, Dev, B. Kannan, X. Yang, K. Harris-Shultz, M. Thudi, R. K. Varshney, F. Altpeter and J. Wang. 2018. Surveying the genome and constructing a high-density genetic map of napier grass (*Cenchrus purpureus* Schumach). *Nature Scientific Reports* 8: 14419.

Paul Chowdhury, S. M. Schmid, A. Hartmann and A. K. Tripathi. 2009. Diversity of 16S-rRNA and nifH genes derived from rhizosphere soil and roots of an endemic drought tolerant grass *Lasiurus sindicus European Journal of Soil Biology* 45: 114-122.

Pupilli, F. and G. Barcaccia. 2012. Cloning plants by seeds: inheritance models and candidate genes to increase fundamental knowledge for engineering apomixis in sexual crops. *Journal of Biotechnology* 159: 291-311.

Quattrocchi, U. 2006. *CRC World Dictionary of Grasses: Common Names, Scientific Names, Eponyms, Synonyms, and Etymology.* CRC Press, Taylor and Francis Group, Boca Raton, USA.

Radhakrishna, A., K.K. Dwivedi, M.K. Srivasatava, A.K. Roy, D.R. Malaviya and P. Kaushal. 2018. Transcriptome data of pre-meiotic stage of floret development in apomictic and sexual types of Guinea grass (*Panicum maximum* Jacq). *Data in Brief* 18: 590-593.

Raheja, P.C. 1966. Rajasthan deserts can bloom with forage. *Indian Farming* 15: 47.

Rajora, M. P. 1998. Variability and character association in Buffel grass. *Annals of Arid Zone* 37: 99-101.

Raman, V.S., P. Chandrasekharan and D. Krishanaswami. 1959. A note on some chromosome numbers in Gramineae. *Current Science* 29: 127–128.

Reddy, P.S. 1967. *Study of Mechanism and Inheritance of Apomixis in Dichanthium*. Ph. D. Thesis, University of Pune, India.

Reddy, P.S. and R. D'Cruz. 1969. Mechanism of apomixis in *Dichanthium annulatum*. *Botanical Gazette* 130: 71-79.

Reid, R. S., K. A. Galvin and R. L. Kruska. 2008. Global significance of extensive grazing lands and pastoral societies: an introduction. In: K. A. Galvin, R. S. Reid, R. H. Behnke and N. T. Hobbs (eds), *Fragmentation in Semi-Arid and Arid Landscapes*. Springer, Dordrecht, The Netherlands. pp. 1-24.

Robert, T., N. Khalfallah, E. Martel, V. Poncet, M. Remigereau and S. Rekima. 2011. Pennisetum. In: C. Kole (ed.). *Wild Crop Relatives: Genomic and Breeding Resources*. Vol. 9. Springer, Heidelberg, Berlin, pp. 217–255.

Roy, A. K, D.R. Malaviya, P. Kaushal, A. Chandra, U.P. Singh, S.K. Mahanta, R. Chauhan and R. Tiwari. 2009. Descriptors for *Dichanthuim Bothriochloa* complex. IGFRI, Jhansi, India. pp. 1- 24.

Roy, A. K. 2004. Genetic variability, character association and path analysis in black spear grass (*Heteropogon contortus* L.) *Range Management and Agroforestry* 25: 11-16.

Roy, A. K. and J.P. Singh. 2013. Grasslands in India: problems and perspectives for sustaining livestock and rural livelihoods. *Tropical Grasslands– Forrajes Tropicales* 1: 240-243.

Roy, A. K., D. K. Agarwal and S. Gupta. 1999. Character association in Sen grass (*Sehima nervosum). Range Management and Agroforestry* 20: 131-135.

Roy, A. K., D. Kumar, A.K. Sharma, A. K. Mall, D.R. Malaviya and P. Kaushal. 2017. *Minimal Descriptors in Forage Crops*. AICRP on Forage Crops and Utilization, Jhansi. pp. 1-136.

Roy, A.K., P. Kaushal, S.N. Zadoo and R.N. Choubey. 2003. Identification of a new cytotype of *Pennisetum squamulatum* Fresen with 2n=56 chromosomes. *Range Management and Agroforestry* 24: 71-73.

Roy, A.K., R.K. Agarwal, S. Ahmed, R.V. Kumar, A.K. Mall, N.R. Bhardwaj, R. Mawar, D.N. Singh, S.R. Kantwa and S.A. Faruqui. 2018. *Database of Forage Crop Varieties 2018*. Technical Publication No. 12/2017-18. AICRP on Forage Crops and Utilization, IGFRI, Jhansi. pp. 1-330.

Roy, R.P., A.P. Singh and S. Kumari. 1965. Pachytene analysis in *Dichanthium*. I. Chromosome morphology in *D. annulatum*. *The Nucleus* 8: 137-148.

Rusdy, M. 2016. Elephant grass as forage for ruminant animals. *Livestock Research for Rural Development. Volume 28, Article #49.* http://www.lrrd.org/lrrd28/4/rusd28049.html.

Sahu, P.P., S. Gupta, D.R. Malaviya, A.K. Roy, P. Kaushal and M. Prasad. 2012. Transcriptome analysis of differentially expressed genes during embryo sac development in apomeiotic non parthenogenetic Interspecific hybrid of *Pennisetum glaucum*. *Molecular Biotechnology* 51: 262-271.

Sailer, C., B. Schmid and U. Grossniklaus. 2016. Apomixis allows the trans-generational fixation of phenotypes in hybrid plants. *Current Biology* 26: 331–337.

Saini, M.L., P. Jain and U. N. Joshi. 2007. Morphological characteristics and nutritive value of some grass species in an arid ecosystem. *Grass and Forage Science* 62: 104-108.

Sampath, S. and K. Ramanathan. 1949. Chromosome numbers in Indian Economic plants. *Current Science* 18: 408-409.

Sanadya, S. K., S. S. Shekhawat, S. Sahoo, A. Kumar and N. Kumari. 2018. Metroglyph analysis in Sewan grass (*Lasiurus sindicus* Henr.) accessions. *Forage Research* 44: 86-89.

Savidan, Y, J.G. Carman and T. Dresselhaus. 2001. *The Flowering of Apomixis: From Mechanisms to Genetic Engineering.* Mexico, D.E: CIMMYT, IRD, European Commission DC VI (FAIR).

Savidan, Y. 1980. Chromosomal and embryological analyses in sexual apomictic hybrids of *Panicum maximum* Jacq. *Theoretical and Applied Genetics* 57: 153-156.

Savidan, Y. and J. Pernes. 1982. Diploid-tetraploid-dihaploid cycles and the evolution of *Panicum maximum* Jacq. *Evolution* 36: 596-600.

Savidan, Y.H. 2001.Transfer of apomixis through wide crosses. In: Y. Savidan, J.G. Carman and T. Dresselhaus (eds). *The flowering of apomixis: from mechanisms to genetic engineering*; 1st edn. Mexico, DF: CIMMYT, IRD, European Commission DG VI (FAIR). pp. 153-167.

Saxena, R. and A. Chandra. 2006. RAPD and cytological analyses and histological changes caused by moisture stress in *Dichanthium annulatum* accessions. *Cytologia* 71: 197–204.

Schmelzer, G.H. 1997. Review of Pennisetum section Brevivalvula (Poaceae). *Euphytica* 97: 1-20.

Schmelzer, G.H. and J.F. Renno. 1997. Genetic variation in the agamic species complex of Pennisetum section Brevivalvula (Poaceae) from West Africa. Ploidy level and isozyme polymorphism. *Euphytica* 97: 23-29.

Schmid, M. W., A. Schmidt and U. Grossniklaus. 2015. The female gametophyte: an emerging model for cell type-specific systems biology in plant development. *Frontier in Plant Science* 6: 907.

Shankar, V. and J.N. Gupta. 1992. Restoration of degraded rangelands. In: J.S. Singh (ed). *Restoration of Degraded lands - Concepts and Strategies*. Rastogi Publication, Meerut, India. pp. 115 -155.

Sharma, R., M. P. Rajora, R. Dadheech, R. K. Bhatt and R. K. Kalia. 2017. Genetic diversity in sewan grass (*Lasiurus sindicus* Henr.) in the hot arid ecosystem of Thar Desert of Rajasthan, India. *Journal of Environment Biology* 38: 419-426.

Sindhe, A.N.R. 1976. Supernumerary chromosomes in *Pennisetum squamulatum* Fresen. *Current Science* 45: 526.

Singh, A.P. and K. L. Mehra. 1965. Cytological analysis of hybrids within the *Dichanthium annulatum* complex. *Cytologia* 30: 307-316.

Singh, S.D. and S. S. Navi. 2000. Genetic resistance to pearl millet downy mildew II. Resistance in wild relatives. *Journal of Mycology and Plant Pathology* 30: 167-171.

Skerman, P. J. and F. Riveros. 1990. *Tropical Grasses.* FAO Plant Production and Protection Series No. 23, FAO, Rome.

Souissi, A.K., S.S. Yakovlev and P. Fatima and C. Mohamed. 2012. Physical mapping of 5S and 18S-5.8S-26S RNA gene families in polyploid series of *Cenchrus ciliaris* Linnaeus, 1771 (Poaceae). *Comparative Cytogenetics* 6: 273-286.

Srivastva, A.K. and Purnima. 1990. Agamospermy in some polyploidy grasses. *Acta Botanica Indica* 18: 240-246.

Takahara, M., E. Ebina, R. Morita, Y. Kazama, T. Abe and T. Takamizo. 2014. DNA marker analysis revealed that the deletion is relatively small in loss-of-apomixis mutants. *RIKEN Accelerator Progress Report* 47: 294.

Takahara, M., R. Morita, Y. Kazama, T. Abe, T. Takamizo and H. Nakagawa. 2016. Sexual reproduction observed in the loss-of-apomixis mutants of guinea grass induced by heavy-ion beam irradiation. *RIKEN Accelerator Progress Report* 49: 260.

Taliaferro, C.M. and E.C. Bashaw. 1966. Inheritance and control of obligate apomixis in breeding buffelgrass, *Pennisetum ciliare. Crop Science* 6: 473-476.

Timbo, A. L. de O. , L. C. Davide, J. E. B. P. Pinto and A. V. Pireira. 2010. Protoplast production from napier grass and pearl millet triploid hybrids. *Ciência Agrotecnologia* 34: 1219-1222.

Tiwari, R. and A.K. Roy. 2005. Exogenous dormancy in *Heteropogon contortus* In: T. Pullaiah, R.R. Venkata Raju, C. Sudhakar, B. Ravi Prasad Rao and S. Thimma Naik (eds). *Recent Trends in Plant Sciences*. Regency Publications, New Delhi. pp. 48-53.

Tran, G. 2016. *Birdwood grass (Cenchrus setiger)*. Feedipedia, a programme by INRA, CIRAD, AFZ and FAO https://www.feedipedia.org/node/481.

Ueno, O., Y.Kawano, M. Wakayama and T. Takeda. 2006. Leaf vascular systems in C_3 and C_4 grasses: a two-dimensional analysis. *Annals of Botany* 97: 611-621.

Van Soest, P. J. 1994. *Nutritional Ecology of the Ruminant.* Comstock Publishing Associates. A division of Cornell University Press, Itacha and London.

Wang xia Wang, B. Basia Vinocur and Aric Altman. 2003. Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. *Planta* 218: 1-14.

Watson, L. and M.J. Dallwitz. 1992. *The Grass Genera of the World.* CAB International, Wallingford, pp. 674-676.

Woodart, K. R. and L. N. Sollenberger. 2015. Production of biofuel crops in Florida: Elephantgrass. IFAS Extension, University of Florida. https://edis.ifas.ulf.edu//pdffiles/AG//AG30200.pdf.

Yadav, S., A. K. Roy, D. R. Malaviya, P. Kaushal, R. Chauhan and R. Tewari. 2010. Genetic diversity analysis in *Sehima nervosum. Range Management and Agroforestry Symposium Issue* 8: 269-270.

Yadav, C. B., A. Dwivedi, S. Kumar and V. Bhat. 2019. AFLP-based genetic diversity analysis distinguishes apomictically and sexually reproducing Cenchrus species. *Brazilian Journal of Botany* DOI:10.1007/s40415-019-00536-z.

Yadav, M. S., K.L. Mehra and M. L. Magoon. 1974. Genetic variability and correlations of a few quantitative characters in pasture grass, *Cenchrus ciliaris. Indian Forester* 100: 512-517.

Yadav, M.S., K.L. Mehra and M.L. Magoon. 1976. Heritability and correlations among fodder yield components in pasture grass, *Dichanthium annulatum. Indian Forester* 102: 64-68.

Young, B. A. 1986. A source of resistance to seed shattering in kleingrass, *Panicum coloratum* L. *Euphytica* 35: 687-694.

Yu, P., N. Prakash, R. D. B. Whalley, S.W.L. Jacobs and J. Everett. 2000. Comparative reproductive biology of vulnerable and common grasses in *Bothriochloa* and *Dichanthium* Grasses: *Systematics and Evolution*: 307-315.

Zadoo, S. N., A.K. Roy and R.N. Choubey. 1997. Cytology of a perennial octoploid cytotype of *Pennisetum pedicellatum* Trin: a new report. *Range Management and Agroforestry* 18:35-39.

Zhaoli, Y. 2004. *Co-Management of Rangelands: An Approach for Enhanced Livelihoods and Conservation*. ICIMOD Newsletter, No. 45. Kathmandu: ICIMOD.