5. PLANT BIODIVERSITY

PLENARY LECTURE

Biodiversity Act-2002 and Agrobiodiversity

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Biodiversity encompasses the variety of all life on earth. India is one of the 17 mega diverse countries of the world with only 20.5% of the land area. India accounts for 8% of the global recorded species. India is also rich in traditional and indigenous knowledge, both coded and informal. Biological diversity is fundamental to agriculture and food production. From the millions of genes that serves as building blocks to the thousands of plants and animals that make up natural ecosystem. Under the contextual reference of modern intensive agriculture demanding many farmers to adopt high yielding varieties of plants and animals, biodiversity makes an essential contribution for feeding the millions of population of the world. When farming communities abandon diversity, varieties, and breeds of animals extinct and the specialized useful traits may be lost. Agricultural diversity forms an important component for developing varieties and animal species withstanding temperature extreme floods, droughts, outbreak of disease reducing the crop productivity and directly causing untold hardship to the farming community.

Agro-Biodiversity:

The country is bestowed with immense agro-Biodiversity and a rich diversity in landraces/traditional cultivators/ farmers varieties. A number of crop plants are reported to be cultivated in India. India is the centre of origin of 30,000-50,000 varieties of cultivated plants including rice, pigeonpea, mango, okra, bamboo etc. There are certain laws in India which are pertaining to Agro-Biodiversity. A new legislation Plant Varieties and Farmers Right Act, 2002 has also been developed by the Ministry of Agriculture which inter alia recognizes and seeks to protect the interest of the traditional rural and farming communities, who have made significant contributions to the conservation and enhancement of genetic diversity particularly at the intra-specific level.

The Biological Diversity Act, 2002:

In pursuance to giving effect to CBD, India has also developed a national legislation for the conservation of Biodiversity i.e. The Biological Diversity Act (BDA), 2002 (Table 2.3). The legislation primarily addresses the issue concerning access to genetic resources and associated knowledge by individuals, institutions or companies, equitable sharing of benefit arising out of the use of these resources and knowledge to the country and the people. It provides for setting up of a three tier structure at national, state and local levels:

- National Biodiversity Authority (NBA)
- State Biodiversity Boards (SBB)
- Biodiversity Management Committees (BMC)

The Biological Diversity Act 2002 also has provision dealing with access and benefit sharing mechanism and protection of traditional knowledge dealing with biological resources. All foreign nationals require prior approval of

NBA for obtaining biological resources and or associated knowledge for any use and similarly, all Indian nationals require approval of NBA for transferring any research results involving any biological resources to foreign nationals/ organizations for commercial purpose. However, there is an exemption under the legislation to collaborative research projects, and exchange of any knowledge and resources under these projects.

BDA also impose an obligation on the Indian Industry to give prior intimation to the SBB about obtaining any biological resource for commercial use. The SBB has the power to restrict the activity if found to violate the objectives of conservation, sustainable use and benefit sharing. However, Indian citizens/local people including vaids and hikims are allowed to have free access to use biological resources within the country for their own use, medicinal purposes and research purposes. The act also has a provision for setting up framework for protecting knowledge. The monetary benefits, fees, royalties as a result of approval by NBA to be deposited in National Biodiversity Fund which will be used for conservation and development of areas from where resource has been accessed, in consultation with the local self government concerned. There is also an important provision in the Act for notifying Heritage Sites by State governments in consulation with local self-government.

INVITED LECTURES

Managing diversity of legumes at genetic, species and ecosystem levels

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Conservation of available diversities of plant species is very important for welfare of mankind. In this paper we have discussed the management of diversity of legumes at genetic, species and ecosystem levels. In Indian subcontinent diversity for many legumes is available in sufficient numbers. The regions rich in diversity of legume crops in India are western Himalayas including cold arid tracts, north eastern regions and eastern Himalayas, eastern peninsular region, western arid/semi-arid region, central tribal region, western peninsular region. Besides, cultivated species India is also rich in diversity of wild relatives of legumes, which mainly occur in western and eastern ghats, north eastern hills, north eastern plains, peninsular region, northern Himalayas, northern plains / gangetic plains. At present NBPGR with network of its 10 regional stations located in various agro-climatic regions of the country and 59 national active germplasm sites (NAGS) manage the plant genetic resources including legumes. Several other international research institutes viz., CIAT, ICARDA, ICRISAT, IITA and AVRDC are also involved in collecting and conserving the enormous wealth of genetic diversity of different legumes crops. All these research institutes, spread all over the world are responsible for exploration, collection, characterization, evaluation and utilization of genetic diversity of different legume crops. The genetic base of legumes is quite narrow and the real challenge, therefore is to convert the collected plant genetic resources through pre-breeding into parental lines, which will be more acceptable to the plant breeders. For management of large collections of diversity of different crops, these could be pruned to a manageable sample or core collection. The core subset should be designed to minimize repetitiveness within collection and it should represent the rich genetic diversity of crop. Molecular markers proved to be useful tools to identify materials by gene pool of origin, to show germplasm diversity, to fingerprint commercial varieties, to show gene flow, to map genomes and to tag genes of economic importance. In context of conflicts arising due to intellectual propriety rights (IPR) registration of germplasm is one of the important activities of diversity management. Therefore it is important to register the germplasm for its uniqueness for their effective utilization in crop improvement programme. NBPGR is nodal institute for registering the unique/useful germplasm

Establishment of core collections of grain legumes: Strategy for effective utilization of genetic resources

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Grain legumes are primarily cultivated for protein-rich edible seeds, green vegetable, fodder and edible oil. A large number of accessions (48,921 of three crops) are conserved in ICRISAT and in NBPGR (66,349 accessions of 16 crops) genebanks. This germplasm have been well characterized and documented. To enhance utilization of germplasm in crop improvement core collections (10% of entire collection) have been developed. In species with large collections, mini-core collection (10% of core, 1% of entire) has been proposed by ICRISAT scientists. Nineteen core/mini-core sets of 11 legume crops have been developed worldwide. Core/mini-core collections of chickpea, groundnut, and pigeonpea have been evaluated for traits of economic importance (yield, early maturity, diseases, drought etc.) and genotyped using SSR markers as component of the composite collections under Generation Challenge Programs. Trait specific genetically diverse germplasm have been identified for mapping the traits and utilization in the crop improvement to develop broad-based cultivars.

Broadening the genetic base of pulse crops: Present status and future strategies

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Pulses are integral components of sustainable agriculture with global production of 61.73 million tonnes from 73.20 million ha area with average productivity of 843 kg/ha. In spite of being the largest producer of pulses, India contributes only 23% to the global kitty mainly because of low productivity which is estimated at 595 kg/ha. In addition to well known productivity constraints, narrow genetic base of the pulse crops have been identified as the major technical constraint in spite of development of more than 550 varieties using various breeding methods. This is basically due to bottlenecks at evolutionary process in nature and in the directed breeding programmes undertaken at different research stations. Pedigree analysis of the released varieties of different pulse crops clearly brought out this fact that the extensive and repetitive use of the superior genotypes with common ancestors as the one of the parents in hybridization is a common phenomenon in pulse crops. This suggests that there is an urgent need to broaden the genetic base of cultivated species of different pulse crops by pre-breeding efforts. Pre-breeding efforts in chickpea, pigeonpea and Vigna crops have started showing its results in the form of enormous variability for useful traits in the breeding material. Some of the varieties released through pre-breeding efforts are HUM 1, Pant Mung 4, Meha and UPM 02-17 in mungbean and Mash 1008 in urdbean. Some of the promising lines like Mash 114 emanating from interspecific cross showed yield superiority of 40% in multilocation trials. The present article summarizes the past successes, current efforts on wide hybridization, and future approaches for broadening the genetic base in pulses crops.

Utilization of potential germplasm and species spectrum in improvement of legumes

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Genetic base of most of the released cultivars of legumes in India is narrow and needs immediate corrective measures by involving potential germplasm accessions, exotics and wild relatives in breeding programme. Enormous variability is available both within the primary species of interest and among related species in almost all the food legumes. More than 62,000 accessions of different food legumes viz., chickpea, pigeonpea, groundnut, lentil, mungbean and urdbean are conserved in genebanks of CGIAR institutes which are available for research and breeding purposes. About 79,000 accessions of these crops are maintained by national programmes and research centres. Global germplasm collections of Soybean is 1,70,000. However, the utilization of potential germplasm is constrained by poor characterization of genetic resources, a widening gap between improved and unimproved material, and disruption of well adapted genotypes during introgression. Over last ten years, for the development cultivars of mungbean 190 parents , of urdbean 186 and of lentil 466 parents have been used as sources for disease resistance and other desirable characters in India. Efficient utilization of exotic germplasm would benefit programmes aimed at producing new improved cultivars from adapted germplasm by providing potential sources of disease and pest resistance alongwith other agronomic traits. A total of 8 exotics of chickpea, two of pigeonpea, five of fieldpea, 11 of mungbean, one of lentil, three of rajmash have contributed in the development of different cultivars of these crops in India. The exotic accession PI 17443 has been widely used as a source of YMV resistance in development of many leading cultivars of soybean. However, rate of infusion of new exotics in breeding programme has been slow. Several exotic accessions with useful traits are yet to be exploited in breeding programme. Utilization of wild species germplasm has an important place in the history of many crop plants. Unfortunately, in cultivar development of food legumes, the role of wild species has been minimal. Recent interspecific hybridization has concentrated more on the transfer of specific adaptive

traits between species rather than combining complete genomes in amphiploid hybrids. Success in this approach depends on the identification of relevant and relatively simple genetic traits as well as good knowledge of species relationships governing the potential for recombination between genomes. Controlled introgression between mungbean and urdbean has been successful in transferring MYMV resistance from urdbean. Also a gene that control the vegetative growth has also been transferred from urdbean. Progress has also been made in the introgression of traits from *Vigna silvestris* into urdbean. Introgression of disease resistance from Arachis cardenassi, A. chacoense and A. batizocoi into groundnut has produced desirable segregants. *Glycine soja* a wild relative of soybean is reported to have desirable traits like high protein and resistance to soybean cyst nematode. Despite the appeal of this species as a source of diversity and easy accessibility, there has been little success in breeding due to undesirable phenotypic traits. A greater challenge for crop improvement is to utilize species outside the primary gene pool. Using monogenic traits is the simplest case for interspecific gene transfer because selection in small population is possible. However, multigenic traits can also be transferred from wild to cultivated species, including yield increases and adaptation traits. New DNA technologies allow more targeted approaches to the use of genetic resources. Possibilities for gene transfer between related species using conventional techniques expand the available gene pool. The present paper describes the status of utilization of potential germplasm, exotics and wild species, target traits for introgression, availability and possible approaches for their utilization in improvement programme.