Vol. 20 No.1 2007

ISSN 0971-8184

Journal of Plant Genetic Resources

An International Journal for Conservation and Use of Plant Diversity

ISPGR 1987

Indian Society of Plant Genetic Resources
New Delhi, India

Neglected and Underutilized Crop Genetic Resources for Sustainable Agriculture*

Bhag Mal
Bioversity International, Sub-regional Office for South Asia, NASC Complex, Pusa, New Delhi-110012, India

The world is presently over-dependent on a few plant species. Diversification of production systems by including a broader range of species can contribute significantly to improved health and nutrition, livelihoods, household food security and ecological sustainability. Hundreds of little known traditional, neglected and underutilized plant species help support the lives of rural people by providing food, fodder, fibre, medicine, fuel wood, and shelter and nutrition benefits especially to women and children. Being low input crops, these are important for agricultural diversification and provide a unique opportunity to combat food and nutritional insecurity within the communities. This review paper highlights the importance of neglected and underutilized species, their role in crop diversification and reducing hunger, research efforts made at the national and international level, and future thrusts for germplasm collection, characterization, conservation, utilization, capacity building and the policies enabling their enhanced role in agricultural production and well being of the people.

Key Words: Neglected, Underutilized, Sustainable, Crop diversification, Characterization, Conservation, Enabling policies

Introduction

The dependence of mankind on plant resources is inevitable. Necessity based gathering of wild plants and their domestication have helped in the evolution of several useful plant species since the dawn of agriculture. Living in close contact with nature, man has learnt to use plants for food, fodder, medicine and other purposes. Out of the global wealth of about 80,000 edible plants, only 3,000 plant species have been used for food and only about 150 species have been commercially cultivated of which about 30 species provide 90% of the world's food (NAS, 1975a; Paroda, 1988). Three crops, namely, rice, wheat and maize provide more than half of the world's calorie requirements. Dependence on a few species involves a high degree of risk of loosing their genetic diversity due to various biotic and abiotic stresses. Hence, there is an urgent need for focused attention on exploiting alternative plant species for food and other purposes in order to widen the food basket to ensure adequate food supply, better nutrition and health to the people.

Underutilized crops are plant species traditionally used by many communities for food, fibre, fodder, oil, medicines and also for several other potential uses. These species are known by various names, e.g. underutilized, underdeveloped, underexploited, minor, lesser known, orphan, new, alternative, traditional, niche, neglected, forgotten, vanishing, lost crops and life saving/support species. Traditionally, these species contribute significantly to the well being and livelihoods of rural households. Many of these species form part of subsistence farming systems, while others are valued for their medicinal uses. Many of these occur in extreme environments and marginal or waste lands, and are being lost through rapid destruction of natural habitats, especially in the tropics.

Underutilized plants, often well adapted to marginal and stress conditions, constitute the lesser known species in terms of trade and research. Generally, they have high nutritional and industrial importance and are useful to humankind in various ways. Their cultivation is restricted to specialized geographical pockets in different agroecological regions, mainly by poor farming communities which derive their sustenance and livelihood from such plants. However their commercial importance and market value is still unknown to the public. Therefore, research on underutilized crops holds promise to attain sustainability, profitability and diversification in agriculture and to restore the balance of trade, reduced dependence on imports and to become more competitive in agricultural exports since our depleting resource can be replaced with renewable ones.

The underutilized plant species of economic importance are the key to sustainable agriculture in most of the developing countries facing resource constraints as well as rapid depletion of natural resources due to ever-increasing population pressure. Poverty at both rural and urban level leads to various health and nutritional problems, respectively. This can be improved upon

** The paper is the sole responsibility of the author and does not necessarily represent the views of Bioversity International*

through wider cultivation and inclusion of underutilized crops in our food habit. Food and Agriculture Organization of the United Nations (FAO) statistics revealed that about 800 million children, women and men suffer from protein-caloric under-nutrition, while over 2 billion suffer from hidden hunger and there is a high frequency of low birth-weight children caused by the deficiency of micronutrients in the diet, particularly iron (Swaminathan, 1999).

Wealth of Less Known Plants

Well documented information is available on genetic resources of less known cultivated food plants (Arora, 1985; Paroda and Bhag Mal, 1989). The genetic diversity in the underutilized and underexploited food plants is represented by native species as well as naturalized alien species, viz., 15 species for seed/nut crops, 21 for vegetable crops, 10 for roots and tubers, 25 for fruit crops, and 10 species for other useful plants as listed below:

Seed/nut crops: The important species that need to be paid attention are *Amaranthus* spp., *Borassus flabellifer*, *Chenopodium* spp., *Coix lacryma-jobi*, *Digitaria cruciata* var. *esculenta*, *Echinochloa colonum*, *Euryale ferox*, *Mucuna capitata*, *Panicum sumatrense*, *Parkia javanica* and *Paspalum scorbiculatum*.

Pulses: The important underutilized pulse crops include *Dolichos uniflorus*, *Psophocarpus tetragonolobus*, *Vigna aconitifolia*, *V. angularis*, *V. umbellata* and *V. trilobata*.

Oilseeds: The important species which need to be paid attention are *Amoora rohituka*, *Azadirachta indica*, *Aesandra butyracea*, *Calophyllum inophyllum*, *Juglans regia*, *Madhuca latifolia*, *Pongamia pinnata*, *Prinsepia utilis*, *Salvadora oleoides*, *Schleichera oleosa*, *Shorea robusta* and *Terminalia catppa*.

Vegetable crops: Amongst these crops, there are two distinct categories: i) plants whose leaves/young shoots are eaten cooked or used in making soups and ii) plants whose tender fruits/pods are consumed as vegetable after cooking. The important species are *Amaranthus polygonoides*, *Bambusa tulda*, *B. spinosa*, *B. vulgaris*, *Canavalia polystachya*, *Corchorus capsularis*, *Crambe cordifolia*, *Dendrocalamus asper*, *Emilia sagitata*, *Houttuyina cordata*, *Lactuca indica*, *Moringa oleifera*, *Mucuna cochinchinensis*, *M. utilis*, *Nasturtium indicum* var. *apetala* and *Wolfa arrhiza*.

Root and tuber crops: Most of these are consumed after boiling – the tubers are usually eaten after cooking and occasionally consumed raw. The useful species are *Allium tuberosum*, *Alocasia cucullata*, *Asparagus sarmentosus*, *Coleus forskohlii*, *Colocasia esculenta*, *Curcuma angustifolia*, *Eleocharis tuberose*, *Moghania vestita*, *Netumbo nucifera* and *Pachyrrhizus erosus*.

Fruit crops: The important lesser known cultivated fruit species identified are *Aegle marmelos*, *Artocarpus lakoocha*, *Carissa congesta*, *Citrus* species, *Elaeocrpus floribundus*, *Emblica officinallis*, *Garcina pedunculata*, *G. tinctoria*, *Grewia asiatica*, *Limonia acidissima*, *Malpighia coccigera*, *Morus alba*, *Pereskia grandifolia*, *Phoenix sylvestris*, *Phyllanthus distichus*, *Rhodomyrtus tometosa*, *Rubus albescens*, *R. ellipticus*, *Syzgium cuminii* and *Zizyphus mauritiana*.

Spices, condiments and beverage plants: The more important species are *Amomum aromaticum*, *A. xanthioides*, *Anethum sowa*, *Areca triandra*, *Caryota urens*, *Euterpe edulis*, *Kaempferia galanga*, *Madhuca indica*, *Osmanthus fragrans* and *Piper longum*.

Fodder and fodder-cum-fuel species: *Agrostis alba*, *Albizia lebbek*, *Desmodium parvifolium*, *Gliricidia sepium*, *Hardwickia binata*, *Indigofera heterantha*, *Kochia indica*, *Leptochloa fusca*, *Polygonum tortuosum*, *Potentilla fruticosa*, *Prosopis cineraria*, *Rhyncosia minima*, *Rivea hypocrateriformis*, *Salvadora persica* and *Zizyphus nummularia*.

Dye yielding plants: *Butea monosperma*, *Kochia indica*, *Wrightia tinctoria*, *Morinda citrifolia* and *Anogeissus pendula*.

Tannin yielding plants: *Acacia nilotica* and *Cassia auriculata*.

Plants used as detergents: *Roots and leaves of Euphorbia thomsoniana*, *Lychnis indica* and *Silene griffithii*.

Gum, wax and resin plants: *Acacia senegal*, *A. nilotica*, *Butea monosperma*, *Commiphora wightii*, *Prosopis juliflora*, *P. cineraria*, *Moringa oleifera* and *Salvadora oleoides*.

Timber and fuel plants: *Acacia jacquemontii*, *A.nilotica*, *A. senegal*, *Calligonum polygonoides*, *Capparis decidua*, *Dalbergia sissoo*, *Azadirachta indica*, *Cordia dichotoma*, *C. gheraf*, *Moringa oleifera*, *Tecomella undulata* and *Boswellia serrata*.

Fibre plants: *Leptadenia pyrotechnica*, *Crotalaria burhia*, *Saccharum munja*, *S. bengalense*, *Calotropis procera*, *C. gigantea*, *Cordia dichotoma*, *Acacia leucophloea*, *Butea monosperma*, *Sida cordifolia*, *S. carpinifolia* and *S. rhombifolia*.

Role of Underutilized Crops

Crop Diversification

The focus of research and development on a few widely used species has helped in meeting the food needs of the rapidly growing human population, but it has narrowed down dramatically the number of species upon which global food security and agricultural incomes depend. The impact of the narrowing species base of global food security is likely to be felt most by the rural poor, particularly in marginal areas where people are faced with a restricted set of livelihood options. With the increasing speed and intensity of social and environmental change, humankind has become more vulnerable now than ever before. Urgent measures for crop diversification need to be taken to promote a wider diversity of crop species to ensure food security and enhanced incomes of the poor.

Many neglected and underutilized species occupy important niches, adapted to the risky and fragile conditions of rural communities and have a comparative advantage in marginal lands where they have been selected to withstand stress and to contribute to sustainable production with minimal inputs. They also contribute to the diversity and the stability of agro-ecosystems and are potential crops for the diversification of agriculture. These species also often have a strategic role in fragile ecosystems, such as those of arid and semi-arid lands, mountains, steppes and tropical forests. To address the needs of these ecosystems, it is imperative to broaden the focus of research and development by including a much wider range of crop species, with the ultimate objective of increasing their sustainable productivity.

Ethnobotanic surveys confirm that hundreds of such species are still to be brought under cultivation in many countries, representing an enormous wealth of agrobiodiversity having the potential to contribute to improved incomes, food security and nutrition. These locally important species generally remain neglected which can lead to genetic erosion of their diversity and usefulness, thus restricting development options for the rural poor. Many of the species ignored for research and development are rich in cultural value. Local communities consider these as essential elements not only in their diet but also in their food culture and rituals. The link between cultural values and plant resources can be important in empowering communities to conserve and develop their biological and cultural assets.

Most of the underutilized crop species do not require high inputs and can be successfully grown in marginal and degraded lands and at the same time can contribute to increased agricultural production, enhanced crop diversification and an improved environment. In addition, such efforts will help in conserving and using the genetic resources of underutilized crop species.

Combating World's Hunger

The member countries of the United Nations (UN) pledged to meet by 2015 a set of international targets known as United Nations Millennium Development Goals (MDGs). The first MDG is to reduce by half the number of people who suffer from hunger. The current focus on just a few crops means there is a strong chance that the global community will miss the first UN Millennium Development Goal (MDG) on hunger by several decades beyond 2015. Hence, the national development plans should make better use of agricultural biodiversity and there should be a better access to traditional foods.

Neglected and underutilized plant species can play a very significant role in reducing hunger the world over. Realizing this, an International Consultation was organized at Chennai in April 2005 by M.S. Swaminathan Research Foundation (MSSRF), Chennai, India and Bioversity International (formerly, the International Plant Genetic Resources Institute – IPGRI) and Global Facilitation Unit for Underutilized Species, both based in Rome, Italy. The main outcome of the Consultation was the adoption of Chennai Platform for Action which is a 10-point strategy, designed to assist the national governments and international agencies to achieve, as soon as possible, the UN MDGs of reducing extreme poverty and hunger by half by 2015. During the consultation, it was emphasized that eradicating hunger will require more research on nutritious but largely ignored crop species. The farmers in developing countries should be encouraged to grow a wider range of native crops to provide local populations with greater dietary diversity. These crops could include varieties of pseudo-cereals, millets and pulses in Asia, tubers and grains such as quinoa, canihua and amaranth in the Andes region of South America; and green leafy vegetables in Africa.

The world increasingly relies on a shrinking food basket of a few crops to fulfill the dietary needs of its people. Tackling malnutrition by increasing dietary diversity would not only help address this 'hidden hunger' but could also help achieve two more of the MDGs, namely, reducing infant mortality and reducing the number of women who die in childbirth (Swaminathan, 2006).

Interpreting the first MDG as meaning that each person gets more food, ignores the fact that malnutrition is also about people not getting enough of micronutrients, vitamins and minerals. Malnutrition contributes to at least half of the 10.4 million child deaths each year. Vitamin A deficiency, which can cause blindness, afflicts 120 million children every year, of whom 250,000-500,000 go blind. Some two billion people are anemic because of iron deficiency. In the past, these deficiencies were tackled through food fortification programmes, but these cannot be replicated in remote rural areas and the dietary diversity is the only way forward (Frison, 2006).

Research Achievements

National Efforts in India

India exhibits extreme diversity for edapho-climatic conditions, agroclimatic regions and ecosystems. The Indian sub-continent is a reservoir of several plant species, which have known uses of future potential for the benefit of human beings. India occupies a unique position among the major gene-rich countries of the world with a bounty of 49,000 species of higher plants known to occur. About 30% of these species–17,500 species are endemic (Gautam and Singh, 1998) occurring in 16 major vegetation types of the country.

Systematic efforts have been made to compile information on lesser known food plants including wild resources used by farmers and tribal communities in different regions of the country. Ethnobotanical investigations have been made to record a large number of wild plant species used by native tribal and aboriginal people, to meet their varied requirements (Jain and Sinha, 1987; MEF, 1994). Immensely rich landrace diversity occurs in major agri-horticultural crops, which is attributed to the farmers' conscious or unconscious selections, inherited and perpetuated over generations. Also, an enormous richness occurs in terms of crop relatives (326 species). Out of a rich floristic wealth of higher plants in the country, over 1000 wild food plants are used, and human association with these has been much older than with crops that emerged with settled agriculture (Arora, 1985; Arora and Pandey, 1996). Over 50 of these species have been domesticated by native communities. Others hold promise as nutritional food supplements for future domestication and exploitation.

In order to strengthen research on underutilized plants at the national level, an All India Coordinated Research Project on Underutilized Crops (AICRP-UUC) was initiated in 1984 with its headquarters at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Under this programme, the priority underutilized crops were identified based on their suitability to the existing cropping systems or their potentiality to supplement the new production systems, and concerted research efforts were made in respect of germplasm collecting, characterization, evaluation, conservation and utilization of selected priority species particularly for crop diversification for food and commerce (Bhag Mal, 1988, 1993, 1994; Bhag Mal and Joshi, 1991; Paroda, 1988; Paroda and Bhag Mal, 1989, 1992; Phogat *et al.*, 2004)

Germplasm Collection, Characterization and Evaluation

Efforts through well-organized multi-crop explorations resulted in sizeable germplasm collections over the years in a few selected species. Under the World Bank funded National Agricultural Technology Project (NATP), priority areas for exploration were identified and germplasm of rice bean (*Vigna umbellata*), buckwheat (*Fagopyrum esculentum*), amaranths (*Amaranthus* spp.), scarlet bean (*Phaseolus multiflorus*) and bhanjira (*Perilla frutescens)*, were collected. Useful germplasm was also introduced from other countries through the National Bureau of Plant Genetic Resources (NBPGR), New Delhi which maintains links with over 70 countries.

In India, over 25,000 accessions of about 60 underutilized crops were introduced during the past 50 years out of which 3361 accessions of 21 crops were evaluated under the aegis of All India Coordinated Project (now a Network) on Underutilized Crops (Rathi *et al.*, 2005; Phogat *et al.*, 2006). Germplasm characterization and evaluation was also done at different research centres in several underutilized species, namely, amaranth (Joshi, 1986; Shukla and Singh, 2000; Verma *et al.*, 2001; Varalaxmi, 2004; Rana *et al.* 2005; Priya *et al.* 2007), buckwheat (Joshi and Paroda, 1991); rice bean (Seyie *et al.* 2006), winged bean (Pan *et al.*, 2005); moth bean (Bhavsar and Birari, 1989) chenopod (Bhargava *et al.*, 2004, 2005); horsegram (Birari *et al.*, 1987; Chahota *et al.*, 2005); and grasspea (Pandey *et al.*, 2000).

Germplasm Conservation

Conservation of germplasm of many neglected and threatened plant species assumes a high priority as the local rural populations inhabiting the extremely harsh environments depend on these crops. In view of large-scale over-exploitation of land resources, fragile ecosystems of the humid tropical and temperate forests

are under threat. In diversity-rich areas, conservation of such plant species assumes greater priority for current and future use. The conservation of plant genetic resources has been accomplished through: i) the farming community (*in situ* conservation through the continued use of local cultivars), and ii) conservation through the formal sector (*ex situ* conservation in the genebanks). Some of the potentially useful wild species have been domesticated and their cultivation initiated in areas where the climatic conditions are similar to the niche of wild species. Valuable germplasm of several neglected and underutilized plant species is maintained by NBPGR, at New Delhi as well as at its Regional Stations located in different ago-climatic zones of the country. Also, a few selected centres of AICRP (UUC) have been assigned the responsibility for maintaining the germplasm of particular species. The current status of germplasm holdings of important underutilized crops in India is given in Table 1.

Germplasm Utilization

The genetic diversity of a few selected native and introduced species has been successfully utilized in developing improved varieties through selection process. The germplasm available in different crops was evaluated for grain yield and other traits at several research stations/ centres and promising lines/cultivars were identified. The selected elite lines were tested through multi-location trials over the years and the most promising varieties were identified/released for cultivation in different agro-climatic zones. The varieties identified/released in grain amaranth (*Amaranthus hypochondriacus*), buckwheat (*Fagopyrum esculentum*), winged bean (*Psophocarpus tetragonolobus*), rice bean (*Vigna umbellata*), faba bean (*Vicia faba*), guayule (*Parthenium argentatum*) and jojoba (*Simmondsia chinensis*) are given in Table 2. Concerted breeding efforts have also been initiated in a few selected potential crops at specified research centres for developing better varieties. Hybridization programmes in amaranth , rice bean, adzuki bean (*Vigna angularis*) and tumba (*Citrullus colocynthis*) and mutation breeding programmes in rice bean, winged bean and tumba are currently underway at different research centres in the country.

International Scenario

Neglected and underutilized plant species play a significant role in crop diversification and sustained/ enhanced agricultural production (Bhag Mal, 1994; Williams, 1995; Padulosi, 1999). Much global awareness currently prevails among not only the researchers but equally among the planners, policy makers, growers and users all over the world about their usefulness and economic potential and concerted efforts in this direction

Table 1. Germplasm assembled and characterized in important underutilized crops**

Crop	No. of accessions	Major source countries	Origin
Amaranth(*Amaranthus* spp.)	4950	India, Russia, Germany, Kenya,, Netherland, Nigeria, Syria, Nepal, Bangladesh, China, Taiwan, USA	South America
Chenopod(*Chenopodium* spp.)	177	India, Poland, USA. Italy. Hungary, Russia	South America
Buckwheat(*Fagopyrum* spp.)	800	India, Nepal, Russia, Hungary, Germany, Japan	Central Asia Near Eastern Region
Winged bean (*Psophocarpus tetragonolobus*)	328	India, Ghana, Papua New Guinea, Nigeria, Indonesia, Philippines, USA, Thailand, Sri Lanka, Puerto Rico	Papua New Guinea
Rice bean (*Vigna umbellata*)	1880	Nepal, China, India, Indonesia, Brazil, Colombia, Costa Rica, Belgium.USA	Indo-Burma/SE Asia
Faba bean (*Vigna faba*)	564	USA, Italy, Germany, Israel, Spain, Syria	Southwest Asia, Near East, Mediterranean
Adzuki bean(*Vigna angularis*)	167	Belgium, Germany, Japan, Thailand, Colombia, USA	India, Japan, China
Bambara groundnut (*Vigna subterranea*)	196	Nigeria, India, Australia, UK	Western Africa
Jerusalem artichoke (*Helianthus tuberosus*)	11	France, USA, Canada, Netherland	North America
Guayule (*Parthenium argentatum*)	113	USA, Mexico, Spain.	Southwest America, Mexico
Jojoba (*Simmondsia chinensis*)	188	USA, Israel, Mexico	South-west America, Mexico
Euphorbia spp.	83	USSR, USA, Philippines, Mexico, Spain	South America
Jatropha spp.	29	India, Brazil, Ghana, Australia, Nigeria	Tropical America
Tumba (*Citrullus colocynthis*)	115	USA, USSR, Nigeria, Sudan, Egypt, Korea, Holland, Australia	Africa, India
Cuphea spp.	13	USA	South America Brazil to Argentina

** Source AICRP (Uniderutilized Crops); NBPGR

Table 2. Varieties released under All India Coordinated Research Project on Underutilized Crops**

Crop	Variety	Year of release/ identification	Economic product	Average yield (q/ha)	Important Characteristics	Recommended areas for cultivation
(1)	(2)	(3)	(4)	(5)	(6)	(7)
GRAIN AMARANTH						
1	Annapurna	1984	Grain	22.50	High grain yield, high protein (15%), drought tolerant, wider adaptability	Hilly region
2	GA-1	1991	Grain	19.50	High seed yield and drought resistant	Gujarat, Maharashtra
3	Suvarna	1992	Grain	16.00	Drought tolerant, high grain yield	Peninsular region (Karnataka, Orissa), Gujarat
4	PRA-1 (PRA 8801)	1997	Grain	14.50	High grain yield	Uttaranchal hills
5	PRA-2 (PRA 9101)	2000	Grain	14.50	High grain yield	Hilly region
6	GA-2	2000	Grain	15.50	High grain yield	Gujarat
7	PRA-3 (PRA 9401)	2003	Grain	16.50	High grain yield	Hilly region
8	IC 35407 (Durga)	2004	Grain	21.00	High grain yield, early maturing	North west hill zone comprising Himachal Pradesh and Uttaranchal states
9	BGA-2 (Kapilasa)	2005	Grain	13.26	High grain yield, early maturing	Karnataka, Orissa and Tamil Nadu
10	VL Chua 44	2006	Grain	13.20	Early maturing (110-120 days), escapes from leaf webber and has non-spiny bract for easy threshability	Hills of Uttaranchal
BUCKWHEAT						
11	Himpriya	1991	Grain	12.00	High grain yield, medium maturity *F. tataricum*	High altitude areas
12	VL Ugal 7	1991	Grain	8.00	Early maturing, moderate grain yield	Mid hills
13	PRB 9001 (PRB 1)	1997	Grain	12.00	High grain yield, medium maturity	Mid hills
14	Shimla B-1 (Himgiri)	2005	Grain	11.12	Early maturing (81-95 days)	Dry temperate region of Himachal Pradesh and J & K
15	Sangla B-1	2005	Grain	12.65	Medium maturity (104-108 days), high grain yield	Mid and high hills of Himachal Pradesh and Uttaranchal
WINGED BEAN						
16	AKWB-1	1991	Green pods	105.00	Dual purpose (seed and vegetable), high pod yield	All winged bean growing areas
FABA BEAN						
17	VH 82-1	1998	Grain	14.55	High grain yield, medium maturity	Northern plains
RICE BEAN						
18	RBL-1	1986	Grain	16.00	High grain yield, medium maturity, light green seeded, resistant to diseases and stored grain pests	Punjab
19	PRR-1	1995	Grain	15.00	High grain yield	Uttaranchal hills
20	PRR-2	1997	Grain	12.00	High grain yield, shining light yellow seed colour	North east and North west hilly areas
21	RBL-6	2000	Grain	13.33	High grain yield medium maturity, light green seeded, resistant to diseases and pests	Entire plain Zone
22	RBL 35	2003	Grain	11.65	Early maturing	Plains

(1)	(2)	(3)	(4)	(5)	(6)	(7)
23	RBL-50	2003	Grain	10.90	Dark green seeds	Plains
24	BRS 1	2003	Grain	14.50	Early maturing, high grain yield	Hills
KALINGADA						
25	Gujarat Karingada-1	2001	Seed and vegetable	10.00	High protein (18%), high oil content (37.1%), high TSS (3.4%)	Arid/semi arid areas of Gujarat
GUAYULE						
26	Arizona-1	1986	Rubber	13.50	Drought resistant, high rubber content (6%), medium vigour	Arid and semi arid areas
27	HG-8	1991	Rubber	15.00	High rubber content (7%), tolerant to root rot, vigorous growth	Arid and semi arid areas
TUMBA						
28	RMT 59 (Mansha Marudhara)	2004	Seed/oil	2.38	High fruit and seed yield	Rajasthan and Gujarat
JOJOBA						
29	EC-33198	1986	Oil	5.00	High seed yield, drought tolerant	Arid regions and coastal areas
KANKODA						
30	Indira Kankoda (RMF-37)	2006	Vegetable	15-20	High fruit yield	Chhatisgarh, Uttar Pradesh, Jharkhand, Orissa and Maharashtra
JATROPHA						
31	Chhatrapati (SDAUJ-1)	2006	Oil	4.00 (3rd year)	High seed yield, high oil percent	Gujarat, Orissa, Haryana and Maharashtra

**Source : *AICRP (Underutilized Crops); NBPGR*

have been made at the international level. Several international organizations such as the Overseas Development Agency (ODA, now Department for International Development (DFID), UK, Bioversity International (formerly, the International Plant Genetic Resources Institute (IPGRI), Rome, Italy, United States Agency for International Development (USAID), US Academy of Agricultural Sciences, International Centre for Underutilized Crops (ICUC), Southampton, UK and British Council encouraged research on underutilized species in order to broaden the range of plant species crop diversification. The National Academy of Sciences (NAS), USA brought out several important publications highlighting the importance of potential underutilized species (NAS, 1975a, b; 1979a, b). The NAS has also brought out a book 'Lost plants of the Incas'; its earlier contributions are well known in this field (Anonymous 1975). The Food and Agriculture Organization of the United Nations (FAO) gathered and documented useful information on underutilized grain legumes and pseudo-cereals through expert consultancies (Bhag Mal, 1994, 2000).

The Commonwealth Science Council (CSC), London, UK organized several international workshops to assess the role of underutilized crops and life support species. The CSC has also organized a workshop jointly with the National Bureau of Plant Genetic Resources (NBPGR) at New Delhi in 1987 and its proceedings were published and widely distributed (Paroda *et al.*, 1988). Further, an International Symposium on 'New Crops for Food and Industry' was organized at the Southampton University, Southampton, UK in September 1987 and its proceedings were published and widely distributed (Wickens *et al.*, 1989). These developments generated lot of renewed interest in this group of crops.

Bioversity International in collaboration with Institute of Plant Genetics and Crop Plants Research (IPR), Germany published crop monographs on physic nut (Heller, 1996), yam bean (Sorensen, 1996), coriander (Diederichsen, 1996), hulled wheat (Padulosi, *et al.*, 1996), Niger (Getinet and Sharma, 1996), pili nut (Coronell, 1996), safflower (Dajue and Hans-Henning 1996), chayote (Saade, 1996), Bambara groundnut (Heller *et al.*, 1997), breadfruit (Ragone, 1997), cat's whiskers (Chweya and Mnzava, 1997), tef (Ketema, 1997), oregano (Padulosi, 1997), sago palm (Flach, 1997), black nightshade (Edmonds and Chweya, 1997), traditional African vegetables (Guarino, 1997), carob tree (Battle and Tous, 1997), grass pea (Campbell, 1997), buckwheat (Campbell, 1997), peach palm (Mora Urpi *et al.*, 1997), aibika/bele

(Preston, 1998), chenopods (Pratap *et al.*, 1998), lupin (Cowling *et al.*, 1998) and Andean roots and tubers (Hermann and Heller, 1997). The major information covered in these monographs include crop description, taxonomy, origin and centres of diversity, plant properties, uses, genetic resources, breeding, production areas, ecology and agronomy, limitations, research needs and future prospects. Bioversity also supported work on less utilized crop genetic resources in East Asia.

In a global initiative, Bioversity International with funding support from the International Fund for Agriculture Development (IFAD) implemented a programme on 'Enhancing the contribution of neglected and underutilized species to food security and to incomes of the rural poor' during 2001-2005. The species included were millets in Asia (India, Nepal), medicinal and aromatic plants in Central West Asia and North Africa (Egypt, Yemen) and Andean grains in Latin America (Bolivia, Ecuador, Peru).The project was successful in: i) working with farming communities, ii) securing and making available the diversity of target crops, iii) improving agronomic practices, iv) reducing drudgery in processing, v) adding value to products, vi) conducting training and building capacity among stakeholder groups, vii) fostering establishment of self-help groups and cooperatives, viii) creating links among various actors in the value chain, ix) raising awareness at local, national and international levels. The project delivered very substantial value and proved to be of interest to the entire development community (Padulosi, 2006)

Based on the success of this initiative, IFAD further supported a three-year follow-up programme 'Empowering the rural poor by strengthening their identity, income opportunities and nutritional security through the improved use and marketing of neglected and underutilized species' started in 2007. This amply demonstrated that biodiversity is important for people's lives, and that one way of protecting biodiversity is by supporting the use and appreciation of plant species that are currently neglected and underutilized.

With funding support from the International Development Research Centre (IDRC), Canada, Bioversity International also implemented a project on dietary diversity in sub-Saharan Africa. The project made substantial contribution in linking traditional food and plant resources to health in urban and rural populations, creating awareness of the benefits of traditional leafy vegetables and providing a platform for discussion for inclusion of dietary diversity and traditional foods in the national policies (Maundu, 2006).The increased use of traditional leafy vegetables in sub-Saharan Africa has clearly established the links between dietary diversity, better nutrition and better health (Eyzaguirre, 2004; Maundu, 2005). The IFAD funded project on minor millets in India and Nepal also demonstrated close links between nutrition, health, conservation and biodiversity and exemplary impact of the project on peoples' well being (Padulosi, 2002; 2006).

The Global Facilitation Unit for Underutilized Species (GFU) which is an initiative of the Global Forum on Agricultural Research (GFAR), the Food and Agriculture Organization of the United Nations (FAO), the International Fund for Agricultural Development (IFAD), Bioversity International and the International Centre of Underutilized Crops (ICUC) was established in 2002 at Bioversity International, Rome, Italy with funding support from the German Federal Ministry for Economic Cooperation and Development (BMZ).GFU encourages wider deployment of underutilized species globally and supports activities on networking, sharing of experiences across regions, creation of synergies, capacity building, socioeconomic backstopping and serves as a platform for discussion, strategy development and cooperation.

The International Centre on Underutilized Crops (ICUC) was established in 1989 at Southampton, U.K. which moved to Colombo, Sri Lanka in 2005. The mission of the centre is to promote the use of underutilized crops for the benefit of humankind and environmental protection. ICUC established Underutilized Tropical Fruit Trees in Asia Network (UTFANET) in 1995 and a regional centre known as the Asian Centre for Underutilized Crops (ACUC) in 2003 (Anonymous, 2006). ICUC published several monographs on minor fruit crops, viz., tamarind (Gunasena and Hughes, 2000), ber (Pareek, 2001), safou (Kengue, 2002), baobab (Sidibe and Williams, 2002), *Annona* spp, (Pinto *et al.*, 2005) and Ndjanssang (Tchoundjen and Atangana, 2006). Several International Conferences had also been organized by ICUC in UK, Argentina, Malta, and Colombo in which the progress and achievements made in different underutilized crops in different countries were shared and the future plans made for their better utilization.

Neglected Crops – a Sustainable Option

In order to make the neglected and underutilized crops a sustainable option, there is a need for concerted action to conserve genetic diversity of these species and to make

better use of it to improve food security, nutrition and income for the rural poor in developing countries. Enhanced research efforts on traditional crops need to be made and the policies to preserve them be integrated into national development plans, and food and nutrition security programmes, especially those providing food aid and school meals. Getting neglected crops back on the menu is important and equally so is ensuring that the poor people get a fair share of any commercial benefits that arise from exploiting these genetic resources.

Undoubtedly, there is a need to broaden the range of plant species utilized by man. An untapped potential of species exists in the forests, grasslands, swamps, rivers, seas and even deserts of the world. This potential is, however, a diminishing resource, diminishing in the face of environmental degradation by human and livestock population pressures and the requirements for food and raw materials on which to survive. Consideration of factors, such as available diversity and its exploitation, cost of domesticating new species, environmental problems and likelihood of their incorporation in the farming systems tends to indicate the need for taking risks for the domestication of new species (Smith, 1988). There are only a few people or organizations prepared to take risks of this nature and even fewer who also have the resources required to make the necessary investment. The farmer himself is unlikely to be able to take the lead in developing a new crop. In such a situation, the Government or established Public Sector agencies should take the lead in research and development related to this category of plants. The resources needed for this type of innovative work need to be critically assessed as the new endeavours would be more demanding.

Another serious concern relates to the fact that no proper data base is available pertaining to these crops. The Bioversity International and Global Facility for Underutilized Crops (GFU), Maccarese, Rome, Italy and the International Centre for Underutilized Crops at Colombo, Sri Lanka need to make efforts to establish such a data base for information on neglected and underutilized plants that are considered potential in different countries.

Future Thrusts

It is imperative that required thrust needs be given to the neglected and underutilized plants for harnessing their potential for various purposes. In order to make these plant species an important component of existing farming systems, several useful suggestions given below are worth considering both at the national and international levels to overcome an array of existing constraints and to improve their cultivation prospects:

Germplasm Acquisition

- Ecogeographic surveys are required to collect data on existing collections and on the distribution of plant species to have a consolidated picture on the available genetic diversity. The areas having rich diversity of land races, primitive cultivars and wild relatives of specific crops need to be identified.
- Germplsam collecting needs to be done through well organized exploration programmes aimed at filling gaps in the collections with particular emphasis on collecting the material possessing specific desirable traits.
- Joint exploration and collecting need to be undertaken involving multinational teams to collect diversity of targeted potential underutilized crops of common interest to participating countries. These should be supported by the respective national governments as well as the concerned international organizations.
- The germplsam of important underutilized crops available in other countries should also be acquired through bilateral/multilateral exchange following standard material transfer agreement (SMTA).

Characterization, Evaluation and Documentation

- Crop descriptor lists, not available for many of the underutilized crops, need to be prepared on priority basis.
- The available germplasm in different crops need to be characterized for important traits and crop catalogues need to be brought out and made available to interested researchers and other users.
- Joint multi-locational evaluation of germplasm needs to be undertaken by the research institutes/centres both within and between countries so as to obtain more useful information based on genotype x environment interactions.
- There is a great need to document the indigenous knowledge (IK) and wisdom available with the communities relating to the traditional cultivation and use of underutilized species

Genetic Improvement

- Well organized breeding programmes based on carefully defined objectives with various end uses of specific underutilized crops should be initiated to develop high yielding and nutritive varieties.

- Greater emphasis needs to be given for developing suitable plant types possessing specific desirable traits to fit well in different cropping systems and to serve specific needs of the users.
- Development of appropriate varieties suitable for non-conventional seasons and areas without disturbing the cultivation of more commonly grown food and cash crops in the region needs to be taken up.
- The problem of antinutrition factors and toxic substances which adversely affect the taste and digestibility needs due consideration while developing new varieties of underutilized species.
- Basic studies which hitherto remained largely ignored in many underutilized species require urgent attention. The genetics of plant, fruit and seed characters needs to be studied

Conservation and Utilization

- The germplasm of different crops scattered at different centres needs to be assembled and conserved in the national seed genebank/field genebank for long-term conservation.
- There is also a greater need to develop and promote suitable mechanisms for sustainable maintenance of genetic diversity of underutilized crop species in the production systems.
- The adaptability studies need to be undertaken in order to find out suitable agro-climatic situations for efficient cultivation of different crops. Standardization of package of cultivation practices also needs to be undertaken.
- Concerted efforts are needed to promote the establishment of seed/grain banks at the level of farmers in the target communities.

Product Development and Marketing

- Utmost attention needs to be paid to post-harvest processing, value addition and product development so as to enable the farmers and communities to make effective use of potential underutilized species for crop diversification.
- There is a great need to establish strategic alliances with agencies and organizations that have experience in marketing, processing and product development of neglected and underutilized species.
- Efforts need to be made to identify opportunities to add value through improved processing methods and product development through low-cost technologies
- Greater emphasis needs to be given to establish market links to enable the farmers to sell their produce at reasonable price and enhance their income from the use of these species
- Identify ways to ensure that the nutritional contributions of selected underutilized species are recognized and integrated into state-level poverty reduction and nutritional programmes

Strengthening Partnerships and Capacities

- Thrust needs to be given to build and strengthen sustainable partnerships with all the stakeholders at national and regional levels and promote close collaboration with National Agricultural Research Systems (NARS), Non-Governmental Organizations (NGOs), Farmers' Organizations, Civil Society Organizations (CSOs), entrepreneurs, private sector and the international organizations.
- The existing collaboration between various stakeholders needs to be strengthened and the initiatives that have delivered relevant outputs at the field-level need to be further geared up.
- There is a great need to play a catalytic role for pooling the scattered efforts and limited resources to address priority actions for developing and conserving neglected and underutilized crops.
- A close collaboration between the researchers, administrators and officials of development departments needs to be established to realize full potential of neglected and underutilized crops.
- In order to popularize cultivation and use of these crops, there is a need for raising public awareness through meetings, demonstrations, fairs, food competitions, TV/radio programmes, newsletters and pamphlets, etc.
- Focused attention needs to be given to develop public-awareness activities for crops and products at local and national levels and integrate such work in development related-activities
- There is a strong need for human resource development and capacity building of stakeholder groups through training/ skill enhancement interventions at the level of farmers, community members, researchers and extension workers.

Enabling Policies

- An urgent attention needs to be given for promoting policies, laws and regulations that ensure benefits from increased use of underutilized crops to the communities particularly women and other disadvantaged members of the society

- There is an urgent need to critically review and address specific aspects of policies on crops and commodities to identify gaps in addressing issues relating to neglected and underutilized species.
- The policies and guidelines for safeguarding access of farmers to the genetic resources of underutilized species need to be developed/strengthened.
- Appropriate measures need to be taken up to integrate policies related to sustainable use of these species by poor farmers including policies related to safeguarding of traditional knowledge base of the farmers

The global struggle against poverty and hunger can not be overcome without national and international commitment. The neglected and underutilized crops hold great promise for overcoming this struggle owing to their varied uses and inherent potential to adapt to harsh edapho-climatic situations. These species can prove to be a boon in agriculture in the changing scenario emerging due to the climate change. Conservation, sustainable and equitable use of genetic resources of these crops is thus imperative for the well being of present and future generations and calls for urgent attention of all concerned to initiate/enhance actions as suggested.

References

Anonymous (1975) Underexploited tropical plants with promising economical value. National Academy of Sciences, USA, 189 p.

Anonymous (2006) International Centre for Underutilized Crops. *Annual Report* 2005-2006. 13 p.

Arora RK (1985) Genetic resources of less known cultivated food plants. *Sci. Monogr.* **10:** 126 p.

Arora RK and Anjula Pandey (1996) *Wild-edible Plants of India: Diversity, Conservation and Use*. NBPGR, New Delhi.

Battle I and J Tous (1997) *Carob tree, Ceretonia siliqua L. Promoting the conservation and use of underutilized and neglected crops*. 17. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 92 p.

Bhag Mal (1988) Underutilized plants programme in India – concepts and future perspective. pp 153-159. In: Kapoor, RK Arora and Bhag Mal (eds.) *Life Support Species: Diversity and Conservation*. Proceedings of the CCS/ICAR International Workshop on Maintenance and Evaluation of Life Support Species in Asia and the Pacific Region, 4-7 April. NBPGR, New Delhi.

Bhag Mal (1993) Genetic resources of underexploited plants. pp 158-164. In: RS Rana, B Singh, U Srivastava, PN Mathur, M Rai, BM Singh, S Kochhar and IS Bisht (eds.) *Exploration, Evaluation and Conservation of Plant Genetic Resources*. National Bureau of Plant Genetic Resources, New Delhi, India, 217 p.

Bhag Mal (1994) *Underutilized Grain Legumes and Pseudocereals – Their Potentials in Asia*, RAPA Publication 1994/14. FAO, Bangkok, Thailand.

Bhag Mal (2000) *Importance and production of tropical and subtropical food grain legumes*. Consultancy Report, PR 15174. FAO, Rome, Italy. 240 p.

Bhag Mal and V Joshi (1991) Underutilized plant resources. pp. 211-229. In: RS Paroda and RK Arora (eds.) *Plant Genetic Resources–Conservation and Management*. Malhotra Publishing House, New Delhi.

Bhargava A, S Shukla and D Ohri (2004) Genetic variability in *Chenopodium*. *Indian J. Plant Genet. Resour.* **17(2):** 133-136.

Bhargava A, S Shukla and D Ohri (2005) Determination of genetic diversity in *Chenopodium* spp. *Indian J. Genet.* **65(3):** 202-206.

Bhavsar VV and SP Birari (1989) Variability, correlation and path analysis in moth bean (*Vigna aconitifolia* (Jacq.). *J. Maharashtra Agric. Univ.* **14(2):** 148-150.

Birari SP, NV Deorukhakar and BM Jamadagni (1987) Genetic parameters and character association in horse gram (*Dolichos biflorus* L). *Indian J. Agric. Res.* **21:** 55-58.

Campbell CG (1997) *Grasspea, Lathyrus sativus L. Promoting the conservation and use of underutilized and neglected crops*. 18. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, 92 p.

Campbell G (1997) *Buckwheat, Fagopyrum esculentum Moench. Promoting the conservation and use of underutilized and neglected crops*. 19. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 93 p.

Chahota RK, TR Sharma, KC Dhiman and N Kishore (2005) Characterization and evaluation of horsegram (*Macrotyloma uniflorum* Roxb.) germplasm from Himachal Pradesh. *Indian J. Plant Genet. Resour.* **18(2):** 221-223.

Chweya JA and NA Mnzava (1997) *Cat's whiskers, Cleome gynandra L. Promoting the conservation and use of underutilized and neglected crops*. 11. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 54 p.

Coronell RE (1996) *Pili nut, Canarium ovatum Engel. Promoting the conservation and use of underutilized and neglected crops*. 6. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 57 p.

Cowling WA, BJ Buirchell and ME Tapia (1998) *Lupinus L. Promoting the conservation and use of underutilized and neglected crops*. 23. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 105 p.

Dajue L and M Hans-Henning (1996) *Safflower, Carthamus tinctorius L. Promoting the conservation and use of underutilized and neglected crops*.7. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 83 p.

Diederichsen A (1996) *Coriander, Coriandrum sativum L. Promoting the conservation and use of underutilized and*

neglected crops. 3. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 83 p.

Edmonds JM and JA Chweya (1997) *Black nightshades. Solanum nigrum L.and related species. Promoting the conservation and use of underutilized and neglected crops*. 15. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 113 p.

Eyzaguirre P (2004) *Getting a grip on nutrition. Bioversity International*. Annual Report 2004. pp 6-7. Bioversity International, Rome, Italy.

Flach M (1997) *Sago palm. Metroxylon sagu Rottb. Promoting the conservation and use of underutilized and neglected crops*. 13. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 76 p.

Frison E (2006) Biodiversity and Livelihoods. Pp. 66-69 In: Bala Ravi S, I Hoeschele-Zeledon, MS Swaminathan and E Frison (eds.) *Hunger and poverty: the role of biodiversity* – Report of an International Consultation on The Role of Biodiversity in Achieving the UN Millennium Development Goals of Freedom from Hunger and Poverty, MSSRF, Chennai, India, 18-19 April, 2005. MS Swaminathan Research Foundation, Chennai, India, International Plant Genetic Research Institute, Rome, Italy, and Global Facilitation, Unit, Rome, Italy. 232 p.

Gautam PL and AK Singh (1998) Agro-biodiversity and Intellectual Property Rights (IPR) related issues. *Indian J. Plant Genet. Resour.* **11(2):** 129-151.

Getinet A and SM Sharma (1996) *Niger, Guizotia abyssinica (L.f.) Cass. Promoting the conservation and use of underutilized and neglected crops*. 5. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 59 p.

Guarino L (1997) *Traditional African Vegetables. Promoting the conservation and use of underutilized and neglected crops*. 16. Proceedings of the IPGRI International Workshop on Genetic Resources of Traditional Vegetables in Africa: conservation and use, 29-31 August 1995. ICRAF-HQ, Nairobi, Kenya. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 171 p.

Gunasena HPM and A Hughes (2000) *Tamarind, Tamarindus indica* (L.). International Centre for Underutilized Crops, Southampton, UK, 170 p.

Heller J (1996) *Physic nut, Jatropha curcas L. Promoting the conservation and use of underutilized and neglected crops*. 1. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, 66 p.

Heller J, F Bagemann and J Mushonga (1997) *Bambara groundnut, Vigna subterranea (L.) Verdc. Promoting the conservation and use of underutilized and neglected crops*. 9. Proceedings of the Workshop on Conservation and Improvement of Bambara Groundnut (*Vigna subterranean* (L.) Verdc.), 14-16 November 1995. Harare, Zimbabwe. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 166 p.

Hermann M and J Heller (1997) *Andean roots and tubers | Ahipa, arracacha, maca, and yacon. Promoting the conservation and use of underutilized and neglected crops*. 21. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, 256 p.

Jain SK and BK Sinha (1987) Ethnobotanical aspects of life support species – some emergency and supplementary foods among aboriginals in India. pp 173-180 In: Paroda RS, Promila Kapoor, Arora RK and Bhag Mal (eds.) *Life Support Species: Diversity and Conservation*. Proceedings of the CCS/ICAR International Workshop on Maintenance and Evaluation of Life Support Species in Asia and the Pacific Region, 4-7 April. NBPGR, New Delhi.

Joshi BD (1986) Genetic variability in grain amaranth. *Indian J. Agric. Sci.* **56(8):** 574-576.

Joshi BD and RS Paroda (1991) Buckwheat in India. *Sci. Monograph* **2:** National Bureau of Plant Genetic Resources, Shimla, India, 117 p.

Kengue J (2002) Safou, *Dacryodes edulis* (G. Don.). International Centre for Underutilized Crops, Southampton, UK, 147 p.

Ketema S (1997) *Tef, Eragrostis tef (Zucc.) Trotter. Promoting the conservation and use of underutilized and neglected crops*. 12. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 50 p.

Maundu P (2005) What is on the menu? Bioversity International. Annual Report 2005, pp 6-7. Bioversity International, Rome, Italy.

Maundu P (2006) *A tasty approach to dietary diversity. Bioversity International*. Annual Report 2006. pp 22-23. Bioversity International, Rome, Italy.

MEF. 1994. Ethnobiology in India – A Status Report. All India Coordinated Research Project on Ethnobiology, Ministry of Environment and Forests, New Delhi.

Mora-Urpi J, JC Weber and CR Clement (1997) *Peach palm, Bactris gasipaes Kunth. Promoting the conservation and use of underutilized and neglected crops*. 20. Institute of Plant genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, 83 p.

NAS (1975a) *Underexploited tropical plants with promising economic value*. National Academy of Sciences, Washington DC. 189 p.

NAS (1975b) *The winged bean: a high protein crop for the tropics*. National Academy of Sciences, Washington, DC 43 p.

NAS (1979a) Rice bean. In *Tropical Legumes: Resources for the future*. National Academy of Sciences, Washington, DC, 331 p.

NAS (1979b) Tropical legumes: Resources for the future. National Academy of Sciences, Washington, DC, 331 p.

Padulosi S (1997) *Oregano. Promoting the conservation and use of underutilized and neglected crops*. 14. Proceedings of the IPGRI International Workshop on Oregano, 8-12 May 1996. CIHEAM, Valenzano (Bari), Italy. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 176 p.

Padulosi S (1999) Priority setting for underutilized and neglected plant species of the mediterranian region. In *Report of IPGRI*

Conference. ICARDA, Aleppo, Syria, 9-11 February, 1998. International Plant Genetic Resources Institute, Rome, Italy.

Padulosi S, K Hammer and J Heller (1996) *Hulled wheats. Promoting the conservation and use of underutilized and neglected crops*. 4. Proceedings of the First International Workshop on Hulled Wheats, 21-22 July 1995. Castelvecchio Pascoli, Tuscany, Italy. International Plant Genetic Resources Institute, Rome, Italy, 262 p.

Padulosi S (2002) Traditional foods, modern diets and the conservation of biodiversity. *Annual Report 2002*, pp 9-11. International Plant Genetic Resources Institute, Rome, Italy.

Padulosi S (2006) Exemplary impact of neglected species project. Bioversity International. *Annual Report 2005*, pp 23-25. Bioversity International, Rome, Italy.

Pan RS, AK Singh, S Kumar and Mathura Rai (2005) Evaluation of winged bean germplasm. *Indian J. Plant Genet. Resour.* **18(1):** 48-49.

Pandey RL, NK Rastogi, AK Geda and RN Sharma (2000) Genetic diversity in relation to grain yield and neurotoxin in grasspea (*Lathyrus* sp.) genetic resources. *Indian J. Plant Genet. Resour.* **13(1):** 33-36.

Pareek OP (2001) Ber. International Centre for Underutilized Crops, Southampton, UK, 292 p.

Paroda RS (1988) The need for life support species: an Indian perspective. pp 153-159 In: Paroda RS, Promila Kapoor, Arora RK and Bhag Mal, (eds.) *Life Support Species: Diversity and Conservation*. Proceedings of the CCS/ICAR International Workshop on Maintenance and Evaluation of Life Support Species in Asia and the Pacific Region, 4-7 April. NBPGR, New Delhi.

Paroda RS, P Kapoor, RK Arora and Bhag Mal (eds.) (1988) *Life Support Species: Diversity and Conservation*. National Bureau of Plant Genetic Resources, New Delhi, India, 190 p.

Paroda RS and Bhag Mal (1989) New plant sources for food and industry in India. pp.135-149. In: New Crops For Food and Industry (eds.) GE Wickens, N Haq and P Day, Chapman and Hall, London.

Paroda RS and Bhag Mal (1992) *Developing national programme for research on underutilized crops in India*. Proceedings of the International Crop Science Congress, 14-22 July, Ames, Iowa, USA.

Phogot BS, GD Sharma and Vandana Joshi (2004) Promising research and development activities in underutilized crops to strengthen food and nutritional security. pp 404-409 In: BS Dhillon, RK Tyagi, Arjun Lal and S Saxena (eds.) *Plant Genetic Resource Management*, National Bureau of Plant Genetic Resources, New Delhi, India, 434 p.

Phogot BS, RP Dua and RK Arora (2006) Germplasm introduction of underutilized and new crops. *Indian J. Plant Genet. Resour.* **19(3):** 404-417.

Pinto AC de QMCR Cordeino, SRM de Andrade, FR Ferriera, HA de C Filgueras, RE Alves and DI Kinpara (2005) *Annona* species. International Centre for Underutilized Crops, Southampton, UK, 263 p.

Pratap T, BD Joshi and NW Galwey (1998) *Chenopodium* spp. *Promoting the conservation and use of underutilized and neglected crops*. 22. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 67 p.

Preston SR (1998) Aibika/Bele, *Abelmoschus manihot (L.) Medik. Promoting the conservation and use of underutilized and neglected crops*. 24. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 97 p.

Priya VP, VA Celine, C Gokulapalan and L Rajamony (2007) Screening amaranth genotypes (*Amaranthus* spp.) for yield and resistance to leaf blight caused by *Rhizoctonia solani* Kuhn. *Plant Genetic Resources Newslett.* **149**, 1-4. Food and Agriculture Organization of the United Nations and the International Plant Genetic Resources, Institute, Rome, Italy.

Ragone D (1997) *Breadfruit, Artocarpus altilis (Parkinson) Forsberg. Promoting the conservation and use of underutilized and neglected crops*. 10. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 77 p.

Rana JC, SK Yadav, S Mandal and S Yadav (2005) Genetic divergence and interrelationship analysis in grain amaranth (*Amaranthus hypochondriacus*) germplasm. *Indian J. Genet.* **65(2):** 99-102.

Rathi RS, HL Raiger, BS Phogot and RP Dua (2005) Evaluating germplasm introductions of underutilized crops. *Indian J. Plant Genet. Resour.* **18(1):** 123-124.

Saade RL (1996) *Chayote, Sechium edule (Jacq.) Sw. Promoting the conservation and use of underutilized and neglected crops*. 8. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 58 p.

Seyie K, GK Handique and AK Handique (2006) Evaluation of indigenous landraces of rice bean (*Vigna umbellate*) from Nagaland for growth and yield attributing characters. *Indian J. Plant Genet. Resour.* **19(2):** 209-214.

Shukla S and SP Singh (2000) Varietal performance and foliage yield in vegetable Amaranth. *Indian J. Plant Genet. Resour.* **13(2):** 147-150.

Sidibe M and JT Williams (2002) *Baobab. Adansonia digitata. International Centre for Underutilized Crops*, Southampton, UK. 96 p.

Smith RW (1988) The place of life support species in hostile or risk-prone environments: An overview, pp. 14-19 In: RS Paroda, P Kapoor, RK Arora and Bhag Mal (Eds.) *Life Support Species: Diversity and Conservation* NBPGR, New Delhi.

Sorensen M (1996) *Yam bean, Pachyrhizus DC. Promoting the conservation and use of underutilized and neglected crops*. 2. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, 141 p.

Swaminathan MS (1999) Enlarging the basis of food security: role of underutilized species. In: Proceedings of the International Consultation organized by the Genetic Resources Policy Committee (GRPC) of the CGIAR. 17-19 February 1999. MS Swaminathan Research Foundation, Chennai 22 p.

Swaminathan MS (2006) Biodiversity and livelihoods. pp 60-65. In Bala Ravi S, I Hoeschele-Zeledon, MS Swaminathan

and E Frison (eds.) *Hunger and poverty: the role of biodiversity* – Report of an International Consultation on The Role of Biodiversity in Achieving the UN Millennium Development Goals of Freedom from Hunger and Poverty, MSSRF, Chennai, India, 18-19 April, 2005. MS Swaminathan Research Foundation, Chennai, India, International Plant Genetic Research Institute, Rome, Italy, and Global Facilitation, Unit. Rome, Italy, 232 p.

Tchoundjeu Z and AR Atangana (2006) *Ricinodendron heudelotii*. International Centre for Underutilized Crops, Southampton, UK, 74 p.

Varalaxmi B (2004) Characterization and preliminary evaluation of vegetable amaranth (*Amaranthus* spp.) germplasm. *Plant Genetic Resources Newsletter* No. **137**, 55-57. Food and Agriculture Organization of the United Nations and the International Plant Genetic Resources. Institute. Rome. Italy.

Verma PK, MK Deen, SN Gupta and GD Sharma (2001) Genetic variation, correlation and path-coefficient analysis for seed yield and quality characters in grain amaranth. *Indian J. Plant Genet. Resour.* **14(2):** 171-172.

Wickens GE, N Haq and P Day (eds.) (1989) *New Crops for Food and Industry*. Chapman and Hall, London. UK.

Williams JT (1995) Underutilized Crops: Cereals and Pseudocereals. Chapman and Hall. London, UK.

Zhou Ming-De (1992) *Less Utilized Crop Genetic Resources of East Asia*. IPGRI Office for East Asia, Beijing.

Phenotypic Variability among the Germplasm Lines of Egyptian Clover (*Trifolium alexandrinum* L.)

DR Malaviya, AK Roy, P Kaushal, UP Singh and Bijendra Kumar
Indian Grassland and Fodder Research Institute, Jhansi-284003, India

Egyptian clover or *Berseem* (*Trifolium alexandrinum*) is a widely adapted good nutritious annual fodder crop. To estimate the genetic variability, 598 lines of *berseem* were evaluated using augmented block design. The material included released varieties, advanced breeding lines, induced tetraploid lines and ecotypes. Although wide range of variation was observed for most of the traits, a closer look indicated that the majority of the accessions centered around the mean leaving little number of accessions on the extremes. The frequency distribution was observed to be symmetrical and unimodal for most of the traits indicating thereby a continuous variation among the population. Similar trend was observed for floral and seed characters. Marked differences were observed among the diploid and tetraploid genotypes for foliar traits such as leaflet shape, size, margin and surface hairiness. The study indicated that the germplasm had derived from narrow genetic base. Promising lines were identified which have high value for particular traits and can be exploited in genetic improvement programme.

Key Words: Genetic variability, *Berseem*, *Trifolium alexandrinum*, Germplasm evaluation

Plant Genetic Resource (PGR) which is the backbone of crop improvement programme has to be given greater importance with the changing scenario due to Intellectual Property Right (IPR) regime under the TRIPS and the National Biodiversity Act. In this context, it has become important to evaluate and document all the germplasm available in the country.

The genus *Trifolium* commonly called clovers comprises of 237 annual and perennial species (Zohary and Heller, 1984) out of which 25 species are agriculturally important as cultivated and pasture crops (Lange and Schifino-Wittmann, 2000). Egyptian clover, popularly known as *Berseem* (name derived from Arabic name 'Bersym' or 'Berzum') is believed to be indigenous to Egypt. Based on the branching behaviour and regeneration potential, three ecotypes of *Berseem* i.e., Mescavi, Fahli and Saidi are reported from Egypt. Out of the two ecotypes `Mescavi' and `Fahli' introduced in India during 1903, the former proved to be highly adaptable because of its multicut nature and is cultivated in approximately 2 million ha in India.

The present work was undertaken to estimate the extent of variability among the existing germplasm lines, maintained at Indian Grassland and Fodder Research Institute, Jhansi, which includes old introductions, its derivatives, selections and mutants.

Material and Methods

Seeds of 598 lines of Egyptian clover (*Trifolium alexandrinum*) including germplasm lines and advance breeding lines were grown in augmented block design in 3 m row plots with row to row distance of 50 cm and plant to plant distance of 5 cm. In total, there were 11 blocks consisting of 58 lines in each block. Wardan, JHB 146, BL 122 and HFB 155 were used as checks in each block and their position was randomized. Sowing was done in the third week of October and green fodder yield data recorded for three cuttings whereas morphological data was recorded on three randomly selected plants at 50 per cent flowering stage and for seed characters at maturity. Plant height was recorded in cm each before second cut, third cut and lastly at 50 per cent flowering stage. The other observations recorded were number of nodes per tiller, internode length between fourth and fifth node, petiole length, leaflet size, occurrence of multifoliate leaves, leaf colour, leaflet margin, leaf hairiness, stipule hairiness, stipule fused and free length and stipule total length, stipule width, total green fodder yield (GFY) per 3 m row recorded during second, third and fourth cut, date of flowering initiation, date of 50 per cent lowering, peduncle length, flower colour, number of flower whorls in a head from base to the top, number of flowers in the first whorl at maturity, date of 50 per cent pod maturity, length and width of the flower head at maturity, seeds/ inflorescence and 1000 seed weight. The mean values of meteorological data of the crop growing period is given in Table 1.

Results and Discussion

The data recorded on various morphological traits and yield are presented in the Tables 2-4 in the form of

Table 1. Mean Values of meteorological data during the years 1996-97

Months	Temperature °C		Relative humidity (%)		Rainfall (mm)	Bright sunshine hrs/day
	Max	Min	1st	2nd		
October	31.0	17.3	92	45	105.7	7.5
November	28.5	9.4	94	27	–	9.4
December	23.5	4.0	96	30	–	8.6
January	22.3	5.3	95	36	–	7.7
February	27.3	8.3	91	32	–	9.9
March	31.3	13.9	86	29	0.5	8.0
April	36.1	18.3	65	26	21.4	9.5
May	39.7	22.9	54	30	17.0	10.1

frequency distribution. For numerical traits the mean value and the maximum and minimum values, kurtosis, standard deviation, skewness and variance have also been presented in Tables 3 and 4. As observed on the basis of leaflet shape and particularly leaflet apex, out of 598 accessions, 329 showed homogeneous populations and 269 heterogeneous populations.

Plant Height and Node Character

The perusal of data revealed that the minimum plant height during three cutting stages ranged between 28 to 37.44 cm and the maximum height ranged from 71.68 to 123.93 cm. Most of the accessions during first and second cut grouped in 41 - 60 cm class whereas in third cut stage, the variation for plant height was observed to be narrowed down and most of the accessions were present in 55-75 cm class. Number of nodes and internodal length recorded during third cut stage ranged from 6.06 to 15.2 and 3.92 to 14.96 respectively but most of the accessions grouped in 6 - 11 nodes class and 6 - 12 cm internodal length.

The total green fodder yield per three meter row over three cuts ranged from 0.32 to 17.02 kg with an average value of 6.80 kg but most of the accessions yielded in the range of 0.32 to 10 kg. Twenty three accessions were identified as high yielders with forage yield of more than 23 kg (Table 5).

Leaf Characters

Petiole length varied from 1.02 cm to 4.54 cm and accessions were distributed more or less uniformly in different classes i.e., <2, 2.1 – 3.0, 3.1 - 4.0 cm with maximum number present in 2.1 - 3.0 cm class. Leaflet length varied from 2.33 to 5.45 cm and most of the accessions grouped in two middle classes. Accessions with too small and too large leaves were less in number. It was invariably observed that the tetraploid accessions possessed bigger leaflets. Similar trend was observed for leaflet width which ranged from 0.79 to 2.35 cm and most of them belonged to 1.0 to 2.0 cm group (Tables 3 and 4).

Leaflets of diploid accessions were entire whereas that of tetraploid accessions were serrate. On visual performance basis, 303 accessions were found to possess medium size leaves. Multifoliate nature of leaves was evident from the presence of pentafoliate, quadrifoliate, heptafoliate and trifoliate leaves in different combinations on the same branch of single plant. A total of 266 accessions were found to possess only trifoliate leaves whereas 234 accessions possessed around 10 per cent plants with multifoliate leaf. Some accessions were observed to have as high as 80 per cent plants multifoliate leaves. The findings are in conformity with an earlier report (Shukla and Malaviya, 1988) accompanying genetic explanation of pentafoliate leaves in greater frequency derived in nature. The leaf colour was recorded as dark, light and medium green. Most of the accessions were light green followed with dark green leaves. The hairiness on upper surface of the leaflets was also variable. A few accessions showed scant hairs whereas maximum accessions (406) were medium hairy and 173 accessions were marked for dense hairiness and most of them were tetraploid in nature. Thus, leaflet shape, size, margin and hairiness were distinguishing characters for diploid and tetraploid accessions.

Stipule length ranged from 1.29 to 3.12 cm and the width ranged from 4.2 to 10.08 mm. In most of the accessions, the stipule length varied from 1.5 to 2.5 cm and width ranged from 5.1 to 9 mm. Stipule hairiness was dense among 419 accessions, medium among 159 accessions and scant among 20 accessions.

Floral and Seed Characters

The initiation of flowering in 10 accessions belonging to Saidi group or its derivative was seen before 28 February. Sixty eight lines were early in flowering i.e. flower initiation noticed between March 1 to 15 and 488 lines

Table 2. Morphological traits observed in *Berseem* accessions

Character	Accessions (No.)
Population	
Homogeneous	329
Heterogeneous	269
Leaf size	
Bold	75
Medium	303
Small	146
Very bold	74
% Plants with multifoliate leaves	
All trifoliate	266
1-10	234
11-20	70
21-30	37
31-40	13
41-50	14
51-60	6
61-70	9
71-80	4
Date of 50% flowering	
Type of leaf	
Hepta/penta/tri	7
Penta/tri	204
Penta/hepta	5
Penta/hepta/tri	2
Fused	1
Penta/tri/hepta	3
Quadri/tri	4
Quadri/penta/tri	106
Trifoliate	266
Leaf colour	
Dark green	151
Medium green	118
Light green	329
Leaflet margin	
Entire	427
Serrate	171
Leaf hairiness	
Dense	173
Medium	406
Scant	19
Stipule hairiness	
Dense	419
Medium	159
Scant	20
Date of flowering initiation	
Before Feb 28	10
March 1-15	68
51-60	6
61-70	9
71-80	4
Date of 50% flowering	
Before Feb 28	6
March 1-15	8
March 16-31	156
April 1-15	427
April 16-30	1
Flower colour	
White	549
Pink/red	49
Trifoliate	266
Date of maturity	
Before March 31	7
April 1-15	434
April 16-30	157

between March 16 to 31. Only 32 accessions were late in flowering i.e. between April 1 to 15. Similarly 50 per cent flowering was noticed in 427 accessions between April 1 to 15 followed with 156 accessions showing 50 per cent flowering between March 16 to 31. Majority of the accessions showed 50 per cent pod maturity between April 16 to 30.

A total of 549 accessions were noticed for white flowers whereas 49 accessions were noticed for different shades of pink/red (Table 2). Beri (1983) in his study reported the purple flower be single gene governed character but in the present study different shades of pink flower indicated involvement of more than one gene. High degree of variation for peduncle length was seen which ranged from 1.64 to 9.92 cm but majority of them were ranging from 2.6 to 7.5cm.

Limited diversity was observed for the number of flowers in first whorl and the number of whorls. In majority of accessions, 6.6 to 8.5 flowers were seen in the first whorl and the number of flower whorls per head ranged from 7.1 to 11. Pod length also did not vary much and ranged between 1.29 to 2.98 cm. Most of the diploid accessions were grouped in 1.6 to 2.0 cm class and tetraploid accessions in 2.1 to 2.5 cm class. Seeds per head varied considerably. Although the maximum number of accessions were observed to have 51 to 75 seeds per head, good number of accessions showed less than 25 and more than 75 seeds per head also. 1000 seed weight ranged from 1.80 to 4.12 g with majority of them ranging between 2.1 to 3.5 g. For, this character too, the tetraploid accessions showed higher seed weight.

In the present study, the characters like plant height at third cutting stage, internode length, leaflet length, leaflet width, stipule fuse length, stipule free length, stipule total length, stipule width, peduncle length, number of whorls, flowers in last whorl, pod length and seeds/ inflorescence showed unimodal type of frequency distribution showing that the variation was of continuous nature and the majority of the accessions grouped near mean value of the population. Plant height recorded during the first two cuts and the total green fodder yield showed amodal type of frequency distribution (Tables 3, 4). The accessions having higher values for various traits are presented in Table 5.

Although the crop suffers from lack of genetic variability, still there are reports on occurrence of variability (Yadav *et al.*, 1974; Sidhu and Mehndiratta, 1976) but Shukla and Patil (1985) indicated that in such

Table 3. Variation in morphological traits observed in 598 accessions of *Berseem*

	Plant height 1 (cm)	Plant height 2 (cm)	Plant height 3 (cm)	Number of nodes	Internode length	Total Green Fodder Yield (kg)	Petiole length (cm)
Average	54.31	58.25	66.27	8.61	9.38	6.80	2.48
Max	87.98	71.68	123.93	15.20	14.96	17.02	4.54
Min	31.23	28.90	37.44	6.06	3.92	0.32	1.02
Kurtosis	0.86	2.59	15.50	3.80	1.56	1.06	-0.07
SD	8.66	5.35	7.56	0.99	1.45	2.07	0.67
Skewness	0.37	-0.76	2.69	1.08	-0.25	-0.32	0.49
CV%	15.94	9.10	11.40	11.55	15.48	30.42	27.04

	Leaflet length (cm)	Leaflet width (cm)	Stipule fuse length (cm)	Stipule free length (cm)	Stipule total length (cm)	Stipule width (mm)	Peduncle length (cm)
Average	3.83	1.34	1.07	0.93	2.00	6.34	4.90
Max	5.45	2.35	1.53	1.81	3.12	10.08	9.92
Min	2.33	0.79	0.54	0.22	1.29	4.20	1.64
Kurtosis	0.18	0.66	-0.11	0.74	0.22	1.22	0.40
SD	0.48	0.26	0.18	0.22	0.31	0.81	1.19
Skewness	0.17	0.97	0.15	0.21	0.57	0.67	0.35
CV%	12.52	19:74	16.18	24.04	15.81	12.71	24.31

	No. of whorls	Flowers in last whorl	Pod length (cm)	Pod width (cm)	Seeds/ inflorescence	1000 seed wt (g)
Average	8.10	7.42	1.94	1.44	55.10	2.76
Max	11.47	8.91	2.94	1.98	115.48	4.12
Min	5.65	6.06	1.29	1.07	5.63	1.80
Kurtosis	0.31	-0.29	0.41	0.52	0.13	-0.85
SD	0.90	0.50	0.26	0.15	19.19	0.45
Skewness	0.30	0.03	0.53	0.33	-0.62	0.61
CV%	11.11	6.73	13.63	9.82	34.82	16.60

Table 4. Frequency distribution for different traits in *Berseem*

Plant height 1		Plant height 2		Plant height 3		Total Green Fodder Yield	
Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions
<45	81	<41	4	<55	16	<5.0	107
46-60	367	41-50	32	55-75	553	5.1-10.0	368
61-75	140	51-60	335	76-95	19	10.1-15.0	22
>75	10	>60	214	96-105	3	>15.0	1
				>105	7		

Number of nodes		Internode length		Petiole length		Leaflet length		Leaflet width	
Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions
<8	165	<6	17	<2	147	<3	19	<1.0	18
8-11	419	6-9	199	2.1-3.0	331	3.1-4.0	367	1.0-1.5	446
12-14	13	10-12	364	3.1- 4.0	106	4.1-5.0	203	1.6-2.0	124
>14	1	>12	18	>4	14	>5	9	>2.0	10

Stipule fuse length		Stipule free length		Stipule total length		Stipule width		Peduncle length	
Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions
<0.75	19	<0.5	19	<1.5	21	<5.0	12	<2.5	10
0.75-1.0	212	0.5-1.0	360	1.5-2.0	316	5.1-7.0	470	2.6-5.0	323
1.1-1.25	275	1.1-1.5	212	2.1-2.5	222	7.1-9.0	113	5.1-7..5	254
1.26-1.5	86	>1.5	7	2.6-3.0	36	>9	3	>7.5	11
>1.5	6			>3.0	3				

No. of whorls		Flowers in last whorl		Pod length		Seeds/inflorescence		1000 seed weight	
Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions	Class	Accessions
<7.0	60	<6.5	18	<1.5	19	<25	72	<2.0	2
7.1-9.0	448	6.6-7.5	311	1.6-2.0	368	26-50	97	2.1-2.5	244
9.1-11.0	88	7.6-8.5	265	2.1-2.5	193	51-75	369	2.6-3.0	162
>11.0	2	>8.5	4	>2.5	18	76-100	55	3.1-3.5	156
						>100	5	3.6-4.0	32
								>4.0	2

Table 5. Selected genotypes possessing higher values for different traits

Character	Criteria	Accession number
Plant height at 50% flowering	>100 cm	IL2001-355, IL2001-356, IL2001-357, IL2001-358, IL2001-359, IL2001-361, IL2001-362, IL2001-364, IL2001-583
Node number	>12	IL2001-356, IL2001-358, IL2001-359, IL2001-360
Internode length	>12 cm	IL2001-1, IL2001-2, IL2001-3, IL2001-6, IL2001-8, IL2001-10, IL2001-11, IL2001-13, IL2001-19, IL2001-20, IL2001-22, IL2001-26, IL2001-28, IL2001-379, IL2001-459, IL2001-461, IL2001-463, IL2001-579
Total Green Fodder Yield	>10 kg/3m row	IL2001-311, IL2001-330, IL2001-332, IL2001-334, IL2001-335, IL2001-345, IL2001-346, IL2001-347, IL2001-354, IL2001-382, IL2001-384, IL2001-385, IL2001-386, IL2001-403, IL2001-427, IL2001-532, IL2001-533, IL2001-534, IL2001-535, IL2001-536, IL2001-559, IL2001-567, IL2001-573
Petiole length	>4 cm	IL2001-119, IL2001-198, IL2001-252, IL2001-286, IL2001-292, IL2001-294, IL2001-305, IL2001-313, IL2001-341, IL2001-362, IL2001-392, IL2001-437, IL2001-443, IL2001-450
Leaflet length	>5 cm	IL2001-183, IL2001-219, IL2001-221, IL2001-227, IL2001-281, IL2001-325, IL2001-327, IL2001-329, IL2001-376
Leaflet width	>2 cm	IL2001-219, IL2001-223, IL2001-232, IL2001-235, IL2001-239, IL2001-259, IL2001-290, IL2001-298, IL2001-299, IL2001-326
Stipule length total	>3 cm	IL2001-219, IL2001-246, IL2001-249
Stipule width	>9 mm	IL2001-333, IL2001-388, IL2001-474,
Peduncle length	>8.5 cm	IL2001-554, IL2001-570
No. of whorls	>10	IL2001-272, IL2001-284, IL2001-285, IL2001-287, IL2001-291, IL2001-295, IL2001-296, IL2001-308, IL2001-320, IL2001-377, IL2001-521
Flowers in first whorl	>8.5	IL2001-87, IL2001-179, IL2001-570, IL2001-584
Pod length	>2.5 cm	IL2001-26, IL2001-230, IL2001-272, IL2001-276, IL2001-284, IL2001-286, IL2001-287, IL2001-288, IL2001-289, IL2001-291, IL2001-295, IL2001-308, IL2001-310, IL2001-311, IL2001-315, IL2001-318, IL2001-322, IL2001-486
Pod width	>1.75 cm	IL2001-116, IL2001-196, IL2001-253, IL2001-273, IL2001-286, IL2001-299, IL2001-324, IL2001-342, IL2001-343, IL2001-366, IL2001-372, IL2001-375, IL2001-446, IL2001-450, IL2001-574, IL2001-584
No. of seeds/inflorescence	>100	IL2001-271, IL2001-298, IL2001-300, IL2001-321, IL2001-574
1000 seed weight	>3.75 g	IL2001-180, IL2001-280, IL2001-285, IL2001-289, IL2001-322, IL2001-323, IL2001-445, IL2001-449, IL2001-589
Seeds/inflorescence and 1000 seed weight	>80&>3 g	IL2001-59, IL2001-296, IL2001-298, IL2001-300, IL2001-307, IL2001-318, IL2001-321, IL2001-438, IL2001-563, IL2001-574, IL2001-584, IL2001-589
Pod length and Pod width	>2.5 cm&1.5 cm	IL2001-26, IL2001-272, IL2001-276, IL2001-284, IL2001-286, IL2001-289, IL2001-295, IL2001-308, IL2001-310, IL2001-311, IL2001-315, IL2001-318, IL2001-486
Leaflet length and Leaflet width	4.5 cm&1.75 cm	IL2001-219, IL2001-220, IL2001-221, IL2001-223, IL2001-224, IL2001-225, IL2001-226, IL2001-227, IL2001-239, IL2001-246, IL2001-252, IL2001-298, IL2001-299, IL2001-325, IL2001-329
Green fodder yield and plant height	>8 kg/3m row &>75 cm	IL2001-564, IL2001-577, IL2001-582, IL2001-586, IL2001-587

studies it was important to ascertain the substantial proportion of genetic variability in the gross variation, wider phenotypic range of variation and normal distribution of the data on one hand and the minimum G x E interaction on the other. The differential agronomic inputs and cutting management systems by and large may change the phenotypic performance.

Variability study conducted by Yadav *et al.,* (1974) indicated genotypic and phenotypic coefficient of variation to be moderate for number of secondary branches and low for others. Sindhu and Mehndiratta (1976) observed genetic differences for forage yield and its components viz., plant height, tiller number, leaf number, leaf length and leaf width. Beri (1983) also reported genetic variability for plant height, stem thickness, tiller number, secondary branches, leaflet length and breadth, green fodder yield, dry leaf weight, dry matter yield, leaf stem ratio, days to flowering, days to maturity, stem rot incidence and crude protein content.

The values of skewness were found to have a substantially low magnitude for the number of flowers in the last whorl, leaflet length and the stipule fused length, which indicated a marginal deviation of modal value from the mean. The respective low value of kurtosis revealed

a platycurtic curve. The values of kurtosis, predominately, were within the range of ± (<3) sketching platykurtic curve except for plant height and number of nodes where a high value of kurtosis was observed. This indicated that the plant height and number of nodes would show a leptokurtic curve meaning thereby less variability in the population besides a broad range of individual means. This is warranted with the respective low values of coefficients of variance (Table 3). The platycurtic curves within the limitations of skewness, otherwise, assure better distribution of individuals yielding a greater variance. The exploitable level of variability, however, may hardly be affirmed.

Most of the characters studied belonged to quantitative trait group. However, the characters like presence of multifoliate plants in population, heterogeneity for leaf shape and flower colour can be considered as qualitative traits and presence of intra-accession variation for these traits expectedly, appeared to be a resultant of out crossing in the population. The species is reported to be cross pollinated by Hossanein (1953), Latif *et al.* (1956) and Narayanan *et al.* (1961) whereas self pollinated by Bogdan (1966), Chowdhary *et al.* (1966) and Beri *et al.* (1985). However, in a recent study existence of different breeding populations in relation to mode of pollination has been reported (Roy *et al.*, 2005). In the present study, out of 598 accessions, 269 were recorded for heterogeneous nature *i.e.*, plants with varying leaflet shape particularly the leaflet tip, 332 accessions showed presence of different percentage of multifoliate plants and 49 accessions with varying shades of pink/red flowers in the population.

Acknowledgements

Authors are grateful to the Director, Indian Grassland and Fodder Research Institute, Jhansi and Head, Crop Improvement Division for facilities and encouragements.

References

Beri SM (1983) Genetic variability and pollination behaviour in Egyptian clover (*Trifolium alexandrinum* L). Unpublished Ph.D. thesis, Punjab Agricultural University, Ludhiana India.

Beri SM, MS Sohoo and HL Sharma (1985) Estimates of natural cross pollination in Egyptian clover. *Euphytica* **34:** 147-151.

Bogdan AV (1966) Pollination and breeding behaviour in *Trifolium ruepellianum* complex in Kenya. *The New Phytologist* **65:** 417-422.

Chowdhary JB, RK Mehta and AB Joshi (1966) Pollination in *Berseem. Indian J. Genet.* **26:** 118-120.

Hossanein MH (1953) Studies on the effect of pollinating insects especially the honey bees on the seed yield of clover in Egypt. *Bull. Soc. Found. Im. Ent.* **37:** 337-344.

Lange O and MT Schifino-Wittmann (2000) Isozyme variation in wild and cultivated species of the genus *Trifolium* L. (Leguminosae). *Ann. Bot.* **86**: 339-345.

Latif A, A Quyyum and Manzoor-ul-Haq (1956) Role of *Apis indica* in pollination of Egyptian clover (*Trifolium alexandrinum* Linn). *Pakist. J. Scient. Res.* **8:** 48-50.

Narayanan ES, PL Sharma, and KG Phadke (1961) Studies on requirements of various crops for insect pollination. Insect Pollinators of *berseem* – Egyptian clover (*Trifolium alexandrinum* L) with particular reference to honey bees and their role in seed setting. *Indian Bee J.* **23:** 23-30.

Roy AK, DR Malaviya and P Kaushal (2005) Pollination behaviour among different breeding populations of Egyptian clover. *Plant Breeding* **124**: 171-175.

Shukla GP and BD Patil (1985) Breeding Egyptian Clover – A Review. *Forage Research* **11(1):** 1-19.

Shukla GP and DR Malaviya (1988) Genetics of multifoliate character in Egyptian clover (*Trifolium alexandrinum*) *Proc XVIth Int Cong Genet* Canada. 83 p.

Sidhu BS and PD Mehndiratta (1976) Genetic analysis of factors influencing forage yield *berseem. Indian J. Agric. Sci.* **46:** 168-170.

Yadav MS, KL Mehra and ML Magoon (1974) Variability and heritability for fodder yield components in *berseem* (*Trifolium alexandrinum* L.) *Indian J. Hered.* **6:** 57-61.

Zohary M and D Heller (1984) *The genus Trifolium.* The Israel Academy of Sciences and Humanities, Jerusalem.

Desiccation Tolerance and Seed Storage Behaviour Studies in Himalayan Rhubarb

Veena Gupta, Anjali Kak and Chitra Pandey
Germplasm Conservation Division, National Bureau of Plant Genetic Resources, Pusa Campus New Delhi-110012

Seed storage studies were initiated on three species of *Rheum*. In all three species, seeds showed good germination when dried upto 5.6% moisture content. Irrespective of the temperature and storage conditions, all three species showed marginal decline in germination percentage (up to 12 %) when stored for twelve months. Based on present studies it seems that *Rheum* exhibit the orthodox type of seed.

Key Words: Desiccation tolerance, Seed storage behaviour, Himalayan Rhubarb, *Rheum*

Introduction

Roberts (1973) categorized the storage behaviour of seeds into recalcitrant and orthodox based on the desiccation sensitivity and desiccation tolerance, respectively. Of the 250,000 known species, the information on seed storage behaviour is known for about 7000 species from 251 families of plants (Hong and Ellis, 1996), which is also not complete. This is true for indigenous medicinal plant species where the information is meagre. The seed storage behaviour determines the survival and longevity of seed under various storage conditions. Therefore, investigating seed storage behaviour is essentially quantifying optimum storage conditions in order to preserve the seed under the best possible conditions while keeping the costs to be minimum. To determine the strategies for germplasm conservation seeds should be first classified according to their storage behaviour.

Although there are some references on seed germination and propagation of endangered medicinal plants, but the seed storage behaviour is still an untouched aspect. Therefore, experiments were conducted to investigate seed storage regimes and storage behaviour in three species of endangered but highly demanded medicinal plant–*Rheum viz., R. emodi, R. moorcroftianum* and *R. australe.*

Material and Methods

Physiologically mature seeds of three *Rheum* species were procured from NBPGR regional station Bhowali.

1. *R. emodi* (IC211665)
2. *R. moorcroftianum* (IC394048)
3. *R. australe* (IC220416)

Seed Germination

The standard germination was conducted as per International Seed Testing Association rules (ISTA, 1993) using three replicates of twenty-five seeds placed on top of the paper in sterilized petri-plates. Preliminary experiments have shown that the seeds showed good germination at 20°C, therefore rest of the germination studies were conducted on this temperature.

Seed Storage Behaviour Studies

Seed moisture was estimated as per the ISTA Rules (1993) at 130°C for one hr in three replicates. The samples were processed and conserved at the National Gene Bank. The extra seed samples were divided into small seed lots and were conditioned to different moisture levels using desiccators containing water viz., 9.82 and 5.6 per cent. Seeds of each species were packed in tri-layered aluminium foil pouches with two moisture levels 9.82% and 5.6% and were stored at ambient, 5°C (MTS) and –20°C (LTS). These are the storage regimes used in gene banks for medium and long term conservation. Samples were drawn after 3, 6, 9 and 12 month from each storage regime and were subjected to seed viability studies.

Desiccation Tolerances

Seeds were kept in desiccators containing freshly charged silica gel and two replicates of 10 seeds each were removed every alternate day for testing moisture content and seed viability.

Result and Discussion

According to the storage physiology, two distinct types of seed have been identified. Those undergo desiccation during the final stage of development, and of low moisture content can be stored successfully at low temperature, have been described as orthodox seeds, while those do not undergo maturation drying upon the parent plant and lose viability at relatively high moisture content upon dehydration after shedding, have been termed as recalcitrant. The extent to which dehydration can be

tolerated varies from species to species (Chin and Roberts, 1980). The widely accepted method to test the recalcitrant nature of seeds is to uniformly desiccate them and withdraw periodically for moisture testing and germination study. In the present study (Table 1) it is observed that freshly harvested seeds showed 15.49% moisture content with 90 percent germination and subsequent drying up to 5.67% showed 86% germination. This indicates that the seeds are desiccation tolerant and seems to be of orthodox nature.

Seeds of all the three species showed negligible decline in germination at low moisture content (5.6%) under all the three storage conditions (Table 2). Seeds with lower moisture contents when stored at lower temperatures of 5°C and –20°C showed insignificant decrease in viability as compared to those with higher moisture content of 9.82 under ambient conditions. When compared to fresh seeds stored for 3, 9 and 12 months showed loss in germination to the extent of 4, 8 and 24 per cent. Irrespective of the temperature and storage conditions, all three species showed marginal decline in germination percentage (up to 12%) in the present investigation. Seeds of all the three species with varying moisture content stored under –20°C showed insignificant difference in germination percentage when compared to control indicating thereby that the seeds of *Rheum* are tolerant to chilling.

Seed storage behaviour is also associated with plant ecology (King and Roberts, 1979) as most of the orthodox species originate from environments subjects to occasional or seasonal drought in which desiccation tolerance of seeds is integrated with seed survival and continued regeneration of the species. On the other hand, recalcitrant species tend to originate from ecosystem in which seeds are subjected to high humidity during seed development, maturation and after shedding. For example, *Coffee arabica*, which is native to the dry and cool region of Ethiopia and showed intermediate seed storage behaviour, whereas *Coffee liberica*, which is native to hotter and humid region of Liberia showed recalcitrant seed storage behaviour (Hong and Ellis, 1996). The same has been observed in the family Palmae, where the species native to dry habitats were orthodox in nature and the species native to relatively moist habitats were recalcitrant in nature whereas in arid habitats, deserts and Savannas environment, the majority of plant species show orthodox seed storage behaviour while a few shows intermediate seed storage behaviour. In the present investigations, all the species were from the sub temperate region which faces a span of at least 2 months dry climate. Further the seed with 9.82% moisture as well as 5.6% moisture content showed 80 to 88% germination under all the conditions of storage. When stored for 12 months, the viability declined by approximately 24% at all storage temperatures. Therefore, it is suggested that all the three

Table 1. Desiccation Tolerance studies in *Rheum* Spp.

S. No	Moisture %	Germination %
1	15.49	90
2	12.58	86
3	11.63	86
4	10.84	82
5	9.32	80
6	9.12	84
7	6.43	84
8	5.67	86

Table 2. Seed germination in different storage conditions in three *Rheum* species.

Storage conditions	Initial		After 3 month of storage		After 6 month of storage		After 9 month of storage		After 12 month of storage	
Moisture content	9.82	5.6	9.82	5.6	9.82	5.6	9.82	5.6	9.82	5.6
R. moorcroftianum (IC394048)										
Ambient	88	80	84	80	72	80	72	80	64	72
MTS	84	84	84	80	80	84	74	78	68	72
LTS	84	84	80	82	80	84	80	80	72	76
R. australe (IC220416)										
Ambient	84	88	84	82	72	88	68	78	68	76
MTS	80	80	84	80	72	80	72	72	68	72
LTS	84	80	80	88	72	72	76	78	68	72
R. emodi (IC211665)										
Ambient	88	84	72	82	72	80	76	88	72	70
MTS	80	72	72	82	76	80	72	80	64	72
LTS	80	92	84	84	68	72	72	76	60	78

species of *Rheum* under investigation tends to exhibit orthodox type of seed storage behaviour and can be stored at ambient conditions by reducing the moisture content up to 5%.

Acknowledgements

The authors gratefully acknowledge the facilities provided by Director, NBPGR, New Delhi.

References

Chin HF and EH Roberts (1980) *Recalcitrant crop seeds*, Kuala Lumpur, Tropical Press Sdn. Bhd. 71 p.

Hong TD and RH Ellis (1996) A protocol to determine seed storage behaviour. *Technical Bulletin on International Board for Plant Genetic Resources, Rome.*

ISTA (1993) International rules for seed testing. *Seed Sci. Technol.* **21:** 288.

King MW and EH Roberts (1979) *The Storage of Recalcitrant Seeds. Achievements and Possible Approaches.* International Board for Plant Genetic Resources.pp 96. Rome.

Roberts EH (1973) Predicting storage life of seeds. *Seed Sci. Technol.* **1:** 499-514.

The Indian Experience in Establishment of National Information Sharing Mechanism for Monitoring the Implementation of GPA

RC Agrawal, Pratibha Brahmi and Sanjeev Saxena
National Bureau of Plant Genetic Resources, New Delhi-110012

The Global Plan of Action (GPA) for conservation and sustainable utilization of Plant Genetic Resources for Food and Agriculture (PGRFA) is an initiative of Food and Agriculture Organization (FAO), signed by 150 countries at Leipzig, Germany in 1996. The GPA is a framework of activities encompassing development of *in situ* conservation of PGRFA, sustaining existing collections, enhancing utilization and increasing capacity of countries regarding education, public awareness and training on these aspects. FAO has developed a monitoring process of implementation of GPA in different countries through a mechanism called National Information Sharing Mechanism (NISM) for monitoring the implementation of GPA. The Indian experience in implementation of this mechanism and its outcome is discussed in this article.

Key Words: Global Plan of Action, Plant Genetic Resources for Food and Agriculture (PGRFA), *In Situ* and *Ex Situ* Conservation, Information Sharing

Introduction

The Global Plan of Action (GPA) is the initiative by the Food and Agricultural Organization (FAO) of the United Nations for the conservation and sustainable utilization of plant genetic resources for food and agriculture (PGRFA). It is essentially a country-driven process and countries having adopted the GPA, are required to take actions within the framework of the defined priority areas depending on their capacity and also on the status of PGRFA management (FAO, 1996). The FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) with inputs from Bioversity International, erstwhile known as International Plant Genetic Resources Institute (IPGRI), in line with recommendations made by the Inter-governmental Technical Working Group on PGRFA of the Commission in 2001 adopted a new approach for monitoring the GPA implementation (FAO and IPGRI, 2001). A project on monitoring the implementation of GPA commenced in June 2003 at FAO, adopting a country-driven, participatory and capacity building process. It was based on a set of internationally agreed indicators and a reporting format for monitoring the GPA implementation, and an information system to facilitate and simplify recording, processing, analysis and sharing of the information addressed by the indicators and the reporting format. The indicators and the reporting format were developed in consultation with an expert group at a meeting convened by FAO and Bioversity International (CGRFA 2004 a).

The main objectives of the new monitoring approach of GPA were to: improve countries' capacities to manage information on PGRFA; allow meaningful analysis of gaps and priorities; improve decision-making on and planning of available resources; build stronger partnerships among stakeholders in the management of PGRFA within each country. Accordingly, the FAO project funded by Government of Japan (GCP\RAS\186\JPN) was implemented in 7 countries of Asia Pacific Region namely India, Thailand, Philippines, Vietnam, Sri Lanka, Malaysia, Bangladesh. The present paper describes the Indian experience of implementing the project

Monitoring of GPA: The Indian Experience

The process for the establishment of the National Information Sharing Mechanism (NISM) in India began in 2004 through a letter of agreement, which was signed between Department of Agriculture and Co-operation (DAC), Government of India and the FAO Regional Office at Bangkok. All activities foreseen under this agreement were coordinated by the National Bureau of Plant Genetic Resources (NBPGR), which was designated as the focal point for the implementation of GPA.

The project was implemented during 2005 with an aim to establish a continuing monitoring framework of the GPA implementation at national level. This was envisaged to be achieved through: (a) thorough assessment of the present status of PGRFA in the country and the region for the identification of needs and effective strategies for conservation and utilization of PGRFA; (b) the establishment of a National Information Sharing Mechanism on the GPA Implementation (NISM-GPA) to enhance coordination of plans and activities on

conservation and utilization of PGRFA amongst stakeholders and for achieving the objective (a); (c) capacity building and training for National PGRFA Programmes; (d) sharing of experiences in PGRFA *in situ* conservation and on-farm management; and (e) the improvement of regional cooperation.

The Role of Stakeholders in India

Stakeholders included governments, ministries of agriculture and of the environment, gene banks, breeders and breeders' associations, seed producers, research and training institutions, rural associations, civil society organizations involved with and related to the conservation and utilization of PGRFA, and focal points of international conventions such as the Convention on Biological Diversity.

As per the FAO guidelines, all activities coordinated by the NBPGR were divided in three distinct phases: (i) a preparatory phase, (ii) an implementation phase and (iii) a conclusion/reporting phase.

The Preparatory Phase

During the preparatory phase, work was focused on reviewing all materials, briefing and raising awareness of authorities and getting necessary permissions to undertake a collaborative information sharing process that includes the national PGR programme, the private sector, NGOs' and other public sector organizations and cross-ministerial collaboration. A committee of key stakeholders was formed to guide the GPA monitoring process and the Country Report preparation, and to identify stakeholders to be involved into this process. A total of 114 stakeholders were identified during the preparatory phase. The First National Stakeholders Workshop of the Project was held during January 2005 at NBPGR. The participants included representatives of key stakeholders Ministries/ Departments, International Crops Research Institute for the Semi-Arid Tropics, Indian Council of Agricultural Research crop based institutes and Dr. Ng Quat, the Chief Technical Advisor of the Project from FAO Regional Office, Bangkok.

The Implementation Phase

During the implementation phase a number of meetings and 6 workshops were held to explain the process and build capacity of stakeholders in the use of the computer application for gathering information. Direct technical assistance to stakeholders was also provided during this phase. During the training workshops, a comprehensive understanding of the Indicators and Reporting Format for monitoring GPA implementation was discussed and practical sessions on the use of the computer application for managing and sharing information among stakeholders were conducted. A detailed timetable for completing the questionnaire by the stakeholders and submitting the information to the National Focal Point was also circulated during each training programme. Each stakeholder was provided with a hard copy of the reporting format and the manual of the NISM software. A copy of the NISM software was given to each Stakeholder after a registration process. A unique key was generated in the NISM-GPA software for each registered stakeholders, which kept track of the data submitted by individual stakeholder.

The stakeholders were trained to edit/enter the information as per the format of the document, including a demonstration of the process of data entry into the National Focal Point Version of the NISM-GPA database through the local area network temporarily created for the purpose of training.

All the stakeholders were given a month's time after attending the training to submit the data. The data received from 91 stakeholders was merged with the National Focal Point version of the NISM-GPA after elimination of the duplicate records. The data after merging was utilized for the preparation of the national report for the implementation of the NISM in India.

The Conclusion Phase

During the conclusion/reporting phase, second round of meetings for the data validation and to discuss the draft report on monitoring the implementation of the NISM were held during the month of November 2005. During these meetings, the data submitted by the stakeholders was reviewed individually with each stakeholder and corrections/suggestions were incorporated in the NISM database accordingly. The draft report based on analysis of data gathered from stakeholders was produced and discussed with all participating stakeholders. A web site (http://www.nbpgr.ernet.in/) describing the Mechanism and including a database search engine was developed and made available to the users. Compact discs including the complete database of the Mechanism were produced and distributed to the stakeholders involved in the process.

The revised draft report (Agrawal *et al.*, 2006) was presented before the National Advisory Committee of the project for approval during March 2006. The final report of India has been submitted to the FAO. This report shall

Table 1. Total accessions conserved *ex situ* and number of safety duplicates for various categories of crop species (1996 – 2005)

Status	No. of crop sp.	No. of accessions	Safety-duplicates as active collections	Safety-duplicates (%)
Traditional cultivar/ Landrace	280	121274	84931	70
Wild	314	15881	4745	30
Weedy	70	267	11	4
Breeders' Line	37	14661	2272	15
Mutant/ Genetic Stock	26	7898	4880	62
Advanced/ Improved cultivar	59	9080	4867	54
Others	73	27662	2378	9

form the basis for the preparation of the second report of India on the state of the world's PGRFA (CGRFA 2004 b).

Some Observations from the Analysis of the NISM Information

Amongst the total accessions of PGRFA conserved in India, about 64.2% were conserved in long-term seed genebank and 33.3% were held either in medium- or short-term storage or in field genebanks. The rest were conserved in cryobanks or *in vitro* genebanks. Stock inventorization and monitoring of viability was performed regularly in most of the accessions, while the genetic integrity were checked occasionally. The data related to *ex situ* collections were predominantly published in the form of printed copy and most of the publications included passport data, characterization and evaluation data. About 60% publications had analyzed data, whereas 34% publications had raw data.

The greatest constraints to sustain *ex situ* collections reported were lack of funding and limited number of trained staff to cover all activities related with management of PGRFA following all possible approaches. Lack of adequate facilities was the other constraint reported by some organizations. For better management practices to reduce genetic changes or loss of genetic integrity, suitable regeneration environment were selected. Adequate population size and proper handling of regenerated material was in close collaboration of crop-based institutes.

There is a built-in duplicity of accessions in the system, wherein the accessions conserved at NAGS and the crop-based institutes as active collection were conserved as base collection in the National Genebank. The active collections used in research and crop improvement and the National Genebank helped in restoration of lost accessions to the active sites. This also served as safety mechanism.

The details of the total accessions and safety duplicates conserved as active collections under *ex situ* are presented in Table 1.

Amongst the *ex situ* conserved accessions which are threatened (low seed number, loss in viability during storage) 38,031 were regenerated according to established standards, while 42,148 still required to be regenerated. In the latter case, where priorities for regeneration have been set and the activities were underway, a maximum of 10 years may be required. Most of the stakeholders (65%) reported good regeneration capabilities of *ex situ* accessions in restricting the loss of genetic diversity. Only 15% reported undertaking of regeneration of existing backlogs.

Planned and targeted collection of PGRFA has been systematically undertaken in India, especially during 2000-2005 under the World Bank funded National Agricultural Technology Project (NATP). The number of accessions collected, districts explored and accessions stored in the long-term storage (LTS) are indicated in the Table 2.

Major gaps in collection reported were under-explored/unexplored areas and incomplete coverage of gene pools of the targeted taxa (Fig. 1). Priorities, needs and constraints in supporting planned and targeted collection of PGRFA, were taken into consideration for further action at national or sub-regional level.

Table 2. Details of collection missions undertaken for targeted collection of PGRFA (1996-2005).

Item	Number
Collection missions	78
Crop species collected	571
Accessions collected	86,005
Accessions in long-term storage	55,595
Total districts covered for the exploration	402

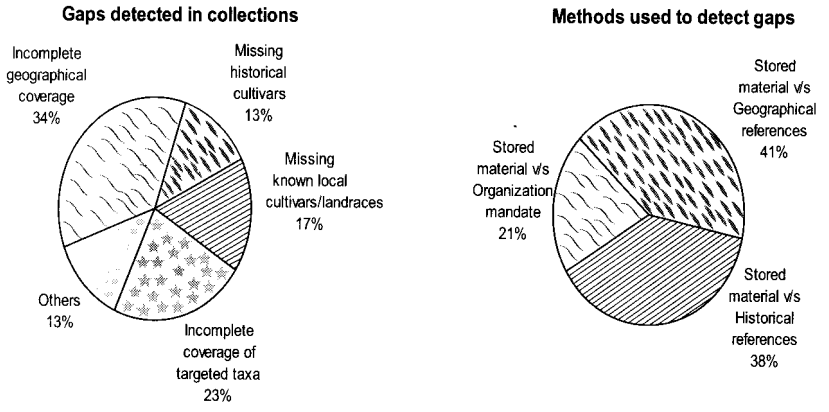


Fig 1: *Gaps detected and methods used in supporting planned and targeted collection of PGRFA*

Conclusions

The NISM in the Monitoring of the Implementation of the GPA has been a very useful project in India. This project has helped in identifying the institutions involved in PGR related activities and the synthesis of all the PGR work in India. This information generated shall be used for effective planning of projects and to identify priority areas. It will also help to eliminate duplication in efforts of the various agencies. Gaps in PGRFA activities would be filled with certainty and not based on speculation. As part of awareness raising and strategic development, policy makers in the country would be supplied with vital information on PGRFA relevant to political debate and interested parties would be given appropriate advice. This will help the promotion of coherence between different sectors, for example environment and agriculture and their support approaches. As much as possible the implementation of the NISM should be strongly linked with other areas of national policy.

Acknowledgements

The financial and technical support of the FAO and Bioversity International for the Establishment of NISM-GPA for the conservation and sustainable use of PGRFA in India is gratefully acknowledged. We also thank the Indian Council of Agricultural Research, Department of Agriculture and Co-operation, Ministry of Agriculture, Government of India and Director NBPGR, New Delhi for giving the opportunity of executing this project at NBPGR. All the nodal officers involved in providing the information for NISM are also gratefully acknowledged.

References

Agrawal RC, Pratibha Brahmi, Sanjeev Saxena, Gurinder Jit Randhawa, Kavita Gupta, DS Mishra and JL Karihaloo (2006) Report on the establishment of the National Information Sharing Mechanism on the implementation of the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture in India. Department of Agriculture and Cooperation and National Bureau of Plant Genetic Resources, New Delhi, 224 p.

CGRFA (2004 a) Indicators and Reporting Formats for Monitoring the implemtation of GPA: Agenda for the Tenth Session of the Commission on Genetic Resources for Food and Agriculture, November (Rome). CGRFA-10/04/Inf.5

CGRFA (2004 b) Preparation of the second report on the state of World's Plant Genetic Resources for Food and Agriculture. Draft Guidelines for Country Reports. Document CGRFA-10/04/Inf. 8.

FAO (1996) Global Plan of Action for Conservation and Utilization of Plant Genetic Resources for Food and Agricuture and the Leipzig Declaration. 1996. Food and Agricultural Organization of the United Nations, Rome, Italy.

FAO and IPGRI (2001) Guide towards national information sharing mechanism on the implementation of Global Plan of Action for the conservation and sustainable utilization of Plant Genetic Resources for Food and Agriculture and its establishment. FAO, Rome, Italy.

Methods for Breaking Seed Dormancy in *Acacia* Species

JS Bamel[1], K Srinivasan*[2], S Saxena[2], M Uprety[2] and Neelam Bhatnagar[3]

[1] *Krishi Vigyan Kendra, Sonepat, Haryana, India*

[2] *National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012*

[3] *NBPGR Regional Station, Jodhpur, Rajasthan, India*

Seeds of six species of *Acacia* namely, *Acacia nilotica* (L.) Delile, *A. tortilis* (Forssk.) Hayne, *A. victoriae* Benth, *A. trachycarpa* E. Pritz., *A. leucophloea* (Roxb.) and *A. holosericea* G. Don were subjected to various physico-chemical treatments to break the hard seed coat imposed dormancy. The treatments included immersing in hot water (different temperatures for varying duration), chemical scarification with concentrated sulphuric acid (varying duration), subjecting seeds to dry heat (16 hrs in an air-circulated oven at 65±1°C), pouring boiling water over seeds and mechanical abrasion and scarification using sand paper. The treatments resulted in significant improvement in the germination percentage in all the species, however, the response of the species differed to the various treatments. Maximum germination (60%) could be achieved in *A. nilotica* by mechanical scarification. In other species better germination (70-100%) could be achieved by various treatments. Sulphuric acid treatment for 20 and 50 minutes produced the best results for *A. leucophloea* and *A. tortilis*. Hot water treatment at 70°C for 30 min was found best for *A. trachycarpa* and *A. holosericea* and 80°C for 10 min was more effective in improving the germination of *A. victoriae*. Other treatments were beneficial to the different species to various extents.

Key Words: *Acacia holosericea, Acacia leucophloea, Acacia nilotica, Acacia tortilis, Acacia trachycarpa, Acacia victoriae,* Dormancy, Hot water treatment, Sulphuric acid treatment, Scarification and seed germination

Introduction

Trees in genus *Acacia* (Leguminosae) are of great importance in the rural economy particularly in the arid and semi arid regions. The trees provide high quality animal fodder, timber, fuel wood, charcoal, gums and other products and contribute to soil stabilization and improvement through nitrogen fixation.

Seeds of *Acacia* species have hard seed coat and are dormant when ripe, failing to germinate under natural conditions for several months to years, thus, resulting in low or staggered germination and consequently poor or uneven plant stand. Natural regeneration through seed is generally considered to be rare in arid and semi arid regions because of hard seed coat, which is highly impermeable to water and oxygen. The depth of dormancy can vary between the seeds from different individual mother trees and between different environments experienced during seed development.

A number of techniques have been developed by horticulturists, foresters, farmers, gardeners and researchers for removing the physically imposed dormancy in seeds for increased germination (Bilsland *et al.*, 1984). These methods include treatments with acid, hot water/ temperature, mechanical scarification etc.

Preliminary germination evaluation in the six species of *Acacia* namely *A. holosericea* G. Don, *A. leucophloea* (Roxb.), *Acacia nilotica* (L.) Delile, *A. tortilis,* (Forssk.) Hayne, *A. trachycarpa* and *A. victoriae* Benth, E. Pritz., revealed that the seeds possessed very high degree of dormancy imposed by hard seed coat. The present study was undertaken to evaluate and develop effective techniques that would soften the hard seed coat and enhance the germination in the above mentioned species.

Materials and Methods

Seeds of *A. leucophloea* (IC424928), *A. nilotica* (IC424927) were procured from Delhi University and *A. holosericae* (EC170441), *A. tortilis* (IC424929), *A. trachycarpa* (EC204733) and *A. victoriae* (EC170453) from National Bureau of Plant Genetic Resources Regional Station, Jodhpur. Cleaned and healthy seeds were subjected to the following dormancy breaking treatments.

Hot Water

Seeds wrapped in muslin cloth were suspended in water bath maintained at 65, 70, 75, and 80°C for 60, 30, 15, 10 and 5 minutes, respectively, with occasional stirring. The seeds were then dried over clean filter papers.

*Corresponding author Email: kaliamnga98@yahoo.com; Present address: IPR Cell, ICAR H.Q.

Concentrated Sulphuric Acid

The seeds were immersed in 98% sulphuric acid for 10, 20, 30, 40 and 50 minutes with intermittent stirring, washed in running water for three to four hours and dried over clean filter papers.

Dry Heat

The seeds were kept over night (16 hours) in an air-circulated oven set at a constant temperature of 65 ± 1°C.

Boiling Water Treatment

Sufficient quantity of water at 100°C was poured over the seeds, kept to cool at room temperature for 24 hours and dried over clean filter papers.

Mechanical Abrasion

The seeds were placed in standard petridishes (11cm dia) lined with sand paper (no 100) in the inner dimension of the base and lid so that the seeds were in contact with sand paper on all the sides. These petridishes were fixed on mechanical shaker set at 240 rpm and allowed to shake for five hours.

Mechanical Scarification

The seeds were manually scarified with fine grained sand paper (no 100) uniformly for five minutes.

Seed Germination Test

One set of seeds was not given any treatment and it served as the control. The untreated and treated seeds were tested for germination by the rolled towel method. Three replicates of 25 seeds each were incubated in a germinator set at 30°C in dark and germination counts were taken on the seventh day. The mean germination values were subjected to analysis of variance using the MSTAC software and comparison of means was carried out through the critical difference values.

Results and Discussion

The response of various *Acacia* species to different dormancy breaking treatments was investigated in the present study. The results of treatment with concentrated sulphuric acid revealed that the best treatment effect was obtained in *A. leucophloea* subjected to acid treatment for 20 minutes. Equally effective for this species were acid treatment for 10 and 30 minutes as compared to untreated seeds. In *A. tortilis*, *A. victoriae* and *A. holosericea*, acid treatment for longer duration that is, 40 and 50 min. resulted in significant improvement in germination over their controls (Table 1). Acid treatment for various lengths of time evoked only inappreciable response in *A. trachycarpa* and *A. nilotica* seeds. Seed mortality increased as duration of treatment increased in *A. leucophloea* whereas in other species the ungerminated seeds remained hard at the end of the germination test. Treatment of many hard seeded leguminous species with sulphuric acid is known to improve the germination (Msamba, 1994 and Teketay, 1996). Karihaloo (1984) reported differential response to acid treatment for 10 minutes in *A. leuophloea* and *A. tortilis* seeds with an increase in germination percentage of 67% and 97%, respectively. It is widely believed that the seed moisture content at the time of harvest, the post harvest storage and the ecological conditions of the habitat at the time of collection influence the degree of seed coat hardness as well as the differences in response to various treatments between species and within species harvested in different years.

The results of hot water treatment for varying lengths or time and temperature on germination of various species of *Acacia* clearly indicate the extent of variation among the species in response to this treatment. By varying immersion time and temperature, hot water treatments have effectively been used to break seed coat dormancy in several related legumes (Werker 1980; Sacheti and Al-Rawhay, 1998). Similarly, in the present study *A. trachycarpa, A. victoriae* and *A. holosericea* showed good response to this treatment. When seeds were immersed in boiling water and kept to cool at room temperature for 24 hours, a remarkable variation in germination response was observed. The maximum increase in germination was obtained for *A. trachycarpa* and *A. victoriae* followed by *A. holosericea*. However, this treatment failed to produce any appreciable effect in other species namely, *A. tortilis, A. nilotica* and *A. leucophloea*. Necrosis was also observed in *A. leucophloea* particularly at higher temperature (80°C). The possibility of hard testa acting as a mechanical barrier to water permeability has been reported earlier (Bewley and Black, 1982; Rana and Nautiyal, 1989).

The effect of mechanical abrasion was found positive in only two species of *Acacia* namely, *A. leucophloea* and *A. holosericea* and to a smaller extent in *A. victoriae*. Most of the ungerminated seeds remained hard at the end of the test. These results are in good agreement with those of Sacheti and Al-Rawahy (1998) in *A. nilitoca* and *A. tortilis*.

Mechanical scarification using sand paper improved the germination significantly in all the species of *Acacia* studied. Best results for this treatment were observed for

Table 1. Effect of various physico-chemical treatments on the germination of *Acacia* species

Treatments	Species					
	A. nilotica	*A. tortilis*	*A. victoriae*	*A. trachycarpa*	*A. leucophloea*	*A. holosericea*
Control	3	4	26	4	9	4
Hot water						
65^{0}C, 30 min	10	12	84	97	44	80
75^{0}C, 15 min	12	9	87	93	31	95
70^{0}C, 30 min	9	6	84	99	25	96
80^{0}C, 5 min	8	20	92	96	31	95
80^{0}C, 10 min	12	12	99	97	32	93
Concentrated Sulphuric Acid						
10 min	13	18	31	21	98	45
20 min	18	53	52	22	100	46
30 min	21	61	57	27	96	68
40 min	27	68	56	36	73	74
50 min	43	70	61	41	70	89
Other Treatments						
Boiling Water	51	6	56	96	28	57
Mechanical abrasion	4	5	30	6	99	68
Mechanical scarification	60	70	90	98	96	56
Dry Heat	50	48	59	98	36	56
Treatment x Species LSD >	1% 6.3	5% 4.8				

A. trachycarpa, *A. leucophloea* and *A. victoriae*. In the other species also the treatment effects were positive to varying degrees. Mechanical scarification has been widely used to improve the germination of several hard-seeded species (Gonzalez-Melero, *et al.*, 1997; Rehman, *et al.*, 1999; Mackay, *et al.*, 2001; Tigabu and Oden, 2001). Mechanical scarification disrupts the barrier for the uptake of water by the seed and facilitates the protrusion of the radical by thinning out the seed coat. Das and Saha, (1999) have demonstrated through electron microscopic studies that mechanical scarification causes the removal of the hilar plug, which not only covers the hilum but also partly hides the micropyle thereby restricting the entry of water only through the fine cracks on the testa surface.

The response of dry heat treatment at 65^{0}C for 16 hours (overnight) was found to be significantly positive for *A. trachycarpa*, *A. holosericea*, *A. victoriae* and *A. nilotica*. On the contrary, dry heat treatment has been reported to play a negative role in dormancy breaking of some *Acacia* species (Gosling *et al.*, 1995).

Present study clearly indicates that seed dormancy in the *Acacia* species is imposed by hard seed coat and there is a great inter-specific variability in the response observed for various treatments to which the species were subjected to overcome this dormancy. Results suggest that the best treatment for achieving maximum germination in *A. leucophloea* and *A. tortilis* is acid immersion for 20 and 50 min. respectively while it is hot water treatment which resulted in highest germination in *A. trachycarpa*, *A. holosericea* and *A. victoriae*. The germination of *A. nilotica* could not be increased to more than 60% by any treatment other than mechanical scarification. Although mechanical scarification improved the germination of various species significantly, the process is labour intensive and time consuming and less feasible for application to bulk samples. Acid treatment although highly effective in breaking seed coat dormancy, requires handling skills and safety measures. Hot water treatment on the other hand is a relatively simple and safe practical germination pretreatment method especially for large seed samples under field conditions.

References

Baskin CC and JM Baskin (1998) Causes of within species variation in seed dormancy and germination characteristics. pp 181-236. In: *Seeds: Ecology, Biogeography and Evaluation of Dormancy and Germination*. Academic press.

Bewley JD and M Black (1982) Viability and longevity. In: JD Bewly and M Black (eds.) *Physiology and Biochemistry of Seed in Relation to Germination, Viability, Dormancy and Environmental Control*, Vol 2, pp 5-11. Springer-Verlag, Berlin.

Bilsland DM, NR Brandenburg and AG Berlage (1984) A procedure for evaluating scarification processes. *J. Appl. Seed Prod.* **2:** 45-49.

Das B and PK Saha (1999) Effect of dormancy breaking treatments on testa ultrastructures and water uptake patterns of *Albizia procera* seeds. *Seed Sci. Technol.* **27:** 615-625.

González Melero, F Pérez-García and Martínez-Laborde (1997) Effect of temperature, scarification and gibberellic acid on seed germination of three shrubby species of *Coronilla* L. (Leguminosae). *Seed Sci. Technol.* **25:** 167-175.

Gosling PG, YK Samuel and SK Jones (1995) A systematic examination of germination temperature, chipping and water temperature/soak duration pretreatments on the seed of *Leucaena leucocephala*. *Seed Sci. Technol.* **23:** 521-532.

Karihaloo JL (1984) Effect of pre-treatment on germination of *Acacia*. *Seed Research* **12:** 112-115.

Mackay WA TD Davis and D Sankhla (2001) Influence of scarification and temperature on seed germination of *Lupinus arboreus*. *Seed Sci. Technol.* **29:** 543-548.

Msamba C (1994) Pre-sowing seed treatment on four African *Acacia* species-Appropriate technology for use in forestry rural development. *Forest Ecology and Management* **64:** 105-109.

Rana U and AR Nautiyal (1989) Coat imposed dormancy in *Acacia farnesiana* seeds. *Seed Research* **17:** 122-127.

Rehman SR NJ Losescher and PJC Harris (1999) Dormancy breaking and germination of *Acacia salicina* Lindl. seeds. *Seed Sci. Technol.* **27:** 553-557.

Sacheti PU and SH Al-Rawhay (1998) The effect of various pretreatment on the germination of important leguminous shrub-tree species of the Sultanate of Oman. *Seed Sci. Technol.* **26:** 691-699.

Teketay D (1996) Germination ecology of twelve indigenous and exotic multipurpose leguminous species from Ethiopia. *Forest Ecology and Management* **8:** 209-223.

Tigabu MR and PC Oden (2001) Effect of scarification, gibberellic acid and temperature on seed germination of two multipurpose *Albizia* species from Ethiopia. *Seed Sci. Technol.* **29:** 11-20.

Werker E (1980) Seed dormancy as explained by the anatomy of embryo envelopes. *Israel J. of Bot.* **9:** 22-44.

Bush Mango (*Irvingia gabonensis*): New Potential Multipurpose Fruit Tree for India

Anil Kumar Singh
Land Water Environment and Engineering Research Programme, (LWEERP), ICAR Research Complex for Eastern Region, Patna-800014, India

Bush mango (*Irvingia gabonensis*) is an African tree with edible yellow fruit resembling mangoes valued for its oil rich seed, fresh fruit, fuel, fibre, medicine, and hardy green termite resistant wood. Grows wildly in forest of tropical Africa. It offers considerable scope for enhancing the nutritional and economic security of subsistence farmers in India. In India, a large area is ideally suited to this tropical and subtropical fruit. In view of this, introduction of such plants from their centre of origin is necessary for enhancing the existing plant wealth. National Bureau of Plant Genetic Resources (NBPGR) New Delhi is nodal organization engaged in the various activities related to exchange of plant genetic resources in the country. Acquisition of germplasm has become a priority due to latest development under Convention on Biological Diversity and other International treaties and laws. Realizing the importance of tropical fruits trees and their future potential in India, an attempt was made to introduce Bush mango (*Irvingia gabonensis*), a new potential tropical fruit and sent to different research station for their preliminary evaluation. Multilocation testing, multiplication and distribution will be done in later stage.

Key Words: Bush mango, Multipurpose tree use, Variability and Tropical fruits

Introduction

Bush mango (*Irvingia gabonensis*) grows wild in forests of tropical Africa. It is truly a multipurpose tree as it provides food, fuel, fibre, medicines and timber. Fruits are edible having yellow pulp. Seeds contain oil used in different culinary purposes and wood is hardy and green having resistance to termites. Bark is used as medicine in arthritis, rheumatism, dropsy, swellings, oedema, gout, eye treatment, fabrifuges, stomach trouble and venereal diseases. This plant offers considerable scope for enhancing the nutritional and economic security of subsistence farmers in India. Formerly known as Simaroubaceae, the Irvingiaceae family has 3 genera (*Desbordesia*, *Irvingia*, *Klainedoxa*) and about 20 species (Oxafor, 1974). In African continent people used numerous local names – wild mango, Dika nut, Bush mango, egili (Igala), oghi (Etsako) and African mango are few of them (Onwuka, 1983).

Origin and Geographic Distribution

I. gabonensis is cohabitant of tropical Africa i.e. from Senegal to Angola often found near riverbanks and reaches its optimum in the dense evergreen rain forest. Commonly found in the forest of Cameroon, Congo, Gabon, Ivory Coast, Nigeria, Yoruba and Zaire. Southeast Nigeria is the centre of diversity of *I. gabonensis* (Atangana *et al.*, 2002).

Irvingia species collectively known as Bush mango or dika nut, are economically important fruit species, native to moist lowland tropical forest in central and west Africa, especially along the Gulf of Guinea. In Africa, *I. gabonenesis* is the commonest one. In Nigeria, two varieties of this species were identified in 1974, *I. gabonensis* var. *gabonensis* (with sweet edible fruit) and *I. gabonensis* var. *excelsa* (with bitter fruit). In a revision of the taxonomy of the Irvingiaceae family, Harris renamed the bitter variety *I. wombulu* Vermoesen and the sweet variety *I. gabonensis* Aubry-Lecomte ex O'Rorke. Other species of the same genera are *I. excelsa, I. robur, I. smithii*, and *I. grandifolia.*

The geographical range of *I. gabonensis* is from southern Nigeria to the Republic of Congo, the centre of concentration being southern Nigeria, southern Cameroon and central Gabon. While for *I. wombulu* the range of distribution is much greater and goes in principle from southern Senegal to the south western part of Uganda, its centre of concentration being southern Nigeria and southern Cameroon. This information is fundamental as a basis on which a farmer-oriented cultivar development process could be built, within the framework of a domestication program for the bush mango species. Found native in Angola, Cameroon, Central African Republic, Congo, Cote d'Ivoire, Democratic Republic of Congo, Equatorial Guinea, Gabon, Ghana, Guinea-Bissau, Liberia, Nigeria, Senegal, Sierra Leone, Sudan, Uganda and as exotic in Benin, Sao Tome.

Domestication

I. gabonensis and *I. wombolu*, the eating and the cooking types, respectively, of bush mango, have been identified by the International Centre for Research in Agroforestry as priority wild fruit tree species for domestication. With information on farmer trait preference, and in collaboration with national agricultural research systems, range wide germplasm collections have been made. The need for conservation, domestication and development of sustainable production systems, such as are possible through agroforestry, has been emphasized if the environment is to recover from this degradation process. The genetic benefits obtained from the domestication in the tropics has shown that large genetic gains are possible. The International Centre for Research in Agroforestry (ICRAF) has organized, with its national agricultural research system (NARS) partners, a systematic collection of good quality seeds from Ghana, Nigeria, Cameroon and Gabon, with emphasis on southeast Cameroon and northern Gabon, the centre of diversity of the trees *I. gabonensis* and *I. wombolu* (Ladipo, 1995).

Botany and Taxonomy

A deciduous tree reaching a height of 100 ft; bole usually straight and cylindrical slightly buttressed; trunk diameter 3 to 5 ft. glabrous in all its parts; ramuli usually sulcate when dries. Leaves coriarceous, shining above, elliptical or oblong-elliptical, shortly acuminate or apiculate, more or less acute, base cuneate or rounded in the broader-leaved forms, 7.5-11.5 cm long, 4-6.5 cm broad, petiole 0.6-0.8cm. Flowers in axillary panicles or loose subfasciculate, divaricate, few or several-flowered hermaphrodite racemes, usually much shorter than the leaves; pedicels 1-3 lines, often 2-5 together, calyx 5-occasionally 3-4-partite, with rotundate lobe petals broadly elliptical, style filiform. Fruit "edible" about 10 cm in diameter. With a fleshy epicarp and bony endocarp. Irvingaceae family comprises three genera viz. *Desboresia* (one species), *Klainedoxa* (two species) and *Irvingia* (six species). Genus *Irvingia* has six species (Table 1).

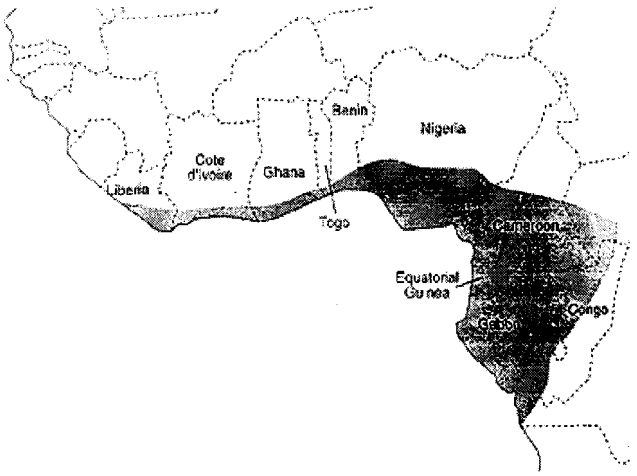


Fig. 1: *Distribution of Irvingia gabonensis in African sub continent (Ladipo et al., 1994)*

Variability in Fruit Shape and Quality

In the domestication of bush mango *I. gabonensis,* special attention needs to be placed on fruit shape and form. Spherical fruits are most common, but a range of other shapes has been recorded (Fig. 2). For example, in Cameroon, an unusual rectangular fruit shape was found, which was later also found to occur in Nigeria and Gabon. Pyriform fruits are also found frequently. This character was recorded for all mother trees. In Onne (Southeast Nigeria), fruit malformation or 'dimpling' was observed on some trees. In fact, it is important to identify this and other characteristics that can reduce the value or quality of *Irvingia* so that they can be eliminated early in the improvement programme for this species.

Variability in Fruit Sweetness

Chemical changes during ripening usually involve the conversion of starch to sucrose and reducing sugars. The extent of this conversion affects the sweetness of ripe and mature fruits as well as their retention on the tree. Fruits were divided into three categories: very sweet, sweet and not sweet. Most were assessed as sweet, but substantial variation in fruit sweetness between accessions was observed.

Table 1. Species and growing countries

Species	Countries
Irvingia gabonensis Bailln (Aubry-Lecomte ex O'Rorke)	Cameroon, Central Africa, Congo, Gabon, Ivory Coast, Nigeria, W. Africa, Yoruba and Zaire
Irvingia grandiflora (Engl.) Engl.	W. Africa, Cameroon, Central Africa, Gabon, Congo: Nigeria, and Zaire
Irvingia malayana Olivex AW Benn	Vietnam and Malaysia
Irvingia robur Mildbr	Congo, Cameroon and Gabon
Irvingia smithii Hook F.	Nigeria and Cameroon
Irvingia wombulu (Aubry-Lecomte ex O'Rorke)	Zaire

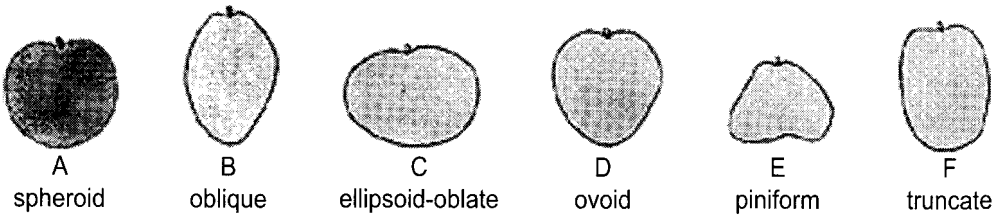


Fig. 2: Variation in fruit shapes of I. gabonensis

Variability in Fruit Colour

Irvingia fruits change from green to yellow as fruits ripen. The mature fruit colour has, however, been found to vary from tree to tree. Fruit pigmentation is a major attribute in fruit marketing. The major pigments responsible for fruit colours are chlorophyll, carotenoids and anthocyanins. The chloroplasts in green immature fruits generally lose chlorophyll on ripening and increase other pigments. This immense variability in colour is a resource that can be utilized for colour selection. The resulting consumer appeal should enhance the commercialization process of this wild fruit. *Irvingia* fruit has found in five colours as Green, Greenish yellow, Yellow, Brownish (cork) yellow and bright reddish yellow (Ladipo *et al.*, 1994).

Variability in Seed Cracking

The endocarp of *Irvingia* needs to be cracked open (shelled) to extract the cotyledons (kernels), which are used as thickening agents in soups and stews. People utilize different techniques to extract *Irvingia* kernels. They can be extracted from fruits in the fresh state, or fruits can be fermented and the kernels extracted wet. Alternatively, they can be fermented and sun dried before extracting, packaging or marketing. All these methods are difficult and hazardous. The whole operation also takes a lot of farmers' time. This useful trait is an early splitting of the hard endocarp, a process that usually takes place much later during germination.

Variability in Crown Shape

The form and shape of tree crowns can vary substantially and is probably due to genetic variation in apical dominance and apical control. Isolated mature (10-25 years) trees of *I. gabonensis* have been assessed for their crown characteristics over the last 4 years in Cameroon, Gabon and Nigeria. Considerable variation is apparent (Fig. 3). The genetic nature of these differences needs to be confirmed. Pruned and plantation trees were not included because of the possibility that their crown form results from competition in a forest type situation. It is not known, however, whether these assessed trees have been isolated throughout their life.

Variability in Leaves Colour

Colour change in the leaves of tropical trees is not uncommon as the leaves expand and mature. In *I. gabonensis* young leaves are usually pale green and sometimes pink. Field and nursery observations have shown that some trees of *I. gabonensis* have red leaves.

Agro Climatic Adaptation

I. gabonensis are very well adapted to the tropical rainforest. Thrives well in almost all-tropical rain forest soil but alluvial, equatorial brown loam soil, mud soils is suited best. Mineral composition of this soil is altisol and ultisol, rainfall should be in between 1250-2500 mm, shady conditions in the understory of water demands are high and there is a good adaptability to dry conditions. *I. gabonensis* is distinguished by a high productivity, which is conforming to the high nutrient and water demands.

Propagation

Propagate through direct seeding/seedling and vegetative methods like cutting, budding and grafting. Because of the plant's allogamy, multiplication by seed involves a large genetic heterogeneity. The techniques of traditional vegetative multiplication give a low propagation rate. *In vitro* technique for cloning of selected individuals open a new way for the consistent production of *I. gabonensis* plantlets, which could be used for the species propagation and domestication. Germination is a major problem owing

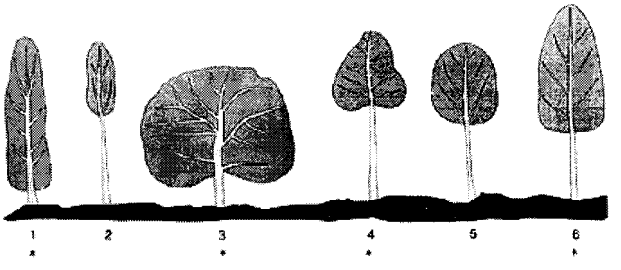


Fig. 3: Variation in crown shape of I. gabonensis

to strong shell and may take on an average about 3-4 weeks time to germinate coupled with low germibility.

Cultivars

Very little work had been carried out in past on improvement of this crop, as a result this is still under domestication and grown in forest, agroforestry system and in kitchen garden only. Now emphasis is given on exploration for selection and collection of superior genotype for systemic breeding programme. Excelsa and Dulices are main cultivars/ varieties but basically these are varieties of *I. gabonensis i.e. I. gabonensis* var. *excelsa and I. gabonensis dulices.*

Cropping System

I. gabonensis can be well accommodated in agroforestry system and silviculture, in kitchen gardens as well as in social forestry system. Inter cropping of food crops, such as maize and cassava takes place with the planting of additional multi-purpose fruit trees.

Nutrient Management

Arbuscular mycorrhizal inoculation as experience points not only to increased growth and nutrient uptake but also to improved water supply (as indicated, for example, by higher SLA). This would stimulate even further the above-mentioned high adaptability to dry conditions.

Training and Pruning

Domesticated *I. gabonensis* acceptable for both agroforestry and intensive orchard management may eventually be required. This might involve the need for different crown and bole forms manipulation of tree to promote flowering and improve fruit yields. Branching and form traits are incorporated into breeding and selection programmes, as they can be of substantial value for orchard development.

Fruiting Age

Precocity in plants is known to be under some degree of genetic control, with considerable variation in the time taken for trees to reach maturity and start fruiting. *I. gabonensis* is generally said to commence flowering after 10-15 years, but it has also reported variation in the commencement of flowering in young *I. gabonensis* in southeast Nigeria, that fruiting could commence much earlier in a precocious tree genotype i.e. it can start from the age of 4 year onwards.

Fruit Production

The flowering and fruiting process consists of a series of sequential stages, the key steps are floral initiation, flower development, pollination, fruit set, fruit development and seed set. Fruit set may depend on the availability of pollen and the efficiency of pollinators, but seed set that is the development of viable seeds from the ovules of pollinated flowers depends on endogenous factors and their interaction with the environment.

Flowering

The flower is hermaphrodite, like other tropical trees, is highly heterozygous. The first stage in the flowering process is floral induction or evocation. It is not known what triggers this process in *Irvingia* species, but a substantial variation was observed in the number of floral flushes within the population, with most trees not flowering at the age of 4-5 year or flowering only once a year, twice a year and few flowering 3-4 times a year.

Harvesting

Maturity of fruits was early in the southwest and littoral regions, while fruiting was late in the central, eastern and southern regions of the humid lowlands of Cameroon. Fruiting can be observed in July-August (early); and August-September (late). However, some out-of-season fruiting seems to occur. In Onne (southeast of Nigeria) few trees fruited in February (4 months before general fruiting). Southeast Nigeria, Research is therefore, needed to understand the genetic basis of this characteristic, so it can be effectively utilized.

Post Harvest Management

Irvingia fruits follow climacteric pattern for its ripening, fruit after harvesting faces several physiochemical change which cut short shelf life of fruit, changes occurred mainly in fruit weight, texture, colour, starch, fermentation of sugar and increase in total carotenoids. Dipping of perclimateric mature green fruits in 0.5% NaS_2O_5 at 55°C, followed by wax packing in wooden boxes overlapped with stretch polyvinyl chloride (PVC) film, delayed ripening, controlled decay, minimized weight losses and extended the shelf life of fruits kept at 22-35°C and 70-95% RH.

Disease and Pest Management

Major diseases pest is *Phytophthora* root rot, root knot nematode (*Helicotylenchus limatus* sp.*nov)* stored pest *(Oryzaephilus mercator)* of nuts and bark eating caterpillar, which can be managed with help of fungicide/ pesticide application coupled with proper crop management techniques.

Fruits Characteristics

Bush mango fruit had variability in all respect of its fruits viz. size, shape and weight which is reflected by fruit mass, flesh nut mass, shell mass, kernel mass, length, width, flesh depth, extent of variability is shown in Table 2.

Table 2. Fruit characteristics

Parameter	Range
Fruit Weight	69.0-419.8 g
Flesh Weight	59.5-388.8 g
Nut Weight	9.5-40.6 g
Shell Weight	4.9-30.9 g
Kernel Weight	0.41-7.58 g
Length	49.2-89.3 mm
Width	46.2-100.5 mm
Flesh depth	12.9-31.4 mm
Fruit Share	
Particular	Share (%)
Mesocarp	89%
Endocarp	8%
Seed	3%

Nutritive Value of Fruit and Kernel Seed

Bush mango has good nutritive valve. It is good source of energy, vitamin A and C, protein, fibre, fat, minerals and essential oils. Composition of fruit pulp and seed (kernel) are given in Table 3.

Fat produced form nuts of bush mango are used in various purposes (Eyo, 1979), physicochemical properties mentioned in Table 4 reflects the potential to use it in different pharmaceuticals confectionery and cosmetic uses.

Aroma Content

More than 35 compound (essential oils) were identified mainly benzoic, cinnamic and methyl-butyric acid derivatives as well as the sesquiterpens, a *Curcumene* and *Zingerberrine* in ripe and unripe fruits (peel and fruit pulp). Study suggested that this could be used as flavoring agent in food (Van Buren, 1970).

General Characteristics Timber Wood

Heartwood pale green brown or orange yellow, fading on exposure to a grey brown, sometimes with dark grey streaks; sapwood lighter, not always differentiated. Texture is fine to medium; grain straight to interlocked and without luster.

Mechanical Properties: (2-cm standard)

- Moisture content, Bending strength Modulus of elasticity, Maximum crushing strength (%) (Psi) (1000psi) (Psi) 12% (47) 23,600 2,710 11,400.
- Amsler toughness 288 in.-Ib at 12% moisture content (2-cm specimen). Growth ring boundaries indistinct or absent. Heartwood basically light brown yellow to white or grey, without streaks. Sapwood colour similar to heartwood colour. Odour indistinct or absent. Basic specific gravity 0.64-0.75 g/cm^3.

Table 3. Nutritive value of fruit pulp and kernel seed

Parameter	Value
Moisture	46.5%
Dry matter	43.5%
Carbohydrate	19.2%
Protein	10.9%
Fiber	8.2%
Ash	1.8%
Vitamin A	67 mg/gm
Vitamin C	65.3 mg/gm
Minerals	Mg, Ca, P, Na, K, Cu, Zn, Ni, Fe and Co
Kernel Seed	
Crude fat	68-75%
Fat	54%
Gum content	67%
Preteen	8-9%
β-Carotene	0.7 mg/gm
Plant sterols	8.08 mg/gm
Phospholipid	14.8 mg/gm
Myristic	21.2%
Palmitic	33.9%
Oleic acid	25.4%
Unsaturated fatty acid	23%
Saturated fatty acid	77%
Minerals	Mg, Ca, P Zn, Ni, Fe and Co

Table 4. Physicochemical properties of Bush mango fat (Omogbai, 1990)

Melting point	**39-40 °C**
Saponification value	212-220 °C
Smoking point	213-210 °C
Free fatty acid value	0.25-0.30%
Iodine Value	3.5-4.2
Peroxide value	1.95-1.99mg/gm
Acid value	13.6
Total Lipid content	71%

Wood Anatomy

Wood type is diffuse-porous. Vessels are arranged in no specific pattern, in multiples, commonly short (2-3 vessels) radial rows. Average tangential vessel diameter 145-220-300 flm; diameter of vessel lumina varies from large to very large. Average number of vessels/mm^2 (2-) 3-5(-7); vessels per square millimeter very few to few. Average vessel element length 400-650(-800) flm.

Average vessel element length medium. Perforation plate's simple. Intervessel pits alternate. Intervessel pits average diameter (vertical) 7-10 flm, medium. Intervessel pits not vestured. Vessel-ray pits with reduced borders or apparently simple, rounded or angular or horizontal to vertical, of uniform size or type or of two distinct sizes or types in the same ray cell, of the same type in adjacent elements or unilaterally compound and coarse. Helical thickenings absent. Tyloses in vessels present. Other deposits in heartwood vessels not observed.

Tracheids and Fibres

Vascular or vasicentric tracheids sporadic to absent. Fibres of medium wall thickness to very thick-walled. Average fibre length 1650-2200 flm. Fibre pits mainly restricted to radial walls, simple to minutely bordered. Helical thickenings absent. Fibres non-septate.

Axial Parenchyma

Axial parenchyma banded. Axial parenchyma bands not marginal (or seemingly marginal), bands much wider than rays, coarse, more than three cells wide. Axial parenchyma as strands. Average number of cells per axial parenchyma strand 6-13. Rays 7-11 per tangential mm, multiseriate (also if only few), 2-4 cells wide, narrow (2-3 seriate) to of medium width (3-5 seriate). Height of large rays up to 500 /lm to commonly 500 to 1000 /lm. Rays composed of a single cell type (homocellular). Homocellular ray cells procumbent. Sheath cells absent. Perforated ray cells absent

Secretory Structures

Intercellular canals absent. Laticifers or tanniniferous tubes absent.

Mineral Inclusions

Crystals present, prismatic, located in ray cells or axial parenchyma cells or tyloses. Crystal-containing ray cells procumbent. Crystal-containing axial parenchyma cells chambered, or not chambered. Number of crystals per cell or chamber one. Silica not observed.

Uses

Bush mango is multipurpose tree, beside it is excellent timber wood it has quality fruit and oil in its kernel is used for (i) Bakery and cosmetic purpose for preparation of dikka fat, chocolate and soap; (ii) Pharmaceutical purposes for preparation of anti ulcer and analgesic medicine;(iii) Bark of this tree has sown ant fungal activities. Polyphenols tannin or saponins could be responsible and (iv) the wood of Bush mango split in to chewing stick approximate 12x2.5x0.5cm is very commonly used for personal dental hygiene in sub Sahara Africa.

Summary

Bush mango, being truly fruit based multipurpose tree if adopted well in tropical and subtropical regions of India has the potential to change the fruit culture scenario as well as living standard of small and marginal framers. Owing to its immense potential to perform well under adverse agro climatic condition and poor and marginal soil as well it proves to be potential multipurpose fruit tree for farming community.

References

Atangana AR, V Ukafor, P Anegbeh, E Asaah, Z Tchoundjeu, JM Fondoun, M Ndoumbe and RRB Leakey (2002) Domestication of *Irvingia gabonensis*. The selection of multiple traits for potential cultivars from Cameroon and Nigeria. *Agroforestry system* **55(3):** 221-229.

Ladipo DO (1995) Management and genetic improvement of MPTS in humid lowlands of West and Central Africa. In: ICRAF 1995 Annual Report. ICRAF, Nairobi, Kenya,79 p.

Ladipo DO, SPK Britwum, Z Tchoundjeu, O Oni and RRB Leakey (1994) Genetic improvement of West African tree species: past and present. 239-248. In: RRB Leakey and AC Newton (eds.) *Tropical trees: the potential for domestication and rebuilding of forest resources*. HMSO, London.

Omogbai FE (1990) Lipid composition of tropical seeds used in the Nigerian diet. *J. of the Sci. of Food and Agric.* **50(2):** 253-255.

Onwuka ND (1983) Solvent extraction and characterization of oils from the breadfruit (AB), the African mango (AM) and the oil bean seed (OB). *Progress in Food Engineering*. 175-179.

Oxafor JC (1974) Varietal delimitation in *Irvingia gabonensis* (Irvingiaceae). *Nigerian J Forestry* **4:** 80-87.

Van Buren J (1970) Fruit phenology. In: The biochemistry of fruits and their products, Vol. 1, AC Hulme (Ed.). Academic Press. New York, pp 269-304.

Formation of Core Set in Finger Millet (*Eleusine coracana* (L.) Gaertn.) Germplasm using Geographical Origin and Morpho-agronomic Characters

Jayarame Gowda[1*], Suvarna[1], G Somu[1], S Bharathi[1] and PN Mathur[2]
[1]*Project Coordination Cell (Small millets), University of Agricultural Sciences, GKVK, Bangalore-560065*
[2]*Scientist, Bioversity International, NASC complex, Pusa Campus, New Delhi-110012*

Finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm collection involving 4511 accessions at National Active Germplasm Collection Site (NAGS), Project Co-ordination Cell (Small millets), UAS, Bangalore were evaluated for different morpho-agronomic characters over the years. A core set of 551 accessions was formed using this evaluated data by cluster analysis and PCA scoring. Majority of the accessions have Indian origin. The core set formed was true representative of the entire collection and the procedure followed in its formation was appropriate as the statistical analysis indicated that core set did not differ significantly from entire collection. The total diversity present in the entire collection was completely captured in core set. Character association studies revealed that the associations among yield and yield contributing characters found in entire collection were also found in core set. The characters *viz.*, plant height, culm thickness, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering and days to maturity could be used as indirect selection for high seed yield.

Key Words: Finger millet, Core Set, Diversity, Correlation

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important food crop in Southern Asia and Eastern Africa. Finger millet popularly known as ragi, ranks third in importance after sorghum and pearl millet, both in area and production providing staple for a large section of farming community in many parts of India. The cultivation of this crop is more widespread compared to other millets and grows from sea level in South India to high lands of Himalayas.

The crop has dual importance as source of food grain as well as straw. Finger millet grain is very nutritious with good quality protein, calcium and other minerals. The cultivated *E. coracana* is a tetraploid (2n=4x=36) and has morphological similarity to both *E. indica* (2n=18) and *E. africana* (2n=36) and is highly variable in its primary centre of origin in Africa and secondary centre of origin in India. India is the major producer of finger millet contributing nearly 60 per cent of the global production.

The success in plant breeding research is closely linked to the availability of appropriate germplasm. Realizing this, National Active Germplasm Collection Site (NAGS), Project Co-ordination Cell, All India Co-ordinated Small Millets Improvement Project (AICSMIP), Bangalore has made an effort in the assemblage of large collection of finger millet germplasm at global level (4511 accessions). Collection and conservation of large number of germplasm pose several problems in various germplasm related activities. To overcome these problems, the concept of developing core collection from the entire germplasm as suggested by Otto Frankel (1984) has been considered as effective strategy for enhancing the utility of germplasm. Considering the importance of finger millet as food and feed crop, especially to harsh agricultural regions in the country, an effort was made to develop a core set from the entire collection of 4511 accessions at Bangalore using all available information on geographical origin and evaluated data on agro-morphological characters.

Materials and Methods

Characterization and Evaluation of Finger Millet Accessions

A total of 4511 accessions of finger millet which includes extensive collections from various parts of Indian subcontinent, African and Asian countries maintained at NAGS, AICSMIP, Bangalore were evaluated at Main Research Station, Gandhi Krishi Vigyan Kendra, Bangalore over the years from 1987 to 2005. The accessions were grown in an augmented design (Federer, 1966) for evaluation. Each accession was grown in one row of 3 m length. The row to row distance was kept at 30 cm and plant to plant distance was kept at 10 cm. Data on 27 descriptors were recorded following the procedures

*Corresponding Author: Email: jg_gene@rediffmail.com

given in the Descriptors for finger millet (IBPGR, 1983), FAO, Rome.

For characterization and evaluation, fifteen quantitative characters *viz.*, plant height (cm), culm thickness (cm), number of productive tillers, number of leaves, flag leaf sheath length (cm), flag leaf sheath width (cm), flag leaf blade length (cm), flag leaf blade width (cm), leaf blade length (cm), leaf blade width (cm), peduncle length (cm), number of fingers per ear, days to 50 per cent flowering, days to maturity, grain yield per plant (g) and twelve qualitative characters *viz.*, growth habit, plant pigmentation at flowering, culm branching, ear size, ear shape, grain covering by glumes, grain colour, grain shape, grain surface, grain uniformity, pericarp persistence on seed at maturity, synchrony of ear maturity in each accession were considered for formation of core set.

Formation of Core Set

The initial grouping of accessions was attempted using characterization data such as plant pigmentation, grain colour, grain shape, ear shape etc. The groups thus formed were further subjected to cluster analysis using SYSTAT 9 package. Cluster having large number of accessions was further subjected to Principal Component Analysis (PCA) using package SPLUS 2000. Using PCA scores, around 10 per cent of the accessions in each cluster were selected for inclusion in the core set. The geographical distribution of germplasm accessions in entire collection and the core set were studied. State wise grouping of Indian collections and country wise grouping were made and per cent contribution of accessions from each region was worked out.

Statistical Analysis

The data on quantitative characters was subjected to statistical analysis to calculate mean, range and variance in the entire collection and the core set. The means of the entire collection and core set were compared using Newman–Keuls procedure (Newman, 1939 and Keuls, 1952) for all the fifteen quantitative characters. The homogeneity of variances in the entire collection and core set was tested with Levene's test (Levene, 1960).

Regarding characterization of qualitative characters; according to the finger millet Descriptors, germplasm accessions were counted for each sub-descriptor and their frequencies were worked out both in the entire collection and the core set. Chi-square (χ^2) test was applied to test whether the expected frequencies of accessions under different sub descriptors were present in the core set formed.

The frequency distribution for 15 quantitative characters and also for 12 qualitative characters under different sub-descriptors was calculated. Using this data, Shannon and Weaver (1949) diversity index (H′) was estimated and used as a measure of phenotypic diversity in the entire collection and core set for each character. The phenotypic correlations among yield and yield contributing characters in entire collection and core set were estimated separately, as suggested by Al-Jibourie *et al.* (1958) to know the extent of character associations.

Results and Discussion

A total of 551 accessions of core set was formed from the global collection of 4511 accessions and it constituted 12 per cent of the entire collection. Based on the origin, the accessions of both entire collection and core set were classified according to state wise and also country wise and are presented in Table 1. In the entire collection, maximum number of accessions were from Asia, especially from India. In Indian collections, maximum accessions were collected from Uttar Pradesh, followed by Karnataka and Tamil Nadu. Other states also contributed in small numbers to the entire collections. Africa contributed 27.87 per cent of accessions to the entire collection. Within Africa, maximum accessions were from Malawi and Kenya.

Regarding geographical distribution of germplasm accessions in core set, same trend was observed as in case of entire collection. Maximum accessions were from India (383) followed by African countries. In India, similar trend of distribution of accessions was observed. More number of accessions was from Uttar Pradesh (24.86%) followed by Karnataka (15.06 %) and Tamil Nadu (9.98%). The distribution of accessions in African countries was also similar to that of entire collection. Two countries *viz.*, Malawi (9.98%) and Kenya (8.71%) contributed more accessions to the core set. The similar trend of distribution of accessions according to their origin in both entire collection and core set indicates that the core set truly represents the entire collection and the procedure followed to constitute the core set was appropriate.

Mean, range and variance for 15 quantitative characters in both entire collection and core set is presented in Table 2. Based on Newman-Keuls test, non-significant differences were observed between the entire

Table 1. Number and Percentage of Accessions Present in Different Countries/Continents of Entire Collection and Core Set of Finger Millet Germplasm

S. No.	Continent / Country / State	Entire	Percentage	Core	Percentage
I. Asia					
1	India				
	a) Andhra Pradesh	168	3.72	21	3.81
	b) Bihar	246	5.45	11	2.00
	c) Delhi	54	1.20	3	0.54
	d) Gujarat	17	0.38	2	0.36
	e) Himachal Pradesh	18	0.40	2	0.36
	f) Jammu & Kashmir	6	0.13	1	0.18
	g) Karnataka	654	14.50	83	15.06
	h) Kerala	36	0.8	4	0.73
	i) Madhya Pradesh	121	2.68	9	1.63
	j) Maharashtra	244	5.41	37	6.72
	k) NEFA	16	0.35	1	0.18
	l) Orissa	85	1.88	11	2.00
	m) Punjab	5	0.11	–	–
	n) Rajastan	1	0.02	–	–
	o) Sikkim	44	0.98	6	1.09
	p) Tamil Nadu	451	10.00	55	9.98
	q) Unknown states	12	0.27	–	–
	r) Uttar Pradesh	1051	23.30	137	24.86
	s) West Bengal	2	0.04	–	–
	Total (India)	**3231**	**71.62**	**383**	**69.51**
2	Japan	3	0.07	3	0.54
3	Nepal	8	0.18	–	–
4	Sri Lanka	12	0.27	3	0.54
	Total (Asia)	**3254**	**72.13**	**389**	**70.60**
II. Africa					
1	Burundi	1	0.02	–	–
2	Ethiopia	16	0.35	2	0.36
3	Kenya	379	8.40	48	8.71
4	Malawi	412	9.13	55	9.98
5	Mozambique	1	0.02	–	–
6	Sudan	7	0.16	–	–
7	Tanzania	23	0.51	4	0.73
8	Uganda	181	4.02	24	4.36
9	Unknown African country	54	1.20	10	1.81
10	Zambia	92	2.04	12	2.18
11	Zimbabwe	91	2.02	7	1.27
	Total (Africa)	**1257**	**27.87**	**162**	**29.40**
	GRAND TOTAL	**4511**		**551**	

and core set for all the quantitative characters studied. The homogeneity test (Levene's test) revealed that the variance of entire collection was homogenous with the variance of core set for all the quantitative characters studied. The range for the characters studied in the core set was similar to the range in the entire collection for all the quantitative characters studied. Scores were recorded for 12 qualitative characters (morpho-agronomic) for both entire and core collection according to the Descriptors for finger millet and presented in Table 3. The chi-square (χ^2) value for frequency distribution of accessions under different sub-descriptors of entire collection and that of core set revealed non significant differences for all the qualitative characters studied. All these tests indicate that the core set formed represents the entire collection of finger millet.

Estimates of Shannon-Weaver diversity index (H′) for all the characters both in entire and core set are presented in Table 4. This index indicates the presence of genetic diversity for a character. The indices for all the characters in core set were similar to that in entire collection. The average of H′ values for 15 quantitative characters and 12 qualitative characters in core set was also similar to that in entire collection. This indicates that the diversity present in the entire collection was represented in the core set formed.

Table 2. Comparison of Mean, Range and Variance for the Quantitative Characters in the Entire Collection and Core Set of Finger Millet Germplasm

S. No.	Character	Mean			Range		Variance		
		Entire	Core	T test	Entire	Core	Entire	Core	F test
1	Plant height (cm)	94.79 ± 0.26	95.85 ± 0.848	NS	33.0 – 153.0	33.0 – 153.0	311.03	396.02	NS
2	Culm thickness (cm)	0.85 ± 0.002	0.86 ± 0.007	NS	0.4 – 1.9	0.4 – 1.9	0.02	0.03	NS
3	Number of productive tillers	3.94 ± 0.019	3.96 ± 0.052	NS	1.0 – 10.0	1.0 – 9.0	1.59	1.60	NS
4	Number of Leaves	9.75 ± 0.028	9.89 ± 0.087	NS	4.0 – 17.0	4.0 – 16.0	3.430	4.22	NS
5	Flag leaf sheath length (cm)	10.15 ± 0.031	10.21 ± 0.086	NS	2.0 – 28.0	4.6 – 17.0	4.28	4.31	NS
6	Flag leaf sheath width (cm)	1.09 ± 0.002	1.095 ± 0.006	NS	0.4 – 1.7	0.7 – 1.7	0.02	0.02	NS
7	Flag leaf blade length (cm)	33.95 ± 0.105	34.63 ± 0.349	NS	11.5 – 60.5	14.9 – 60.5	49.90	67.20	NS
8	Flag leaf blade width (cm)	1.03 ± 0.002	1.047 ± 0.008	NS	0.5 – 2.0	0.6 – 2.0	0.02	0.03	NS
9	Leaf blade length (cm)	45.92 ± 0.114	45.1 ± 0.390	NS	20.9 – 70.2	21.0 – 70.2	58.12	83.60	NS
10	Leaf blade width (cm)	1.18 ± 0.002	1.196 ± 0.008	NS	0.5 – 2.0	0.6 – 2.0	0.03	0.03	NS
11	Peduncle length (cm)	22.82 ± 0.055	22.92 ± 0.162	NS	9.2 – 41.0	9.2 – 34.0	13.84	14.43	NS
12	Finger number	7.01 ± 0.018	7.01 ± 0.053	NS	3.0 – 13.0	3.0 – 11.0	1.44	1.54	NS
13	Days to 50% flowering	59.79 ± 0.106	60.45 ± 0.337	NS	40.0 – 79.0	44.0 – 78.0	50.79	62.59	NS
14	Days to maturity	102.20 ± 0.146	103.06 ± 0.468	NS	80.0 – 129.0	80.0 – 128.0	96.51	120.87	NS
15	Grain yield per plant (g)	12.90 ± 0.100	13.54 ± 0.342	NS	1.0 – 48.8	1.7 – 45.2	45.37	64.43	NS

NS: Non significant at P = 0.05

Table 3. Descriptors, Descriptor State, Score Code and Phenotypic Proportions in Entire Collection (E) and Core Set (C) of Finger Millet Germplasm

S.No.	Descriptor	Descriptor state	Score code	E	C	χ^2
1	Growth habit	Decumbent	3	1786	228	
		Erect	5	2671	314	1.7809^{NS}
		Prostrate	7	54	9	
2	Plant pigmentation	Non pigmented	0	3049	377	
	at flowering	Pigmented	1	1462	174	0.1736^{NS}
3	Culm branching	Absent	0	2170	286	
		Present	1	2341	263	3.4958^{NS}
4	Ear shape	Droopy	1	93	17	
		Open	2	1581	190	
		Semi-compact	3	2381	274	8.1047^{NS}
		Compact	4	379	56	
		Fist	5	77	14	
5	Ear size	Small	3	1108	127	
		Intermediate	5	2865	340	4.6398^{NS}
		Large	7	538	85	
6	Grain covering by	Exposed	3	647	93	
	Glumes	Intermediate	5	2252	264	2.9585^{NS}
		Enclosed	7	1612	194	
7	Grain colour	White	1	16	5	5.0450^{NS}
		Light brown	2	1795	212	
		Copper brown	3	1710	210	
		Purple brown	4	990	123	
8	Grain shape	Round	1	2959	364	
		Reniform	2	1498	181	0.1215^{NS}
		Ovoid	3	54	6	
9	Grain surface	Smooth	1	4120	506	
		Wrinkled	2	391	45	0.2185^{NS}
10	Grain uniformity	Not uniform	0	1075	122	
		uniform	1	3436	429	0.8235^{NS}
11	Pericarp persistence	Non persistent	0	903	108	
	on seed after	Partially persistent	3	2950	370	1.0007^{NS}
	threshing	Persistent	7	657	73	
12	Synchrony of ear	Non synchronous	0	1863	227	0.0050^{NS}
	maturity	Synchronous	1	2648	324	

^{NS}: Non significant at P = 0.05

Table 4. Shannon–Weaver Diversity Index (H') for 15 Quantitative and 12 Qualitative Characters in the entire Collection and Core Set of Finger Millet

S.No.	Character	Shannon–Weaver Index	
		Entire	Core
	Quantitative character		
1	Plant height	1.808	1.917
2	Culm thickness	1.283	1.445
3	Number of productive tillers	1.613	1.588
4	Number of Leaves	1.504	1.651
5	Flag leaf sheath length	1.214	1.220
6	Flag leaf sheath width	1.528	1.588
7	Flag leaf blade length	1.782	1.904
8	Flag leaf blade width	1.415	1.500
9	Leaf blade length	1.857	2.013
10	Leaf blade width	1.386	1.448
11	Peduncle length	1.535	1.536
12	Number of fingers	1.583	1.620
13	Days to 50% flowering	1.975	2.057
14	Days to Maturity	2.069	2.187
15	Grain yield	1.646	1.802
	Mean ± SE	**1.613 ±0.064**	**1.698 ±0.070**
	Qualitative character		
1	Growth habit	0.730	0.753
2	Plant pigmentation at flowering	0.630	0.624
3	Culm branching	0.692	0.693
4	Ear size	0.887	0.924
5	Ear shape	1.062	1.148
6	Grain covering by glumes	0.993	1.020
7	Grain colour	1.087	1.113
8	Grain shape	0.696	0.688
9	Grain surface	0.295	0.281
10	Grain uniformity	0.549	0.529
11	Pericarp persistence on seed at maturity	0.880	0.854
12	Synchrony of ear maturity	0.678	0.677
	Mean ± SE	**0.765 ±0.066**	**0.775 ±0.072**
	Overall mean ± SE	**1.236 ±0.094**	**1.288 ±0.103**

The effect of each yield contributing characters on yield improvement in finger millet was analyzed through character association studies. Estimates of phenotypic correlation coefficients for 15 quantitative characters in both entire and core set are presented in Table 4. Out of 105 correlations, 64 correlations were significant in both entire and core set. This indicates a good representation of phenotypic correlations of characters from entire collection to the core set. The characters namely, culm thickness, number of productive tillers, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering, days to maturity were positively associated and flag leaf sheath length was negatively associated with grain yield in both entire and core set. But, plant height was positively correlated with grain yield only in core set.

Among different characters studied, the significant correlations between characters found in entire collections were also found in core set. Characters *viz.*, plant height, culm thickness, number of leaves, flag leaf blade length, flag leaf blade width, days to 50% flowering and days to maturity were correlated with each other in both entire collection and core set. Hence in future characterization of finger millet germplasm, plant height, culm thickness, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering and days to maturity could be used as indirect measure to select for high yield.

It can be concluded that the core set involving 551 accessions formed from 4511 accessions of entire collection of finger millet is a true representative of entire collection and has all the diversity present in the entire collection. The core set thus selected comprised accessions with higher diversity representing the entire coverage of variability giving accurate reproducible list of entries of core whenever repeated. This avoids the repeating of useful alleles thus enhancing their richness. Hence this core set can be used in future for effective screening of the finger millet germplasm for identifying the sources of desirable characters. The method followed in the formation of core set was correct and core set represents the entire set.

References

Al-Jibourie HA, PA Miller and HF Robinson (1958) Genotype and environmental variances in an upland cotton crosses of interspecific origin. *Agron. J.* **50:** 633-637.

Federer WT (1956) Augmented designs. *Hawaiian Planters' Record* **55:** 191-208.

Frankel OH (1984) Genetic perspective of germplasm conservation. In: Arber W, K Llimensee, WJ Peacock and P Starlinger (eds.), *Genetic manipulations: Impact of man and society*. Cambridge University Press, Cambridge, England, pp 161-170.

IBPGR (1983) *Descriptors for finger millet*. International Board for Plant Genetic Resources, Rome.

Keuls M (1952) The use of 'studentized range' in connection with an analysis of variance. *Euphytica* **1:** 112-122.

Levene H (1960) Robust tests for equality of variances. In: Oklin, I (ed.) *Contribution of Probability and Statistics*. Essays in Honour of Harold Hotelling. University Press, Stanford, pp 278-292.

Newman D (1939) The distribution of range in samples from a normal population expressed in term of an independent estimate of standard deviation. *Biometrika* **31:** 20-30.

Shannon CE and W Weaver (1949) The mathematical theory of communication. University of Illinois Press, Urbana.

Selection Response for Fruit Yield in Okra (*Abelmoschus esculentus* (L.) Moench)

M Abdul Nizar*, K Joseph John[1] and R Karuppaiyan[2]

**National Bureau of Plant Genetic Resources Regional Station, PDKV Campus, Akola-444104 (Maharashtra)*

[1] National Bureau of Plant Genetic Resources Regional Station, Vellanikkara, Kerala Agricultural University Thrissur P.O.-680656 (Kerala)

[2] ICAR Research Complex for NEH Region, Tadong, Gangtok-737102 (Sikkim)

Field trials were conducted with 904 accessions of indigenous and exotic okra (*Ablemoschus esculetus* (L.) Moench) germplasm from 1999 to 2001 to identify high yielding genotypes and to study the selection response for fruit yield. Both inter and intra population selection was carried out. Fortyone out of 904 accessions recorded high yield over check variety Arka Anamika. Accessions IC 45802 exhibited significantly more fruits per plant (13.00) followed by EC 329386 and EC 305609. Three accessions namely, IC 69304, EC 305609 and IC 140929 II outperformed for fruit weight per plant. Accession EC 305609 registered consistently superior yield over years and is hence worthy for commercial exploitation. The direction of selection response was positive as well as negative. Selection response was high and positive when fruit yield per plant in the parental population (X_0) was low and *vice versa*. The results of the study revealed that in the initial phase of breeding programme, selection between accessions for yield might be useful. However, once the yield level reached a ceiling limit or plateau point, recombination breeding or heterosis breeding would be most effective as this trait was governed by polygene with additive as well as non-additive gene action.

Key Words: Selection response, Genetic gain, Okra, *Abelmoschus esculentus*

The genetic composition of a population can be changed in many ways. Selection is one among them. There are two agencies involved in carrying out selection; one is by nature known as natural selection and the other is by man known as artificial selection. The purpose of artificial selection is to isolate superior genotypes from the population with diverse genetic base. While doing so the phenotypic value of the selected population *vis-à-vis* the frequency of yield contributing alleles are shifted towards favourable direction. Bhindi, being often cross pollinated crop, offer much scope for genetic improvement through breeding methods that are normally applicable to self as well as cross pollinated crops including by selection (Hussein, 1994). This study was conducted to identify high yielding okra genotypes from 'active germplasm collection' and to assess the response to selection for fruit yield.

Materials and Methods

The study was conducted in the Research Farm of NBPGR Regional Station, Thrissur. Nine hundred and four accessions of okra germplasm collected from several Asian countries constituted the base population for the study. The base population was derived from open pollinated flowers. Twelve seeds from each of the 904 accessions were sown in augmented design during 1999. Simple phenotypic selections for fruit yield have been exercised to identify high yielding accessions. Arka Anamika was considered as check variety. The selected high yielding accessions henceforth referred as parental population (X_0). Twenty-four seeds from each of the X_0 population were raised in replicated trial during June 2000. Observations on individual plants were recorded and high yielding individual plants within each accession (X_0) were selected, selfed and harvested separately. They are henceforth, referred as progeny (X_p) population. During May 2001, seeds from X_p and X_0 populations were planted in RBD with two replications. Observations on number of fruits per plant and fruit weight per plant were recorded from each of the X_p and X_0 population. Selection response (R) was calculated as the differences between the mean phenotypic value of (X_p) and (X_0) population (Sharma, 1994). Selection response as percentage of mean of parents was also calculated.

Results and Discussion

The analysis of variance for number of fruits and fruit weight per plant for 904 accessions (base population) showed significant differences. The accessions had high degree of variability. Number of fruits per plant varied from 3.25 to 18.67, while fruit weight ranged from 39.50 g to 418.33 g. Accessions in the base population recorded, on an average, 6.62 fruits per plant while the check variety Arka Anamika recorded 4.67 fruits per plant. Arka

Anamika yielded 119.26 g fruits per plant whereas the grand mean for base population was 75.40 g. Forty-one out of 904 accessions that recorded significantly high yield (number and weight basis) than Arka Anamika were selected. These 41 accessions constituted parental (X_0) populations for next cycle of selection. The selection intensity between accessions was therefore, 4.5 per cent. In the subsequent trial, high yielding plants (X_p) within each accession were selected. The selection intensity within accessions varied from 4.1 to 8.2 per cent.

The fruit yield from replicated trial laid during May 2001 for each of X_0 and X_p plants are given in Table 1 and 2. The grand mean for parents was 8.6 fruits per plant while it was 9.6 fruits for plants selected from each of the X_0 accessions. Among the parents, IC 45802 exhibited significantly more fruits per plant (13.00) followed by EC 329386 and EC 305609. Accessions IC 218896, IC 218896 II and EC 305746 had few fruits per plants and on par. Among the progenies IC 282298 and IC 140929 were the poor yielders. They were at par. An exotic collection EC 305609 recorded the maximum of 17 fruits per plant followed by three indigenous collections *viz.*, IC 218887, AA selection and IC 43736.

As regard to fruit weight per plant, the range was from 56.67 g to 246.15 g among parents and from 49.5 g to 332.50 g among progenies. Three accessions namely, IC 69304, EC 305609 and IC 140929 II outperformed for this trait and were at par. This was followed by accessions EC 329386 and IC 140929. For number of fruits per plant, IC 140929 did not figure in the top list,

Table 1. Passport information of the selected parental lines

S. No.	Accession No.	Collector's No./NIC No.	Place of Collection	District	State/Country
1	IC 32855 C			Dhule	Maharashtra
2	IC 33182			Singli	Madhya Pradesh
3	IC 33206 A			Nasik	Maharashtra
4	IC 33340				Madhya Pradesh
5	IC 33350				Madhya Pradesh
6	IC 43736				Kerala
7	IC 45791				Tamil Nadu
8	IC 45802				Tamil Nadu
9	IC 45813				Tamil Nadu
10	IC 45824				Tamil Nadu
11	IC 69242	105/82-8	Pazhayannur	Thrissur	Kerala
12	IC 69250	109/82-48	Thonippadam	Palakkad	Kerala
13	IC 69272				Kerala
14	IC 69304				Kerala
15	IC 218874	V-4549		Kannur	Kerala
16	IC 218874 A	V-4549 A		Kannur	Kerala
17	IC 282240	V-89/O-22		Coimbatore	Tamil Nadu
18	IC 218887	V-89/O-59		Cuddappah	Andhra Pradesh
19	IC 218896	V-90/O-81	Thekkumpadam	Malappuram	Kerala
20	IC 218896 II	V-90/O-81 II		Malappuram	Kerala
21	EC 305746				Bangladesh
22	IC 140915	TZA/91-231	Payyanadu	Malappuram	Kerala
23	IC 140915 II	TZA/91-231 II	Payyanadu	Malappuram	Kerala
24	IC 140920	TZA/91-330	Meenkolli	Wynad	Kerala
25	IC 140929				Kerala
26	IC 140929 II				Kerala
27	IC 282298	TZA/91-412		Calicut	Kerala
28	IC 128055	T 91/75	Barestri	Goa	Goa
29	IC 128075	PSR 2043	Mohammadnagar	Nizamabad	Andhra Pradesh
30	IC 128078	NIC 9494	Bussapur	Nizamabad	Andhra Pradesh
31	IC 140877				Kerala
32	EC 329380	V 91/O-294	Piple	Makwanpur	Nepal
33	IC 128096	PSR 2163	Kudurupaka	Karimnagar	Andhra Pradesh
34	IC 140897	H 2150	Shimpong	West Siang	Andaman & Nicobar
35	EC 329386	V 91/O-290	Darimtar	Makwanpur	Nepal
36	EC 329406	V 91/O-316	Parbas	Palpa	Nepal
37	EC 329406 II	V 91/O-316 II	Parbas	Palpa	Nepal
38	EC 305609				Bangladesh
39	AA Selection				Bangladesh
40	IC 69242 II	105/82-8 II	Pazhayannur	Thrissur	Kerala
41	IC 43736 II				Kerala

Table 2. Selection response for number of fruits per plant

S.No.	Accession No.	Number of fruits/plant		Selection response	Selection response
		Progeny (X_p)	Parents (X_o)	$R= X_p - X_0$	as % of parent mean
1	IC 32855 C	8.62 cd	10.00 abcd	- 1.38	- 16.05
2	IC 33182	9.60 bcd	7.33 bcd	2.27	26.40
3	IC 33206 A	8.41 cd	8.67 abcd	- 0.26	- 3.02
4	IC 33340	8.90 cd	11.00 abcd	- 2.10	- 24.42
5	IC 33350	7.02 cd	7.67 abcd	- 0.65	- 7.56
6	IC 43736	11.62 bc	7.33 bcd	4.29	49.88
7	IC 45791	9.69 bcd	9.00 abcd	0.69	8.02
8	IC 45802	11.25 bcd	13.00 a	- 1.75	- 20.35
9	IC 45813	10.91 bcd	7.00 bcd	3.91	45.47
10	IC 45824	9.43 bcd	9.67 abcd	- 0.24	- 2.79
11	IC 69242	8.90 cd	6.67 bcd	2.23	25.93
12	IC 69250	10.37 bcd	8.00 abcd	2.37	27.56
13	IC 69272	7.50 cd	8.31 abcd	- 0.81	- 9.42
14	IC 69304	10.51 bcd	9.00 abcd	1.51	17.56
15	IC 218874	9.43 bcd	10.00 abcd	- 0.57	- 6.63
16	IC 218874 A	9.57 bcd	9.67 abcd	- 0.10	- 1.16
17	IC 282240	9.97 bcd	9.33 abcd	0.64	7.44
18	IC 218887	14.25 ab	7.67 abcd	6.58	76.51
19	IC 218896	7.37 cd	6.00 d	1.37	15.93
20	IC 218896 II	8.78 cd	6.00 d	2.78	32.33
21	EC 305746	10.88 bcd	6.00 d	4.88	56.74
22	IC 140915	10.50 bcd	7.00 bcd	3.50	40.70
23	IC 140915 II	8.08 cd	7.00 bcd	1.08	12.56
24	IC 140920	7.01 cd	6.33 cd	0.68	7.91
25	IC 140929	7.11 cd	8.00 abcd	- 0.89	- 10.35
26	IC 140929 II	6.30 d	8.00 abcd	- 1.70	- 19.77
27	IC 282298	6.25 d	9.00 abcd	- 2.75	- 31.98
28	IC 128055	8.66 cd	9.33 abcd	- 0.67	- 7.79
29	IC 128075	11.03 bcd	10.67 abcd	0.36	4.19
30	IC 128078	10.18 bcd	9.33 abcd	0.85	9.88
31	IC 140877	10.43 bcd	9.00 abcd	1.43	16.63
32	EC 329380	9.16 bcd	10.67 abcd	- 1.51	- 17.56
33	IC 128096	8.07 cd	9.33 abcd	- 1.26	- 14.65
34	IC 140897	10.32 bcd	8.67 abcd	1.65	19.19
35	EC 329386	11.03 bcd	12.00 ab	- 0.97	- 11.28
36	EC 329406	9.57 bcd	7.67 abcd	1.90	22.09
37	EC 329406 II	9.00 bcd	7.67 abcd	1.33	15.47
38	EC 305609	17.00 a	11.67 abc	5.33	61.98
39	AA Selection	12.10 bc	7.65 abcd	4.45	51.74
40	IC 69242 II	9.34 bcd	8.90 abcd	0.44	5.12
41	IC 43736 II	9.85 bcd	7.33 bcd	2.52	29.30
Mean	9.62	8.60			
Check: Arka Anamika		5.66			

Values followed by same alphabet do not differ significantly

however, due to high individual fruit weight its yield was high. T-test comparisons between parents and progenies for fruit yield showed significant mean differences indicating a shift in the phenotypic value of selected population from the base population for both these traits. Bagchi (1995) reported similar results in Teak.

Selection response (R) is the deviation of the progeny mean from the original population mean. It is often reflected as genetic gain under selection, which is the real success of a selection exercise. The value for R varied from - 2.75 to 6.58 fruits per plant and - 43.95 g to 108.77 g fruit weight per plant. The direction of selection response was both positive as well as negative, suggesting that response to selection need not always be positive. In fact, 16 and 21 out of 41 accessions showed negative response for fruit number and fruit weight per plant respectively. Wu (1999) observed decline in response after each generation of selection in forest trees.

An appraisal of heritability values and genetic advance gives an idea on the nature of gene action governing a particular trait. High heritability (h^2= 68.20 %) and moderate genetic advance (28.63 %) among parents for number of fruits per plant suggests the importance of additive gene action. Hence, simple

Table 3. Selection response for fruit yield (g)/plant

S. No.	Accession No.	Fruit weight (g)/plant		Selection response $R = X_p - X_0$	Selection response as % of parent mean
		Progeny (X_p)	Parents (X_o)		
1	IC 32855 C	95.06 nop	125.90 ijk	−30.84	−20.43
2	IC 33182	118.06 lmn	101.37 kl	16.69	11.05
3	IC 33206 A	107.42 no	126.32 ijk	−18.90	−12.52
4	IC 33340	97.29 nop	136.18 hi	−38.89	−25.76
5	IC 33350	155.38 efghijk	198.58 bc	−43.20	−28.61
6	IC 43736	188.46 cd	130.62 hij	57.84	38.31
7	IC 45791	136.62 ijklm	142.11 ghi	−5.49	−3.64
8	IC 45802	141.67 ghijkl	181.09 bcdef	−39.42	−26.11
9	IC 45813	115.14 mno	82.95 lm	32.19	21.32
10	IC 45824	161.97 efghi	186.53 bcde	−24.56	−16.27
11	IC 69242	165.70 defg	140.27 ghi	25.43	16.84
12	IC 69250	169.05 def	145.04 ghi	24.01	15.90
13	IC 69272	146.42 fghijk	188.14 bcde	−41.72	−27.63
14	IC 69304	259.24 b	246.15 a	13.09	8.67
15	IC 218874	163.54 defgh	194.80 bcd	−31.26	−20.70
16	IC 218874 A	49.52 q	56.67 n	−7.15	−4.73
17	IC 282240	166.42 defg	174.19 cdef	−7.77	−5.15
18	IC 218887	266.00 b	157.24 fgh	108.77	72.04
19	IC 218896	159.79 efghi	122.34 jjk	37.45	24.80
20	IC 218896 II	169.24 def	124.08 ijk	45.16	29.91
21	EC 305746	93.62 nop	88.74 lm	4.88	3.23
22	IC 140915	137.21 ijklm	119.00 ijk	18.21	12.06
23	IC 140915 II	142.54 ghijkl	134.47 hi	8.07	5.35
24	IC 140920	99.77 nop	134.13 hi	−34.36	−22.76
25	IC 140929	159.82 efghij	201.52 b	−41.70	−27.62
26	IC 140929 II	195.41 c	239.36 a	−43.95	−29.11
27	IC 282298	157.03 efghij	144.00 ghi	13.03	8.63
28	IC 128055	161.19 efghi	196.77 bcd	−35.58	−23.57
29	IC 128075	159.90 efghij	170.83 def	10.93	−7.24
30	IC 128078	82.04 p	83.97 lm	−1.93	−1.28
31	IC 140877	131.38 klm	126.63 ijk	4.75	3.15
32	EC 329380	138.12 hijklm	181.39 bcdef	−43.27	−28.66
33	IC 128096	80.21 p	106.46 jkl	−26.25	−17.38
34	IC 140897	139.52 hijklm	130.40 hij	9.12	6.04
35	EC 329386	169.51 def	203.64 b	−34.13	−22.61
36	EC 329406	180.99 cde	162.68 efg	18.31	12.13
37	EC 329406 II	134.66 jklm	129.09 ij	5.57	3.69
38	EC 305609	332.50 a	242.50 a	90.00	59.61
39	AA Selection	260.70 b	180.39 bcdef	80.31	53.19
40	IC 69242 II	166.28 defg	178.09 bcdef	−11.81	−7.82
41	IC 43736 II	90.96 op	75.87 mn	15.09	10.00
Grand mean		152.32	150.98		
Check: Arka Anamika		128.67			

Values followed by same alphabet do not differ significantly

selection would be rewarding for improvement of this trait. However, progenies after one cycle of selection exhibited high heritability (h^2= 71.40 %) and low genetic advance (3.12 %) thus suggesting the contribution of non-additive gene action and improvement of this trait warrants heterosis breeding as also reported by Hussein (1994).

A perusal of Table 3 shows interesting results. Selection response was high and positive when number of fruits per plant was below nine in parents. Lower the yield of parental accession greater was the genetic gain in the progeny derived from them as exemplified in IC Nos. 33182, 43736, 45813, 69242, 69250, 218887, 218896-II, 140915, 140915-II and EC 305746. Selection response was approaching unity when the number of fruits per plant in the parents was nine as in IC Nos. 282240, 128078, 69242-II and 45791. When number of fruits per plant exceeds nine in the parents, selection response was low and negative. It was also observed that more the fruits per plant in the parents greater would be the genetic gain but in negative direction. Yield data recorded from IC Nos. 32855 C, 45802, 33340, 218874, EC 329380 and EC 329386 could testify this point.

The above results could be interpreted as follows. The accessions in the parental generation with fruit number less than nine fruits per plant were the unimproved populations, derived from open pollinated seeds. They are the rich sources of variability and contain high amount of additive genetic variance as also explained by Sharma (1994). As a matter of fact, the frequency of desirable alleles available for selection was high and hence they responded positively for selection pressure. On the other hand, accessions (parents) with around nine fruits per plant might be considered as partially improved accessions. As a consequence of previous selection, they are expected to carry low or moderate additive genetic variance. This was reflected in the gradual approach in performance of these accessions to the ceiling or plateau point of nine fruits per plant under Kerala conditions. As selection proceeds for greater than six fruits per plant, it is obvious that they may not respond positively since the residual variation in the parental population is additive. The same holds good for fruit weight per plant. Therefore, from the results it is clear that the number of fruits and fruit weight per plant in okra is conditioned by polygenes with additive as well as non-additive gene action. Under such circumstances, at initial stage of breeding programme, selection between accessions (inter-population selection) of large germplasm collection would be effective. However, after few cycles of selection, recombination breeding or heterosis breeding would be more effective.

Acknowledgements

The authors are grateful to Dr. B.S. Dhillon, Former Director, NBPGR, New Delhi for the facilities provided. We are also thankful to Dr. Mahendra Singh, Former Head, Germplasm Evaluation Division, NBPGR, New Delhi, Dr. Z. Abraham, Officer-in-charge, NBPGR Regional Station, Thrissur and Shri. K.C. Velayudhan, Principal Scientist (Retd.) for their encouragements and valuable suggestions. The financial assistance provided by the USIF is gratefully acknowledged.

References

Bagchi SK (1995) Selections differential and predicted gain in *Tectona grandis*. *Indian Forester* **121 (6)**: 482-490.

Hussein HA (1994) Variation, heritability and response to selection in okra. *Assiut J. agric. Sciences* **31(1)**: 12-17.

Sharma JR (1994) *Principles and Practice of Plant Breeding*. Tata McGraw-Hill Publishing Co., New Delhi, 599 p.

Wu HX (1994) Study of early selection in tree breeding 2. Advantages of early selection through shortening the breeding cycle. *Silvae Genetica*. **489(2)**: 78-83.

Molecular Characterization of Hill Maize Inbreds Using RAPD Markers

Jai Dev*, Samuel Jeberson M, Munish Sharma[1], R Rathour[1] and SR Thakur[1]
Department of Plant Breeding and Genetics, CSK HP Krishi Vishvavidyalaya-176062 (HP), India
[1]Advanced Centre of Hill Bioresources and Biotechnology, CSK HP Krishi Vishvavidyalaya, Palampur-176062 (HP), India

The genetic diversity of 82 hill maize inbreds of Almora, Bajaura and Ranichauri centers was evaluated using random amplified polymorphic DNA (RAPD) markers. Thirty seven decamer random primers were selected out of more than 100 primers screened, which resulted in the amplification of 196 fragments, out of which 160 (81.63 %) were polymorphic. The data were used to generate the similarity matrix using Jaccard's similarity coefficient and a dendrogram was constructed using UPGMA. The similarity among the inbreds ranged from 0.50 to 0.89 with an average of 0.70. The dendrogram clustered the inbreds into three major groups. The inbreds from different centers, generally, clustered in different groups. The results showed that RAPDs can be used as a tool for determining the extent of genetic diversity among maize inbreds and the diverse inbreds from different groups may be utilized successfully in the development of maize hybrids so as to aid in the choice of superior crosses to be made among the inbred lines.

Key Words: Maize, RAPD, Inbreds, Genetic similarity, Polymorphism

Introduction

Maize (*Zea mays* L.) has been under cultivation traditionally since long in the North-Western Himalayan region of the country. It is one of the most important cereal crops of the world for food, feed and industrial uses. It is a crop of tropical and subtropical areas but can be cultivated successfully under temperate climate conditions. One such example is its cultivation in dry temperate region of Himachal Pradesh in India.

Knowledge of genetic diversity in maize inbreds is useful in planning crosses for hybrid development, assigning lines to heterotic groups and plant variety protection (Pejic *et al.*, 1998). This information can be obtained from pedigree of the lines, heterosis estimates, morphological traits, biochemical markers and DNA based markers (Smith and Smith, 1992). The developments in molecular biology techniques have allowed the use of DNA markers for analyzing diversity in different crops. DNA markers offer several advantages over other methods. They show higher degree of polymorphism *vis-à-vis* environmental neutrality and can be evaluated at any stage of plant development. Moreover, DNA markers are quicker, more reliable and effective than other marker types.

Random amplified polymorphic DNA (RAPD) is a class of molecular markers that involves random amplification of DNA from the genome using a single arbitrary primer generating several DNA fragments, which can be used as genetic markers. Besides its simplicity, speed and good degree of polymorphism as well as wide genome coverage, the RAPD technique also facilitates automation and has low operational cost (Dias *et al.*, 2004).

Keeping this in view, the RAPD marker system was employed in the present study for the assessment of genetic diversity among maize inbreds lines of three different hill research stations (Almora, Bajaura and Ranichauri) of India.

Materials and Methods

Eighty-two maize inbred lines (Table 1) collected from CSK HPKV Regional Research Station, Bajaura, Kullu (HP), Vivekanand Parvatiya Krishi Anushandhan Shala (VPKAS), Almora (Uttrakhand) and Hill Campus of GB Pant University of Agriculture and Technology, Ranichauri (Uttrakhand) were analyzed for RAPD polymorphism during 2005-06.

DNA of each inbred was isolated by using the CTAB method (Hahn *et al.*, 1995) with minor modifications. More than 100 decamer random primers were initially screened for their ability to amplify the DNA of maize inbreds. Out of these, 37 primers (Table 2) giving reproducible amplification products were selected for the present study. DNA amplification was carried out by making final reaction volume to 20 µl containing 1.6 µl of dNTP mix (0.2 mM of dATP, dGTP, dCTP and dTTP),

*Author for correspondence: Email: jdhp@rediffmail.com; jd@hillagric.ernet.in

Table 1. List of hill maize inbred lines used in the present study

S. No.	Inbreds	Procured from/ Source
1.	CM-212	Almora[1] (DMR[2])
2.	CM-145	-do-
3.	CM-141	-do-
4.	V-25	-do-
5.	CM-152	-do-
6.	CM-153	-do-
7.	CM-128	-do-
8.	CM-129	Almora[1]
9.	V-12	-do-
10.	V-13	-do-
11.	V-21	-do-
12.	V-128	-do-
13.	V-178	-do-
14.	V-190	-do-
15.	V-198	-do-
16.	V-261	-do-
17.	V-273	-do-
18.	V-337	-do-
19.	V-359	-do-
20.	V-365	-do-
21.	PRM-401	Ranichauri[3]
22.	PRM-402	-do-
23.	PRM-403	-do-
24.	PRM-404	-do-
25.	PRM-405	-do-
26.	PRM-406	-do-
27.	PRM-407	-do-
28.	PRM-408	-do-
29.	PRM-409	Ranichauri[3]
30.	PRM-410	-do-
31.	PRM-411	-do-
32.	PRM-412	-do-
33.	BJIM-1	Bajaura[4]
34.	BJIM-2	-do-
35.	BJIM-3	-do-
36.	BJIM-4	-do-
37.	BJIM-5	-do-
38.	BJIM-6	-do-
39.	BJIM-7	-do-
40.	BJIM-8	-do-
41.	BJIM-9	-do-

Table 1 contd.

S. No.	Inbreds	Procured from/ Source
42.	BJIM-10	-do-
43.	BJIM-11	-do-
44.	BJIM-12	-do-
45.	BJIM-13	-do-
46.	BJIM-14	-do-
47.	BJIM-15	-do-
48.	BJIM-16	-do
49.	BJIM-17	-do-
50.	BJIM-18	Bajaura[4]
51.	BJIM-19	-do-
52.	BJIM-20	-do-
53.	BJIM-21	-do-
54.	BJIM-22	-do-
55.	BJIM-23	-do-
56.	BJIM-24	-do-
57.	BJIM-25	Bajaura[4]
58.	BJIM-26	-do-
59.	BJIM-27	-do-
60.	BJIM-28	-do-
61.	BJIM-29	-do-
62.	BJIM-30	-do-
63.	BJIM-31	-do-
64.	BJIM-32	-do
65.	BJIM-33	-do-
66.	BJIM-34	Bajaura[4] (DMR[2])
67.	BJIM-35	-do-
68.	BJIM-36	Bajaura[4]
69.	BJIM-37	-do-
70.	BJIM-38	Bajaura[4] (CIMMYT[5])
71.	BJIM-39	Bajaura (DMR[2])
72.	BJIM-40	Bajaura[4]
73.	BJIM-41	-do-
74.	BJIM-42	Bajaura[4] (DMR[2])
75.	BJIM-43	Bajaura[4]
76.	BJIM-44	Bajaura[4] (DMR[2])
77.	BJIM-45	-do-
78.	BJIM-46	Bajaura[4] (CIMMYT[5])
79.	BJIM-47	-do-
80.	BJIM-48	Bajaura[4]
81.	BJIM-49	Bajaura[4] (DMR[2])
82.	BJIM-50	-do-

[1]Almora– Vivekanand Parvatiya Krishi Anushandhan Shala
[2]DMR– Directorate of Maize Research, New Delhi
[3]Ranichauri– Hill campus of GB Pant University of Agriculture and Technology, Pantnagar
[4]Bajaura– Regional Research Station of CSK HP Krishi Vishvavidyalaya
[5]CIMMYT– International Center for Maize and Wheat Improvement, Mexico

0.16 µl of *Taq* DNA polymerase (5 U/µl l), 1.6 µl (20 ng) DNA template, 0.8 µl of 5 pmole primer, 2.0 µl of 10x PCR buffer, 1.6 µl MgCl2 and 12.64 µl of sterilized distilled water.

PCR amplification was carried out in a thermal cycler (Applied Biosystems) using the following temperature profile: initial denaturation at 94°C for 5 minutes followed by 40 cycles of 94°C for 1 minute, 37°C for 1 minute, 72°C for 1 minute and a final extension at 72°C for 5 minute followed by rapid cooling to 4°C. Ten µl of each PCR products mixed with gel loading dye (0.25% bromophenol blue and 40% sucrose), was electrophoresed using 1.4% agarose gel in 0.5x Tris borate EDTA (pH 8.0). The gel was run at a constant voltage of 100 volts for 2 hours. The gel was stained with ethidium bromide (0.5 µg/ml) for 10 minutes after completion of electrophoresis. The gel was destained for 30 minutes by keeping under distilled water. The resolved PCR products were visualized on an ultraviolet transilluminator and a photograph of gel was stored in Gel Doc (Bio-rad).

RAPD profiles of 82 maize inbreds were analyzed by scoring the presence or absence of each RAPD band.

Table 2. Number of RAPD bands generated by 37 decamer oligonucleotide primers used for the analysis of 82 maize inbreds

Sr. No.	Primer	Sequence (5' to 3')	N_f	N_p	N_m	% polymor-phism
1.	OPC-08	5'-TGGACCGGTG-3'	3	1	2	33.30
2.	OPD-05	5'-TGAGCGGACA-3'	8	8	0	100
3.	OPE-03	5'-CCAGATGCAC-3'	4	3	1	75
4.	OPX-04	5'-CCGCTACCGA-3'	5	5	0	100
5.	OPF-19	5'-CCTCTAGACC-3'	7	7	0	100
6.	OPJ-04	5'-CCGAACACGG-3'	8	8	0	100
7.	OPJ-06	5'-TCGTTCCGCA-3'	7	7	0	100
8.	OPJ-08	5'-CATACCGTGG-3'	6	6	0	100
9.	OPJ-10	5'-AAGCCCGAGG-3'	5	3	2	60
10.	OPP-06	5'-GTGGGCTGAC-3'	7	0	7	0.0
11.	OPP-08	5'-ACATCGCCCA-3'	7	3	4	42.86
12.	OPP-10	5'-TCCCGCCTAC-3'	9	8	1	90
13.	OPP-11	5'-AACGCGTCGG-3'	7	7	0	100
14.	OPE-06	5'-AAGACCCCTC-3'	7	7	0	100
15.	OPD-11	5'-AGCGCCATTG-3'	9	9	0	100
16.	OPF-17	5'-AACCCGGGAA-3'	4	4	0	100
17	OPU-17	5'-ACCTGGGGAG-3'	3	0	3	0.0
18.	OPU-14	5'-TGGGTCCCTC-3'	3	0	3	0.0
19.	OPC-12	5'-TGTCATCCCC-3'	3	0	3	0.0
20.	OPP-01	5'-GTAGCACTCC-3'	4	3	1	75.00
21.	OPD-01	5'-ACCGCGAAGG-3'	4	4	0	100
22.	OPJ-01	5'-CCCGGCATAA-3'	7	7	0	100
23.	OPQ-10	5'-TGTGCCCGAA-3'	4	3	1	75
24.	OPQ-12	5'-AGTAGGGCAC-3'	4	1	3	25
25.	OPQ-13	5'-GGAGTGGACA-3'	4	4	0	100
26.	OPF-7	5'-CCGATATCCC-3'	5	5	0	100
27.	OPJ-17	5'-ACGCCAGTTC-3'	4	2	2	50
28.	OPP-14	5'-CCAGCCGAAC-3'	4	3	1	75
29.	OPA-5	5'-AGGGGTCTTG-3'	3	2	1	66.66
30.	OPQ-8	5'-CTCCAGCGGA-3'	7	7	0	100
31.	OPP-4	5'-GTGTCTCAGG-3'	4	4	0	100
32.	OPQ-16	5'-AGTGCAGCCA-3'	6	6	0	100
33.	OPJ-15	5'-TGTAGCAGGG-3'	4	4	0	100
34.	OPA-14	5'-TCTGTGCTGG-3'	4	4	0	100
35.	OPQ-15	5'-GGGTAACGTG-3'	6	6	0	100
36.	OPJ-9	5'-TGAGCCTCAC-3'	6	5	1	83.33
37.	OPA-9	5'-GGGTAACGCC-3'	4	4	0	100
Total			196	160	36	-
Average			5.30	4.32	0.97	77.06

N_f: Total number of fragments, Np: Number of polymorphic fragments, N_m: Number of monomorphic fragments

A binary data matrix with '1' indicating the presence of particular band and '0' indicating its absence was constructed. The binary data were used to generate a similarity matrix using Jaccard's similarity coefficient, $J_{ij} = C_{ij}/(n_i+n_j-C_{ij})$, where '$C_{ij}$' is the number of positive matches between two genotypes, while n_i and n_j is the total number of bands in the genotype i and j, respectively, in SIMQUAL programme of NTSYS-pc package version 1.80 (Rohlf, 1993). The data were subsequently used to construct a dendrogram using the unweighted pair group method with arithmetical averages (UPGMA) in SHAN programme of NTSYS-pc package version 1.80.

Results and Discussion

The random amplified polymorphic DNA (RAPD) profiling of 82 maize inbreds using 37 decamer random primers generated a total of 203 RAPD bands (Table 2), of which 160 were polymorphic (81.63%). On an average, 4.32 polymorphic bands were generated per primer. Primers OPP-10 and OPD-11 generated the maximum number of bands (9) and OPC-08, OPU-17, OPU-14, OPC-12 and OPA-5 produced the least number of bands (3). As many as 21 primers generated 100% polymorphic products, whereas four primers gave only monomorphic bands. A representative RAPD profiles generated with OPD-05 primer are shown in Fig. 1.

The RAPD data were used to discern genetic relationship among the inbreds using Jaccard's similarity coefficient. The genetic similarity coefficient among the inbreds ranged from 0.50 (genetic distance, GD=0.50) between CM 128 and BJIM 40 to 0.89 (GD=0.11) between PRM 403 versus PRM 404 (Data not shown). The similarity matrix was used to construct a dendrogram

using UPGMA method (Fig. 2). The cluster analysis revealed that the inbreds were clustered in three major groups A, B and C. The dendrogram showed that the cluster A comprised 28 inbreds out of which 20 were from Almora (out of a total of 20) and eight (out of a total 12) from Ranichauri. The other four inbred lines from Ranichauri and 24 inbreds (out of a total 50) from Bajaura were grouped in cluster B. The cluster C included 26 inbreds which were all from Bajaura. The genetic similarity ranged from 0.79 (GD=0.21) between inbreds CM 128 versus V 13 to 0.89 (GD =0.11) between inbreds PRM 403 and PRM 404 in cluster A, from 0.76 (GD=0.24) between inbreds BJIM 19 versus BJIM 20 to 0.85 (GD=0.15) between lines BJIM 14 and BJIM 15 in cluster B, whereas it ranged from 0.75 (GD=0.25) between inbreds BJIM 41 versus BJIM 42 and BJIM 40 versus BJIM 43 to 0.83 (GD=0.17) between lines BJIM 49 and BJIM 50 for cluster C. The inter cluster similarity between clusters A and B was 70 % (GD=30 %), while both A and B clusters showed a similarity of 67 % (GD=33 %) with cluster C.

The 82 maize inbreds used in the study were obtained from Almora, Ranichauri and Bajaura. Some of these lines have been developed at these centres while others are from Directorate of Maize Research (DMR), New Delhi and International Centre for Maize and Wheat Improvement (CIMMYT), Mexico. According to the observations of the present study, the inbreds from different centres showed a tendency to fall into separate groups indicating their different genealogies. The inbreds from Almora

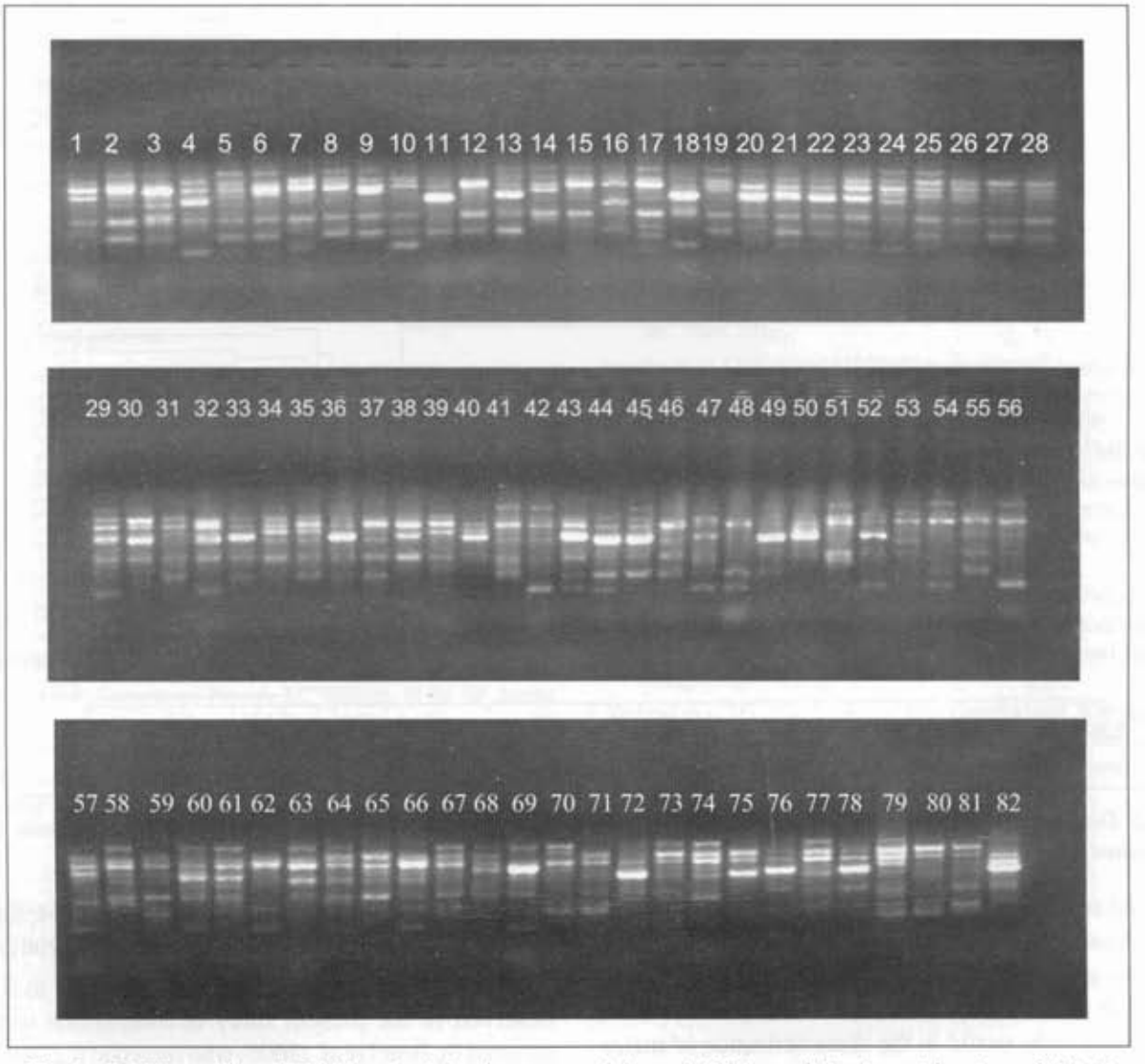


Fig. 1: *RAPD profiles of 82 hill maize inbreds generated through DNA amplification with primer OPD-05*

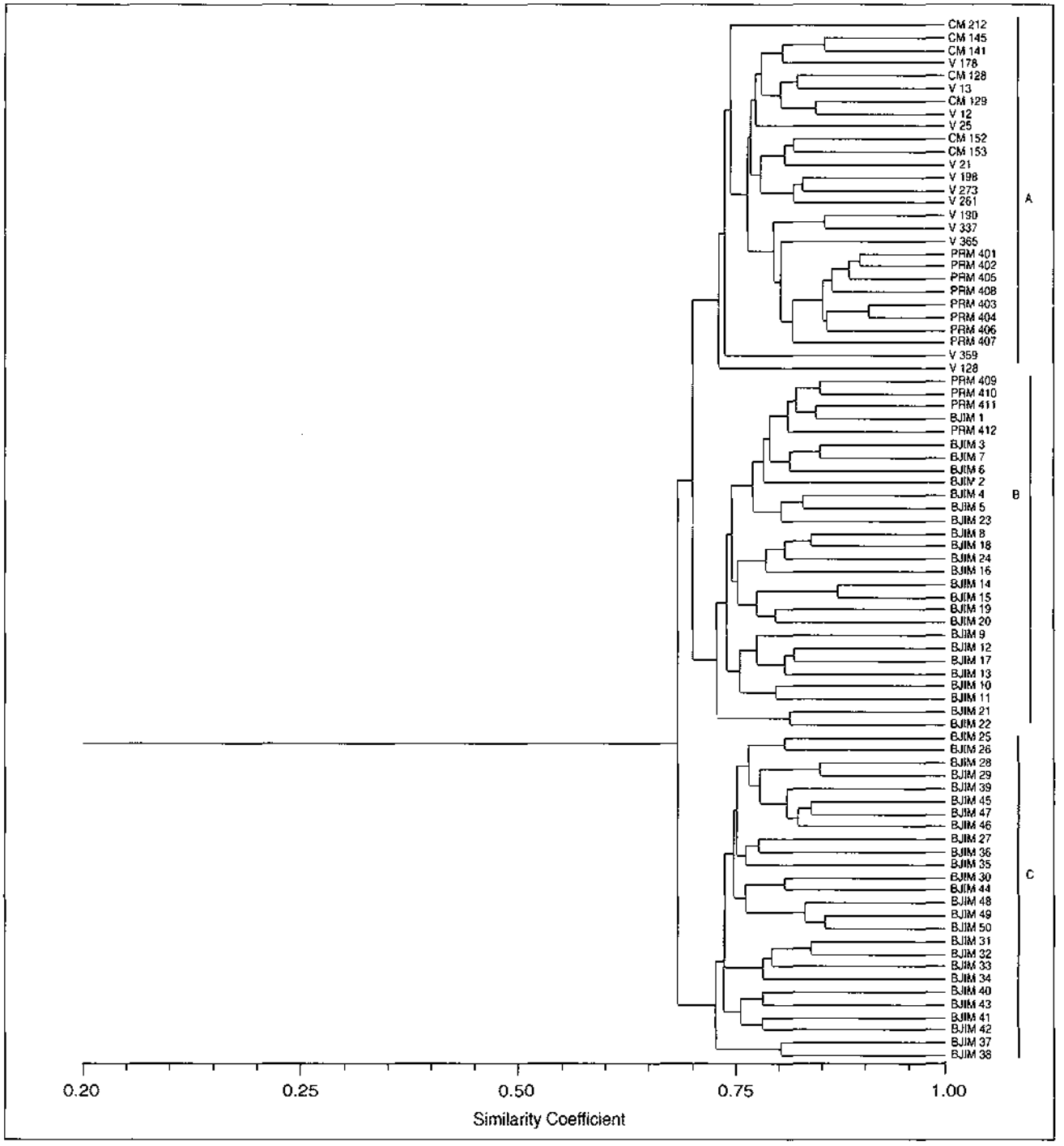


Fig. 2: *Dendrogram depicting the genetic relationship among 82 hill maize inbreds based on similarity coefficients calculated from 37 RAPD marker profiles*

grouped separately along with most of the inbreds from Ranichuari. The inbreds from Bajaura formed two separate groups. The results of the current study are in line with previous reports where RAPD markers have been found to be useful in the characterization of maize germplasm and inbreds and assigning these to different groups (Messmer *et al.*, 1992; Burstin *et al.*, 1994; Smith *et al.*, 1997; Senior *et al.*, 1998 and Sun *et al.*, 2001).

The level of genetic divergence (GD=0.11 to 0.50) observed in the present study is comparable to that reported by Bruel *et al.* (2006) who recorded 0.27 to 0.64 GD among maize inbreds of Brazil and observed

relationships between genetic divergence in parental inbreds and single cross hybrid performance. Various other workers have also found a positive correlation between the hybrid yield and RAPD based genetic distance within the heterotic groups (Lanza *et al.*, 1997 and Verbitskaya *et al.*, 1999). Therefore, RAPDs can be used as a tool for determining the extent of genetic diversity among maize inbreds and the diverse inbreds from different groups may be utilized successfully in the development of maize hybrids so as to aid in the choice of superior crosses to be made among the inbred lines. For example, hybrids involving inbred parents from Almora and Bajaura; Ranichuari (except the inbreds PRM 409, 410, 411 and 412) and Bajaura or from two groups of Bajaura may be expected to be heterotic.

It may be concluded that based on RAPD analysis using 37 decamer primers, the 82 hill maize inbreds from Almora, Ranichauri and Bajaura were clearly classified into three different clusters. The RAPD profiling has revealed the existence of sufficient genetic variability in the maize inbreds studied in the present investigation. This information may be used in hybrid maize breeding program to maximize the use of genetic resources and exploit heterosis for effective and quick development of maize hybrids.

Acknowledgments

The work was carried out under a DBT, Government of India, funded project. The authors are thankful to Dr. H.N. Gupta and Dr. Vinay Mahajan of VPKAS, Almora (Uttrakhand), Dr. B. Bandopadhaya of GBPUA&T Hill Campus, Ranichauri (Uttrakhand), and Dr. B.K. Sharma and Dr. S.K. Guleria of CSK HPKV Research and Extension Centre, Bajaura, Kullu (HP) for providing the maize inbred lines for this study.

References

Bruel DC, V Carpentieri-Pipolo, AC Gerage, N da SF Junior, CEC Prete, C de F Ruas, PM Ruas, SGH de Souza and DD Garbuglio (2006) Genetic distance estimated by RAPD markers and its relationship with hybrid performance in maize. *Pesq agropec bras, Brasilia.* **41(10):** 1491-1498.

Burstin J, D de Vienne, P Dubreuil and C Damerval (1994) Molecular markers and protein quantities as genetic descriptors in maize: I. Genetic diversity among 21 inbred lines. *Theor. Appl. Genet.* **89:** 943-950.

Dias LAS, EA de T Picoli, RBR Rocha and AC Alfenas (2004) A priori choice of hybrid parents in plants. *Genet. Mol. Res.* **3:** 356-368.

Hahn V, K Blakenhorn, M Schwall and AE Melchinger (1995) Relationship among early European maize hybrids: III. Genetic diversity revealed with RAPD markers and comparison with RFLP and pedigree data. *Maydica* **40:** 299-310.

Lanza LLB, CL de Jr Souza, LMM Ottobni, MLC Vieira and AP de Souza (1997) Genetic distance of inbred lines and prediction of maize single cross performance using RAPD markers. *Theor. Appl. Genet.* **94:** 1023-1030.

Messmer MM, AE Melchinger, J Boppenmaier, RG Herrmann and JE Brunklaus (1992) RFLP analyses of early-maturing European maize germplasm. I. Genetic diversity among flint and dent inbreds. *Theor. Appl. Genet.* **83:** 1003-1012.

Pejic I, MP Ajmone, M Morgante, V Kozumplick, P Castiglioni, G Taramino and M Motto (1998) Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. *Theor. Appl. Genet.* **97:** 1248-1255.

Rohlf FJ (1993) NTSYS-pc: Numerical taxonomy and multivariate analysis System Version 1.80. Exeter Software: Setauket, New York.

Senior ML, JP Murphy, MM Goodman and CW Stuber (1998) Utility of SSRs for determining genetic similarities and relationships in maize using an agarose gel system. *Crop Sci.* **38:** 1088-1098.

Smith OS and JSC Smith (1992) Measurement of genetic diversity among maize hybrids: A comparison of isozymic, RFLP, pedigree and heterosis data. *Maydica* **37:** 53-60.

Smith JSC, ECL Chin, H Shu, OS Smith, SJ Wall, ML Senior, SE Mitchell, S Kresovitch and J Ziegle (1997) An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.): comparison with data from RFLPs and pedigree. *Theor. Appl. Genet.* **95:** 163-173.

Sun GL, M William, J Liu, KJ Kasha and KP Pauls (2001) Microsatellite and RAPD polymorphisms in Ontario corn hybrids are related to the commercial sources and maturity ratings. *Mol. Breed.* **7:** 13-24.

Verbitskaya TG, YM Sivolap, DV Guzhva and VM Sokolov (1999) Analysis of the elationship between the genetic divergence of the DNA of corn lines and hybrid productivity. *Russian Agril. Sci.* **5:** 28-33.

Identification of Groundnut (*Arachis hypogaea* L.) Varieties through Biochemical Markers

BN Motagi, MVC Gowda*, GK Naidu and J Salim
Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad-580005, Karnataka, India

Sixteen groundnut cultivars were assessed for protein (seed and hypocotyl) and glutamate oxaloacetate transaminase (GOT) polymorphism. Seed protein profiles produced six (S1-S6) electrophoretic phenotypes compared to three (G1-G3) of GOT. While, hypocotyl proteins produced twelve (H1-H12) electrophoretic patterns. Individually, seed and hypocotyl proteins can identify three and nine cultivars, respectively. However, combination of protein (seed and hypocotyl) and GOT isozyme profiles fingerprinted all the sixteen cultivars.

Key Words: Groundnut, Varietal identification, Biochemical markers

Introduction

Electrophoresis of storage and functional proteins has emerged as an efficient, simple and reliable tool supplementing traditionally used morphological parameters. International Rules for Seed Testing (ISTA) has adopted standard SDS (sodium dodecyl sulphate), PAGE (Polyacrylamide gel electrophoresis) and IEF (Iso Electric Focusing) methods into the international rules (ISTA, 1996) for cultivar identification. Seed proteins and isozymes because of their stability and reproducibility have potential to serve as tools for fingerprinting of genotypes. Therefore, the present study was carried out to determine the protein (seed and hypocotyl) and Glutamic Oxaloacetate Transaminase isozyme (GOT) variation in groundnut cultivars and their potential for fingerprinting.

Materials and Methods

Sixteen groundnut varieties belonging to Spanish bunch (Spanish Improved, TMV 2, S 206, Dh 3-30, JL 24, KRG 1, K 134, Dh 8, R 8808, Dh 40, TAG 24 and GPBD 4), Virginia runner (S 230 and DSG 1) and Valencia (ICGV 86590 and mutant 28-2) botanical types released for cultivation were assessed for protein (seed and hypocotyl) and isozyme (GOT) polymorphism.

The analysis of proteins and isozyme was performed by polyacrylamide gel electrophoresis (PAGE) technique. Gels were prepared according to the method of Hames and Rickwod (1984). To study seed protein polymorphism, one-dimensional SDS-PAGE (12.5% separating gel and 2.5% stacking gel) was carried out following the procedure given by Laemmli (1970) in a vertical gel system. For this purpose total protein was extracted after suspending seed flour for 1 hour in an extraction buffer (65mM Tris-HCl, pH 6.8) followed by centrifugation at 10,000 rpm at 4 ÚC for 20 minutes. Then the protein sample was heated for 3 min in boiling water and gradually cooled. 100¼ g of protein was loaded with micropipette along with 10 ml sample buffer containing bromophenol blue in each sample well. The gel was run at 70 Volts for 3 h followed by staining in Coomassie Brilliant Blue R 250 for 6-8 h. Relative mobility (Rm) of the protein band was determined. For hypocotyl protein and GOT, native PAGE was done with 7.5% separating gel. One gm of fresh hypocotyl sample from 6 days old seedling was macerated in phosphate buffer (pH 8.0) at 4 ÚC. The homogenate was centrifuged at 10,000 rpm for 10 min and the gel was run at 70 Volts for 3 h. Staining was done using Coomassie Brilliant Blue for total protein and Fast Blue BB salt for GOT.

Results and Discussion

Hypocotyl Protein

A total of 15 bands with Rm values ranging from 0.218 to 0.945 were resolved. Of these, seven bands (0.345; 0.545, 0.600, 0.625, 0.636, 0.691 and 0.945) were polymorphic. Based on presence/absence of these bands, 12 electrophoretic phenotypes (H1-H12) were identified (Fig. 1 and Table 1). Nine cultivars (K 134, KRG 1, Dh 40, DSG 1, Dh 3-30, TMV 2, ICGV 86590, Mutant and GPBD 4) exhibited unique banding pattern. Two groups had two cultivars each {Spanish Improved and JL 24 (H3), and S 206 and S 230 (H6)} and one group (H12) had three cultivars [Dh 8, R 8808 and TAG 24].

*Author for correspondence: E-mail: mvcgowda@satyam.net.in

Seed Protein

SDS-PAGE of seed proteins showed differences in number and intensity of bands for different groundnut cultivars. A total of 17 bands appeared with Rm values ranging from 0.300 to 0.970. Of these, only four bands with Rm values 0.529, 0.567, and 0.962 were polymorphic forming six electrophoretic phenotype patterns (S1-S6; Fig. 1 and Table 1). Among the 16 cultivars, three (Mutant, R8808 and TAG 24) exhibited unique banding patterns and thus could be identified solely by the cultivar specific electrophoretogram. Pattern I (S1) had Valencia Mutant; Pattern II (S2) had Virginia runner (S 230 and DSG 1) and Valencia (ICGV 86590) cultivars. While, other electrophoretic patterns (S3-S6) had Spanish bunch cultivars. GPBD 4 and its female parent KRG 1 showed similar banding pattern and formed a separate group (S5). Hartzook *et al.* (1969) also observed differences in seed protein content among three botanical types and concluded that PAGE of seed proteins could be used as tool in establishing cultivar identification.

GOT Isozyme

GOT revealed four bands (Rm values 0.338, 0.385, 0.431 and 0.492). Presence and/or absence of first two bands resulted in three banding patterns (G1-G3; Fig. 1 and Table 1). The pattern I (G1) comprised five cultivars having both the polymorphic bands (0.338 and 0.385). Grieshammer and Wynne (1990) and Lacks and Stalker (1993) reported that these two polymorphic bands were present only in Virginia types. Pattern II (G2) with eight genotypes had only one polymorphic band (0.385); while, pattern III (G3) comprised three genotypes lacked both the polymorphic bands.

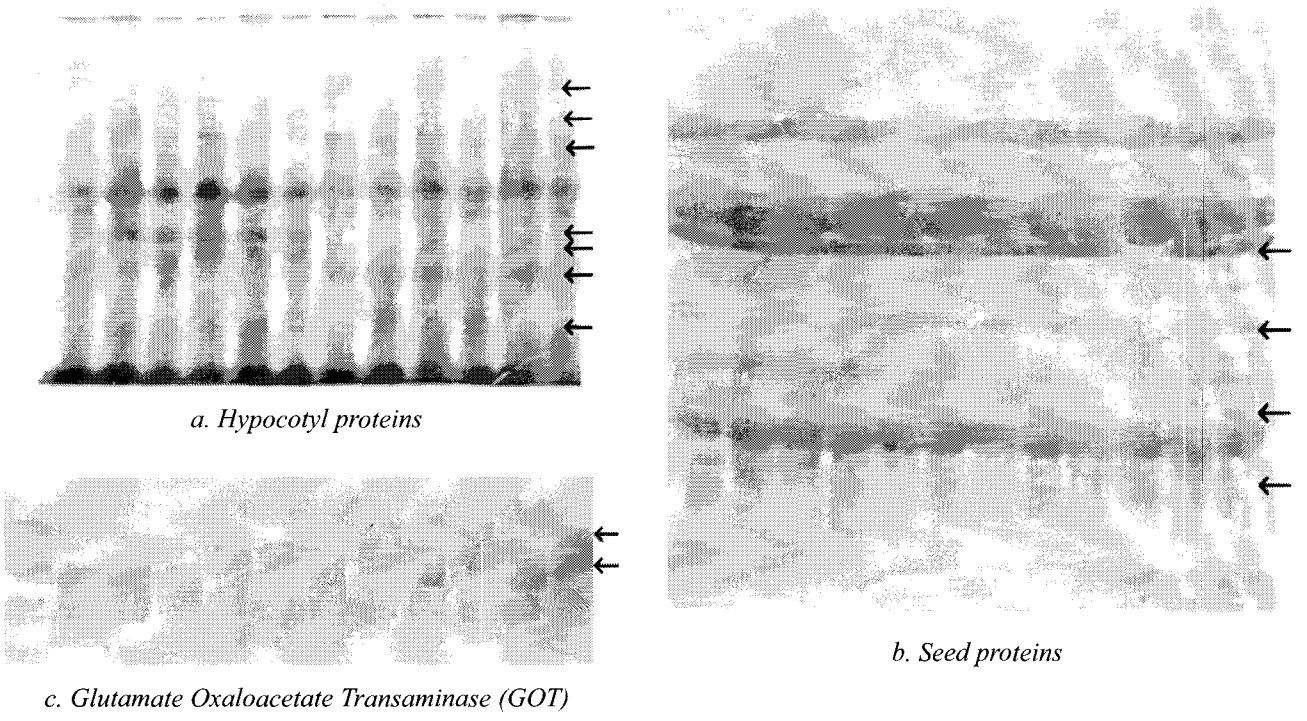
Pattern I that is specific to Virginia botanical type had cultivars belonging to Virginia (S 230 and DSG 1) with some Spanish cultivars (R 8808, TAG 24 and Mutant 28-2). TAG 24 is a cross derivative from two mutants TGE 1 and TGS 2, which in turn derived from Virginia cultivars *viz.*, TG 1 and M 13, respectively. R 8808 had ICGS 11 in its pedigree, which is a selection from Robut 33-1, a Virginia bunch cultivar. 28-2 is a secondary mutant of Dharwad Early Runner (DER). While pattern II and III had Spanish bunch cultivars.

Cultivar Fingerprinting

Hypocotyl protein profile has an advantage of twelve (H1-H12) electrophoretic phenotypes compared to six (S1-S6) of seed protein and three (G1-G3) of GOT, which can be used to identify the groundnut cultivars. Hypocotyl and seed protein together identified 14 cultivars. While, Spanish Improved could not be differentiated from JL 24 as they formed a separate group (H3S6). Combination of hypocotyl protein and GOT profiles formed fifteen groups and identified 14 cultivars. Cultivars R 8808 and TAG 24 formed a single group (H12G1). Seed protein and GOT profiles together resulted in eight groups identifying four cultivars. Two groups (S2G1 and S5G2) had two cultivars each, one group each with three (S6G3) and five (S6G2) cultivars. However, proteins (seed and hypocotyl) and GOT profiles together identified all the sixteen groundnut varieties (Table 2). Thus, electrophoresis can be used successfully as a tool for varietal identification in groundnut.

Table 1. Pattern of polymorphic bands for proteins (hypocotyls and seed) and Glutamate Oxaloacetate Transaminase (GOT) isozyme in groundnut cultivars

Variety	Hypocotyl protein							Seed protein				GOT	
	0.345	0.545	0.600	0.625	0.636	0.691	0.945	0.529	0.567	0.739	0.962	0.338	0.385
Spanish Improved	+	+	+	+	+	+	-	-	+	-	-	-	+
TMV 2	+	+	-	+	-	+	-	-	+	-	-	-	-
S 206	+	+	+	-	+	+	-	-	+	-	-	-	+
Dh 3-30	+	+	-	-	+	+	-	-	+	-	-	-	+
JL 24	+	+	+	+	+	+	-	-	+	-	-	-	-
KRG 1	+	+	-	+	+	+	+	-	+	-	+	-	+
K 134	+	-	+	+	+	+	+	-	+	-	-	-	+
Dh 8	+	+	-	-	-	-	-	-	+	-	-	-	-
S 230	+	+	+	-	+	+	-	-	+	+	+	+	+
R 8808	+	+	-	-	-	-	-	+	-	-	+	+	+
Dh 40	+	-	-	+	+	+	+	-	+	-	-	-	+
DSG 1	+	-	+	-	+	+	+	-	+	+	+	+	+
TAG 24	+	+	-	-	-	-	-	-	+	+	-	+	+
ICGV 86590	-	+	-	-	+	-	+	-	+	+	+	-	+
Mutant (28-2)	-	+	-	-	-	-	+	+	+	+	+	+	+
GPBD 4	-	+	-	+	-	-	-	-	+	-	+	-	+



a. Hypocotyl proteins

b. Seed proteins

c. Glutamate Oxaloacetate Transaminase (GOT)

Fig. 1: *Banding patterns with polymorphisms for protein (hypocotyl and seed) and GOT isoenzyme*

Table 2. Protein fingerprint of groundnut cultivars

Protein fingerprint	Cultivar
H1 S6 G2	K 134
H2 S5 G1	KRG 1
H3 S6 G2	Spanish Improved
H3 S6 G3	JL 24
H4 S6 G2	Dh 40
H5 S2 G1	DSG 1
H6 S2 G1	S 230
H6 S6 G2	S 206
H7 S6 G2	Dh 3-30
H8 S6 G3	TMV 2
H9 S2 G2	ICGV 86590
H10 S1 G1	Mutant (28-2)
H11 S5 G2	GPBD 4
H12 S3 G1	R 8808
H12 S4 G1	TAG 24
H12 S6 G3	Dh 8

References

Grieshammer U and JC Wynne (1990) Isozyme variability in mature seeds of US peanut cultivars and collection. *Peanut Sci* **18**: 72-75.

Hames BD and D Rickwood (1984) *Gel Electrophoresis of Proteins: A Practical Approach* IRL Press, Washington DC, USA, 91 p.

Hartzook A, T Birk and S Hurwitz (1969) Electrophoretic investigation of proteins from three groundnut (*Arachis hypogaea* L.) types. *Israelian J. of Agric. Res.* **19**: 135.

ISTA (1996) International Rules for Seed Testing. *Seed Sci. Tech.* **24(Supplement):** 253-270.

Lacks GD and HT Stalker (1993) Isozyme analyses of *Arachis* species and interspecific hybrids. *Peanut Sci.* **20:** 76-82.

Laemmli UK (1970) Cleavage of structural proteins during the assembly of head of bacteriophage T_4. *Nature* **227:** 680-685.

Response of Assam Rice Varieties to Low Temperature Stress

D Dutta and PK Pathak*
Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785 013, Assam, India

Low temperature induced injury, slow growth and prolongation of crop duration are some of the most important problems of *boro* rice cultivation in Assam and other eastern states of India. Any variety to be ideally fitted to the *boro* rice season must have cold tolerance at the vegetative stage of growth. In the present study, a set of rice varieties, randomly drawn from Assam rice collection, was evaluated for their response to low temperature stress at germination, post-germination and seedling growth stages. Several varieties, both modern and traditional, distributed across different classes and sub-classes of Assam rice germplasm, exhibited desired degree of tolerance to low temperature stress at one or the other stages of growth. Sufficient genetic diversity was observed among the varieties with Eucledian coefficient of dissimilarity ranging from 0.60 to 8.61 and average being 3.88 across the 56 genotypes. In this study, no ecotype-specific clustering was observed among the Assam rice varieties.

Key Words: Rice (*Oryza sative* L.), Low temperature stress, Genetic diversity, Assam rice germplasm, Boro rice

Introduction

Low temperature is a major climatic problem for growing rice in 25 countries (Kaneda and Beachell, 1974). More than 15 million hectares of rice throughout the world suffers from cold damage at one or the other stage of growth. In South and Southeast Asia alone, low temperature limits production of modern rice cultivars on an estimated area of 7 million ha (Kaw and Khush, 1985). It is one of the most serious constraints to cultivation of *boro* rice crop in the entire eastern India including Assam (Thakur, 1995; Chatterjee, 1995; Pathak *et al.*, 1999). In Assam, *boro* rice is adversely affected by low temperature in its vegetative stage with the impacts such as poor germination, stunted seedling growth and poor vigor, seedling chlorosis and mortality and prolongation of duration (Pathak *et al.*, 2003). These factors have direct bearing on the grain yield per unit area. Moreover, stunted seedling growth makes manual uprooting and transplanting operations very cumbersome. Hence, identification of genotypes with desired degree of tolerance to low temperature stress has become very important for recommendation of suitable varieties to the farmers and also for utilization in the breeding programs. Though, about 4000 accessions of rice germplasm are being maintained in Assam (Pathak, 2001) no effort has, so far, been made to systematically evaluate the varieties for their response to low temperature stress. The present study was undertaken to evaluate a set of rice varieties of Assam for their response to low temperature stress and to understand the nature and extent of genetic diversity among the varieties in relation to their response to cold.

Materials and Methods

Altogether, 56 rice genotypes were taken for the study. Of these, 53 *indica* varieties, both modern and traditional, chosen randomly from different classes and sub-classes of Assam rice, were collected from Regional Agricultural Research Station, Titabar and three *japonica* varieties were collected from College of Bioresource Sciences, NIHON University, Japan. The field and laboratory experiments were carried out in the Assam Agricultural University, Jorhat during 2005-06 to assess their response to low temperature stress at germination, post-germination and seedling growth stages using several cold tolerance indices.

Twenty healthy seeds of each variety were placed on filter paper moistened with distilled water in a 50 mm diameter Petri dish and incubated at 17°C in the dark by wrapping the Petri dishes with black polythene bags for a period of 168 hours with an interruption at 96 hours after initiation of the incubation process. The black polythene bags were removed after 168 hours and the germinated seeds were exposed to normal daylight and temperature for 48 hours for allowing the etiolated plumules to turn green. At germination and post-germination stages, response of the varieties was estimated based on the observations on rate of germination (RG) index following the method of Krishnasamy and Seshu (1989) and plumule length and plumule greening following McWilliam *et al.* (1979). According to the methods, RG index (%) = $(N_{96}/ N_{168})' 100$ where, N_{96} =

* *Corresponding author's E-mail: pathakpk_aau@yahoo.co.in*

number of seeds germinated in 96 hours (as against 72 hours in the original method) and N_{168} = number of seeds germinated in 168 hours. The plumule length was measured on 5 germinated seeds from the point of plumule emergence to the tip of the plumule after 168 hours of germination at 17°C. Plumule greening was visually scored as the average performance of the 5 germinated seeds on a 1 to 9 scale, where 1 = dark green; 3 = light green; 5 = pale green; 7 = pale white with a tinge of greenness and 9 = plumule brown or dead.

Pre-germinated seeds of each variety were also sown on well-puddled seedbeds in two replications in Randomized Block Design (RBD) on 26 December 2005 when the average temperature fell below 20°C. On 30 days after sowing (d), seedlings were assessed for leaf yellowing, electrolyte leakage and chlorophyll content following the methods described by IRRI (1996), Patterson *et al.* (1976) and Arnon (1949), respectively. The weekly average temperature during the period of experimentation was 15.8°C-16.8°C.

The mean data of each of the characters were subjected to analysis of variance and calculation of genotypic and phenotypic correlation coefficients among the parameters in all possible combinations. Diversity among the varieties was studied through cluster analysis using unweighted pair group method using arithmetic average (UPGMA). Since observed traits were measured in different scales, the data were standardized with STAND module to have a mean of zero and variance of one. Euclidean distance was computed by running SIMINT with standardized data following Sneath and Sokal (1973). The phenetic representation of genetic relationship among the genotypes as revealed by Euclidean distance was produced through cluster analysis using UPGMA.

Results and Discussion

Analysis of Variance

The analyses of variance revealed the existence of significant variation among the varieties for all the characters except chlorophyll b. The varieties were randomly chosen from diverse classes and sub-classes of rice germplasm conserved at the Regional Agricultural Research Station, Titabar that staggers to a volume of more than 1000 accessions. The result reflects the variation in the rice germplasm stock of Assam. Earlier works have already established that the indigenous rice germplasm of the region is endowed with wide genetic diversity and represents a wealth of valuable gene systems (Sharma *et al.*, 1971; IRRI, 1974 and Das *et al.*, 1981).

Germination Index

Germination index, measured to assess the varieties' tolerance to low temperature stress at germination, varied from 0-100% (Table 1). Among 56 varieties, only two *viz.*, Satkora lahi, and Ranjit scored 100 per cent for the index. These two varieties were, however, statistically *at par* with the varieties, Sail borak (97.5%), Gitesh (97.22%), Basundhara (95%), Jahinga (92.5%), Khoirajuli (92.5%), Kumol sali (92.5%) and Disang (92.5%). Other 14 varieties, belonging to different classes of rice, scored 80 or more for the index and differed significantly from the rest of the varieties. On the other end, 11 varieties *viz.*, Khoiya boro, Kolagoria, Akitakomuchi, Dusri ahu, Iharsal, Jagli boro, Majeni chembi, Kolamanik, Kola boro, Mokon boro, with a germination index score of 0 and Koshihikari (*japonica*) with a score of 5, were the worst in their response to low temperature stress at germination (Table 1).

Seventeen varieties including five traditional *boro* rice varieties of Assam scored 20% or less for rate of germination index. This clearly indicates that the traditional *boro* rice varieties of Assam are highly susceptible to low temperature stress at germination which is quite contrary to expectation. Because, the traditional *boro* rice varieties of Assam are being grown under low temperature from a very long past they are believed to possess desired degree of tolerance to low temperature stress at this stage. However, it did not appear so. Nevertheless, good performance during germination is important to guarantee fast establishment and uniform crop stand (Krishnasamy and Seshu, 1989) which was not observed in case of most of the traditional varieties from *boro* as well as other classes of rice varieties of Assam.

It is also important to note that the varieties recording high score for germination index (> 80) belong mostly to the traditional *sali* and modern varieties. The *sali* rice varieties are, normally, sown during June-July when Assam experiences reasonably high temperature. It can, therefore, be assumed that environment-neutral mutant should be abundantly available in the rice germplasm of Assam and mass screening of the state's rice germplasm should allow identification of varieties with desired degree of low temperature tolerance at germination. The fact that several popular modern varieties like Ranjit, Basundhara and Gitesh showed desired degree of tolerance should

Table 1. Mean performances of the varieties for various cold tolerance indices

Varieties	Germination index (%)	Plumule length (mm)	Plumule greening score (1-9)	Leaf yellowing score (1-9)	Electrolyte leakage (C.per cent)	Chlorophyll a (ml/g)	Chlorophyll b (ml/g)	Total Chlorophyll (ml/g)
Guni ahu	80.00	4.50	3.00	4.00	6.44	1.68	0.79	2.47
Iharsal	0.00	4.00	5.00	4.00	4.86	2.28	1.39	3.67
Kolagoria	0.00	5.00	1.00	3.00	2.66	1.93	0.35	2.28
Bongaldoria	28.89	1.33	4.00	5.00	2.70	2.15	0.39	2.54
Dusri ahu	0.00	0.50	6.00	5.00	2.56	1.98	0.98	2.96
Gorupotia ahu	25.00	1.00	6.00	5.00	4.14	1.27	0.81	2.08
Malbhog	29.71	1.17	7.00	6.00	3.36	2.07	1.07	3.14
Goalbhog	50.00	1.17	5.00	4.00	5.08	1.71	1.04	2.75
Dubaichenga	84.61	8.33	1.00	5.00	2.50	2.40	0.73	3.12
As 313/4	13.33	3.50	4.00	3.00	2.35	2.83	0.59	3.42
Garumoina	47.50	4.17	1.00	5.00	3.16	2.37	0.71	3.09
Garem-1	60.00	4.67	6.00	5.00	6.20	2.01	0.38	2.39
Majeni chembi	0.00	1.67	7.00	4.00	1.79	2.00	0.38	2.39
Bairing	11.11	4.17	4.00	5.00	2.43	2.03	0.60	2.63
Bizor-2	20.00	1.17	6.00	4.00	2.84	2.17	0.28	2.45
Sorainokhia bora	32.50	8.50	6.00	5.00	5.33	1.60	0.36	1.96
Saudang bora 2	27.50	4.67	5.00	4.00	2.69	1.69	0.37	2.07
Ranga bora 2	56.11	8.17	5.00	5.00	4.61	1.76	0.60	2.36
Ranga bora	45.00	7.33	6.00	4.00	3.79	1.90	0.51	2.41
Khamti bora	20.00	4.83	8.00	5.00	3.15	1.41	1.22	2.63
Til bora	87.50	9.83	1.00	4.00	3.55	1.27	1.13	2.40
Jahinga	92.50	4.17	4.00	5.00	3.76	1.93	0.33	2.27
Satkora lahi	100.00	11.83	1.00	4.00	5.38	1.60	0.63	2.23
Sarkari lahi	87.50	10.67	3.00	4.00	6.78	1.28	0.75	2.03
Sail borak	97.50	9.67	6.00	6.00	2.73	2.03	0.60	2.63
Khoirajuli	92.50	5.00	3.00	5.00	2.76	1.10	0.06	1.15
Kanaimuluk	75.00	6.67	3.00	6.00	4.68	1.76	0.63	2.39
Baterueeri-2	32.50	5.00	8.00	6.00	6.43	1.58	1.09	2.66
Ahom Sali	28.16	4.33	3.00	5.00	4.60	1.49	0.77	2.26
Nirokadam	51.47	6.17	1.00	4.00	2.74	1.58	0.89	2.47
Khaja Sali	72.50	3.50	4.00	5.00	4.08	0.97	0.56	1.53
Dholamukh sali	90.57	7.50	1.00	4.00	3.18	1.59	0.34	1.93
Kumol Sali	92.50	3.50	4.00	4.00	3.11	1.98	0.63	2.61
Manohar Sali	30.00	3.33	1.00	4.00	5.48	1.57	0.50	2.07
Sial Sali	15.83	6.00	1.00	3.00	5.50	2.47	0.82	3.30
Hati Sali	41.94	4.83	2.00	4.00	3.79	1.98	0.54	2.52
Nolchuti	57.50	9.50	1.00	5.00	4.03	2.16	0.61	2.77
Kolamanik	0.00	2.50	4.00	5.00	4.71	0.66	0.56	1.22
Mokon boro	0.00	1.67	4.00	3.00	2.24	1.10	0.19	1.30
Jugli boro	0.00	1.33	5.00	5.00	3.13	1.60	0.31	1.91
Gaji boro	11.11	2.67	8.00	4.00	3.67	1.74	0.33	2.07
Khoiya boro	0.00	2.92	5.00	4.00	3.43	2.27	1.89	4.16
Kola boro	0.00	7.17	1.00	3.00	3.29	2.23	1.41	3.64
Lahi boro	52.50	10.00	1.00	4.00	2.52	1.32	0.45	1.77
Mahsuri	62.50	5.00	3.00	5.00	2.80	1.13	0.69	1.82
Bahadur	60.13	7.83	4.00	5.00	3.59	0.94	0.48	1.42
Prafulla	65.00	6.17	5.00	4.00	3.97	2.23	0.66	2.89
Gitesh	97.22	11.67	1.00	4.00	6.63	2.03	0.56	2.59
Keteki joha	65.00	6.83	2.00	4.00	2.59	1.99	0.67	2.66
Disang	92.50	5.83	1.00	5.00	3.14	1.39	0.38	1.77
Luit	59.50	6.17	1.00	5.00	5.69	1.20	0.36	1.56
Ranjit	100.00	13.00	3.00	5.00	3.56	1.80	0.47	2.27
Basundhara	95.00	10.17	1.00	5.00	3.71	0.76	0.24	1.00
Akitakomuchi	0.00	7.33	1.00	1.00	4.08	2.53	0.52	3.05
Nekken 2	55.00	7.50	1.00	1.00	3.77	2.17	0.62	2.79
Koshihikari	5.00	8.00	2.00	2.00	3.06	2.08	0.60	2.67
$CD_{0.05}$	7.89	1.97	1.79	1.85	1.73	1.03	NS	1.49

make the situation quite easy for breeding varieties with low temperature tolerance at germination.

In the present study, the varieties were assessed for germination index at low temperature following method of Krishnasamy and Seshu (1989) with small modification. The number of seeds germinated at 96 hours was taken in the study as the initial count instead of the count at 72 hours used in the original method. Considering the fact that only two varieties showed germination at 72 hours in the first trial of the present study the period for initial germination was extended to 96 hours for allowing better discrimination of the tested varieties for their response to low temperature stress at germination. More experiments will have to be conducted with diverse varieties to confirm the requirement of extending the time or otherwise.

Post-germination Evaluation

Plumule length varied from as low as just 0.5 mm (sign of germination only) to as high as 13 mm (Table 1). Ranjit with the highest plumule length (13 mm) was statistically at par with Satkora lahi (11.83 mm) and Gitesh (11.7 mm). Following these, other good performing varieties for plumule length were Sarkari lahi (10.67 mm), Basundhara (10.2 mm), Lahi boro (10.0 mm), Til bora (9.8 mm) and Sail borak (9.7mm) which were at par with Satkora lahi and Gitesh. The worst variety, Dusri ahu showed just sign of germination and was at par with 10 other varieties *viz,* Gorupotia ahu, Bizor-2, Malbhog, Goalbhog, Bongaldoria, Jagli boro, Majeni chembi, Mokon boro, Kolamanik, Gaji boro, recording plumule length less than 2.7 mm.

The *boro* rice varieties performed poorly for plumule length. At least three of them (Jagli boro, Mokon boro and Gaji boro) found place among the poorest of the varieties. Of course, Lahi boro and Kola boro could find place among the better performing varieties indicating variation among the *boro* varieties in this count. In this case also, the traditional *sali* varieties, *viz.*, Satkora lahi, Sarkari lahi, and Sail borak and the modern variesties, *viz.*, Ranjit, Basundhara and Gitesh performed better. Of course, early germination of these varieties might have positive impact on this trait as reflected from the significantly positive correlation between the two parameters (Table 2).

Altogether 18 varieties *viz.,* Akitakomuchi, Nekken 2, Koshihikari, Til bora, Sial sali, Luit, Disang, Nolchuti, Gitesh, Garumoina, Manohar sali, Nirokadam, Dalamukh sali, Lahi boro, Kola boro, Dubrichinga, Kolagoria, Satkora lahi scored 1 for plumule greening in a scale of 1-9. The worst among the varieties were Khamti bora, Baterueeri-2 and Gaji boro with average score of 8 which were at par with Malbhog, Majeni chembi, Gorupotia ahu, Garem-1, Dusri ahu, Bizor-2, Sorainokhia bora, Ranga bora and Sail borak with score of 6-7 (Table 1). Plumule greening has been suggested as a selection criterion for chilling tolerance in a range of di- and monocotyledonous species (McWilliam *et al.*, 1979) including rice (Sthapit and Wilson, 1992; Sthapit and Witcombe, 1998). In the present study, all the three *japonica* varieties, known to be cold tolerant, had score of 1 confirming the usefulness of the parameter to screen rice varieties for tolerance to low temperature stress.

Notably, only two *boro* rice varieties, Lahi boro and Kola boro, were found to be tolerant to low temperature stress with plumule greening score of 1 indicating that the traditional *boro* rice varieties as a class could not generally be considered cold tolerant contrary to the general belief. On the other hand, several traditional *ahu, sali* and modern varieties exhibited high degree of clod tolerance indicating that the varieties with tolerance to low temperature stress might be randomly distributed across the classes and subclasses of Assam rice germplasm.

The plumule greening score had significant correlation ($r = -0.48$) with plumule length. It was, of course, as expected since ability of a variety to rapidly synthesize chlorophyll under chilling stress should lead to its quicker plumule growth as reported earlier also (Sthapit and Wilson, 1992).

Evaluation at Seedling Stage

Leaf yellowing is one of the earliest symptoms of cold temperature damage in rice during the vegetative stage (IRRI, 1982). In the present study, the *japonica* varieties Nekken 2 and Akitakomuchi scored 1 for leaf yellowing in the scale of 1-9 and appeared to be the most tolerant to low temperature stress during seedling stage of growth. Six more varieties *viz.,* Koshihikari (*japonica*), Kolagoria, Sial sali, Mokon boro, Kola boro and As 313/4, with score 3 (Table 2), were at par with the top ranking *japonica* varieties. Among the 53 *indica* varieties of Assam, only 5 varieties exhibited high degree of tolerance to low temperature stress with leaf yellowing score less than 3. Again, these 5 varieties belong to different growing seasons and classes leaving no scope to consider any class of varieties to be superior to the others in respect of their response to low temperature stress at the seedling stage

of growth like that in the germination and post-germination stage. In the study, however, none of the varieties scored 9 for leaf yellowing indicating that temperature lower than what was experienced during the period of study would have probably allowed better discrimination among the varieties at the seedling stage of growth.

Among numerous screening procedures applied to evaluate chilling sensitivity at various stages of growth, the most widely used technique consists of direct exposure of plants to chilling followed by visual damage assessment though some subjectivity, is sometimes associated with visual rating systems. Leaf yellowing score is one of such techniques most widely used for screening rice plants for their response to low temperature stress at the vegetative stage of growth. However, a reliable laboratory based screening technique would certainly be of significant utility for evaluation of large number of varieties and breeding materials. In this context, plumule greening may be considered as a useful method. The significant positive correlation (r = 0.30) of this parameter with leaf yellowing score (Table 2) enhances its importance as a screening criterion for low temperature tolerance as it would be easier to employ this criterion much earlier at the laboratory without the influence of temporal variation of field temperature.

The variety with the least electrolyte leakage (1.79 %) was Majeni chembi which was *at par* with 25 more varieties drawn from different classes and subclasses of Assam rice. The variety showing the highest electrolyte leakage (6.78%) was Sarkari lahi. This variety was *at par* with 9 other varieties *viz.*, Gitesh, Guni ahu, Baterueeri-2, Garem 1, Luit, Sial Sali, Manohar Sali, Satkora lahi and Sorainokhia bora (Table 1). This result, however, did not show correspondence with the result obtained with the application of leaf yellowing score. This was reflected by non-significant correlation coefficient (r_g = 0.06) between the two parameters (Table 2). Even, the *japonica* varieties Akitakomuchi, Nekken 2 and Koshihikari with electrolyte leakage of 4.08%, 3.77% and 3.06%, respectively seemed susceptible to low temperature stress based on this parameter though the same varieties exhibited very high degree of cold tolerance at post-germination and seedling stages of growth based on plumule greening and leaf yellowing score, respectively.

At low temperature, chlorophyll content tended to decrease in rice leaves (Baruah and Medhi, 1993). Yoshida *et al.* (1996) reported that chlorosis, where the newly emerging leaves lack chlorophyll, is a symptom of cold injury at the seedling stage of rice. The variety As 313/4 (2.83 ml/g of fresh weight) and Kolamanik (0.66 ml/g of fresh weight) recorded the highest and lowest amount of Chlorophyll a content. The best variety As313/4 was *at par* with 27 other varieties. With 4.16 ml/g of fresh weight, Khoiya boro hade the highest total chlorophyll content which was at par with 14 other varieties *viz,* Akitakomuchi, Iharsal, Kola boro, As 313/4, Sial Sali, Malbhog, Dubrichinga, Garumoina, Koshihikari, Dusri ahu, Prafulla, Saudang bora 2, Sorainokhia bora and Nekken 2 (Table 1). This result, unlike the one obtained with electrolyte leakage, maintained very good correspondence with the result obtained with leaf yellowing score, which was also reflected by significant correlation (r_g = −0.30) between the two parameters. Apparently, in this study, electrolyte leakage could not prove itself as a suitable parameter for evaluating a variety for its tolerance to low temperature stress.

Table 2. Estimates of genotypic correlation coefficient (r_g) (upper diagonal) and phenotypic correlation coefficient (r_p) (lower diagonal) for cold tolerance parameters

Traits	Germination index (%)	Plumule length (mm)	Plumule greening score	Leaf yellowing score	Electrolyte leakage	Chl. a	Chl. b	Total Chl.
Germination index	1	0.61**	-0.35**	0.39**	0.26	-0.40**	-0.85**	-0.46**
Plumule length	0.59**	1	-0.54**	-0.10	0.28	-0.01	-0.10	-0.05
Plumule greening score	-0.32*	-0.48**	1	0.52**	-0.05	-0.06	0.33*	0.09
Leaf yellowing score	0.26	-0.08	0.30*	1	0.06	-0.55**	0.51**	-0.17
Electrolyte leakage	0.20	0.22	-0.02	0.13	1	-0.32*	0.47**	-0.03
Chlorophyll a	-0.20	-0.09	0.03	-0.30*	-0.07	1	0.62**	0.95**
Chlorophyll b	-0.20	-0.09	0.07	-0.14	0.05	0.19	1	0.84**
Total Chlorophyll	-0.25	-0.11	0.06	-0.30*	-0.02	0.84**	0.69**	1

*Significant at 5 per cent level of significance, **Significant at 1 per cent level of significance

Diversity in the Rice Varieties

The Eucledian coefficient of dissimilarity between 56 rice genotypes in all possible combinations based on 8 morpho-physiological parameters used for evaluation of rice varieties for their response to low temperature stress showed that the average dissimilarity coefficient was 3.88 across all the 56 genotypes. Maximum coefficient of dissimilarity was observed between Basundhara and Khaiya Boro (8.61). These two varieties differed greatly for almost all the traits except leaf yellowing score and electrolyte leakage. The difference between these two varieties was particularly wide for germination index, plumule length and plumule greening score indicating that these parameters mainly contributed to place the two varieties so apart from each other. The minimum coefficient of dissimilarity was observed between Kumol sali and Jahinga (0.60).

The diversity analysis based on Eucledian distance separated the 56 varieties into two distinct clusters and placed one variety Mokon boro distinctively away from both the groups of varieties. The larger cluster 'A' comprised of 46 genotypes and the smaller cluster 'B' comprised of 9 genotypes (Fig. 1). The larger cluster A could further be classified into two sub-clusters 'A_1' and 'A_2' comprised of 31 and 15 varieties, respectively. All these clusters and sub-clusters included the varieties from all the rice seasons and classes. Incidentally, all the three *japonica* varieties fell in the smaller cluster 'B' along with six *indica* varieties drawn from all the three rice seasons of Assam. The result clearly exhibited the closer relationship among the *japonica* varieties in respect of their response to low temperature stress. At the same time, the result also clearly indicated that there was no cohesive relationship among the varieties of any specific class or

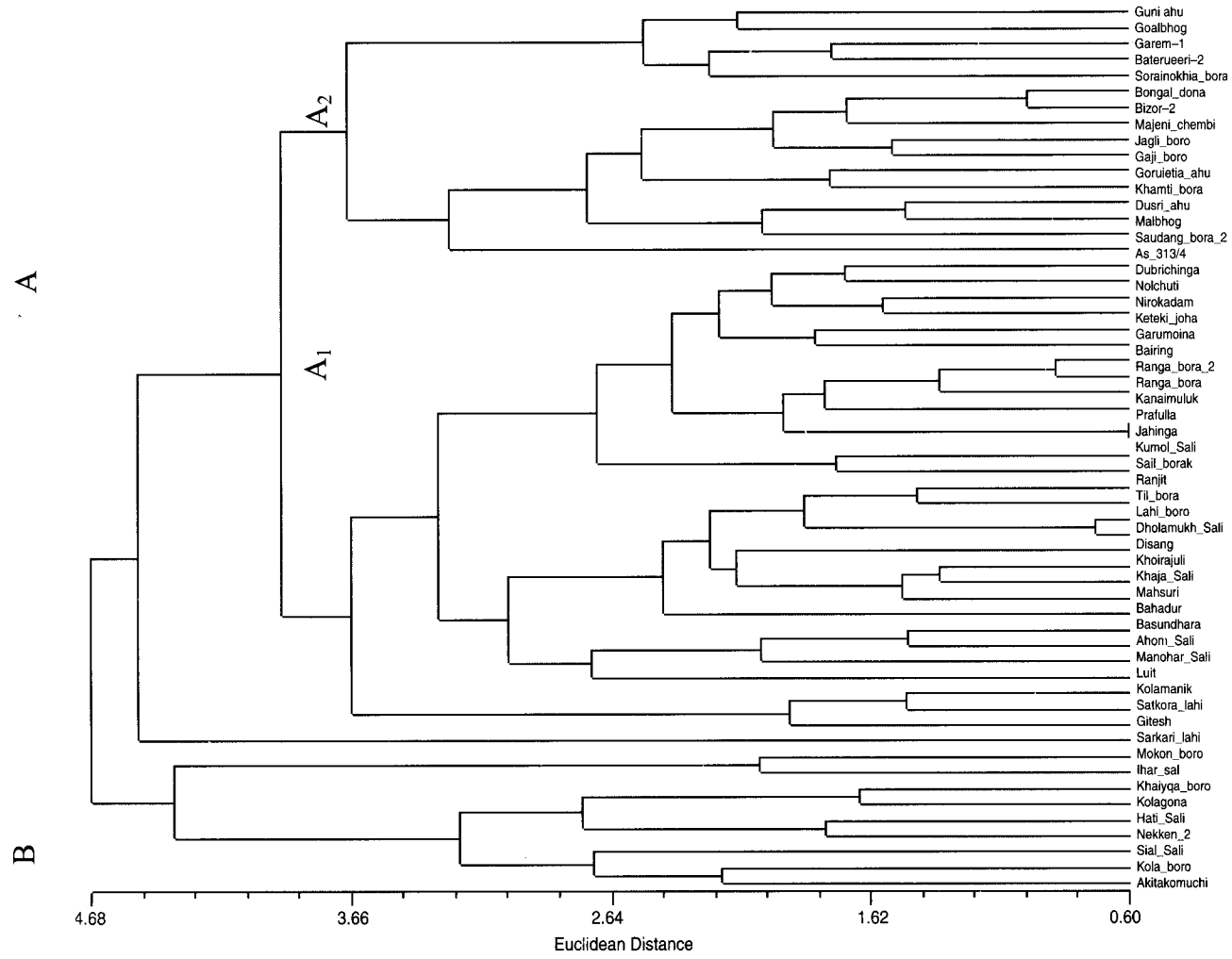


Fig. 1: *Dendrogram of 56 rice varieties based on Euclidean distance*

sub-class of Assam rice in respect of their response to low temperature stress. Even, the traditional *boro* rice varieties of Assam, which constitute a small seasonal group based on their cultivation by the farmers, over generations, in the low temperature affected *boro* season, did not fall in the same cluster.

Conclusion

Among the 53 rice varieties of Assam, the varieties showing tolerance to low temperature stress at different growth stages were found to be distributed across different seasons, classes and sub-classes leaving little scope to consider any class of varieties to be particularly good in respect of their response to low temperature stress. This clearly suggests that a thorough search in the rice germplasm of Assam would allow to identify varieties with desired degree of tolerance to low temperature stress at early growing stages for utilization in the breeding program for improvement of the *boro* rice of Assam. It has also been observed that same set of varieties did not show tolerance to low temperature stress at different stages of growth indicating that different gene systems might be involved with the varietal response to low temperature stress at different growth stages needing use of multiple parental sources for breeding varieties with tolerance to low temperature stress at different stages of growth. The varieties Ranjit, Gitesh, Basundhara and Disang among the improved varieties and Satkora lahi, Sail borak, Sial Sali, Kolagoria, Lahi boro, Kola boro, Mokon boro etc. among the traditional varieties were found to be tolerant to low temperature stress at more than one stage of growth. All the three *japonica* varieties proved themselves to be highly tolerant to low temperature stress at post-germination and seedling stages of growth.

References

Arnon DI (1949) Copper enzymes in isolated chloroplasts. Polyphenoloxidase in Beta vulgaris. *Plant Physiol.* **24:** 1-15.

Baruah KK and A Medhi (1993) Growth and metabolic responses of rice to low temperature stress. *Indian J. Plant Physiol.* **34:** 53-55.

Chatterjee SD (1995) Status of Boro Rice in West Bengal. In: *Report of an INGER Boro Rice Monitoring Visit of India, Bangladesh and Myanmar.* International Rice Research Institute, Los Baños, Manila, Philippines, pp 32-35.

Das GR, T Ahmed, HC Bhattacharyya and BC Barthakur (1981) Evaluation of germplasm: I. Characterisation and evaluation of *ahu* rice for important quantitative characters in relation to yield. *J. Res. Assam Agri. Unv.* **2:** 156-164.

IRRI (1974) *Annual Report.* International Rice Research Institute, Los Baños, Manila, Philippines.

IRRI (1982) *Annual Report.* International Rice Research Institute, Los Baños, Manila, Phillipines, pp 116-118.

IRRI (1996) Standard Evaluation System for Rice. International Rice Research Institute, Los Baños, Manila, Philippines, 36 p.

Kaneda C and HM Beachell (1974) Responses of Indica-Japonica rice hybrids to low temperature. *SABRAO J.* **6(1):** 17-32.

Kaw RN and GS Khush (1985) A modified technique of screening for cold tolerance in rice. *International Rice Research Newsletter* **10(3):** 15-16.

Krishnasamy V and DV Seshu (1989) Seed germination rate and associated characters in rice. *Crop Sci.* **29:** 904-908.

McWilliam JR, W Manokarna and T Kipnis (1979) Adaptation to chilling stress in sorghum. In: Lyons JM, D Graham and JK Raison (eds.) *Low Temperature Stress in Crop Plants: The Role of Membrane* Academic Press, New York.

Pathak AK, PK Pathak and KK Sharma (2003) Recent development in boro rice improvement and production for raising rice yield in Assam. In: RK Singh, M Hossain and R Thakur (eds.) *Boro Rice* IRRI-India Office, New Delhi, pp 73-82.

Pathak PK (2001) Major cereal crops of Assam In: AC Thakur (ed.) Agriculture in Assam, Assam Agricultural University, Jorhat, pp 53-74.

Pathak PK, RK Saud, DK Bora, KD Singh and AK Pathak (1999) Status of *boro* rice in Assam: A case study. *International Rice Commission Newsletter* **48:** 60-66.

Patterson BD, T Murata and D Graham (1976) Electrolyte leakage induced by chilling in *Passiflora* sp. tolerant to different climates. *Aust. J. Plant Physiol.* **3:** 435-442.

Sharma SD, JMR Vellanki, KI Hakim and RK Singh (1971) Primitive and current cultivars of rice in Assam – a rich source of valuable genes. *Curr. Sci.* **40:** 126-128.

Sneath PHA and RR Sokal (1973). Numerical taxonomy. W.H. Freeman and Co; San Francisco.

Sthapit BR and JM Wilson (1992) Chilling tolerance in February seeded Chaite rices of Nepal. *Ann. Appl. Biol.* **121:**189-197.

Sthapit BR and JR Witcombe (1998) Inheritance of tolerance to chilling stress in rice during germination and plumule greening. *Crop Sci.* **38:** 660-665.

Thakur R (1995) Status of Boro Rice in Bihar, India. In: *Report of an INGER Boro Rice Monitoring Visit of India, Bangladesh and Myanmar.* International Rice Research Institute. P.O. Box 933, Manila, Philippines. pp 23-26.

Yoshida R, A Kanno, T Sato and T Kameya (1996) Cool temperature induced chlorosis in the rice plants I. Relationship between the induction and disturbance in etioplast development. *Plant Physiol.* **110:** 997-1005.

Important Crop Germplasm Introduced in India during 2006

RV Singh, IP Singh, Deep Chand, Vandana Tyagi, AK Singh, SP Singh and Surender Singh
Germplasm Exchange Unit, NBPGR, New Delhi-110012

Indian agriculture has been tremendously benefited in the past though exotic germplasm introduced and utilized in developing better crop varieties and hybrid. But most of the crop improvement programmes have now reached at the threshold of dramatic advances and an access to exotic germplasm for import is becoming all the more harder from other countries after an enactment of IPR Act, various national and international agreement, and stringent quarantine measure operative. The Indian agriculture production scenario is also confronting numerous other problem which calls upon national strategic approaches to the Global Plan of Action such as broadening the genetic base of the major crops; increasing the range of genetic diversity available to farmers; strengthening the capacity to develop new crop and varieties that are specifically adapted to local environments; exploring and promoting the use of underutilized crops; and developing genetic diversity to reduce crop vulnerability.

Keeping in the view all these above considerations, an information on the potential useful exotic germplasm has been accessed from various sources and the Bureau imported 16,146 accession from 45 countries, including diverse and trait specific germplasm, in rice, wheat, barley, maize, sorghum, sunflower, soybean, french bean, cowpea, chickpea, chillies, watermelon, tomato, cabbage, strawberry, poppy, cotton, clovers, *Glaucium* and *Elytrigia repens*. Crop species wise account is tabulated below.

Table 1. Promising material introduced during 2006

Crop	Country	Traits	Distribution
		Resistant to biotic stress	
CEREALS			
Oryza sativa			
EC572259-67	USA	Resistant to blast disease, kernel smut, rice water weevil and rice stalk borer	DRR, Hyderabad
EC580364-373	Philippines	Brown Plant Hopper (BPH) resistant lines	Pioneer Overseas Corporation,
EC582484			PAU, Ludhiana
EC580374-375	Philippines	Blast resistant	Pioneer Overseas Corporation
EC580376-390	Philippines	Bacterial blight resistant lines	Pioneer Overseas Corporation,
EC582443-44			PAU, Ludhiana
49-53, 86-92			
EC582455-61	Philippines	Stem borer tolerant lines	PAU, Ludhiana
EC583878-410	Philippines	Bacterial blight and Rice Tungro disease resistant virus	DRR, Hyderabad
EC58341 1-453	Philippines	Resistant to Grassy stunt virus	DRR, Hyderabad
EC592058	Sri Lanka	Resistant to bacterial leaf blight, brown plant hopper and blast	DRR Hyderabad
Triticum aestivum			
EC580485-86	Canada	Sawfly resistant	DWR, Karnal
EC582225-441	USA	Resistant to yellow brown rust and powdery mildew	DWR, Karnal
EC589025 (1)	USA	Resistance to stripe rust and leaf rust	DWR, Karnal
EC589389-91 (3)	USA	Isogenic for stripe rust resistance gene Yr 36, leaf rust resistance gene Lr 47 and leaf, stripe and rusts resistance gene complex	DWR, Karnal
EC589421 (I)	USA	Resistant to stem, leaf and stripe rusts	DWR, Karnal
EC592591	China	Resistant to yellow, brown, black rusts and powdery mildew	DWR, Karnal
Triticum aestivum			
EC586941	USA	Resistant to wheat stem sawfly	DWR, Karnal
EC586942	USA	Resistant to stripe rust	DWR, Karnal
Triticum turgidum* var. *durum			
EC592592	USA	Genetic stock rusty, useful for studying genetics of stem rust resistance in tetraploid wheat or in crosses designed to select monogenic progeny from a parent containing multiple genes for stem rust resistance	DWR, Karnal

Crop	Country	Traits	Distribution
Hordeum vulgare			
E 586943	USA	Resistant to all known greenbug biotypes	PC (Wheat), DWR, Karnal
Zea mays			
EC583148-167	Nigeria	Resistance to foliar disease, gray leaf spot, maize streak virus, northern leaf blight and common rust	NBPGR, New Delhi
OILSEEDS			
Helianthus annuus			
EC586972	USA	Resistant to downey mildew	DOR, Hyderabad
Glycine max			
EC592181- 212	Taiwan	White fly and downy mildew resistant	NRC Soybean, Indore
EC586966	USA	Resistant to stem canker and soybean mosaic virus	,,
EC5 6967	USA	Resistant to southern stem canker, soybean cyst nematode, reinform nematode, sudden death syndrome, frog eye leaf spot	,,
GRAIN LEGUMES			
Phaseolus vulgaris			
EC589388 (I)	USA	Resistant to all known strains of virus (BCMV), Bean common Mosaic Necrosis virus, root rot	IIPR, Kanpur
EC589468	USA	Resistant to BCMV and CTV and tolerant to bean rust	IIPR, Kanpur
EC590327	Canada	Resistant to BCMV, tolerant to white mold,	IIPR, Kanpur
EC592938	USA	Resistant to common bacterial blight	IIPR, Kanpur
Vigna unguiculata			
EC587822	Senegal	Resistant to cowpea aphid borne mosaic virus (CABMV), bacterial blight	IIPR, Kanpur
VEGETABLES			
Capsicum annum			
EC572236,39	Taiwan	Resistant to Chilli Veinal Mosaic Virus and Poty Virus Y	J.K.Agri. Genetics, Hyderabad
EC572238,43-45	Taiwan	Anthracnose resistant lines	J.K.Agri. Genetics, Hyderabad
Capsicum baccatum* var. *pendulum			
EC572240-42	Taiwan	Anthracnose resistant lines	J.K.Agri. Genetics, Hyderabad
Capsicum chinense			
EC589469	Taiwan	Resistant to anthracnose and bacterial wilt	UAS, Bangalore
Citrullus lanatus			
EC572745-47	Taiwan	Disease resistant	Vibha Agrotech Ltd., Hyderabad
Cucumis melo			
EC589374 (I)	USA	Resistant to powdery mildew	IIVR, Varanasi
Lycopersicon esculentum			
EC571821-829	Taiwan	Resistant to whitefly transmitted gemini virus, bacterial wilt, tomato mosaic virus and fusarium wilt	Centre for Plant Biotech and Mol. Biology, Thrissur
EC580001	Taiwan	Resistant to bacterial wilt, tomato mosaic virus, gray leafspot, fusarium wilt (race 1)	MAU, Parbhani
EC580988-020	Taiwan	Resistant to bacterial wilt, Tomato mosaic virus, fusarium wilt and gray leaf spot, late blight, white fly transmitted gemini virus, early blight	Nodai Seeds India Pvt. Ltd., Gurgaon
EC586975	Taiwan	Resistant to Gemini virus, bacterial wilt, tomato mosaic virus, fusaruim wilt, gray leaf spot and early blight	VNR Seed, Raipur
EC588212-230	Taiwan	Resistant to late blight, bacterial wilt, mosaic virus, fusaruim wilt	Ankur Seeds Pvt, Nagpur
FRUITS			
Fragaria ananassa* subsp. *Ananassa			
EC 571812	USA	Resistant to leaf spot, leaf scorch, powdery mildew and red stele	NBPGR, Regional Station, Shimla
EC 571816	USA	Resistant to botrytis, verticillium wilt, red stele, powdery mildew and spotted spider mite	NBPGR, Regional Station, Shimla
EC571820	USA	Resistant to red stele races A-I, A-3, A-4 and fruit rots	NBPGR, Regional Station, Shimla

Crop	Country	Traits	Distribution
MEDICINAL & AROMATIC PLANTS			
Papaver sp.			
EC587085-88	Denmark	Resistant to downey mildew	NRC M&AP, Anand
		Resistant to Abiotic Stress	
CEREALS			
Oryza sativa			
EC571081-155	Philippines	Drought tolerant lines	Barwale Foundation,
EC571211-227			Hyderabad
EC571228-238	Philippines	Submergence tolerant lines	Barwale Foundation, Hyderabad
EC580501-509	Philippines	Deep water lines	Rice Research Station Chinsurah, WB
EC581120-23	Philippines	Submergence tolerant lines	CSSRI, Karnal
EC581124-27	Philippines	QTL lines	CSSRI, Karnal
EC582463-64,68-69,71	Philippines	Fe toxicity tolerant lines	PAU, Ludhiana
EC582211-24	Philippines	Aerobic, moderate drought tolerance	PAU, Ludhiana
Triticum aestivum			
EC582225-441	USA	Tolerant to frost and lodging	DWR, Kamal
EC589421 (1)	USA	Var. Oropos tolerant to lodging, low temperature and diverse climatic conditions	DWR, Kamal
EC592591	China	Variety Jimnmai-5, tolerant to cold and drought	DWR Kamal
EC586941	USA	Tolerant to lodging	DWR, Kamal
EC586942	USA	Variety Jerome tolerant to lodging and stripe rust	DWR, Kamal
OILSEEDS			
Helianthus annuus			
EC586971	USA	Excellent lodging resistance	DOR, Hyderabad
GRAIN LEGUMES			
Phaseolus vulgaris			
EC589468	USA	Resistant to lodging	IIPR, Kanpur
VEGETABLES			
Capsicum annuum			
EC582593	USA	Heat and drought tolerant	IIVR, Varanasi
Lycopersicon esculentum			
EC581 035-1 043	Taiwan	Heat tolerant	Nodai Seeds India Pvt. Ltd., Gurgaon
EC581525, EC592058-59	Sri Lanka	Heat tolerant varieties	IIVR, Varanasi
MEDICINAL AND AROMATIC PLANTS			
Apium graveolens			
EC587045	China	Tolerant to high temperatures	IIVR, Varanasi
		Lines for Heterosis Breeding	
CEREALS			
Oryza sativa			
EC571 539-48	Philippines	Cytoplasmic Male Sterile (CMS) and maintainer lines	NBPGR, New Delhi,
EC573166-200	Philippines		Pioneer Overseas Corporation, Hyderabad,
EC571 553-58	Philippines	Thermogenic Male Sterile (TGMS) lines	
EC581124-27	Philippines	QTL lines	CSSRI, Kamal,
EC582493-500		Maintainer and restorer lines	Annapurna Seeds, West Bengal ,
EC588896-935			M/s Errika Seeds, Hyderabad ,
EC588992-9027			M/s Rasi Seeds, TN
Triticum aestivum			
EC580487-489	Germany	Double Haploid lines, true isogenic and homozygous having different cytoplasm	IGFRI, Jhansi
Sorghum bicolor			
EC582502-508	USA	Isogenic lines for brown midrib genes	• NRC, Sorghum, Hyderabad • IGFRI, Jhansi
EC582509-513	USA	Male sterile lines	• NRC, Sorghum, Hyderabad • IGFRI, Jhansi

Crop	Country	Traits	Distribution
OILSEEDS			
Helianthus annuus			
EC586970	USA	Maintainer	DOR, Hyderabad
EC586973	USA	Restorer line having gene for fertility restoration	DOR, Hyderabad
GRAIN LEGUMES			
Pisum sativum			
EC581505-514	USA	Differential lines	CSKHPKV, Palampur
FIBRES			
Gossypium hirsutum			
EC561526	USA	Male Sterile lines	Proagro Seed Company, Andhra Pradesh
VEGETABLES			
Capsicum annuum			
EC571257-266	Taiwan	Cytoplasmic Male sterile (CMS) lines and maintainers	AAU, Gujarat IIVR, Varanasi
Lycopersicon esculentum	USA	Male sterile lines	IIVR, Varanasi,
EC572692-708			NBPGR, New Delhi.
		Agronomic Traits	
CEREALS			
Oryza sativa			
EC571549-52	Philippines	Early and late maintainer population	NBPGR, New Delhi
EC571549-52	USA	Early maturing	DRR, Hyderabad
EC580391-396	Philippines	High yielding	Pioneer Overseas Corporation, Ghaziabad
EC582473-81	Philippines	Introgression line for high yield	PAU, Ludhiana
EC582482	Philippines	Acid Sulfate tolerant line	PAU, Ludhiana
EC592058	Sri Lanka	High yielding and early maturing	DRR Hyderabad
Triticum aestivum			
EC582225-441	USA	High yielding, non shattering type	DWR, Karnal
EC589025 (1)	USA	Good grain yield	DWR, Karnal
EC589421 (1)	USA	High yielding, semi dwarf, broad, adaptation	DWR, Karnal
EC592591	China	Variety Jimnmai-50 high yielding, wide spread adaptation, early maturing	DWR, Karnal
EC586941	USA	Variety Choteav, superior yield	DWR, Karnal
EC586942	USA	Variety Jerome, early maturing	DWR, Karnal
Hordeum vulgare			
EC586943	USA	Variety Post 90, high yielding, widely adapted	PC (Wheat), DWR, Karnal
OILSEEDS			
Helianthus annuus			
EC581515-519	USA	Tolerant to soil salinity and for genetic base broadening for agronomic and oil content characters in development of hybrids, parents or improved germplasm	DOR, Hyderabad
Helianthus annuus			
EC586970	USA	Short statured type	DOR, Hyderabad
EC586971	USA	Short statured line	DOR, Hyderabad
Glycine max			
EC592181-212	Taiwan	Vegetable type, early & late maturing	NRC Soybean, Indore
EC586966	USA	Variety Desha, early maturing	NRC Soybean, Indore
EC586967	USA	Variety Lonoke high yielding, good standability, shattering resistance	NRC Soybean, Indore
GRAIN LEGUMES			
Phaseolus vulgaris			
EC589388 (1)	USA	Variety Quincy -high yielding	IIPR, Kanpur
EC589468	USA	Variety silver cloud, high yielding	IIPR, Kanpur
EC590327	Canada	Semi determinate growth habit with very short vines or no vines, upright plant and canopy, higher podding nodes on stems	IIPR, Kanpur
EC590328	Canada	Non nodulation genetic stocks	IIPR, Kanpur

Crop	Country	Traits	Distribution
Vigna unguiculata			
EC582501	USA	Variety EIN-El Ghazal, good for grain production under rainfed conditions	IIPR, Kanpur
EC587822	Senegal	Early maturing	IIPR, Kanpur
VEGETABLES			
Brassica oleracea* var. *botrytis			
EC572748	Taiwan	Early maturing (40-45 days)	Vibha Agrotech Ltd, Hyderabad
FRUITS			
Fragaria ananassa* sub sp. *ananassa			
EC571820	USA	Early ripening	NBPGR, Regional Station, Shimla
FORAGES			
Trifolium pratense			
EC578957	USA	Variety Freedom, free from pubescence, good for hay making, faster drying & reduced dustiness	IGFRI, Jhansi
Elytrigia repens			
EC 586940	USA	Variety Eversett, advanced generation synthetic cultivar for high rhizome production ability to spread by rhizomes and used for land stabilization and reclamation	IGFRI, Jhansi
		Quantitative/ Qualitative Traits for Value Addition	
CEREALS			
Oryza sativa			
EC572269	Philippines	Iron rich line	IARI, New Delhi DRR, Hyderabd
Triticum aestivum			
EC589025 (1)	USA	Excellent bread and noodle making quality	DWR, Karnal
EC592591	China	Variety Jimnmai-50 better quality for bread & noodle making	DWR Karnal
Hordeum vulgare			
EC586943	USA	Variety Post 90, good straw quality	PC (Wheat), DWR, Karnal
EC586944	USA	Variety Radiant proanthocyanidin free, potential malting barley and carry the gene that controls a high amount of thermostable beta amylase	PC (Wheat), DWR, Karnal
Zea mays			
EC592161	USA	Yellow kernels, white cobs, good husk coverage	DMR, IARI, New Delhi
ECS86945-47	USA	High amylase, high oil content, high protein quality and waxy with specialty starches, populations of vegetable type	DMR, IARI New Delhi
ECS83148-167	Nigeria	Tropical mid altitude lines	NBPGR, New Delhi
OILSEEDS			
Helianthus annuus			
EC586970	USA	High oleic fatty acid	DOR, Hyderabad
Glycine max			
ECS92181- 212	Taiwan	Vegetable type	NRS, Soybean Indore
ECS922ll-19	Taiwan	High oil content	,,
GRAIN LEGUMES			
Cicer arietinum			
EC571855-572003	Syria	Large seeded kabuli type germplasm	PAU, Ludhiana IIPR, Kanpur
Cicer arietinum			
EC583236	USA	Extra large kabuli variety	ICRISAT, Patancheru

Crop	Country	Traits	Distribution
VEGETABLES			
Brassica oleracea* var. *botrytis			
EC572748	Taiwan	Globular shaped	Vibha Agrotech Ltd, Hyderabad
Capsicum annuum			
EC582593	USA	Variety Tangerine dream, non pungent, banana type peppers, heat and drought tolerant, excellent keeping quality suitable for ornamental and culinary applications	IIVR, Varanasi
Citrullus lanatus			
EC572745-47	Taiwan	Globular shaped, firm fleshed, small seeded, sugar content 11-12% and disease resistant	Vibha Agrotech Ltd. Hyderabad
Lycopersicon esculentum			
EC572692-708	USA	Carotene rich and high lycopene content	IIVR, Varanasi, NBPGR NR, New Delhi.
FRUITS			
Fragaria x ananassa* subsp. *ananassa			
EC 571812	USA	Large fruited	NBPGR, Regional Station, Shimla
EC 571814, 817	USA	Large fruited, good flavor, outstanding fruit quality	NBPGR, Regional Station, Shimla
MEDICINAL AND AROMATIC PLANTS			
Glaucium flavum			
EC587081	Denmark	High glycoyrrhizin content	NRC M&AP Anand

Collection and Characterisation of Plus Trees of *Persea bombycina* (King ex. Hook f.) Kost., the Host Plant of Muga Silkworm in Northeast India

SN Gogoi, Meghali Barua and R Chakravorty
Central Muga Eri Research and Training Institute, Central Silk Board, Lahdoigarh, Jorhat-785700, Assam, India

Key Words: *Persea bombycina*, Host plant, Muga silkworm, Collection, Characterisation

Persea bombycina (King ex. Hook f.) Kost. locally known as Som (Assam), is an economically important and principal food plant of muga silkworm, *Antheraea assamensis* Helfer. It is evergreen, perennial, medium sized and pollinated tree. The species is known to have a great genetic variability. It grows up to an elevation of 500 m amsl and grows widely in Assam, Khasi and Jaintia Hills (Kanjilal *et al.*, 1984), Garhwal and Kumaun hills (Sengupta and Srivastava, 1995) and along the lower Himalayan tract in India and extended to the west of Nepal (Hooker, 1885). North East India seems to be the centre of diversity of this species because of large variation found both in cultivated and wild population. However, details of quantitative data on natural population of Som are still to be studied.

Muga silkworm, *A. assamensis*, the glittering golden silk producer of the world is semi domesticated in nature and endemic to the Northeast India more particularly Brahamaputra valley of Assam (Choudhury, 1981). Perhaps due to congenial climatic condition and wide range of distribution of the principal and primary food plants i.e. Som (*Persea bombycina*) and Soalu (*Litsea polyantha* Juss.) it is found nowhere else on the globe (Choudhury, 1981; Gogoi, 1980 and Bharali *et al.*, 1972).

Presently the eight selected genotypes of Som from natural population (Ram *et al.*, 1993) and four tetraploid genotypes evolved through polyploidization (Gogoi *et al.*, 2005) are maintained in field germplasm bank of Central Muga Eri Research and Training Institute (CMER&TI), Lahdoigarh, Jorhat, Assam, India. Information on morphology and propagation (Ram *et al.*, 1993; Jolly *et al.*, 1992; Choudhury, 2005 and Seth, 2000), floral biology (Yadav *et al.*, 1985), diseases (Das *et al.*, 2005), cytology (Gogoi *et al.*, 2005) and silkworm palatability (Siddique *et al.*, 2000) of the species are available. However, identification of plus trees, distribution in natural habitat and establishment of clonal seed orchard is not yet done unlike in other forest trees species (Kumar *et al.*, 2003; Sindhu, 1996; Sindhu, 1987 and Zobel and Talbert, 1984). Generally, plus trees are selected from the base population for obtaining immediate genetic gain in terms of better quality, wide adaptability, higher productivity and maintaining broad genetic base for continued improvement. Selection of plus tree is first step towards selection of elite genotypes of a species. Therefore, it is worthwhile to study for (i) identification and collection of plus trees of Som in Northeast India and (ii) establishment of field germplasm bank of Som plus tree clones for use in future breeding programme.

A survey was conducted during 2005 - 2007 to identify plus trees of Som in five different states of North East India viz., Assam, Arunachal Pradesh, Meghalaya, Mizoram and Nagaland (Table1). The surveyed area lies between 23°8 and 29°2N longitude and between 90°5 and 97°E latitude and altitude range from 50 to 1832 amsl. Besides the natural habitat, traditional muga growing pockets/sites along with plantations were selected for the purpose of survey (Fig. 1).

During the survey the species were found scattered along roadsides, grazing fields, jungles and forest peripheries but found rare in occurrence inside the big forest, reserve forests and national sanctuaries. The

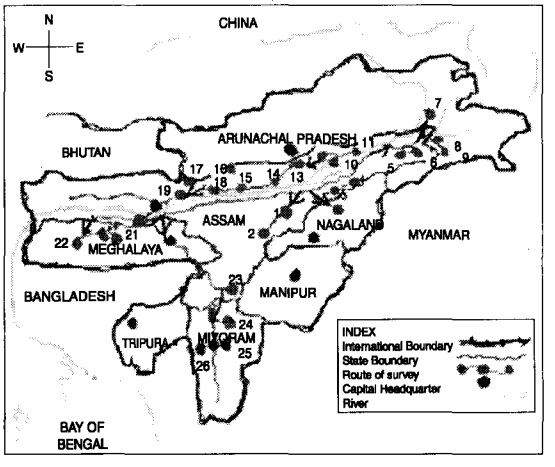


***Fig. 1:** Route map of survey for plus trees of som in Northeastern region of India*

Table 1. Geographical detail of different locations of collection sites

State	District	Locations	Geographical locations			Hill slope/
			Altitude(m)	Longitude	Latitude	Valley
Assam	Golaghat	Bogidhola	58	93.9	26.4	Valley
	Jorhat	Jogdowar	55	94.2	26.6	Valley
	Sibsagar	Borahibari	58	95	26.8	Valley
	Dibrugarh	Bordubi	55	95.6	27.5	Valley
	Tinsukia	Tingrai,	55	95.5	26.5	Valley
	Lakhimpur	Dhakuakhana	54	94.5	27.4	Valley
	Cachar	Thaligram,	55	93.1	24.8	Valley
Arunachal Pradesh	Lohit	Namsai	182	96.2	27.5	Hill slope
	Changlang	Bordumsa	185	96.3	27.4	Hill slope
Nagaland	Mokokchung	Mokokchung,	1832	94.8	26.5	Hill slope
Meghalaya	East Garo Hills	Rompara	350	91.1	25.9	Hill slope

vegetation of different parts of study areas were thoroughly explored by repeated visits to study sites (covering all ecological habitats) through out period of investigation.

Survey areas of Assam belong to subtropical region and are influenced by the southeast monsoon. The state receives large quantity of rainfall from June to August (450 mm to 600 mm). A small quantity of rainfall is received during pre-monsoon (April and May) ranging from 75 mm to 228.5 mm and post monsoon (September and October) ranging from 195 mm to 218 mm. Rainfall is scanty in winter months from November to February. Soils of survey areas of Assam were collected and analyzed for soil texture and pH and were found to be clay-loamy and acidic (pH 4.2-5.9), respectively. The mean annual rainfall of Changlang and Lohit districts of Arunachal Pradesh vary from 1485 mm to 2508 mm which is confined mostly to rainy season (May-September). Soils are clayey in texture, strongly to moderately acidic (pH 4.3-6.2) and rich in organic matter. On the other hand, East Garo Hills of Meghalaya is characterized by hot and moist summers and cool winters with high rainfall. The average rainfall ranges between 2000 mm to 4000 mm which is confined mostly from April to October and scanty in the dry winter months from November to February. The soils are loamy to clayey and acidic (pH 4.4-6.1). The climate of Mokokchung of Nagaland is subtropical with heavy summer monsoon rainfall (April to September). The mean annual precipitation varies from 1960 mm to 3450 mm. Soils are alluvial, non-laterite, forest soil and sandy loam and strongly to moderately acidic (pH 4.8-6.2).

Identification of Plus Tree

Phenotypically superior trees (Fig. 2) (plus trees) were selected from the diverse regions, collected and introduced in field germplasm bank through air layering technique. During selection of plus trees, base population of Som was divided into various grids for effective selection and identification. In each grid, trees with good height, girth at breast height (gbh), maximum crown height (ch), number of healthy branches and free from any diseases and pest attack were marked using point grading method of selection (Zabal, 1993). The candidate trees were selected by comparing to standard check of the base population (Table 2) of Som and awarded points accordingly.

A minimum distance of 100 m between two candidate plus trees (CPTs) was maintained. Equally phenotypically healthy superior trees (five) growing nearby the CPTs were selected as companion trees. Height, gbh, ch, number of branches, pest and disease infection and leaf biomass were measured and assessed for both CPTs and companion trees. Trees stem infected with disease or infested with insect were not considered for selection. While selecting the plus trees adopting the point grading method, one plus tree out of five comparison trees is selected. The points for different characteristics were described in Table 3.

The CPTs that received more than 90 points were finally selected as plus trees and analyzed for superiority

Table 2. Characters of standard check base population of *Persea bombycina*

Parameters	Height (m)	Diameter (cm)	No. of branches of tree	Crown height (m)	Leaf disease incidence (PDI)	Leaf biomass (Kg)
Mean of standard check	7.63±0.642	24.78±1.058	8.68±1.112	4.59±0.894	12.94±1.749	17.95±2.20

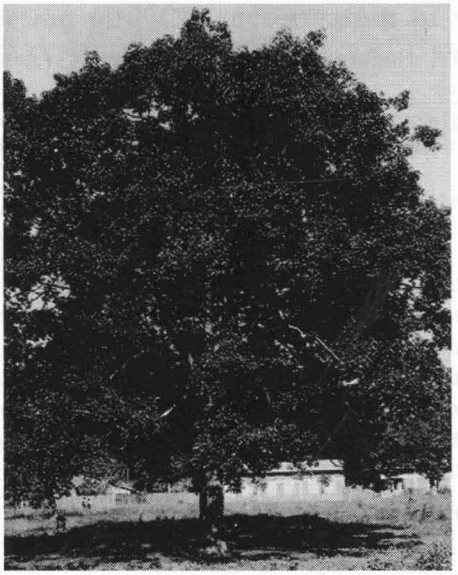


Fig. 2: Plus tree of Som (Persea bombycina)

over companion trees. Tree height, gbh, ch, number of branches, pest and major diseases infection (leaf rust, leaf spot & powdery mildew) and leaf biomass were recorded for all plus trees and companion trees in all the sites.

The mean, range, SD of plus trees (PT) for tree height, gbh, cbh, no. of branches, leaf diseases infection and leaf biomass and % increase in plus trees over companion trees, average % increase in plus trees over companion trees were analyzed (Table 4).

Thirty-nine plus trees, approximately 20 years old plants were identified through Point Grading Methods in 11 different locations (Table 1). Occurrence of plus trees were not observed in Mizoram. Passport data and number of plus trees were prepared by using the standard method (Kumar *et al.*, 2002).

Collection of Propagules and Establishment of Germplasm Bank

Clones of plus trees were collected through air layering

Table 3. Scoring point awarded for different characteristics of candidate and companion trees of *Persea bombycina*

Characteristic	Description	Points
Leaf biomass (40 points)	Less than average	5
	Equal to average tree	10
	More than average but less than biggest check tree	30
	More than largest check tree	40
Health	Infection (Percent Disease Index)	
(a) Leaf disease infection (15 points)	0-1	15
	2-5	12
	6-25	10
	26-50	8
	51-75	4
	75-100	2
(b) Pest infection (15 points)	Infection (%)	
	0-1	15
	2-5	12
	6-25	10
	26-50	8
	51-75	4
	75-100	2
Height (5 points)	Less than average	1
	More than average	2
	More than average but shorter than largest check tree	4
	Taller than tallest check tree	5
Girth at breast height (5 points)	Less than average	1
	Equal to average	2
	Between average and largest check tree	4
	More than largest check tree	5
Crown height (10 points)	Shorter than average	2
	Equal to average	4
	Between average and tallest trees	6
	More than tallest tree	10
No of branches (10 points)	Less than average	2
	Equal to average	4
	More than average	6
	More than largest check tree	10

Table 4. Variability in different characters of 39 plus trees of *Persea bombycina* at different geographical locations

Parameters	Height (m)	Diameter (cm)	No. of branches of tree	Crown height (cm)	Leaf disease incidence (PDI)	Leaf biomass (kg)
Mean	10.18±1.82	30.24±2.19	15.46±6.52	7.80±1.35	1.31±0.63	27.08±6.23
Range	4.8-13.8	26.42-34.8	8-27	2.5-9.5	0.103-2.08	19.8-36.8
Increase in plus trees over companion trees (%)	1.67-62.84	7.58-56.76	6.67-95.67	1.96-69.29	77.76-99.22	7.38-84.17
Average increase in plus trees over companion trees (%)	24.23	27.55	37.66	37.75	89.72	44.50

technique and planted in field gene bank at CMER&TI, Lahdoigarh, Jorhat, Assam, India with recommended spacing of (3x3m). Clones of plus trees showed survivability range of 12.5 % (PT11, PT16, PT23) to 100% (PT15) in field gene bank (Fig.3) and these new entries of PT clones were assigned a new accession number as PB013, PB014, PB015 upto PB051.

The study depicted the variation of growth characters among the plus trees in different study sites. Among the different plus trees, PT18 showed highest improvement in leaf biomass (87.64%) followed by PT5 (84.17%) while PT32 (1.04%) revealed lowest improvement (Fig. 4) over companion tree among the different plus trees in the study sites.

In case of height (Fig. 5), plus trees showed maximum improvement in PT12 and PT36 (62.84%) followed by PT15 (58.98%) over companion trees and lowest was found in PT7 (1.05%).

Girth at breast height of plus trees revealed wide variation (Fig. 6) and maximum improvement was found in PT6 (56.76%) while lowest was found in PT29 (8.57%).

Similarly, plus trees showed wide variation in number of branches (Fig. 7) and revealed maximum improvement in PT15 (95.65%) followed by PT34 (71.87%) over companion trees and minimum was found in PT18 (5.26%).

These plus trees showed variation in improvement of crown height (Fig. 8) range from PT20 (6.67%) to 81.24% (PT2) over companion trees.

Moreover, plus trees showed resistance in various leaf diseases viz. leaf spot, leaf rust and leaf blight (Table 5) ranging from 77.66% (PT4) to 99.22 % (PT2) over companion tree.

In the present study, a total of 39 plus trees and 195 companion trees were selected from different study sites. Growth of tree is influenced by many characteristics and thus it is highly complex trait to be used for selection. Moreover, selection based on single trait may not be very effective to screen elite genotypes in many forest species.

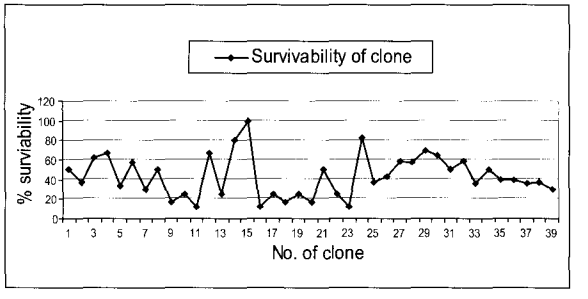


***Fig. 3:** Survivability of clones of Persea bombycina in field gene bank*

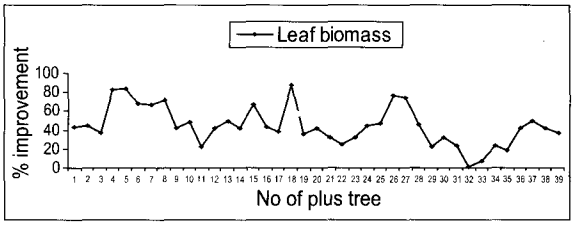


Figure 4

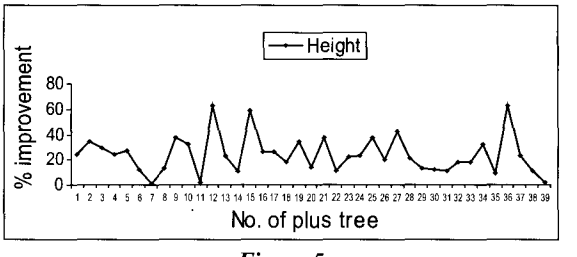


Figure 5

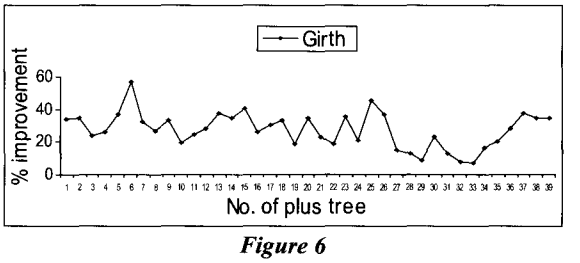


Figure 6

Table 5. Percent disease index (PDI) and resistance to leaf diseases of plus trees over companion trees at study sites

Collection number	PDI		% disease reduction in plus trees over companion tree
	Plus tree	Companion tree	
PT1	0.234	10.53	97.78
PT2	0.103	13.32	99.22
PT3	0.234	9.52	87.35
PT4	2.086	9.34	77.66
PT5	1.096	8.99	87.80
PT6	2.086	9.92	78.98
PT7	0.22	14.22	98.48
PT8	1.02	10.04	89.84
PT9	1.94	15.61	87.57
PT10	1.84	13.14	85.99
PT11	0.24	13.33	98.19
PT12	1.24	12.38	89.99
PT13	1.64	13.32	87.68
PT14	1.92	13.01	85.24
PT15	0.218	10.96	98.01
PT16	1.52	14.57	89.57
PT17	1.72	13.10	86.87
PT18	1.64	13.66	87.99
PT19	2.08	11.67	82.14
PT20	1.21	11.32	89.30
PT21	0.942	10.99	91.43
PT22	1.25	16.98	90.56
PT23	1.62	24.34	93.34
PT24	1.24	20.46	93.93
PT25	1.82	12.27	85.16
PT26	0.94	5.25	93.83
PT27	1.45	3.52	89.28
PT28	1.5	13.12	88.56
PT29	1.75	13.12	83.73
PT30	1.9	14.66	87.04
PT31	1.56	13.16	88.15
PT32	1.24	10.08	85.41
PT33	1.03	14.34	92.81
PT34	1.05	12.7	91.73
PT35	0.95	12.71	93.31
PT36	1.24	12.38	89.99
PT37	1.64	13.32	87.6
PT38	1.92	13.01	85.24
PT39	1.90	8.80	85.24

However, selection based on leaf yield and yield attributing characteristics results in higher expected response (Baker, 1986). In multi traits selection method, each trait plays an important role and all the individuals are ranked according to one scoring system. Genotypes selected by this method are expected not only to have desired qualities but will also have genetically divergent base for future breeding programme.

The current holdings of *P. bombycina* in genetic resources centre are small and likely to represent a fraction of the available genetic diversity. Though the muga silkworm farmers are traditionally interested in the domestication of *P. bombycina* but very less germplasm has been collected and reported previously. Thus, current evaluation of the species is limited to a small number of accessions. Further development of *P. bombycina* would require a greater and better documentation of genetic resource base. The wide distribution of plus trees of *P. bombycina* across the North East India and their occurrence provides an opportunity for targeted collections to regions most likely to yield adapted germplasm. This is only possible when the extensive survey is executed.

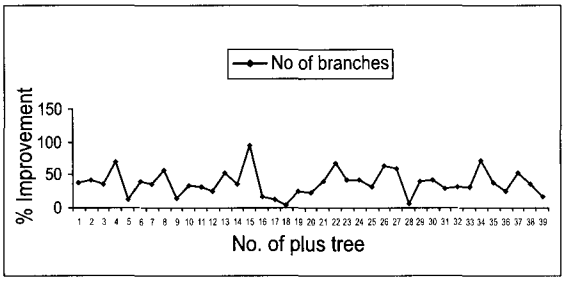


Figure 7

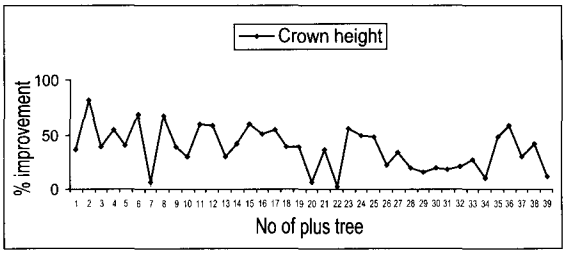


Figure 8

The success of a genetic improvement programme largely depends on the existence of variability in the base population which can easily be utilized through selection of proper genotypes. Hence, a selection methodology of plus trees for a *P. bombycina* has been evolved so that a significant improvements can be achieved in yield and other traits of economic importance. Further, these genotypes shall have immense use when multiplied through clonal technique and established in the clonal seed orchards to meet the immediate demand for seed. The wider genetic base and high variability in *P. bombycina* PT for various traits provide further opportunities to select the elite *P. bombycina* genotypes in subsequent evaluation.

References

Baker RJ (1986) *Selection Indices in Plant Breeding*. Press Inc., Boca Raton, Florida, 218 p.

Bharali N, P Bora and BS Nath (1972) Studies on the growth and development of muga silkworm (*Antheraea assamensis* Westwood) on the different varieties of som plant (*Machilus bombycina* King). *Indian Silk* **19(10):** 7-8.

Choudhury S (1981) Muga Silk Industry. Directorate of Sericulture and Weaving, Govt. of Assam, Gawahati, Assam, India, pp 1-31.

Choudhury SN (2005) Som [*Persea (Machilus) bombycina* King. *M odoratissima* Nees]. In: *Biology of Silkworms and Host Plants*, Dibrugarh, Assam, pp 299-305.

Das R, K Das and R Chakravorty (2005) Reaction of different cultivars of *Persea bombycina* Kost towards leaf spot disease caused by *Phyllosticta perseae* Ell.& Mart. *Sericologia* **45(3):** 345-347.

Gogoi JK (1980) *Assamor Muga Silpo* (Assamese), Jyoti Press, Titabor, Assam, India.

Gogoi SN, R Chakravorty, KN Neog and PL Ghosh (2005) Induced autotetraploidy in som *Persea bombycina* Kost. and its rearing performance of muga silkworm, *Antherea assamensis* Helfer. In: *Perspectives in Cytology and Genetics 2006* Vol. XII, Proceeding of the Twelfth All India Congress of Cytology and Genetics, Mumbai, October 28-31, pp 169-183.

Hooker JD (1885) *The Flora of British India* Vol. V. William Clowes and Sons Ltd., London, England, pp 155-180.

Jolly MS, SK Sen, TN Sonowalkar and GK Prasad (1992) *Sericultural Manual*. FAO Agricultural Service Bulletin (Reprinted by Central Silk Board, Govt. of India, Bangalore) **29:** 121-126.

Kanjilal UN, PC Kanjilal and RN De Das (1984) *Flora of Assam*. Vol. IV Reprinted by Periodical Expert Book Agency, D-42, Vivek Vihar, New Delhi, India, pp 66-67.

Kumar A, PH Chawhaan and AK Mathroo (2003) Improvement through selection of plus tree in *Gmelina arborea*. *J. Trop. For. Sci.* **15(3):** 441-449.

Kumar A, KG Prasad and AK Mathroo (2002) Strategies for testing, registering and releasing genetically improved forestry planting stock. *Indian Forester* **128:** 619-634.

Ram R, AK Sengupta, R Das, M Devnath and MV Samson (1993) Collection, identification and evaluation of *Machilus bombycina* King (Laurales: Lauraceae), germplasm of muga food plant. *Sericologia* **32(32):** 109-124.

Sengupta AK and AK Srivastava (1995) Muga-New Strides. *Indian Silk* pp 28-32.

Seth MK (2000) Food plants of muga silkworm. In: *Sericulture in India, Vol. IV Non-Mulberry sericulture* (Eds: HO Agarwala and MK Seth) pp 887-893.

Siddique AA, Lal, A Bhattacharya and PK Das (2000) Evaluation of leaf quality of som Germplasm through chemoassay and bioassay. In: GK Manna and SC Roy (Eds.) *Prospective in Cytology and Genetics*. (Eds: GK Manna and SC Roy) pp 263-268.

Sindhu DS (1987) Selection of plus trees for genetic improvement of stem form in shisham (*Dalbergia sissoo*) *Indian J. For.* **56:** 815-825.

Sindhu DS (1996) Method of plus tree selection for raising first generation population for a tree-breeding programme. *Indian Forester* **122:** 476-485.

Yadav GS, Md Isa and K Thangavelu (1985) Studies on taxonomy and floral biology of som, *Machilus bombycina* King (Laurales: Lauraceae). *Sericologia* **25(1):** 63-70.

Zabal NQ (1993) Methods of selection of plus trees in plantations and natural stands. In: P Havmoller & L Schmidt (Eds.) *Proceeding of the Regional Training Workshop on selection and Management of Plus Tree and Seed Stands and Establishment of Seed Orchards.* FAO, UNO, Philippines, pp. 17-28.

Zobel BJ and J Talbert (1984) Applied Forest Tree Improvement. John Wiley and Sons, New York.

SHORT COMMUNICATION

D^2 Analysis for Physiological Traits in the Progenies of Urdbean (*Vigna mungo* (L.) Hepper)

Mohar Singh[1] and SK Sharma[2]

[1] *Department of Fruit Breeding & Genetic Resources, Dr Y.S. Parmar University of Horticulture & Forestry, Nauni-Solan-173230 (H.P)*

[2] *National Bureau of Plant Genetic Resources, PUSA Campus, New Delhi-110012*

Keywords: D^2 statistics, Genetic divergence, *Vigna mungo*, Physiological traits

Minor genes, whose effects could be identified by plant morphology have been exploited for genetic improvement of grain legumes, but this has not led to spectacular gains in the yield potential. The analysis of constraints to increasing genetic potential of these crops reveal the existence of wide differences between the actual biological potential and the highest levels achieved through the present available base. Further, the selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for the quantitative inherited physiological traits. The D^2 analysis measures the amount of genetic diversity in a given population in respect of several physiological characters including seed yield considered together. In urdbean, D^2 statistics has been studied in the parents and their F_2 progenies. The intermating of unlike leads to greater opportunity for crossing over which releases latent variation by breaking up the predominantly repulsion phase linkages (Thoday, 1960).The present study aims at analyzing the genetic divergence among progenies and their parents in urdbean, using Mahalanobis, $^sD^2$ statistics by a software (SPSS programme), a powerful tool in discerning divergence among groups based upon multiple growth characters and assessing the relative contribution of different components to total divergence (Rao, 1952; Murty and Arunachalam, 1966). Such a measure will eventually help in breeding programme, aimed at evolving superior genotypes.

The materials for the present study comprised twelve genetically diverse lines of urdbean (HPU-1, VB-17, HPBU-124, HPBU-125, HPBU-126, HPBU-128, HPBU-129, HPBU-130, HPBU-131, HPBU-133, UL-338 and MX-17) which were crossed with four diverse pollen parents (T-9, PDU-1, UG-218 and Palampur-93) in a line x tester mating design (Kempthorne,1957). The resultant 48 F_2, along with 16 parents were evaluated for their performance at the Regional Research Station, Himachal Pradesh Agricultural University, Bajaura (31°48′ N 77°00′E, 1099 amsl) during *kharif* 2003. The experiment was laid out in Randomized Block Design with three replications. All the agronomic practices were followed for raising the crop.

Data for physiological traits were recorded on 20 randomly selected plants within each replication of each cross, 40 and 60 days after sowing. The following physiological traits were included in the study,

1. Leaf Area Plant^{-1} (LAP)

Leaf area plant^{-1} (cm^2) was computed by leaf area meter (Delta-T-Devices, Cambridge, England). After completing the observations on leaf area, clipped leaves and stem portions of each plant were dried in an oven for 48 hours at 65°C. The samples of dried leaves stem and branches were weighed on the Electronic Balance (ADCO Model-AD200B). The following physiological traits were computed using the formulae of Redford (1967).

2. Crop Growth Rate (CGR), (g day^{-1})

$$CGR = (W_2 - W_1)/ (t_2 - t_1)$$

where W_2 and W_1 are dry plant weights measured in two consecutive harvests over time interval $t_2 - t_1$.

3. Leaf Growth Rate (LGR), (cm^2 day^{-1})

$$LGR = (A_2 - A_1)/ (t_2 - t_1)$$

where A_1 and A_2 are the leaf areas at times t_1 and t_2, respectively.

4. Net Assimilation Rate (NAR), (mg dm^{-2})

$$NAR = (W_2 - W_1) (InA_2 - InA_1)/ (A_2 - A_1) (t_2 - t_1)$$

where, InA_2 and InA_1 are the natural log values of leaf area at times t_2 and t_1, respectively.

5. Leaf Area Ratio (LAR), (dm^2 g^{-1})

$$LAR = \frac{\text{Leaf area (A)}}{\text{Total dry plant weight (W)}}$$

6. Seed Yield Plant^{-1} (SYP), (g)

Twenty plants per replication were selected at random and seed yield plant^{-1} was recorded.

Following analysis of variance, genetic divergence was studied using Mahalanobis D^2 statistics as described by Rao (1952). D^2 values based on uncorrelated variables were used to classify the parents and crosses. The constellation of groups was formed according to Tocher, s method (Rao, ibid). The relative contribution of each trait to the total D^2 value between each pair of genotype was determined following the procedure outlined by Bhatt (1970).

The analysis of variance revealed significant differences among genotypes for all characters studied indicating the potentiality of population to isolate parents that may produce heterotic progenies. On the basis of physiological parameters 64 genotypes (16 parents and 48 F_2 crosses) were classified into 9 clusters (Table 1). The maximum number of genotypes (13) was accommodated in cluster 1, followed by 10 genotypes each in cluster II and IX, and 9 genotypes each in cluster VI and VIII. The clustering pattern of progenies was independent of parental cross-combinations, i.e. progenies of a cross and their parents were grouped in different clusters. The estimates of inter-cluster distance between two clusters comprising progenies may be greater than those between clusters comprising progenies derived from two distinct parentages. This suggests that forces other than the divergence of the parents have operated in the differentiation of these progenies (Table 2). Intra-cluster

Table 1. Distribution of parents and their progenies in different clusters

Cluster	Number of genotypes	Parents	Progenies
I	13	T-9, PDU-1	HPU-1 x Palampur-93, HPBU-124 x T-9, HPBU-125 x T-9, HPBU-128 x UG-218, HPBU-126 x T-9, HPBU-128 x Palmpur-93, HPBU-130 x UG-218, HPBU-133 x Palampur-93, UL-338 x PDU-1, UL-338 x UG-218, MX-17 x Palampur-93
II	10	HPU-1, HPBU-130, HPBU-131, UL-338, MX-17	VB-17 x T-9, VB-17 x PDU-1, HPBU-126 x Palampur-93, HPBU-128 x PDU-1, HPBU-130 x T-9
III	08	–	HPU-1 x UG-218, HPBU-124 x UG-218, HPBU-125 x UG-218, VB-17 x UG-218, HPBU-128 x T-9, HPBU-128 x UG-218, HPBU-128 x Palampur-93, UL-338 x T-9
IV	02	–	HPBU-131 x PDU-1, HPBU-133 x UG-218
V	02	–	VB-17 x Palampur-93, HPBU-125 x Palampur-93
VI	09	HPBU-128, HPBU-129, VB-17	HPU-1 x PDU-1, HPBU-131 x T-9, HPBU-131 x UG-218, HPBU-131 x Palampur-93, HPBU-133 x PDU-1, MX-17 x PDU-1
VII	01	–	HPBU-130 x PDU-i
VIII	09	HPBU-126	HPBU-125 x PDU-1, HPBU-125 x UG-218, HPBU-125 x PDU-1, HPBU-128 x T-9, HPBU-124, Palampur-93, HPBU-130 x Palampur-93, MX-17 x T-9, MX-17 x UG-218
IX	10	HPBU-124, HPBU-125, HPBU-133, UG-218, Palampur-93	HPU-1 x T-9, HPBU-124 x PDU-1, HPBU-129 x PDU-1, HPBU-133 x T-9, UL-338 x Palampur-93

Table 2. Inter and intra cluster D^2 values in urd bean progenies

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**13.13**	20.89	44.16	13.46	53.50	44.54	18.34	23.80	34.33
II		**6.89**	34.51	31.68	48.61	39.93	20.63	32.93	32.37
III			**8.98**	49.38	24.00	11.30	38.28	42.35	19.88
IV				**9.48**	56.60	48.11	18.90	22.70	39.86
V					**5.41**	19.62	48.65	56.62	23.67
VI						**10.12**	40.68	41.84	15.20
VII							**5.45**	25.33	35.60
VIII								**12.32**	38.39
IX									**7.65**

Table 3. Cluster means of physiological characters in urd bean progenies.

Cluster	Character					
	LAP	CGR	LGR	NAR	LAR	SYP
I	12.14	0.31	46.62	75.41	15.85	6.48
II	10.46	0.23	38.91	54.77	17.16	9.04
III	8.11	0.18	29.72	58.92	19.11	6.58
IV	11.00	0.25	42.62	81.59	16.78	11.34
V	12.53	0.30	47.21	36.52	15.23	7.15
VI	12.62	0.30	48.23	72.59	16.39	8.63
VII	13.41	0.31	52.04	69.12	16.03	9.97
VIII	14.73	0.37	56.23	62.07	16.13	8.61
IX	8.24	0.19	30.18	73.42	15.82	8.01

average D^2 values varied from 5.41 to 13.13. However, the low values of intra-cluster average D^2 suggested the presence of narrow genetic variation within a cluster. Further, inter-cluster D^2 is a measure of genetic divergence between the two clusters and was observed to be the highest (56.60) between cluster IV and V and the lowest (11.30) between cluster III and VI (Table 2). Cluster means (Table 3) indicated that cluster IV, V and VII revealed highest values for almost all the characters including seed yield. Direct relationships between progeny mean and number of superior genotypes to best check has been reported by Bakshi *et al.* (1996). Therefore, the mean of progenies is very important in deciding which of the crosses should be repeated in order to get better segregants. This will provide opportunity to select better recombinants for various physiological characters and in breeding for obtaining better genetic gains.

References

Bhatt GM (1970) Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement on self-pollinated crops. *Aust. J. Agric. Res.* **21:** 1-7.

Bakshi R, BS Chaudhary and S Singh (1996) Optimum sample size for estimating population mean and variance at ratoon of seedling stage in sugarcane. *Natnl. J. Pl. Improv.* **1:** 80-84.

Kempthorne O (1957) Genetic analysis and crop improvement. John Wiley and Sons, New York. 345 p.

Murty BR and V Arunachalam (1966) The nature and genetic divergence in relation to breeding system in crop plants. *Indian J. Genet.* **26:** 188-198.

Rao CR (1952) Advanced Statistical Methods in Biometrical Research, Ed. I, New York, John Wiley and Sons.

Redford PJ (1967) Growth analysis formulae, their use and abuse. *Crop Sci.* **7:** 171-175.

Thoday JM (1960) Effect of disruptive selection. III. Coupling and repulsion. *Heredity* **14:** 35-49.

SHORT COMMUNICATION

Studies on Variability in Chilli (*Capsicum* spp.) in Central Himalaya

Vandana Pandey, Tribhuwan Pant and Z Ahmed
Defence Agricultural Research Laboratory, Pithoragarh (Uttarakhand), India

There is rich variability in Chilli (*Capsicum* spp.). Defence Agricultural Research Laboratory , Pithoragarh has assembled and evaluated the variability available in *Capsicum* spp., with the objective to find out the promising genotypes on the basis of high yield, biochemical parameters and capsaicin contents. The genotypes which were found promising can be used in further breeding programme for improvement in various yield and nutritional parameters in *Capsicum* spp.

Key Words: *Capsicum* spp., Variability, Genotype, Capsaicin

The cultivated *Capsicum* spp. are herbaceous, frost resistance plants that in temperate areas are annual in growth pattern but in tropical areas may continue to grow and produce yield over several years (ratoon crop). *Capsicum* is a member of Solanaceae, includes many cultivated forms such as pungent peppers , paprika, mild pickle type and bell shaped, non pungent forms known as bell pepper or shimla mirch. At present five species of *Capsicum* are known to have been brought under cultivation (Smith *et al.*, 1987). They include *Capsicum annuum* L., *C. frutescens* L., *C. baccatum* L., *C. chinense* Jacquin and *C. pubescens* Ruiz and Paven. *Capsicum* is a good source of capsaicin and used in the manufacture of selected commercial products known for their pungency and colour (Andrews, 1984). There is great variability among size, shape, color and pungency of fruits of *Capsicum* spp., which can be exploited through conventional breeding (Pickersgill, 1989). Since critical assessment of nature and magnitude of variability is prerequisite for efficient breeding programme and provides an opportunity to identify promising lines with desirable yield and quality parameters. Identification of superior genotypes among relatively new ones becomes imperative for promoting production, productivity and quality of the produce (Mishra *et al.*, 2005). Such type of study was conducted at DARL, Pithoragarh during the year 2006-2007 for identification of promising genotypes which can be used in further breeding programme.

Fifty genotypes of *Capsicum* were collected from different national, international and state agricultural universities to enrich the pedigree. Collected germplasm from IARI, New Delhi, IIHR, Banglore, GBPUA&T, Pantnagar, IARI, Katrain , Gujrat Agricultural University, Kerala Agricultural University and Asian Vegetable Research & Development Center, Taiwan was sown in the nursery and transplanted in the field in three replications in randomized block design. Spacing within plants and rows was 60 cm x 60 cm. Morphological data such as corolla colour, corolla throat spots, anther colour , seed colour and flowers per node were recorded. Data were also recorded on quantitative characters viz, fruit length (cm), fruit width (cm), fruit number per plant and fruit yield per plant. Biochemical characterization for total soluble solids (TSS%), ascorbic acid (mg/100 g) and Capsaicinoid contents (SHU) was performed. T.S.S was studied with the help of Erma Hand Refractometer. Ascorbic acid determination in the fruit was done using Di nitro phenyl hydrazine (DNPH method) (Sadasivam and Balasubraminam, 1987). Capsaicinoid content was determined by high pressure liquid chromatography (HPLC method) (Estrada *et al.*, 1997). There was great variation in morphological characters among collected germplasm (Table1).

Table 1. Morphological characters of collected *Capsicum* spp.

S.No.	*Capsicum* species	Corolla color	Corolla throat spots	Anther color	Seed color	Flowers per node
1	*Capsicum annuum*	White	None	Blue purple	Tan	1
2	*Capsicum frutescens*	Greenish white	None	Blue	Tan	1-3 or 5
3	*Capsicum baccatum*	White	Yellow	Yellow	Tan	1-2
4	*Capsicum chinense*	White to greenish-white	None	Blue	Tan	1-5
5	*Capsicum pubescence*	Purple	None	Purple	Black	1

Table 2. Yield attributing characters in different species of *Capsicum* spp.

Species	Characters	Fruit length (cm)	Fruit width (cm)	Fruit number/ plant	Fruit yield plant (kg)
C. annuum	Minimun	6.2	5.3	10.0	0.400
	Maximum	17.3	25.5	58.0	2.000
	Mean	11.75	15.4	34.0	1.200
C. frutescens	Minimun	2.5	2.1	25.0	0.085
	Maximum	8.5	6.7	80.0	0.300
	Mean	5.5	4.4	52.5	0.192
C. chinense	Minimun	2.5	5.0	40.0	0.100
	Maximum	10.6	7.2	70.0	0.500
	Mean	6.5	6.1	55.0	0.300
C. baccatum	Minimun	3.7	4.0	30.0	0.310
	Maximum	11.3	10.3	50.0	0.425
	Mean	7.5	7.15	40.0	0.367
C. pubescens	Minimun	6.2	3.5	17.0	0.185
	Maximum	9.6	11.0	50.0	0.370
	Mean	7.9	7.3	33.5	0.278

Table 3. Bio-chemical characters in different species of *Capsicum*

Species	Characters	Total soluble solids %	Ascorbic acid (mg/100g)	Capsaicinoids SHU
C. annuum	Minimun	3.46	41.73	1602.00
	Maximum	8.14	112.00	14564.0
	Mean	5.80	76.86	8083.00
C. frutescens	Minimun	5.20	50.86	30445.00
	Maximum	7.92	129.85	2,76,750.00
	Mean	6.56	90.35	153597.50
C. chinense	Minimun	4.50	87.23	43500.00
	Maximum	6.25	99.20	2,54896.00
	Mean	5.37	48.215	1,49,198.00
C. baccatum	Minimun	4.68	42.75	15,885.00
	Maximum	6.20	50.92	52,250.00
	Mean	5.44	46.83	34067.50
C. pubescens	Minimun	4.12	45.72	52,220.00
	Maximum	7.28	118.20	1,08076.00
	Mean	5.70	81.96	80148.00

Minimum and maximum values along with means, with respect to yield, yield attributing characters and bio-chemical characters are given in (Table 2 and 3). Data revealed that in *C. annuum* fruit yield per plant (kg) ranged from 0.400–2.00. The highest yield was recorded in CO-3837. The TSS % was highest in the fruits of red capsicum (8.14). PBC-280 exhibited highest ascorbic acid (112.0 mg/100 g). Maximum fruit length (cm) was recorded in CO-6763 (17.3). In *C. frutescens*, DARL-210 exhibited maximum number of fruits per plant (105) with highest capsaicinoid content (2,76,750 SHU) and TSS (7.92%). PBC-926 showed maximum ascorbic acid (129.85 mg/100g). In *C. chinense* CC-2 showed maximum TSS % (5.37) with ascorbic acid (99.20 mg/100g). Maximum capsaicinoid contents was exhibited by Tejpur chilli (2,54,896 SHU). In *C. baccatum* CO-4180 exhibited maximum TSS (6.20%) and ascorbic acid (50.92mg/100g). Genotype KT-14 showed maximum capsaicinoid (52250 SHU). In *C. pubescens* NBPGR-1 showed maximum TSS (7.28%), ascorbic acid (118.20mg/100g) and capsaicinoid content (1,08076 SHU). The genotypes which were found promising, represent a potential source for future development and can be used as donor parents for further breeding programme.

Acknowledgements

Authors are grateful to Dr. Paul Gniffke, Plant Breeder (Pepper/Allium), Asian Vegetable Research & Development Center, Taiwan, Director IARI, New Delhi, Director, IIHR, Bangalore, Director, DRL, Tejpur, Head Horticulture Division GBPUA&T, Pantnagar, Dr. SK Verma, NBPGR Bhowali, Head, IARI, Katrain, Head, Vegetable Crops, Gujrat Agricultural University, Head, College of Horticulture, Kerala Agricultural University for providing us seeds of different *Capsicum* spp.

References

Andrews J (1984) *Peppers, the Domesticated Capsicums*. University of Texas press, Austin.

Estrada B, F Pomar, J Diaz, F Merinip and A Bernal (1997) Evaluation of capsaicinids in *Capsicum annuum* L. Var. annuum cv. Padron at different growth stages after flowering. *Capsicum Newslett.* **11:** 63-69.

Mishra AC, RV Singh and HH Ram (2005) Studies on genetic variability in Capsicum under mid hiils of Uttranchal Indian *J Hort* **62(3):** 248-252.

Sadasivam S and T Balasubraminam (1987) In *Practical Manual in Biochemistry*. Tamil Nadu Agricultural University, Coimbatore, 14 p.

Smith PG, B Villalon and PL Vuilla (1987) Horticultural classification of peppers grown in United States. *Hort. Sci.* **22:** 11-13.

Pickersgill B (1989) The archaeological record of chilli pepper (*Capsicum* spp.) and the sequence of plant domestication in Peru. *Am. Antiq.* **34:** 543-61.

SHORT COMMUNICATION

Diversity and Selection of Persian Walnut (*Juglans regia* L.) from Ladakh Region of India

OC Sharma, L Ali, NA Ganai and SB Ahmed
Krishi Vigyan Kendra, Regional Agricultural Research Station, SKUAST-K, Leh (Ladakh)
Post Box No. 146, (J&K)-194101, India

Investigations were carried out during 2006 on 91 seedling trees of Persian walnut growing at high altitude (more than 300 mamsl.) at various locations of Ladakh region in India. Data were collected on 26 nut and kernel characters. A great magnitude of variability was noticed for various traits. Maximum coefficient of variability was recorded for kernel weight while minimum for nut width. Based upon the existing variability, selection criteria was made and elite genotypes were selected virk Tree No. 1 at Domkhar, Tree No. 1 and 2 at Nurla; Tree No. 4 and 10 at Saspol and Tree No. 4, 6, 9 and 19 at Khalsi. These selected types will be vegetatively propagated and released as cultivars for commercial cultivation in Ladakh region of India in future to boost the cultivation of walnut at high altitudes.

Key Words: Diversity, Seedling trees, Walnut, Nut characters, Kernel, Variability

Persian walnut (*Juglans regia* L.) is one of the most important nut crops grown in temperate climate and belongs to family Juglandaceae. In India mostly walnuts of seedling origin are being grown. However, in last twenty years a lot of work on variability, selection and propagation has been carried out and now the systematic orcharding with superior cultivars has been started but with low pace. Walnut is monoecious and pollination takes place through wind which exhibit a great variability for various nut and kernel characters in the plants raised from seed. Past selection work has resulted to a number of present day cultivars throughout the world. Although walnut is successfully cultivated from 1,200 to 2,200 meters amsl, but also seedling trees of walnut were found growing at more than 3,000 meters above mean sea level (amsl). So, in present study an effort was made to study the extent of diversity and selection of elite genotypes of walnut from Ladakh for future use in high altitudes.

The present investigations were carried out during 2006 in some of the seedling walnut growing in Ladakh region of India. Nut samples were collected from Saspol (34°14.666' N and 77°10.165' E), Nurla (34°17.968' N and 76°59.473' E), Khaltsi (34°19.218' N and 76°52.972' E) and Domkhar (34°24.179' N and 76°45.995' E) area of district Leh in Jammu and Kashmir. These areas are more than 10 kilometers situated at an elevation of 3075, 3005, 3031 and 3045 meters amsl. These places are apart from each other. A sample size of 20 sun dried nuts were randomonly collected from each bearing tree. The samples were taken from 10 bearing seedling trees from Saspol, 13 from Nurla, 26 from Khaltsi and 42 from Domkhar area. Data on various nut and kernel characters were recorded on total 91 seedling trees as per descriptors of UPOV (1988) and IPGRI (1994). Data were analyzed as per Panse and Sukhatme (1985). The criteria used for selection of important traits were as per Sharma and Sharma (2000).

Data on range, mean, standard deviation and coefficient of variability on various metric nut and kernel characters are presented in Table 1. Maximum and minimum values for various characters were recorded from nuts produced by Tree No. 4 at Khaltsi and Tree No. 5 at Nurla, Tree No. 1 at Domkhar and Tree No. 10 at Nurla, Tree No. 19 at Khaltsi and Tree No. 3 at Domkhar,

Table 1. Range, Mean, Standard Deviation and Coefficient of Variability for Various Metric Nut and Kernel Characters

Characters	Range	Mean	Standard deviation	Cofficient of variability (%)
Nut weight (g)	5.61-18.47	11.30	2.65	23.42
Nut width (mm)	21.97-35.61	29.40	2.72	9.26
Nut height (mm)	26.92-47.30	35.98	4.31	11.99
Nut thickness (mm)	20.39-36.40	29.90	2.91	9.74
Index of roundness	0.65-1.00	0.83	0.08	9.93
Pad thickness (mm)	2.69-6.89	4.46	0.89	19.88
Pad width (mm)	1.76-6.91	4.50	1.11	24.29
Shell thickness (mm)	0.97-2.34	1.63	0.34	20.86
Kernel weight (g)	1.83-10.13	4.53	1.43	31.60
Kernel width (mm)	24.25-27.66	20.11	2.44	12.15
Kernel height (mm)	17.34-36.57	26.96	3.69	13.70
Kernel thickness (mm)	15.44-33.44	23.89	3.28	13.72
Kernel percentage	13.51-63.36	39.96	7.87	19.70

*Corresponding author: E-mail: ommandi@yahoo.co.in

Tree No. 10 at Nurla and Tree No. 2 at Nurla, Tree No. 11 at Nurla and Tree No. 8 at Domkhar, Tree No. 19 at Domkhar and Tree No. 28 at Domkhar, Tree No. 4 at Khaltsi and Tree No. 29 at Domkhar and Tree No. 7 at Domkhar and Tree No. 31 at Domkhar, respectively. Kernel weight, kernel width, kernel height, kernel thickness and kernel percentage varied between 1.83 g (Tree No. 5 at Nurla) to 10.13g (Tree No. 4 at Khaltsi), 14.25 mm (Tree No. 10 at Nurla) to 27.66 mm (Tree No. 4 at Khaltsi), 17.34 mm (Tree No. 10 at Nurla) to 36.57 mm (Tree No. 2 at Nurla), 15.44 mm (Tree No. 10 at Nurla) to 33.44 mm (Tree No. 36 at Domkhar) and 13.51% (Tree No. 2 at Khaltsi) to 63.36% (Tree No. 1 at Saspol) with their mean and coefficient of variability at the tune of 4.53 g and 31.60%, 20.11 mm and 12.15%, 26.96 mm and 13.70%, 23.98 mm and 13.72% and 39.96% and 19.70 %, respectively. The coefficient of variability extremes between 9.26% (nut width) to 31.60% (kernel weight).

Nut shape in longitudinal section perpendicular to suture and through suture on various locations were circular, triangular, broad ovate, ovate, short trapezoid, long trapezoid, broad elliptic and obovate. The percentages of trees at different locations were different. Most of the nuts produced at various locations were circular and broad elliptic for nut shape in cross section except one tree at Nurla which produced nuts having narrow elliptic shape in cross section. Shapes of nut base and apex also varied at various location as pointed, rounded, truncate and emarginated with varied frequencies at various places. The prominence of pistil point was weak, medium and strong at various location with varied number of trees while the position of pad on suture extremes as up to upper half, upper 2/3 and whole length of the fruit. The structure of shell surface was slightly grooved, moderately grooved, strongly grooved and embossed while grooves along pad on suture were shallow, medium and deep at various locations with different frequencies of trees falling in each category. Similarly adherence of two shell halves observed was weak, medium, strong and very strong while inner dividing primary and secondary membranes were thin, medium and thick at various locations with varied percentage of trees in each category. The kernel recovery was very easy, easy, medium, difficult and very difficult while the intensity of brown colour on kernel was very light, light, medium, dark and very dark.

Based on the existing variability for various nut and kernel characters in the region, 9 seedling trees were found elite trees. The various nut and kernel characters of selected types are presented in Table 2. The number of selected types at different locations is one at Domkhar (Tree No. 1), 2 at Nurla (Tree No. 1 and 2), 2 at Saspol (Tree No. 4 and 10) and 4 at Khaltsi (Tree No. 7, 6, 9 and 19). All the selected types produced nuts having nut weight more than 15 g. Tree No. 4 at Khaltsi and Tree No. 1 at Domkhar had maximum nut weight (18.47 g) and nut width (35.61 mm, respectively. Similarly Tree No 19 at Khaltsi and Tree No 2 at Nurla produced nuts with maximum height (47.30 mm) and thickness (36.40 mm), respectively. Minimum pad thickness 3.84 mm), pad width (1.76 mm) and shell thickness (1.05 mm) among selected types was found in Tree No. 9 at Khaltsi, Tree

Table 2. Nut and kernel characteristics of some elite walnuts of Ladakh

Characters	Locations and Tree Number								
	Domkhar	Nurla		Saspol		Khaltsi			
	Tree	Tree No. 1	Tree No. 2	Tree No. 4	Tree No. 10	Tree No. 4	Tree No. 6	Tree No. 9	Tree No. 19
Nut weight (g)	16.64	15.44	17.63	15.28	15.21	18.47	15.42	15.22	16.66
Nut width (mm)	35.61	31.58	34.02	33.15	31.01	35.21	25.05	31.38	35.21
Nut height (mm)	37.54	42.62	44.43	41.65	45.88	45.01	32.86	35.32	47.30
Nut thickness (mm)	36.39	33.73	36.40	33.70	30.93	35.30	28.23	32.79	36.10
Shell thickness (mm)	1.74	1.07	1.29	1.18	2.21	1.09	1.58	1.45	1.05
Kernel weight (g)	6.14	5.89	6.94	7.13	5.97	10.13	5.64	6.57	8.78
Kernel percentage	36.90	38.15	39.36	46.66	39.25	54.85	36.58	43.17	52.70
Structure of shell surface	Strongly grooved	Slightly grooved	Slightly grooved	Moderately grooved	Slightly grooved	Moderately grooved	Embossed	Embossed	Slightly grooved
Adherence of two halves	Strong	Medium	Medium	Strong	Very strong	Strong	Very strong	Medium	Strong
Kernel removal	Medium	Easy	Easy	Very easy	Easy	Very easy	Medium	Very difficult	Very easy
Intensity of brown colour	Very light	Very light	Very light	Very light	Light	Medium	Medium	Medium	Light

No. 4 at Khaltsi, and Tree No. 19 at Khaltsi, respectively. Maximum kernel weight (10.13g) and kernel percentage (54.85%) was found in nuts produced by Tree No. 4 at Khaltsi. All the selected types have medium, strong and very strong adherence of two shell halves; very easy, easy and medium ease of kernel removal. The intensity of brown colour on kernel in selected types was medium, light and very light. Only two trees (Tree No. 10 at Saspol and Tree No. 9 at Khaltsi) had value of shell thickness (2.21 mm) and ease of kernel removal (very difficult) beyond the desirable limits but they have other all characters superior, hence they were selected.

In the present study a great range of variability was observed for various nut and kernel characters. Similar variations for these characters were recorded by various workers in seedling trees (Sharma and Sharma, 1998; 2001a and Mehta *et al.*, 2005). The nut shapes observed were as per UPOV (1988) description. Besides, one more shape "obovate" has been observed. The existence of this shape has been earlier reported in seedling trees in Himachal Pradesh by Sharma (1999) and Mehta *et al.* (2005). Similar type of diversity for various non metric nut and kernel traits was also observed by Sharma and Sharma (2000). The existence of variability is the pre requisite for any breeding program. To evolve a cultivar through hybridization is a long process in the fruit crops like walnut. As the cultivar requirement of every region differ and cultivar in one region may not do well in another place. So, the most easy and fast method of improvement is selection of superior types from the existing variability. In the present study nine elite types of walnuts were selected from Ladakh region of India. Similar types of selection work from the existing variability were carried out Sharma and Sharma, 2000; 2001b; Sharma and Sharma, 2005 and Mehta *et al.*, 2005) in Himachal Pradesh. Although criteria used in present study slightly differed from earlier studies because selection was made from the existing population at very high altitudes (more than 3000 meters amsl.) As growing of walnuts was not reported at such height, so the cultivar requirements of this region might be totally different from elsewhere. Although among the selected, one type had more shell thickness than the criteria fixed and other had very difficult kernel removal but these were selected because they were superior in all other characters. The continuous cross pollination and seed propagation has resulted to this variability for various nut and kernel characters. These selected types can be used as cultivars to boost walnut production in the region in future.

References

IPGRI (1994) Descriptor for walnuts (*Juglans* spp.).

Mehta K, OC Sharma, AS Kashayap and BS Thakur (2005) Variability for various nut and kernel characters in some promising seedling walnuts (*Juglans regia* L.) in Himachal Pradesh. *Acta. Hort.* **696**: 91-95.

Panse VG and PV Sukhatme (1985) *Statistical Methods for Agricultural Workers*. ICAR, New Delhi, India.

Sharma OC (1999) Studies on variability and selection of superior walnut (*Juglans regia* L.) seedling trees in Himachal Pradesh, Solan, Dr. YS Parmar University of Horticulture and Forestry. Thesis (Ph.D.).

Sharma OC and SD Sharma (2000) Variation for various non metric characters of walnuts (*Juglans regia* L.) of seedling origin growing in Himachal Pradesh. *Him. J. Agric. Res.* **26(1-2):** 156-165.

Sharma OC and SD Sharma (2001a) Genetic divergence of seedling trees of Persian walnuts (*Juglans regia* L.) for various nut and kernel characters in Himachal Pradesh. *Sci. Hort.* **88:** 163-171.

Sharma OC and SD Sharma (2005) Description of elite selections of walnuts (*Juglans regia* L.) from intra specific population of seedling trees in Himachal Pradesh. *Acta. Hort.* **696:** 79-84.

Sharma SD and OC Sharma (1998) Studies on variability in nuts of seedling walnuts (*Juglans regia* L.) in relation to tree age. *Fruit Varieties J* **52**(1)**:** 20-23.

Sharma SD and OC Sharma (2000) Selection of superior walnut (*Juglans regia* L.) from a seedling population in Himachal Pradesh. *Adv. Hort. Sci.* **14:** 197-200.

Sharma SD and OC Sharma (2001b) Studies on variation in nut and kernel characters and selection of superior walnut seedling (*Juglans regia* L.) from Garsa and Jogindernagar area of Himachal Pradesh. *Acta. Hort.* **544**: 47-50.

UPOV (1988) General Information: International Union for Protection of New Varieties of Plant/TG/125/1 (Proj), Geneva, Switzerland.

Journal of Plant Genetic Resources

ISSN 0971-8184

Vol. 20 No.1 2007

CONTENTS

Published by the *General Secretary,* Indian Society of Plant Genetic Resources, NBPGR Campus, New Delhi-110 012 and printed at *Angkor Publishers (P) Ltd.,* B-66, Sector 6, NOIDA