Principles, strategies and practices of exploration, collection, characterization, evaluation and cataloguing of Plant Genetic Resources important fruit crops

Dr. P. C. Tripathi
Principal scientist and Head
Division of Plant Genetic Resources
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bangalore-89, Karnataka
E-mail: prakaashtripathii2000@yahoo.co.in

India has a rich and varied heritage of biodiversity, encompassing a wide spectrum of habitats from tropical rainforests to alpine vegetation and from temperate forests to coastal wetlands. Out of 18 biodiversity hot spots identified in the world, four hotspots, i.e. Western Ghats, Eastern Himalaya, Western Himalaya, and Nicobar islands are in India. Apart from this, India has 26 recognized endemic centres which are home to one - third of all the flowering plants from identified and described so far. It is estimated that there are 8.7 million species of the world's biota. Out of them only 1.7 million have been described to date, and their distribution is highly uneven. About seven per cent of the world's total land area is home to half of the world's species, with the tropics alone accounting for 5 million . India contributes significantly to the biodiversity of the world by accounting 7.31 % of the global plant diversity from 2.4% of the world's area.

India has two major realms called the Palaearctic and the Indo-Malayan, and three biomass namely, the tropical humid forests, the tropical dry/deciduous forests, and the warm desert/semi-deserts. The endemism of Indian biodiversity is high. About 33% of the country's recorded flora are endemic to the country and are concentrated mainly in the North-East, Western Ghats, North-West Himalaya and the Andaman and Nicobar islands. Of the 49,219 plant species, 5150 are endemic and distributed into 141 genera under 47 families corresponding to about 30% of the world's recorded flora, which means 30% of the world's recorded flora is endemic to India. Of these endemic species, 3,500 are found in the Himalayas and adjoining regions and 1600 in the Western Ghats alone. India is a centre of crop diversity - the homeland of 167 cultivated species and 320 wild relatives of crop plants. India's record in agro-biodiversity is equally impressive that it has 167 crop species and wild relatives. India is considered to be the centre of origin of 30,000-50,000 varieties comprising of rice, pigeon-pea, mango, turmeric, ginger, sugarcane, gooseberries etc and ranks seventh in terms of contribution to world agriculture. India is one of the 17 mega diverse countries of the world holding approximately 8% of global biodiversity with about 45000 plant species in 16 agro-climatic zones. Historically, the Kings and rulers used to conserve many of this diversity in the gardens around their palaces or in the vicinity of temples. Several fruit plant species have originated in Indian subcontinent (Table 1). While many fruits crop species such as pineapple, papaya, guava, cashew, Grapes, pomegranate, litchi, longan, avocado, apple, peach, plum, kiwifruit etc. were introduced by travellers, preachers and invaders

during last 6-7 centuries and several are naturalized in Indian conditions. India holds the world's larger germplasm of several tropical and subtropical fruits such as mango, guava, jackfruit, etc.

Table 1. India-Centre of Diversity of fruit Crops

Primary centre	Mango, citrus, jack fruit, bael, aonla, ber, khejri, jamun, tamarind, phalsa, Lasoda, karonda, wood apple, pilu, bilimbi, *Garcinia,* Under utilized fruits
Secondary centre	Banana, pomegranate, mulberry, *Malus, Pyrus, Prunus, Rubus*

(Source: Singh *et al*. 2009)

Conservation and planned utilization of plant genetic resources is essential for the survival of human beings and other living organisms. Over 24,000 plant species have been reported which have importance for human being. Yet only about 3000 of them are grown for human use and only 30 plant species are feed 90 percent population of the world. Human and natural selection for thousands of years have resulted in establishment, improvement and differentiation of numerous types within each crop species, which is described as genetic resource.

1.0 Plant genetic resources

Plant Genetic resources refer to genetic material of actual or potential value. Plant Genetic material is any material of plant, animal, microbial or other origin containing functional units of heredity. Germplasm are living genetic resources such as seeds or tissues that are maintained for the purpose of plant breeding, preservation, and other research uses. Plant genetic resources include i) Land races and primitive cultivars, ii) Obsolete Farmer's named and old released varieties, iii) Recently released varieties, iv) Parental lines of released hybrids, v)Genetic stocks with known desirable attributes, vi)Wild and weedy relatives of cultivated crops.

Plant genetic resources management involves broadly five stages, viz. exploration and collection, characterization and evaluation, conservation, exchange and utilisation, and documentation. In addition, it is also concerned directly or indirectly with the plant quarantine. At each of the various stages in the above process, information about plant material is used for communication and decision making.

2.0 Exploration and collection

The explorations are carried out in the hot spots areas for collection of plant species and germplasm. Earlier these were done on the basis of experience and previous literature. Now the satellite base imagery and techniques are used for identification of species diversity in a particular locality or region**.** The objectives of the various institutes engaged in plant and/or germplasm collecting activities are different. It would be worthwhile considering the scope of the two activities, the similarities and differences and their complementarily taken together, viz. plant exploration as undertaken by Botanical surveys of India, National Botanical Research Institute , Forest Research Institute etc. as against the specific activity of crop germplasm collection. Plant exploration in its traditional sense is distinct from plant genetic resources collection. This will be evident from the study/survey targets as specified/exemplified in Table 2. Thus, traditional plant exploration is complimentary to PGR collecting. The two aspects together help in locating more

plant diversity of known and untapped potential of current and future use to mankind. Let us compare the two activities (Table 3).

Table 2. Plant exploration and collection *vs.* germplasm collection

Plant exploration and collection	Germplasm collection
Areas of floristic richness-biomes, vegetation/floristic regions, formation, etc.	Areas/regions of genetic diversity-primary, secondary centres; specific attributes represented therein in relation to ecogeography/agro-ecology
Collection based on ecogeographic/phyto-geographic surveys; more static/geographic approach	As above; more dynamic geographic approach
Floristics/flora of an area or region, etc.	Crop resources - their distribution and diversity as per utilisation, (cereals, pulses, fruits, vegetables, oilseeds, fibres, forages, etc.)
Monographic works on taxonomic groups/taxa	Studies on crop domestication/evolution (including archaeological, palaeobotanical evidences)
Taxonomic diversity includes mainly species and supra-level representation (taxonomic approach)	Crop genepool including its wild relatives in one basic unit; involves population structure, incompatibility barriers etc., crop germplasm includes landraces, primitive cultivars, introgressed forms, obsolete and promising plant genetic resources (genetic approach).
Economic taxa-synthesis on basis of uses; ethnobotanical information, collection of wild ornamental plants, study of potential elements of flora	Utilisation linked with agro-botanical/agronomic attributes-plant type, promising traits etc., landrace (s) diversity also linked with ethnic diversity/anthropogenic factors

(Source :Paroda &Arora, 1991)

Table 3. Comparison of approaches in collection of plants and/or germplasm diversity

Plant species collection	Germplasm collection
Wide range of species collected and all ecogeographic regions surveyed for collection	Narrow range of taxa-crop and wild plants collected; collection done in agro-ecological zones/areas with different agricultural practices
Specific and supra-specific categories represented	Material collected mainly at infra-specific levels
Variation represented in commonly available plants and extreme variants, either end of range of variation, is represented (cultivated taxa represented are an extreme type of variation)	Within the unit of collection/genepool, full range of variation represented - common types through random collection and rare types through biased collection
Functional unit of study/collection is species, largely characterized by differences in morphological traits and geographic distribution	Functional unit is a population and unit of demarcation is barrier to geneflow
Collection for flowering/fruiting materials, i.e., limited range of variation represented	Collection surveys taken up based on life cycle pattern - seed producing, vegetatively propagated, annuals/perennials etc.
Periodic surveys of area through the year for full representation of material	Repeated surveys in season of occurrence/ maturity for full representation of variability

Data recorded on limited scale-habitat, locality, size, colour, of plant/plant parts, uses, etc.	Exhaustive data recording done-site/habitat, habit, other characteristics etc.
Material collected and preserved as dried, mounted and identified specimens in Herbarium; in live state, species represented in botanic gardens; phenological data recorded	Material collected as seed, pollen, embryos, vegetative tissue for multiplication/conservation; live material represented in field genebank/plots; regrown material used for evaluation

(Source :Paroda &Arora, 1991)

The collection of plant genetic resources primarily aims at tapping germplasm variability in different agri-horticultural crops, their wild relatives and related species. The germplasm so collected reveals the nature and extent of variability in different species, within species, cultigens, etc. and also their agro-ecological/phyto-geographical distribution. These explorations differ from the floristic surveys which are mainly undertaken to study the flora or plants of an area or its vegetation so as to list out the species diversity. Such botanical studies are generally of taxonomic and ecological relevance and do not deal with the genetic diversity concepts, whereas the botanical collector may look for uniformity or trueness to type. The field sampling procedures in plant genetic resources exploration are aimed at the fullest possible recovery of genetic variation within species, irrespective of the relative frequency or rarity of any genes. Thus, exploration and collection of plant genetic resources must be based on the application of sound scientific principles. The objectives of the botanical collector and the plant genetic resources collector are not the same. Hence, more meticulous planning is required in dealing with germplasm collecting so that the explorer is in the right area at the right time and can search for and collect germplasm - ripe seeds, tubers, vegetative propagules, etc. and study the existing variability in the field. Knowledge of agro-ecology, crops and their distribution and harvesting time in areas of survey, local contacts, equipment required, transport arrangements and routes to be followed, distances involved, places of halt/camping sites available, transport of material, besides team-composition etc. is to be acquired before setting out on a collecting expedition. It is also important to acquire knowledge on diversity in crop plants *vis-a-vis* its distribution to tap target areas and/or target species and the variability.

By and large, germplasm collecting missions are broadly of two kinds: **Specific missions** which aims to collect variability in a particular crop or cultigen, or material of specific attributes, say mango ; e.g. types adaptable to saline tracts of western Indian plains or to collect specific wild relatives, weedy types and related taxa of agri-horticultural relevance e.g. *Mangifera*, *Citrus*, *Musa* and others. The other kind of are **Broad based missions** which are aimed is to tap maximum diversity in different crops (multi-crop collecting missions) occurring in the region to be explored, and maturing almost at the same time. Both kinds of explorations are taken up by the agencies depending on the priorities assigned to crops/regions, specific needs of the breeders to enrich germplasm variability with desired attributes, and to salvage endangered/endemic resources, landraces, wild types, etc.

2.1Types of collections

Currently three types of collections are held at most genetic resources centres.

2.1.1 Base collection

The base collection is defined as a set of accessions, which in terms of genetic integrity, is as close as possible to the sample provided originally, which is preserved for long term future. Normally seeds will not be distributed from the base collection directly to users and it acts as a backup to an active collection.

2.1.2Active collection

An active collection comprises accessions which are immediately available for multiplication and distribution for use. Accessions are stored for short to medium periods of time (generally upto 20 years) as is often the case for breeder's collection. Active collections should be kept at such a conditions at least 65% germination can be obtained after for 10 to 20 years. Active collections are generally held at temperatures between 0-10^{o}C depending upon the species stored, the· prevailing ambient environment and cost factors.

2.1.3 Working germplasm

The genetic material held by the breeders to carry out comprehensive evaluation, testing and section and hybridization**.**

2.2 Strategies and Techniques in collection of Plant Genetic Resources

The collection strategies involve planning the activities required in collection of Plant Genetic Resources during plant explorations. The most important aspects of explorations are:

2.2.1 Sampling Strategy

The sampling strategy primarily depends upon the type of exploration (multi crops/ region specific crop specific/trait specific), objectives of the collection (gene pool/ specific), reproductive system of the crop (Whether cross pollinated/ self pollinated/ vegetatively propagated), extent of gene exchange between the populations and the pattern and distribution of genetic variations. The theory of sampling suggests extensive knowledge of the pattern of genetic variations. In general, there are relatively few species for which this type of information is available. Most species exhibit extensive geographical variation and superimposed on this is the variation within populations. Ecological habitat and/or factors are a major determinant of genetic diversity, and agro-ecotypes are most clearly distinguished in primitive cultivars and landraces. Climatic factors, such as maximum and minimum average temperatures, precipitation and the seasons of dormancy and growth, light intensity, and day length are all reflected in corresponding developmental characteristics. Such factors generally lead to clinal variation patterns, whereas topographically or edaphically determined differentiation may lead to either a clinal (as in the case of altitude) or a mosaic distribution. Consequently, the distribution of variation as affected by such factors should be reflected in the frequency of sampling. The variation within populations, especially at the local level, will depend on the interaction of the breeding system of the species and the forces by which variation is maintained, the maintenance of heterozygosity in out breeding species and genetic structure of inbreeding species. There is now considerable evidence which shows that such populations also contain much genetic variation and heterozygosity. Sampling methods must be used to ensure the collection of representative within-population variation as well as that associated with geographical patterns of variation.

The following methods of sampling are generally followed for the collection of diversity during plant explorations.

2.2.1.1 Random Sampling

Random sampling is usually carried out by randomly selecting a starting point at a collection site and taking a single spike or few pods/ball/puts at every second and third place along a number (50-60) transacts evenly dispersed in a target sets and bulking them to form a random sample. Random sampling at pre determined intervals will be satisfactory.

2.2.1.2Biased sampling

This method is generally followed for sampling rare phenotype variants or observable spontaneous mutants occurring in the target population. The attention is given to identify specific variants for direct utilization.

2.2.1.3 Clustered Sampling

This method is applicable for collection of well relatives or weedy species. The collection site is divided into several evenly spread clusters. Samples are taken independently from each cluster and then bulked together to form a multiple sample.

2.2.1.4 Coarse Grid Sampling

This technique of sampling is used to collect random bulk samples from a site by harvesting parts/plants from several spots of the site. In coarse grid sampling is made at wide interval over the entire region.

2.2.1.5 Fine grid sampling

This sampling technique is used in interested or intensive areas of variation identified after the coarse grid survey. Collector may walk across the site or field twice in cross or zigzag manner avoiding sampling from borders.

2.3 Sampling frequency and size:

The number of sample per site and size of the sample is governed by the extent of genetic diversity and gene flow will be taken and the agro ecology of the site. The collector should use a practical approach and utilize on the spot observation to devise the best sampling technique. The optimum size of sample per site would be the number of plants required to obtain 95 per cent certainty. For smaller seeds very much large samples should be collected whenever possible the seeds should be collected from disease free plants. Immature parts should not be collected whenever there is doubt about the viability, large sample may be collected. The general sample size may be 200-250g seed /sample but large seed crop 500g seed/sample may be collected while small seeds 50-100g seed / sample is may be optimum.

2.4 Collection sites

There are four main collecting sites i.e. (i) farmers field, (ii) kitchen garden (iii) market and iv) wild habitant. Among these, farmer's fields are most important as it provide larger wealth of cultivated and primitive cultivars.

2.5 Collecting Wild Relatives of Crop Species

By and large, wild relatives and related taxa can be classified into primary, secondary and tertiary gene pools.

2.5.1 Primary genepool

Wild species in the primary genepool can produce fertile hybrids with cultivated types and hence are easy to exploit. These are wild progenitors closely related to crops.

2.5.2 Secondary genepool

The wild species are relatively distantly related and cross compatible and hence contribute germplasm less easily.

2.5.3 Tertiary genepool

Distantly related and unrelated taxa of different genra/ species which can only be used with difficulty for some crops for a limited number of genetic traits are considered as tertiary gene pool. The wild species and the weed races represent the highest level of genetic heterozygosity and heterogeneity among the different classes of germplasm. They generally have higher rates of natural out crossing than their domesticates.

2.5.4 Collection techniques

a) Seed propagated, cultivated and wild species

i. Randomly selected sample of 50-100 plants of self pollinated crop and 100-200 plants of cross pollinated crops.
ii. Collect fully and physiologically mature seeds.
iii. Collect about 50 seeds (as per the availability) from each plant and bulk to make a population sample of 2000-4000 seeds in self pollinated and 4000-8000 seeds in cross pollinated crops.
iv. Record passport data and important plant traits for each sample.
v. Sample as many sites as possible as per the .availability of time.
vi. If considerable morphological variation is present make separate samples of each type.
vii. Add biased sample if some morphotypes are not included in random
viii. Take whole inflorescence whenever necessary as voucher samples
ix. Make herbarium specimens wherever possible.
x. Take photographs of the important variants materials.
xi. Write desired field notes

b) Vegetatively propagated crops:

i. Sample each distinct morphotype in the area.
ii. Supplement with seed collections wherever possible give separate number for same plants or seeds from several plants (bulk samples)
iii. The collected materials for grafting with 3-4 days send by speed post or special messengers

c) Vegetatively propagated species

i. Collect just a propagules sample from each 10-15 individual as bulk sample from n area of 100x100m
ii. Choose sampling sites as broad as possible over the environmental range.
iii. Sample as many sites as possible
iv. Supplement with seed samples wherever possible

2.6 Field data recording

The sample forms which were developed by Bioversity International and modified the NBPGR is used for recording the passport data in India. The amount of information which can be recorded during collecting activities is very much dependent upon, the time available. There is a minimum amount of information which must be recorded regardless of time. But other details may be

regarded as being of only secondary importance by some, and to be kept to a minimum so that the time spent actually on collecting can be maximized. Others argue that extra time spent on recording additional information will save time later by avoiding some aspects of evaluation. Clearly, a compromise can and must be made in this respect. Various designs of collecting forms, sheets or books have been used by collecting missions. The details given are more applicable to multicrop collecting. Specific crop missions will need different forms depending on the crop and wild species collecting, forage collecting, etc.

3.0 Characterization

The main aims of germplasm characterization are to describe accessions and establish accessions diagnostic characteristics ,classify accessions into groups using sound means , assess inter - relationships among accessions or among traits and among geographic groups of accessions, estimate the extent of variation in the gene bank collection, identify duplicates in a collection. The characterization of plant genetic resources for purposes of identification and evaluation of plant varieties includes morpho-agronomic characterization, biochemical characterization and molecular characterization.

3.1 Morpho-agronomic characterization

The morpho-agronomic characterization consists in the analysis of germplasm, using specific descriptors developed by IPGRI (Bioversity International), the UPOV or other international consortia, and subsequent morphometric analysis. The data obtained is used in the phenotyping of the characterized germplasm, in assessing diversity and variability of biological resources, leading to the identification of regional and/or conservation plant varieties. The morpho-agronomic specific information is used in the elaboration of passports and reports. Characterization of each sample involves a description of the special characteristics that are inherited, easy to score and expressed consistently in all environments. Most germplasm characterization is carried out in precision fields by spaced planting under adequate agronomic conditions and plant protection with proper statistical analysis yield further information.

The characterization of the collections/germplasm should be done on the basis of the descriptor or minimum descriptor. Bioversity international in collaboration of national genetic resource agencies have developed descriptor for more than 100 crops. They are available at http://www.bioversityinternational.org/elibrary/publications/categories/descriptors/

3.2 Biochemical characterization

The biochemical characterization performed in the analysis of germplasm, uses processes such as protein fractions (storage proteins) or other biochemical markers (antioxidants). These descriptors are proposed by IPGRI (Bioversity International) to assess the diversity of germplasm, the International Seed testing Association for quality control of seeds and propagating material, and by the Community Plant variety Office for identification of marketed plant material or plant varieties.

3.3 Molecular characterization

Molecular characterization consists in the analysis of germplasm, using different molecular markers (microsatellites, ITSs or SNPs). These descriptors are proposed by IPGRI (International Bioversiy) to assess the genetic variability of germplasm, allowing detection of specific markers for identification of regional varieties or misrepresentation of material through genetic

modification (GMO Detection). The obtained data is used in the typing of regional varieties and control of the integrity of the collection of germplasm accessions. Specific molecular information is gathered in passports and reports.

4.0 Multiplication

Most of the time the quantity of seeds, propugules, obtained during survey, exploration and collection is not sufficient for characterization and conservation. In these cases these collections are grown to produce required quantity of seeds. Strict guidelines should be followed for this purpose as per the nature of the crops.

5.0 Evaluation

Main aim of evaluation is to reveal potentially useful variability for further use in genetic enhancement of crops. Evaluation may be expensive and time consuming but is of great value for a precise phenotyping of genebank accession(s) of interest .It is more comprehensive than characterization. It usually includes agronomic performance, yield and reaction to biotic and abiotic stresses, such as drought or pests. These traits are important to plant breeders and researchers in crop improvement. It may require special biochemical techniques or DNA-based methods to analyse a plant's genetic diversity. The information obtained is used for verifying that an accession belongs to the original description, supplying users with the most suitable accession or with information that will allow them to select their own accessions, defining diversity patterns and relating them to the origin and history of the crop. The initial evaluation may be undertaken in small nursery plots followed by a more detailed field trial to assess useful traits that show quantitative variation. Screening techniques are required to assist in identifying sources of host plant resistance to main pathogens and pests. Control or heck line often the most used locally adapted cultivar should be included as a reference standard for comparisons with the accessions being evaluated.

6.0 Conservation

The management of human use of the biosphere so that it may yield the greatest sustainable benefit to present generations, while maintaining its potential to meet the needs and aspirations of future generations. The fundamental objective of genetic resources conservation is the maintenance of broad based genetic diversity within each of the species (i.e., intra-specific genetic diversity) with a known or potential value in order to ensure availability for exploitation by present and future generations. There are broadly speaking two basic approaches to genetic resources conservation, namely, *in-situ* and *ex-situ* conservation. The choice of *in-situ* and *ex-situ* conservation is sometimes seen in terms of exclusive alternate strategies but the two alternatives may be more constructively viewed as mutually complementary activities and each can play an important part in safeguarding particular plant populations. It would be an ideal situation where both may be used to best advantage to ensure both long-term species survival and an adequate supply of germplasm for improvement of related crops.

6.1 *In- situ* conservation

In-situ means the setting aside of natural reserves, where the species are allowed to remain in their ecosystems within a natural or properly managed ecological continuum. The natural biosphere reserve is a useful solution for species that are endangered and nearly on the point of extinction. However, for species more widely distributed, the conservation of total genetic diversity of

species *in-situ* is difficult. Although species conserved in their natural habitats have the potential for continued evolution of a particular trait within the species and are subject to natural selection, there are indeed many problems in establishing this type of reserve, for example, cost, size and maintenance aspects, political and social issues and the danger of genetic wipe out as a result of natural disasters, fire, etc. In particular, this method of conservation is of significance to the wild relatives of crop plants and a number of other crops, especially tree crops and forest species where there are limitations on the effectiveness of *ex-situ* methods of conservation. The crops of immediate interest for *in-situ* conservation are the perennials that are vegetatively propagated and those with seeds that cannot survive cold storage. Wild species maintain their original characteristics best in the habitat to which they are adapted, which necessitates the formation of nature reserves in appropriate climatic, altitudinal and latitudinal zones. Establishment of forest area reserves and national parks and protected areas is being promoted which will facilitate in situ conservation of plant species. *In-situ* On farm conservation of useful plant genetic resources is another important concept to promote in situ conservation of valuable plant varieties developed and protected by fanners for centuries in certain areas.

6. 2 *Ex- situ* conservation

The *ex-situ* form of conservation includes field gene banks , botanic gardens and storage of seed or vegetative material in gene banks or other complementary methods of conservation such as pollen cryopreservation, *in- vtiro* conservation, DNA conservation etc.

The field gene banks where clonal materials are maintained as living collections in a field/orchard or plantation are major form of ex-*situ* conservation in fruit crops. The field gene banks need large amount of space and labour to maintain a small proportion of diversity. The field gene banks have the potential risk of germplasm being lost due to disease, stress or disaster. In India National Active Germplasm Sites (NAGS) have been indentified for the conservation of germplasm (Table 4).

Table 4. Designated National Active Germplasm Sites (NAGS) for horticultural crops

Crop(s)	**Designated NAGS**
Arid fruits	Central Institute of Arid Horticulture, Bikaner
Banana	NRC Banana, Tiruchirapalli
Citrus species	Central Institute of Citrus Research, Nagpur
Grapes	NRC for Grapes, Pune
Aonla, Bael& Litchi	NRC Litchi , Muzaffarpur
Jackfruit	Indian Institute of Horticultural Research, Bangalore
Mango	Central Institute for Sub-Tropical Horticulture, Lucknow Indian Institute of Horticultural Research, Bangalore
Subtropical fruits	Central Institute for Sub-Tropical Horticulture, Lucknow Indian Institute of Horticultural Research, Bangalore
Mulberry	Central Silk and Mulberry Genetic Resources Centre, Hosur
Temperate horticulture Crops	Central Institute of Temperate Horticulture, Srinagar NBPGR RS, Shimla
Tropical fruits	Indian Institute of Horticultural Research, Bangalore

Seed storage is one the most important methods of conservation of seed propagated crops. The seed are generally of two types i) orthodox type (desiccation tolerant seeds) and ii) Recalcitrant seeds as per their of storage behaviour. For orthodox or desiccation tolerant seeds, lower seed moisture content is associated with an increase in storage life of a sample within certain limits. The viability of these seeds can be maintained by drying the seeds and storing these at low temperature and Conservation of these seeds is relatively easy for seeds. The recalcitrant seeds are relatively short lived (few weeks to months) even under high moisture conditions and require different storage technique. These are desiccation sensitive and are generally killed if dried below a critical moisture content value, usually between 12 and 35 percent moisture. Most of the tropical fruits have seeds with recalcitrant behaviour.

Efforts to conserve genetic resources *ex-situ* in seed gene banks have accelerated in the past few decade. In the gene bank, the aim is to provide ideal storage conditions so that the mean viability period of the seeds is greatly extended by reducing the life processes to a low level. Successful seed storage depends on effective control of several factors including temperature, seed moisture content, storage atmosphere, etc. in response to storage conditions. Seeds within heterogenous germplasm accessions frequently deteriorate at different rates thereby causing selection within the samples to favour genotypes more amenable to given storage conditions. The selection within the germplasm accession during seed conservation and subsequent regeneration has a strong influence on the genetic composition of an accession. This is one aspect of *ex-situ* conservation in genebanks that makes it desirable to ensure indefinite maintenance of some wild populations of most crops *in-situ.*

In-vitro cultures offer promising avenues to overcome the several constraints. However, the genetic stability of *in-vitro* cultures has yet to be fully ascertained before an entire collection is committed to this storage technique. Cryogenic preservation of vegetative material is another mode of *ex-situ* conservation and it holds promise, especially for base collections.

Some major issues related to plant genetic resource Conservation include

i. Ensuring adequate facilities and technologies for long-term *ex- situ* conservation
ii. All collections should be stored in at least two base collections under sub-zero temperatures
iii. Ensuring accuracy of passport and evaluation data in gene bank.
iv. Developing core and reserve sub sets for each major crop to increase efficiency and to reduce operational costs
v. Collecting additional landraces and wild relatives to fill gaps from important ecogeographical areas
vi. Development of procedures to minimize genetic changes during *ex situ* conservation
vii. Development of protected *in situ* reserves for wild relatives.

7.0 Documentation

Plant genetic resources provide base material to plant breeders for the development of new and superior crop varieties. During the last four decades, a growing awareness has been witnessed to collect and conserve these fast depleting, irreplaceable resources for the good of the present and future generations. At the same time, it has been accepted that the success of the entire genetic resources activities is dependent upon the descriptive information of the conserved material which enables plant breeders to make decisions regarding the material to be used in breeding

programmes. This dependence on information grows exponentially with the size of the collections.

A genetic resources centre generally handles germplasm samples with all information associated with it and this information can be broadly classified into four major categories depending upon their use. The information is available is the form of Passport data, Characterization, preliminary and further evaluation data, Conservation management data, exchange data. The passport data includes information on the site where sample has been collected, including ecological and habitat data, altitude and climate, etc. Morphological and evaluation data on various collections includes extent of the variability observed in the field, agro-botanical and economic characters, quality traits, and reaction to various diseases and pests, etc. The conservation management data includes details of each sample stored in the gene bank, quantity, its placement in the gene bank, germination and viability percentage when stored, period of storage, to whom the parts of the samples were supplied in the past, rejuvenation date and next probable date for further replenishment of seed stocks. The exchange data includes information related to import and export of germplasm for inventory control. It is different to handle the data form large number of germplasm and crops. This is need a gene bank information system for proper retrieval and use of the data. Efficient gene bank information system should be i) Ease of data input (registration) into a storage medium ii) Data validation during input phase iii) Flexible data storage and retrieval procedures iv) Availability of data for multiple analysis and use v) Exchange of information with other genebanks vi) Basing the system and its terminology on genetic and biological principles vii) simple and user friendly, economical and adoptable .

Two basic types of database management systems can be identified, namely, hierarchical and relational. A hierarchical system tends to be extremely complex because of superior-subordinate type of relationship between data elements in a hierarchical (tree) structure. In comparison to hierarchical structuring technique, the relational technique is much simpler. Data are represented in the form of two dimensional tables and the relationships can be established between these tables. Information contained in any two or more separate files (for example, one for the passport data and the other for the evaluation data) can be related or linked if there are common fields or descriptors in these tables or files. For instance, a unique identifier for each and every accession in germplasm collection e.g. the accession number is such a common field. As a genebank preserves and provides genetic material for a multitude of purposes, the relational Data Base Management Systems is more appropriate in a genetic resources environment as it easily permits the establishment of linkages between different files and change of relationships at any moment.

During recent years, the term documentation is appropriately known as Information System. An information system is much more than simply documenting information. The information system has to be dynamic, vital and flexible and ensuring the reliability and integrity of the data and providing effective methods for their handling. Presently, a good number of genebanks are operating in the entire world. Some of them have developed their own information system, fitting to their requirements and based on the availability of the computer system, and tailored Database Management System (DBMS) software used for other purposes. One of the front runners in the

management of genetic resources data is the Nordic Gene bank at Weibullsholm Plant Breeding Institute in Sweden.

8.0 Exchange of germplasm

Plant introduction activities have been carried out throughout the world for the past few centuries. In the earlier days, the agencies for plant introduction activities were travellers, pilgrims, invaders, explorers or naturalists. The movement of plants within the old world countries was possible much earlier because of geographic contact compared to the exchange of plants between the new world and the old world which was possible only after the discovery of the Americas and the European colonisation soon after. There is enormous diversity of the old world and new world economic plants which have been exchanged not only between Western and Eastern hemisphere but also among countries constituting the two hemispheres. The last five centuries have witnessed much give and take among the economically useful flora of different regions in the world. In India, systematic activities of introduction and exchange of plant genetic resources of agri-horticultural crops is coordinated by National Bureau of Plant Genetic Resources (NBPGR).All requests for indenting germplasm from abroad are to be made to the NBPGR giving specific details of the required material, stating the source/country as well as address of organisation/scientist through a prescribed application so that the Import Permit is issued and sent to concerned scientist(s) for sending the same to exporting organisation or the Bureau be requested to pursue the import of desired material(s) from abroad. Exchange of germplasm involves not only introductions but also the supply of seed and other materials to collaborating scientists/organizations abroad. The requests for seed/planting material received from concerned organizations/agencies abroad have to be forwarded to the NBPGR with relevant information so that prompt decision on the supply of desired materials could be taken.

9.0 Quarantine

Quarantine is a strategy of control to prevent the spread of pests and diseases. It covers all regulatory actions taken to exclude animal or plant pests or pathogens from a site, area, country, or group of countries. when plant genetic resources are imported from another country or region, there is a risk that they may contain or carry pests or pathogens that could be damaging to agriculture. For this reason, countries use quarantine practices to protect their agriculture and living natural resources from potential damage or destruction. Quarantine is usually a government responsibility, and the manner in which quarantine is executed differs among nations. National agencies responsible for plant quarantine may have other responsibilities, such as domestic pest control; research; pesticide registration, safety, and residue monitoring; or seed quality and labeling. At present, India have domestic regulations against potato cyst, potato wart disease, banana bunchy top , apple scab and codling moth. All these pests still have a restricted distribution in our country.

Several types of arguments are used to promote conservation of plant genetic resources. Plants are valuable resource for humanity both now and in the future, role of plants in maintaining a stable environment. Plant genetic resources has attained global, regional and national importance in the last four decades. The International Agricultural Research Centres and the national Genetic agencies are playing great role in the collection, conservation and utilisation and utilization of crop genetic diversity. These agencies are coordinating for several policy issues to

ensure the efficiency of operating a global system in full coordination with national, regional and international organisations.

Selected References

Archak, S., Gaikwad, A.B., Gautam, D., Rao, E.V.V.B., Swamy, K.R.M. and Karihaloo, J.L. 2009. Comparative assessment of DNA fingerprinting techniques (RAPD, ISSR and AFLP) for genetic analysis of cashew (*Anacardium occidentale* L.) accessions of India. Published on the NRC Research Press Web site at http://genome.nrc.ca

Arora, R.K .1991. Plant diversity in the Indian gene centre. In: Paroda, R.S. and Arora, R.K., (eds) Plant Genetic resources-conservation and management. Concept and Approaches. IBPGR, Regional Office for South & SE Asia, News Deli pp 25-54.

Arora, R.K. and Nayar, E.R. 1984. Wild Relatives of Crop Plants in India. NBPGR Sci., Monograph No. 7, 90p.

Dhillon, B.S. and Saxena, S. 2003. Conservation and Access to Plant Genetic Resources. In: Conservation biotechnology of Plant Germplasm. BB Mandal, R Chaudhury, F Engelmann, B. Mal, KL Tao, BS Dhillon (eds.). NBPGR, New Delhi/IPGRI, Rome/ FAO, Rome, pp. 3-18.

Engels, J. and Visser, B. 2006. Genebank Management: Effective management of germplasm collection Training manual on "Conservation, Management and use of Plant Genetic resources in food and Agriculture'. Wageningen University and Research, Wageningen, the Netherlands.

Engelman, F. 1997. Present development and use of in vitro culture techniques for the conservation of Plant Genetic Resources. Acta Hort. 447:471-75.

Paroda, R.S. and Arora, R.K. 1991. Plant Genetic Resources Conservation and Management Concepts and Approaches. IBPGR Regional office, New Delhi

Rai, M. and Gupta, P.N. B. 1996. Distribution and diversity of indigenous tropical fruits. In: Genetic Resources of Tropical Fruits. NBPGR, New Delhi pp 19-43.

Singh, H.P., V.A. Parthasarathy, V.A. and Prasath, D. 2009. Horticultural Crops – Varietal wealth. Studium Press (India) Pvt Ltd, New Delhi pp.450.

Wilson, E.O. 1992. The Diversity of Life. Penguin Books, England.