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Plant genetic resources network in East Asia

Proceedings of the Meeting for the Regional Network for Conservation and Use of Plant Genetic Resources in East Asia
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Foreword

East Asia is one of the main centres of crop diversity in the world. There are many cultivated species which originated in this region, including grains, industrial crops, fruits, vegetables, forages, green manure crops and flowers. In addition, the region is also rich in wild species and wild crop relatives. There is also significant diversity in genepools of forest species as well as medicinal plants. Due to a long cultivation history and diversified ecogeographical environments in East Asia, a considerable amount of landraces or primary cultivars are available in the region. In remote areas of China and Mongolia, in particular, landraces adapted to local environments are still used by farmers. These varieties have strong adaptability to local diversified environments and special characteristics such as disease resistance, high quality and cultural adaptability. However, the landraces of many crop species have disappeared in the more developed areas and replaced by modern cultivars, which are usually much more uniform, have a narrow genetic basis and result in loss of genetic diversity in the region.

The Regional Network for Conservation and Use of Plant Genetic Resources in East Asia (EA-PGR) was established in 1991 and has provided an effective mechanism for sharing and exchanging information, discussing and identifying common interests, and initiating and developing collaborative activities among member countries including China, Japan, Republic of Korea, Democratic People's Republic of Korea and Mongolia. IPGRI East Asia Office services as interim secretariat of the network and works closely with the national coordinators for implementing collaborative programmes initiated by the network involving several member countries. Examples of such collaborative activities are the studies on adzuki bean genetic diversity and collecting and characterization of millet genetic resources. These have played a critical role in enhancing sharing of resources, information and technologies for implementing the Global Plan of Action (GPA) among member countries of the network through joint activities on research, training and germplasm exchange.

The current proceedings is the result of the meeting of the Regional Network for Conservation and Use of Plant Genetic Resources in East Asia held in Ulaanbaatar, Mongolia, 13-16 August 2001. The meeting aimed to exchange views on current status of the conservation and use of plant genetic resources (PGR) in each country and improve mutual understanding, review the progress of joint activities in the region, and identify priority areas for future collaboration. The elaboration of the presentations was given in two sessions: country reports and thematic reports. In the session of country reports, the topics included the status reports on conservation and use of plant genetic resources in all member countries of EA-PGR. The other topics in this session included a regional synthesized report on progress and activities in EA-PGR Network and a discussion paper on germplasm exchange and intellectual property rights (IPR) issues. In the session of thematic reports, the topics covered research work on conservation and use of genetic diversity of millets, barley, soybean and adzuki bean, and cryopreservation of temperate fruit tree species in member countries in the region. It also covered some thematic issues discussed by IPGRI staff, e.g. characterization, ***in situ*** conservation, forest genetic resources, documentation and public awareness. Through a series of discussions on common needs and interests, a number of priority actions had been recommended for EA-PGR activities involving ***in vitro*** conservation research, germplasm collecting and exchange, documentation and public awareness.

I would like to take this opportunity to thank everyone for their valuable contributions to this proceeding and their active participation in the network.

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Country reports

The status and progress of activities on plant genetic resources in China

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Introduction

Geography and climate

China is the largest country in Asia, with an area of about 9.6 million km^2 spanning 50 degrees of latitude (4°N - 52°23’N) and 62 degrees of longitude (73°E - 135°10’E). With highlands in the west, and lowlands in the east, China has a varied topography composed of 33% of mountains, 26% plateau, 10% hills, 19% basins and 12% plains.

The climatic conditions in the country are also diversified, including the cool zone, the temperate zone and the sub-tropics and the tropics from north to south, and the humid area, the semi-humid area, semi-arid area, and arid area from southeast to northwest. China is influenced by the monsoon climate. In northern part of China, winters are dry and cold, and summers hot while in the south it is warm and wet weather. The difference in temperature could be as much as over 40°C between the North and the South. There are large differences in annual rainfall as well among different regions of China. The annual rainfall can reach over 1500 mm in the coastal areas of the Southeast, and it gradually decreases to 50 mm in the Northwest. The wet monsoon comes during the summer and brings much rainfall to the country.

Thus the varied geography and climatic conditions have given rise to diverse ecological conditions for the speciation and evolution of many different kinds of plants and animals.

Socioeconomic conditions

China has 1.3 billon of population, the largest in the world. There are 56 different ethnic groups of people in the country. About 70% of the population live in rural areas. The farmers, agricultural industry and rural development are key issues in economic development in the country.

In China, the economy has been progressed dramatically in recent years. The Gross Domestic Products (GDP) reached about $1100 billion in 2000. However, the average GDP per capita is still very low. Also there is a large difference in the level of economic development between eastern and western regions. The agricultural products accounted for 16% of the GDP in China in 2000.

Diversity

Biodiversity

China is rich in biological diversity, which provides the basic resources of living materials for Chinese people. Table 1 shows the comparison of number of species of living forms found in China and those in the world (EGAPCBC, 1994). There are more than 30 000 seed producing species, of which about 17 000 are native to China.

Agrobiodiversity

There are about 10 000 plant species used for the various purposes in agricultural development in China, including food, oil, medicine and industrial materials (Table 2). Due to the long history of agriculture in China, not only have a large number of crops been domesticated in China, but also a considerable number of crop landraces have been developed in different environments. For example, more than 50 000 accessions of rice landraces have been collected in China. Many of the landraces possess useful characteristics such as disease resistance, stress tolerance, early maturity, high yield and high quality, which are very important economic traits for crop improvement and production (Liu and Dong, 2001).

Table 1. Numbers of species found in China and the world

Taxa	Species in China (SC)	Species in the world (SW)	SC/SW (%)
Mammals	499	4 000	12.5
Birds	1 186	9 040	13.1
Reptiles	376	6 300	6.0
Amphibians	279	4 184	6.7
Fishes	2 804	19 056	14.7
Insects	40 000	751 000	5.3
Bryophytes	2 200	16 600	13.3
Pteridophytes	2 600	10 000	26.0
Gymnosperms	200	520	37.8
Angiosperms	25 000	220 000	11.4
Fungi	8 000	46 983	17.0
Bacteria	500	3 060	16.3
Algae	5 000	26 900	18.6

Table 2. Species used for various purposes in China

Group of crops	No. of species
Direct use for food	
Field crops	100
Oil crops	100
Sugar crops	50
Vegetables	700
Fruits	300
Drinks	50
Indirect use for food	
Feed crops	500
Forages	2 500
Industrial use	
Timbers	2 000
Fibres	1 200
Rubbers	50
Gums	100
Aromatic oils	350
Industrial oils	500
Tanning oils	300
Pigments	60
Parasitic creatures	300
Weaving	50
Medicinal use	
Human's medicines	5 000
Animal's medicines	500
Agricultural chemicals	200
Use for environmental protection	
Horticultures	500
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China is the original centre for more than 200 crop species such as rice, wheat, millet, common millet, buckwheat and Chinese cabbage, and special characters such as dwarf genes, male sterility genes, glutinous genes and compatible genes of various crops (SCGR-CAASS, 1994).

Agriculture

In China, the grain yield was increased from 1035 kg ha^{-1} in 1949 to 4500 kg ha^{-1} in 1999, about 4.4 times increased in 50 years. The total production was increased from 113.2 million tons in 1949 to 508.4 million tons in 1999, about 4.5 times increase in 50 years. The total planting area has remained unchanged, i.e. around 100 million ha. However, due to the faster increase of population, the availability of food per capita is still quite low (Fig 1).

The constant increase in grain production has attributed to the upgrading of farming technologies, particularly the new cultivars developed through the exploitation and utilization of the elite genes in crop germplasm collections.

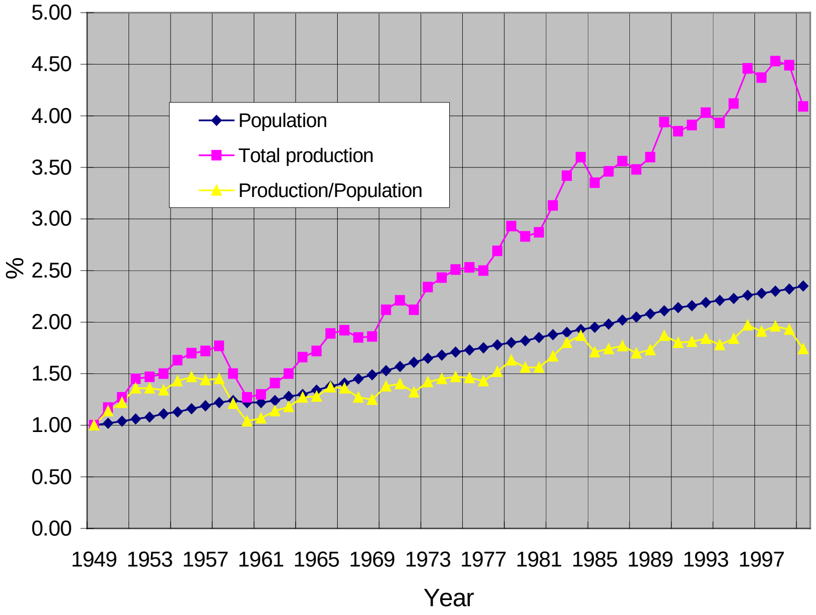

Fig. 1. Trends in population growth, total grain production and per capita food availability in China

PGR management system

From the foregone discussion it is clear that China needs to increase its food and agricultural production and plant germplasm plays a key role in doing so. The country's plant genetic resources (PGR) need to be managed and used and a system for this purpose is in place in China. The national PGR management system is very complicated and usually operated by several relevant ministries in China. The forest genetic resources programme is managed by the State Forestry Administration. The medicinal PGR programme is managed by the Ministry of Health and the State Administration of Traditional Medicine. The crop genetic resources programme is managed by the Ministry of Agriculture. The Ministry of Science and Technology operates PGR programmes in cooperation with all other relevant ministries (Fig. 2).

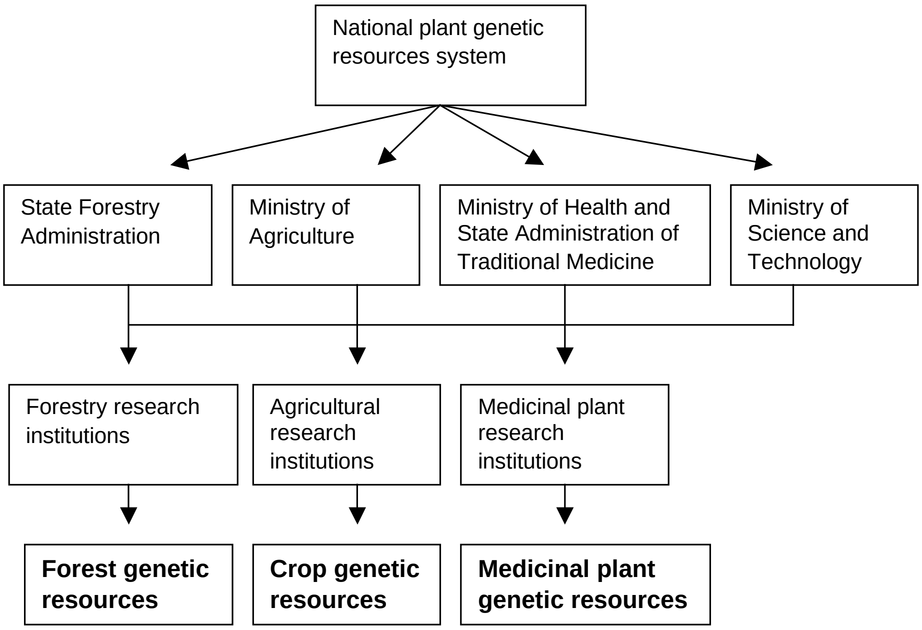

Fig. 2. National plant genetic resources system

The Institute of Crop Germplasm Resources (ICGR) of the Chinese Academy of Agricultural Sciences (CAAS) plays the coordinating role in implementing the national programmes on conservation and use of crop genetic resources in China with particular responsibilities as follows:

- Coordinate the activities of seed propagation, and characterization and evaluation;
- Take charge of nationwide long-term conservation;
- Process germplasm introductions and international exchange;
- Organize nationwide germplasm exploration and collecting; and
- Manage national information system of crop genetic resources.

The National Crop Germplasm Conservation Centre that is being established at ICGR will be responsible for implementing the activities on ***ex situ*** and ***in situ*** conservation of crop germplasm resources and operating national crop genetic resources information network (Fig 3). There are independent research programmes on PGR in each province, which are implemented by relevant research organizations at provincial level.

The national genebank at ICGR-CAAS is responsible for the long-term storage of national collections of all crop germplasm, while the medium-term genebanks maintained by different provinces are responsible for conserving germplasm collected in their own provinces.

China also has established a number of medium-term genebanks or field genebanks for specific crops, which are managed by related institutes of CAAS as follows:

Cotton: Institute of Cotton of CAAS, Anyang, Henan
Fibre crops: Institute of Bast Fibre Crops of CAAS, Changsha, Hunan
Forages: Institute of Grassland of CAAS, Huhhot, Inner Mongolia
Fruit trees: Xingcheng Institute of Pomology of CAAS, Xingcheng, Liaoning; Zhengzhou Institute of Pomology of CAAS, Zhengzhou, Henan; and Institute of Citrus of CAAS, Beipei, Chongqing
Oil crops: Institute of Oil Crops of CAAS, Wuhan, Hubei
Tea: Institute of Tea of CAAS, Hangzhou, Zhejiang
Vegetables: Institute of Vegetables and Flowers of CAAS, Beijing

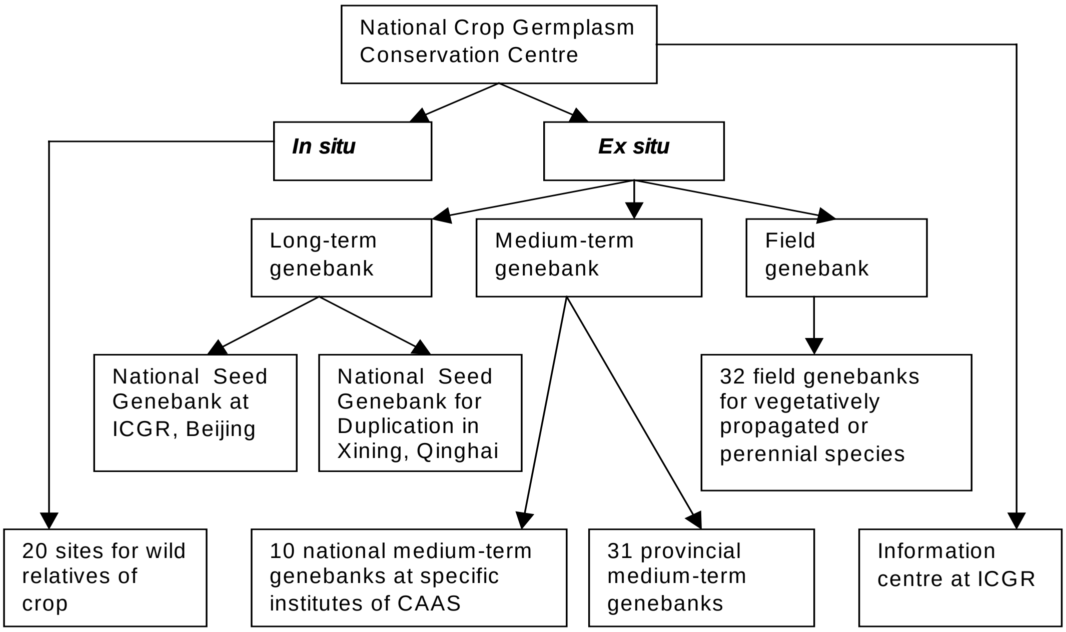

Fig. 3. Crop genetic resources management system

Overall progress of PGR activities

Germplasm collecting

From 1998 to 2000, the collecting activities were carried out mainly in central and southern parts of the country, including Three-Gorge Region, Southern Jiangxi Province and northern Guangdong Province. The collecting missions were organized by ICGR in cooperation with the research institutes in relevant regions. During the collecting missions, the teams visited 38 counties in Three-Gorge Region, southern Jiangxi Province and northern Guangdong Province. A total of 3956 accessions of various crop germplasm were collected in the last three years.

Through other activities, 952 accessions were collected by different institutions throughout the country during 1998 - 2000.

International cooperation and exchange resulted in the acquisition of 3150 accessions of various crops, introduced from 24 countries and international organizations.

Germplasm conservation

The conservation facilities in China for crop germplasm are composed of long-term genebanks, medium-term genebanks and field genebanks. All these genebanks are complementary to each other. During the last three years, more than 21 800 accessions of different crops were entered into the National Genebank at ICGR for long-term storage. By the end of 2000, the total collection of germplasm stored in National Genebank has reached 334 250 accessions belonging to 600 species or sub-species and 174 genera (Table 3).

In the same period, the viability of 12 010 accessions of 10 crops stored in the National Genebank have been monitored. The results indicate that the accessions are stored under good conditions. However, attention should be given to short-lived crops such as carrot and lettuce (Lu ***et al.,*** 2001).

The medium-term genebanks are responsible for maintaining and distributing the active collections. To promote distribution and utilization, 31 200 accessions of germplasm were regenerated in medium-term genebanks from 1998-2000.

Table 3. Accessions of crop germplasm conserved in the National Genebank at the end of 2000

Crops	Accessions	Genera	Species/ sub-species
Wheat	38 224	1	16
Wheat Relatives	1 599	10	102
Rice	64 390	1	17
Wild rice	6 944		
Corn	15 223	1	1
Soybean	30 098	1	4
Wild soybean	6 172		
Cotton	6 264	1	19
Rape	5 446	5	13
Food legumes	23 541	11	27
Sorghum	16 546	1	2
Millets	35 043	6	8
Barley	18 838	1	1
Sesame	4 410	1	1
Peanut	5 426	1	14
Sunflower	2 541	2	2
Forage	3 021	98	265
Green manure	663	25	68
Vegetables	29 153	67	85
Oat	3 171	1	3
Barnyard millet	663	1	1
Buckwheat	2 363	1	3
Kenaf	445	1	1
Jute	566	1	2
Flax	2 639	1	2
Hemp	219	1	1
Caster	1 652	1	1
Safflower	2 378	1	2
Perilla	471	1	1
Watermelon	961	1	1
Sweetmelon	883	1	1
Amaranth	1 459	1	5
Others	2 838	1	22
Total	**334 250**	**174**	**600**

Characterization and evaluation

The characterization of crop germplasm was focused on identification of accessions with useful characters that are interesting to various users. In the last three years, a total of 15 541 accessions were evaluated for agroeconomic characters, 13 037 for quality traits (42 152 items of data obtained), 10 832 for stress tolerance (25 331 items of data obtained), 15 336 for resistance to pests and diseases (53 818 items of data obtained). From the characterization and evaluation, about 241 elite accessions identified, which have been provided for further tests or utilization in breeding programmes and production.

Genetic diversity assessment was carried out using molecular techniques and 24 useful molecular markers have been identified in certain crops. These markers will be useful to evaluate germplasm collections and analyze the relationships between different materials. The evaluation for identifying core collection of rice, wheat, soybean and adzuki bean are being carried out. The fingerprinting techniques have been successfully used for 1000 accessions of rice, wheat, corn, soybean and cotton.

Documentation

The web site for Chinese Crop Germplasm Information System (CCGIS) (http://icgr.caas.net.cn/) has been established at ICGR. It services as a platform for disseminating information on on-going PGR activities in China, accessing on-line database of characterization and evaluation of Chinese germplasm collections, and discussing issues and problems. The passport data of 17 476 accessions have been added to CCGIS in the last three years. The Characterization Geographic Information System has been developed by ICGR and provided service for identifying useful characters that are closely associated with geographic conditions in China. Fingerprinting Automatic Recognizing System was further improved. This system helps to analyse molecular data. The Regeneration Expert System is being developed and will be used to manage and plan the regeneration activities for germplasm stored in the long-term genebank (Cao, 2001).

Distribution and utilization

In the last three years, more than 50 000 samples of various crop germplasm were distributed to the relevant organizations in the country and abroad, of which there were about 241 accessions of elite germplasm with different useful characteristics. It was estimated that 80% of these elite germplasm had been used for breeding purpose, and 20% directly used in agricultural production. More than 200 new varieties (lines) have been developed by breeders using the elite germplasm and released for production.

Regional and international cooperation

China and IPGRI

The cooperation between China and IPGRI has been strengthened in many areas. The IPGRI Office for East Asia has played an important role in coordinating and promoting the collaborative activities. The cooperative researches on cryopreservation of vegetatively propagated crop species have obtained good progress on grape, apple and kiwi fruit. The technical protocols for cryopreservation of these species are being developed. Application of cryopreservation for the conservation of vegetatively propagated crops will greatly improve the complementary conservation strategy and safeguard the crop diversity in the country. The study on ultradry seed storage has improved the knowledge on optimum seed moisture content for storage at different levels of temperature.

The researches on ***in situ*** conservation and indigenous knowledge have contributed to developing methodologies and models for such researches in large scale. The development of Regeneration Expert System will use computer technology to improve the efficiency of genebank management in general and of the regeneration of accessions stored in the large genebank (such as the one at ICGR) in particular.

China and other international cooperation

China has made efforts to develop cooperation on PGR with other countries or international organizations. The collaborative researches on rice, soybean and food legumes have been established between China and Republic of Korea. China also has cooperative activities with many other countries on rice, wheat, corn, soybean, food legume, oil crop, fibre plant, vegetables, fruit trees, tea and mulberry in many areas including molecular markers and stress resistance.

Strategy on conservation and use

Survey and collecting

The surveys for collecting crop germplasm nationwide will be continued in China. The future surveys will mainly focus on the remote areas where many crop landraces are still used by local farmers. The surveys also aim to collect the special crop species or characters such as resistance to extreme environments. These species or characters will be very important for the sustainable agricultural development in the western region of China. About 10 000 accessions are expected to be collected and catalogued in next 5 years.

Conservation

NCGCC of ICGR will be established with extended conservation facilities for long-term storage, including the facilities for ***in vitro*** and cryopreservation. The ***in situ*** conservation will focus on the wild relatives of crop species including wild rice, wild wheat and wild soybean and 20 sites will be identified and protected in cooperation with local communities.

For the security of the germplasm stored in different genebanks, a Monitoring and Early Warning System will be developed and installed at the National Genebank at ICGR and 32 national field genebanks in different locations.

Regeneration and distribution

Regeneration and multiplication will be carried out for about 300 000 accessions of germplasm stored in the National Medium-term Storage from 2001-2005. About 20 000 samples of various crop germplasm will be distributed every year to breeders and other users.

Information network

The National Germplasm Resources Information Network will be established by linking 2 long-term storages, 10 medium-term storages, 32 field genebanks and 20 ***in situ*** conservation sites. The germplasm samples could be ordered through the network. The Diversity of Crop Germplasm Resources in China and Catalogue of Rare and Distinct Crop Germplasm Resources in China will be published.

Evaluation and enhancement

The evaluation and enhancement of crop germplasm will focus on the development of new cultivars through interspecific crosses, improvement of the potential underutilized crops and genetic enhancement of cultivated plants by introgressing genes from their wild relatives or other species.

Capacity analysis

Strengths

- Increased awareness of people on the importance of diversity in food security, poverty elimination and environmental protection.
- The facilities established for long-term storage, medium-term storage, field repositories, which have provided the basic conditions for implementing the

complementary conservation strategy by establishing ***in vitro*** and ***in situ*** conservation facilities in the country.

- The available expertise in advanced technologies, including molecular techniques for gene identification, isolation and utilization, and information and communication technology.
- Financial support for PGR activities has increased continuously.

Weaknesses

- Short of technicians.
- The medium-term storages and field genebanks are not well coordinated.
- Lack of ***in vitro*** or cryopreservation facilities.
- Lack of ***in situ*** conservation technologies and methodologies.
- Weak capacity in monitoring technologies for the viability of seeds stored in the long-term genebank.

Opportunities

- The reform of science and technology system of China will enhance the capacity of the research on PGR.
- A special national programme on germplasm resources has been proposed and submitted to the central government for consideration.
- The establishment of the National Crop Germplasm and Improvement Centre at ICGR will enhance the research and use of crop genetic resources.
- A proposal for ***in situ*** conservation of crop germplasm in China has been submitted to GEF who has shown the interests and will provide support to the activities.

Threats

- Developing the West China may result in the loss of PGR and ecosystems.
- The fast economic development in rural areas may worsen the environments in some areas.
- Imported cultivars will increase after entry into WTO and many local varieties will be lost.
- Increased transgenic plants may damage biosystem and threat to compatibility of local germplasm.

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Plant genetic resources status and progress of activities in Japan

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Introduction

Japan is an island nation lying off the east coast of Eurasia continent. It has the general shape of a crescent and extends 3000 kilometres from north to south. The country is made up of four main islands (Honshu, Hokkaido, Kyushu and Shikoku) together with more than 4000 smaller islands that are collectively referred to as the Japanese Archipelago. Japan's land area is of about 378 000 km^2.

The Japanese climate differs greatly from region to region. Although this is largely due to the length of 3000 km from north to south that puts one of its ends in the sub-frigid zone and the other in the sub-tropic zone, a complex topography and the influence of ocean currents are also important factors. Most of Japan has a temperate, oceanic type of climate with four distinct seasons. On the side of Pacific, the summers are hot and humid with prevailing seasonal winds from the southeast. The winters are dry and marked by many clear days. On the side of Japan Sea, north-western winter winds blowing off the Asian continent bring regular, heavy snows that make it one of the countries with heaviest snowfall on the earth. In Niigata Prefecture, annual snowfall is usually of 4 to 5 meters. All areas except the northern-most islands of Hokkaido have a hot and very humid rainy season that lasts from early June to middle July. Between August and October, the southwestern part of the archipelago is often hit by typhoons. The islands of Japan are bounded by the Pacific Ocean on the east and the Japan Sea on the west. Several volcanic ranges running through the country have contributed to diverse topographical features in Japan. About 67% of Japan's land area is mountainous and is mostly covered with forest. Agricultural land accounts for 15% and residential land for 3%. Gross Domestic Product (GDP) was $3884 billion and the contribution by agriculture was only 1%. The area of cultivated land in Japan is 4.87 million hectares and is decreasing every year. Japan has over 24 million hectares of forest, about two-thirds of the nation's total land area. Of this, 30% is owned by the state and 70% by private sector (Miscellaneous, 1990).

Japan's population was 126.48 million in 1998. The population is mainly concentrated along the Pacific seaboard where the weather is mild and the transportation and industrial facilities are highly developed. Advances in industrialization have been accompanied by a population shift toward the large cities and a remarkable population decline in the agricultural areas, with only 11.31 million (8.9%) living in agricultural areas. The farming population accounted for 4.7% of the total population (1998). The percentage of farmers over 65 years old was 46% and only a small number of younger people were taking up agriculture.

A working party of the Science Council of Japan is playing an important role for coordinating the domestic committee concerned with technological infrastructure as to the academic activity of agricultural genetic resources (Nakagahra ***et al.***, 1998). However, a national committee for genetic resources is yet to be established. The Ministry of Agriculture, Forestry and Fisheries (MAFF), Japan is the nodal ministry for conserving agricultural genetic resources and developing Genebank Project for plants, micro-organisms and animals with the collaboration of National Institute of Agrobiological Resources (NIAR) as a central bank in coordination with 14 other institutions as sub-banks since 1983. DNA section was later added to the Genebank Project. This project focuses on exploration/collecting, evaluation, preservation, data management and distribution/utilization of these genetic resources. All the genetic resources activities have been conducted under the auspices of Japan's first 8-year project and the second 8-year project.

After the Third Meeting of National Coordinators of Plant Genetic Resources for East Asia held in Suwon, Republic of Korea in 1998, the most notable change in the areas of plant genetic resources (PGR) in Japan was the reform of government organizations.

Research Institutes under the MAFF were re-organized as Independent Administrative Agency on April 1, 2001. The former NIAR was reorganized into the National Institute of Agrobiological Sciences (NIAS) that includes the Genome and Biodiversity Research Centre, the Institute of Plant Science and the Institute of Insect and Animal Sciences.

The Genebank was established as a department responsible for genetic resources in the Genome and Biodiversity Research Centre, which also includes other two departments: Genetic Diversity Department and Genome Research Department.

The NIAS Genebank has the overall responsibility for all the PGR activities as a central bank, in collaboration with sub-banks. The PGR Laboratory is in charge of all the PGR related activities in the Genebank. Independent Administrative Institutions involving in PGR activities are shown in Table 1. We developed a new 5-year Genebank project from 2001 to 2005, which includes all PGR activities, i.e. exploration/collecting, evaluation, database management, conservation/preservation, rejuvenation, distribution and utilization.

Table 1. Network of plant genetic resources

Central bank

National Institute of Agrobiological Sciences, Tsukuba

Sub-banks

National Institute of Crop Sciences, Tsukuba
National Institute of Fruit Tree Science, Tsukuba and others
National Institute of Vegetables and Tea Sciences, Anou and others
National Institute of Floricultural Sciences, Tsukuba and others
National Institute of Livestock and Grassland Science, Nishinasuno
National Agricultural Research Institute, Tsukuba and Joetsu
National Agricultural Research Institute for Hokkaido Region, Sapporo and Memuro
National Agricultural Research Institute for Tohoku Region, Morioka and others
National Agricultural Research Institute for Western Region, Fukuyama and Zentsuji
National Agricultural Research Institute for Kyushu Okinawa, Nishigoshi and others
National Centre for Seed and Seeding, Tsukuba and others
National Livestock Breeding Centre, Shirakawa and others
Prefecture Agricultural Experiment Stations, All Japan

Overall progress of national PGR activities

Exploration and collecting

The MAFF Genebank has been actively conducting exploration and collecting in Japan and abroad since 1985. Four collecting missions abroad and six missions in Japan are being dispatched from the MAFF every year (Table 2). We explored and collected rice, elephant yam and millets in Myanmar, ***Lolium*** and ***Festuca*** in Italy, French and Spain, and legumes in Vietnam in the fiscal year of 2000. Exploration activity in Myanmar was performed in good collaboration with the Seed Bank Project assisted by the Japan International Cooperation Agency (JICA). After the introduction of collected materials into Japan, morphology and several useful characters of the materials were evaluated in the network of Genebank.

In the new 5-year project of Genebank, we prioritised crop species to be explored based on crop improvement needs and the degree of genetic erosion in each crop in Japan and planned the long-term programme for exploration/collecting. The NIAS Genebank seeks possibilities of exploration/collecting not only in East Asian countries but also in countries in other regions. Since the importance of endemic crop species in each country and the responsibility of conservation of the species agreed in the Convention of Biological Diversity (CBD), the NIAS Genebank reviewed the present situation on the conservation of indigenous crop varieties in Japan and the result was reflected in the new 5-year project. We are aiming to collect local varieties of food legumes, fruit trees and vegetables mainly.

Table 2. Plant genetic resources collectings

Year	Country	Targeted plants
1998	Greece	Wheat and Barley
	Armeniya, Gruziya	Fruit tree
	Vietnam	Rice, Fruit tree
1999	Greece	Vegetables
	Thailand	Sugarcane
	Myanmar	Rice, Millet, Elephant yam
	Spain	Fruit tree
2000	France, Italy, Spain	Forage crops
	Myanmar	Rice, Millet, Elephant yam
	Vietnam	Food legumes
	Bhutan	Preliminary survey
2001	Myanmar	Food legumes, Forage crops
	Taiwan of China	Vegetables
	Australia	Wild rice

Conservation and preservation

After the CBD, the NIAS Genebank has been focusing on the research of ***in situ*** and/or on-farm conservation as well as ***ex situ*** conservation.

Monitoring of germplasm conserved on-farm was conducted at Fukushima and Ibaraki Prefectures in northern Japan. The results revealed that most indigenous varieties of crops including rice, foxtail millet, barnyard millet and etc. were already extinct although some local varieties of soybean and adzuki bean were still maintained by farmers. These results highlighted the importance of complementary ***ex situ*** conservation in genebanks (Nagamine ***et al***., 2001). Based on results of the monitoring, we have recognized that a large amount of farmer's knowledge on the usage of local genetic resources and cultural/historical stories surrounding crops and local communities were quickly becoming extinct due to the aging of farmers and that this knowledge needs to be collected, documented and used for efficient conservation and use of PGR.

A total of 209 816 accessions of germplasm are now preserved in the Genebank. Of them 169 751 are seed propagated plants, and 40 016 are vegetatively propagated (Table 3). Base collection (long-term storage) at NIAS Genebank has 184 765 accessions, of which 110 624 have been duplicated as active collection (medium-term storage). Vegetatively propagated plants are preserved at each sub-bank. We are planning to preserve the vegetatively propagated species at two different sites in the Genebank Network and we have already established the duplicate preservation system for fruit trees, potatoes and sweet potatoes.

The International Symposium on Cryopreservation for Tropical Crops was held at the Japan International Research Centre for Agricultural Sciences (JIRCAS) with the sponsorship of IPGRI in 1999 (Engelmann and Takagi, 2000). Recent progress on cryopreservation for several plants was presented and discussed at the symposium. The NIAS Genebank started the cryopreservation of winter buds of mulberry in liquid nitrogen as a base collection (Miyashita ***et al.,*** 2000). In the new 5-year Genebank project, the NIAS Genebank is planning to apply the cryopreservation technique to shoot tips of chrysanthemum and mat rush (***Juncus effusus*** L.).

Table 3. The present status of preservation of plant genetic resources (NIAS Genebank, 2001)

Crop group	Base collection	Active collection	Total
Rice	36 104	22 885	36 458
Wheat and barley	55 897	33 731	57 198
Food legumes	15 464	10 955	16 118
Root and tuber crops	6 821	3 696	7 049
Millets and industrial crops	15 277	9 043	16 561
Forage plants	22 399	14 038	28 015
Fruit tree	6 712	4 365	8 574
Vegetables	15 570	9 449	22 765
Ornamental plants	2 264	371	5 582
Tea	5 563	1 032	6 958
Mulberry	983	771	1 386
Tropical plants	266	14	318
Miscellaneous	1 445	274	2 942
Total	**184 765**	**110 624**	**209 816**

Distribution

Distribution of PGR for users is one of the most important tasks of our Genebank. Active collections are distributed upon the requests from users such as researchers from institutes, universities, private sector and overseas. Approximately 7000 - 8000 accessions are distributed annually to users (Table 4). Among the East Asian countries, 45 and 93 accessions were distributed from our Genebank to China and Korea, respectively from 1998 to 2001. The request form for PGR distribution is now available at the web site of the NIAS (http://www.gene.affrc.go.jp).

Table 4. Distribution of plant genetic resources from NIAS Japan in 2000

Crop groups	Institute	University	Private	Abroad	Total
Rice	1 111	75	128	16	1 330
Wheat and barley	1 728	-	2	23	1 753
Food legumes	989	2 006	28	2	3 025
Root and tuber crops	2	3	-	-	5
Millet and industrial crops	336	7	1	23	367
Forage crops	68	7	-	9	84
Fruit tree	-	-	5	-	5
Vegetables	368	305	33	77	83
Ornamental plants	-	1	13	-	14
Tea	-	-	1	-	1
Mulberry	5	-	13	-	13
Total	**4 607**	**2 404**	**224**	**150**	**7 385**

Evaluation and utilization

Passport data and evaluation data of Japanese accessions preserved in the Genebank Network are now available on the Internet. Every user can now access these data and utilize them for the screening of materials.

Utilization through evaluation and genetic enhancement is the ultimate purpose of conserving PGR in genebanks. Agronomically useful genes from wild crop relatives are tried being introduced to modern varieties by backcross method and/or using bridge-species between wild species and crop species at several crop-breeding laboratories.

A joint activity on the evaluation and utilization of ***Vigna*** species was undertaken under the auspices of EA-PGR (See page 58 in this volume: Norihiko Tomooka, ***et al.***, 2002).

From screening different ***Zoysia japonica*** ecotypes collected in Kochi Prefecture, a new turf grass variety named "Asagake" was bred and released for commercial production. Asagake is very vigorous and is expected to adopt for the rapid turf creation.

Upland rice varieties have so far been utilized to improve the resistance to rice blast disease of paddy rice varieties. Based on the improvement of DNA analysis on the field resistance gene(s) involved in upland rice, "Owarihatamochi", three QTLs were found on the chromosome 2, 4 and 12 and the function of QTLs are now being analyzed (Fukuoka and Okuno, 1998).

Japanese sweet potato variety, Hichifuku, which is resistant to black and stem rots and has good storage ability, has been used in breeding varieties, including "Hi-Starch" popular in Japan (Nakagahra ***et al.,*** 1998).

We are expecting that many users from various societies will access our homepage of NIAS Genebank. We are now examining all the passport data and evaluation data carefully. The access to PGR through the Internet will be available soon.

Regional and international cooperation

The NIAS Genebank has collaborated with foreign institutions on field survey and collecting of PGR. Recently ***in situ*** conservation has become one of the important issues and our collaboration has focused on ***in situ*** conservation and related research activities.

In situ conservation research of indigenous rice in Vietnam was initiated between the NIAR and the Vietnam Agriculture Research Institute in 1998. Inter- and intra-varietal differences of RAPDs and morphological characters were investigated. Under the MAFF Genebank project, ***in situ*** conservation research activities on legumes and rice were initiated between the NIAR of Japan and the Plant Genetic Resources Centre (PGRC) of Sri Lanka in

2000. In these Projects, Japanese researchers joined the missions for monitoring genetic diversity of wild ***Vigna*** species and wild rice and researchers from the collaborative countries were trained in carrying out DNA analyses such as RAPD for studying genetic diversity at the NIAS.

From 1999, an ***in situ*** conservation project on ***Fagopyrum*** species, sponsored by IPGRI, has been conducted in Nepal for three years and genetic diversity of natural populations of ***Fagopyrum cymosum*** were investigated using RAPDs after the exploration/collecting. From the results of monitoring genetic diversity in populations, the most feasible site for ***in situ*** conservation of the relevant species would be identified.

A bilateral technical cooperation on PGR has been carried out by the Japan International Cooperation Agency (JICA) in Myanmar since 1997. Four long-term experts have been dispatched to transfer techniques on PGR to the Myanmar Seed Bank of the Central Agriculture Research Institute, and several Myanmar researchers have been invited to Japan for training every year. The Third-Country Training on PGR has been organized by the JICA at Plant Genetic Resources Centre (PGRC) of Sri Lanka since 1999 and researchers from several neighbouring countries benefited from this training. An aftercare project on PGR was newly started at the Plant Genetic Resources Institute of Pakistan in 2001 for 2 years in order to promote sustainable PGR activity in the Institute. The NIAS is strongly supporting these JICA PGR activities from technical aspects.

Public awareness activities

By launching the PGR website on the NIAS Homepage in 1997, we already started the public announcement of MAFF Genebank activities on PGR nationally, regionally and internationally, while we published totally 17 volumes of Annual Report of Exploration and Introduction of Plant Genetic Resources and 2 volumes of The Descriptors for Characterization and Evaluation of Plant Genetic Resources (Nagamine and Takeda, 1999). Passport and evaluation data of Japanese accessions can now be accessed on our website, and the data available from other countries will be provided soon. The same kinds of databases of barley, wheat, rice and ***Arabidopsis*** are open to public on the websites of the Okayama University, Yokohama City University, the National Institute of Genetics and Miyagi Education University, respectively (URL: http://www.nig.co.jp).

We conducted two international symposia on PGR in 1999 and 2000 at NIAR and the themes of the symposia were ’Wild Legumes‘ and ’the Integration of Biodiversity and Genome Technology for Crop Breeding‘, respectively. The International Symposium on Cryopreservation was also conducted in 1999 at JIRCAS. The Japanese Society of Breeding will have an open-symposium for public awareness of the importance of PGR in October 2001. These kinds of public awareness activities are now becoming important to enhance the understanding of citizens on the conservation and utilization of PGR in Japan.

National strategy on conservation and use of PGR

After the re-organization into the Independent Administrative Agency, a strong cooperation is needed among institutions conserving PGR under MAFF. Furthermore, we have to develop good collaboration with universities and private sector organizations to exchange information. By distributing PGR, we would like to promote our activity aggressively as a central bank under MAFF in collaboration with sub-banks and also with other friendly organizations in Japan and abroad.

NIAS Genebank has so far been playing an important role of complementary ***ex situ*** conservation for IPGRI designated long-term storage of wheat, barley and other crop species.

Recently we expanded our complementary ***ex situ*** conservation efforts on rice collections conserved at the Governmental University in Japan based on mutual understanding of the importance of its conservation.

New evaluation methods or new ideas on PGR are urgently required for the further utilization of accessions for breeding and other purposes. We need to distribute a lot more collections, which have more reliable genetic traits and cultural information.

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Plant genetic resources in the Democratic People's Republic of Korea

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Introduction

The Democratic People's Republic of Korea (DPR Korea) is located in Korean peninsula of East Asia. Approximately 80% of the territory is mountainous area, particularly in northern and inland areas. The average altitude is 482 m.

Our country is situated in an area that links Asian continent and the Pacific Ocean. As a result, both continental and coastal climatic features exist in the country. The average annual temperature and precipitation are 8-12°C and 1000-1200 mm, respectively, but their distribution pattern is considerably varied depending on the season and locality. The main climatic stresses for agricultural production are severe cold during the winter, drought during the spring, much rain combined with high temperature and strong winds during the summer.

The country is very rich in biodiversity owing to its high diversity in terms of climate and soil. There are about 4200 species of higher plants, including 450 species of industrial plants, 200 medicinal plants, 60 aromatic plants, 200 vegetables and 370 forage species. Particularly, there are 500 species, which can be only found in our country.

Self-sufficiency in food for meeting national demand is one of the important government policies in agriculture. The Government sets forth the policy of giving priority to seed revolution, potato farming and double cropping. Rice, potato, wheat and soybean will be major stable foods in near future and more efforts are being made to develop superior varieties as well as to improve cultural practices.

Approximately, 200 crops including food, vegetable and industrial crops are in cultivation in cooperative farms. For main crops, the effective national seed production system was established, through which breeder's seed, original seed, registered seed and commercial seed are supplied to cooperative farmers.

Plant genetic resources (PGR) work in the country is a multi-disciplinary activity, which includes agricultural, forestry and medicinal plants. At present, national programme for agricultural genetic resources research is coordinated by the Pyongyang Crop Genetic Resources Institute (PCGRI), Academy of Agricultural Sciences, in collaboration with provincial agricultural academies and specialized institutes for rice, maize, etc. PCGRI is mandated for collecting, characterization, evaluation, conservation and utilization of agricultural crops. The institute has a national genebank with capacity of preserving 10 000 accessions.

Overall progress of national plant genetic resources activities

Germplasm collecting

Great emphasis was laid on collecting local germplasm. Several multi-crop germplasm collecting missions were organized, with focus on northern mountainous areas to collect landraces of some important food crops such as potato, wheat, barley and underutilized crops.

IPGRI supported research programmes on adzuki bean and millet also resulted in collecting of 100 accessions of adzuki bean and about 30 of millet, including wild relatives from different areas of the country.

In addition, germplasm from abroad were acquired through scientific exchange programmes and with support from international research centres, governmental and non-governmental organizations. The total collection of crop germplasm has reached 57 000 accessions (Table 1).

PCGRI is planning to increase the number of germplasm collections to about 100 000 accessions in the next couple of years. Priority will be given to collecting local and important food crop germplasm.

Table 1. Status of germplasm collection

Crops	***Accessions***
Rice	7 860
Maize	12 100
Cereals	11 990
Legumes	4 870
Potato	1 150
Industrial crop	1 690
Vegetables	12 000
Others	5 340
Total	**57 000**

Characterization and evaluation

Germplasm characterization and evaluation work was done for 50 000 accessions. Normally 20-45 quantitative and qualitative characters such as yield and yield components, plant height and colours of different plant organs were recorded according to the Descriptor lists published by IPGRI with slight modification. For quantitative characters, the evaluation was usually conducted for 3 years.

Due to lack of facilities and equipment, little work has been done for evaluation of tolerance or resistance to major biotic and abiotic stresses.

Germplasm evaluation work is in progress at germplasm research units of provincial academies in order to identify germplasm adapted to the specific agro-ecological environments and use for specific breeding purposes.

Genetic diversity assessment

Genetic diversity of selected main crops was assessed using some of the simple statistical approaches such as mean, standard deviation, coefficient of variation and more complicated multivariate statistics such as principal component analysis for major quantitative characters. It was found that considerable amount of genetic diversity is available, for example, maturity from less than 90 days to more than 180 days in rice.

It is planned to apply biotechnology to biodiversity study, for instance, PCR and RFLP methods to study genetic relationships of local maize germplasm and to determine main heterotic patterns.

Documentation

PCGRI has established central genetic resources database. At present, all the available passport data are input into computer. Documentation of characterization and evaluation data is going on, but its slow progress due to lack of computer facilities.

PCGRI elaborated a 3-step plan to form national PGR information network. During the first step, the network within institute will be established by linking genebank, 17 crop germplasm research programmes and information laboratory. The second step is to link crop research institutes within the Academy of Agricultural Sciences in capital and provincial agricultural academies. Finally, it is planned to form a full network by linking with other institutes as well as universities working on genetic resources of forestry, medicinal and other plant species.

The national PGR information network will be connected to national network to provide information to agricultural policy makers and users.

Conservation and utilization of crop germplasm

PCGRI hosts a medium-term storage with capacity of preserving about 10 000 accessions under the conditions of temperature controlled at -5°C and relative humidity 50%. Other accessions are conserved at short-term storage at the temperature of 18-22°C, and are regenerated in field every 2-3 years depending on the crop. Research on conservation strategy of vegetatively propagated crops such as potato and sweet potato are under progress using tissue culture.

It was estimated that crop breeders used about 15% of germplasm collection. For some crops like rice, maize, soybean, wheat for which active breeding programmes exist, germplasm are mainly used as breeding material to transfer superior genes to new cultivars. For some of the minor crops, germplasm are mainly used in production for commercial purpose.

Regional and international cooperation

Important projects with International Plant Genetic Resources Institute are as follow:

- Analysis of genetic diversity in the ***Vigna angularis*** complex, 1999-2000.
- PGR documentation training course, August 1999.
- Collecting and evaluation of millet genetic resources, April 2001-March 2002.
- National Workshop on Conservation and Use of PGR, August 2001.

Such cooperative projects have contributed greatly to building the national capacity on PGR research and facilitated collecting and evaluating important local germplasm of traditional crops.

Public awareness activities

- Field days were held twice each year at PCGRI. Participants are researchers, teachers, government officials.
- Had visiting students from agricultural universities.
- Produced various publications of research results on PGR.

National strategy on conservation and use of PGR

Establishment of long-term storage at national genebank

With current storage capacity, the germplasm seed regeneration has to be carried out every two years, which costs a lot of money, labour, and resources and runs the risk of losing genetic integrity. There is an urgent need to set up a long-term storage facility with capacity of 90 000 accessions for safe and efficient conservation of PGR in the country.

Establishment of national germplasm bio-laboratory

Lack of information on resistance or tolerance to important biotic and abiotic stresses is one of the main constraints to the use of PGR. In recent years, crop breeders are seeking hard for the source of resistance to different stresses. Therefore, it is necessary to establish a bio-laboratory for germplasm research in order to reveal genetic diversity and identify valuable genes for important agroeconomic characters of various crops.

Establishment of national information network on PGR

Lack of PGR information system is also one of the reasons for poor utilization of germplasm by breeders and other users. Therefore it is very important to establish national PGR information network to make information of PGR freely available to whoever interested.

Upgrading experimental farm for crop genetic resources research

Poor facility and infrastructure in experimental farm of PCGRI is also one of constraints limiting the progress of germplasm research and activity in the country.

Machines such as tractor, planter and harvester are needed for assisting in fieldwork on germplasm evaluation and reducing the demand for human labour. Seed processing facilities such as dryer, threshing and cleaning machines are required for processing good quality seed for storage as well as for supply to users.

Capacity analysis

Strengths

- Good government policy on PGR.
- Established system of PGR including PCGRI and germplasm units at provincial academies.
- Research staff well educated and experienced.
- Good working relationships among germplasm research organizations, and
- Strong breeding research.

Weaknesses

- Lack of training on advanced PGR technologies.
- Lack of facilities and equipment for PGR research and activity.
- Lack of facilities for PGR documentation and information services.
- Insufficient information in terms of books and publications.

Opportunities

- Strong government support to PGR work.
- Cooperation with IPGRI and other international organizations.
- Bilateral cooperation with other countries.

Threat

- Risk of natural disasters.

Current status of conservation and use of plant genetic resources in the Republic of Korea

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Introduction

The Korean peninsula stretches about 1100 kilometres from north to south, bordered by the Yellow Sea on the west and by the East Sea on the east. The land area of Republic of Korea is 99 800 km^2, covering about 45 percent of the total area of the Korean peninsula.

Annual average temperature shows a great variation from 14°C in the south to 5°C in the north. The annual precipitation ranges from 1400 mm in the south to 400 mm in the northern high land. The climatic conditions are diverse ranging from subtropics in the southern coastal area of the Cheju island to frigid high land zone in the northern mountains. Such a diverse environment makes the country a habitat for diversified flora.

The population of the Republic of Korea in 1999 was about 46.9 million. Farm population stood at 4.2 million in 1999, about 9.0% of the total population. GNP grew, on average, by almost 9% annually during 1963 – 1990, about 7% on per capita basis. Export volumes was increased sharply from around US$1 billion in 1970 to around US$65 billion in 1990. It reached US$132 billion in 1998. However, per capita GNP decreased to US$ 8551 in 1999.

The ecological and botanical status of Korean plant species has not been well documented except for flowering plants. It is estimated that the numbers of higher plants and lower plants in Korea are 4662 and 3609 species, respectively. Korea is relatively small in size, but the flora is very rich in composition with approximately 4000 vascular plant species and contains a number of unique taxa that are endemic to Korea. Six genera and more than 640 plant species are known to be strictly confined to Korean Peninsula. In addition, Korea has many elements of older flora and hence 27 of 56 genera show floristic disjunction between eastern Asia and eastern North America.

The agricultural land is 1899 thousand ha in 1999, about 19% of total landmass of Korea. Paddy fields with constant water condition during growing season make up 60% of the total agricultural land. In the south, except of a small area of winter crops (wheat and barley), the most arable land is used for rice planting, some times double rice planting during a year. It is possible to plant corn, minor grains, vegetables and fruits. The annual average harvest rate of ordinary fields in Korea is only 108%.

Plant genetic resources (PGR) management system

The Rural Development Administration (RDA) plays a major role in planning and supporting the national programme on the conservation and use of crop genetic resources in the country. RDA Genebank (RDAGB) was established in 1988 and it is a main part of National Institute of Agricultural Science and Technology (NIAST) of RDA. The genebank undertakes researches on germplasm collecting, characterization, evaluation, conservation, documentation and use.

The Genetic Resources Council (GRC) and the Germplasm Advisory Committee (GAC) provide advice on developing national strategies for germplasm conservation and use by setting up priorities for collecting missions and providing recommendations for characterization, evaluation and utilization of PGR for the whole country. Evaluation and multiplication of the PGR is invariably done at related research institutions jointly with RDAGB. The seeds multiplied and the data recorded at those institutions are sent to RDAGB for conservation and utilization (Fig 1).

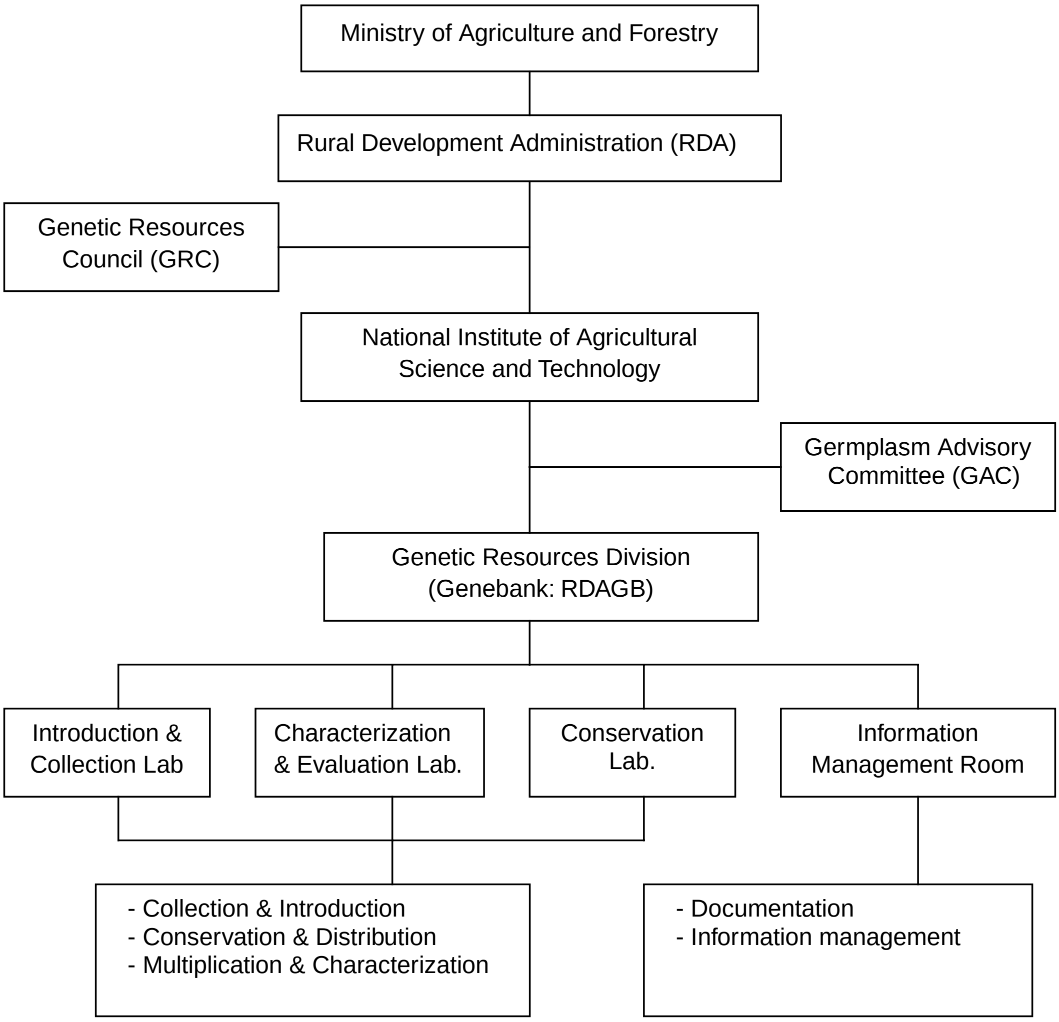

Fig. 1. Organization and function for national genetic resources system in Korea (RDA genebank)

Germplasm collecting

Collecting for landraces has been conducted extensively before the establishment of RDA genebank and up to now. Several collecting missions were organized annually in various parts of Korea and abroad. PGR collecting in 1998 covered western coastal area and western islands of Korea. PGR in southern coastal area, southern island and Jeju island were collected in 1999-2000 (Table 1). Several international collecting missions were also organized by RDA in Russia, Uzbekistan, Thailand, Canada and Germany.

Table 1. Plant germplasm collectings, 1998-2000

Year	Regions collected	No. of accessions	Major crops collected
1998	Western coastal area and islands	1 541	Legumes, oil crops
1999	Southern coastal area	980	Legumes, vegetable, cereals
2000	Southern mountainous area, Cheju island	943	Vegetables, legumes
Total		**3 464**	

Germplasm conservation

RDA conserves 146 154 accessions of germplasm at RDA genebanks (Table 2). RDA seed genebank holds 111 011 accessions of cereal crops, including rice, barley, wheat, soybean and legumes, and miscellaneous crops. There are 13 713 accessions of vegetables and fruit trees, 17 779 accessions of industrial and medicinal plants, 3651 accessions of forage crops and other germplasm which were introduced from other parts of the country or foreign countries. With respect to the vegetatively propagated crop germplasm, there are 41 field genebanks maintaining 11 010 accessions of fruit trees, flowers, vegetables, medicinal plants, tuber crops, shrubs, grasses and other germplasm (Table 3).

Table 2. Germplasm conserved in the RDA genebank

Crops	Number of species	Number of accessions	Ratio (%)
Cereal & legumes	414	111 011	76
Industrial & medicinal plants	258	17 779	12
Vegetables & fruit trees	462	13 713	9
Forage crops & others	643	3 651	3
Total	**1 777**	**146 154**	**100**

Table 3. Vegetatively propagated plant germplasm conserved in the RDA field genebanks

Crops	Number of species	Number of accessions
Fruit trees	164	5 811
Flowers	236	1 245
Vegetables	10	1 461
Others	586	2 423
Total	**996**	**11 010**

Characterization and evaluation

Characterization and evaluation data help researchers to identify desired combinations of traits and meet the requests for appropriate germplasm. Scientists working in RDGB as well as in various crop experiment stations under RDA carried out characterization and evaluation of the stored germplasm. The RDA descriptors (partially modified IPGRI descriptors) were used for recording data during characterization and evaluation germplasm. National project for regeneration and characterization is progressing well with the cooperation of all the institutes under the RDA. The 35 000 accessions were characterized and evaluated for physiological responses, disease and insect resistances, yield traits, and other agronomic characters during 1998-2000 (Table 4).

Table 4. Characterization of germplasm conserved in the RDA genebank during 1998-2000

Year	No. of crops	No. of characterized accessions
1998	28	12 237
1999	30	11 493
2000	31	11 400
Total	**44**	**35 130**

From 2001, regeneration and evaluation activities have been going on under a national mega project at 14 institutes under the RDA. Establishment of core collections for Korean landraces of 6 major crops (rice, barley, soybean, sesame, red pepper and cabbage) is underway.

Passport data of all conserved accessions and characterization data have been computerized on databases. Registration data and management data including distribution, the amount of preserved seed in stock and viability of conserved seeds were managed by computerized system.

Distribution and utilization

The major justification for conservation of PGR, especially in ***ex situ***, is for their utilization in plant improvement programmes. The benefits of using native PGR lie in breeding of cultivars that are adapted to Korean climates and environments, resistant to diseases and superior quality to meet consumer's tastes.

As for the access of PGR, the RDA genebank opts for free-distribution/exchange under appropriate mutually agreed terms. The 102 423 samples have been distributed to public institutes or private researchers during 1996-2000. Among those, 4828 samples were distributed in response to the requests received from foreign institutes (Table 5).

Table 5. Germplasm distribution to users from RDA genebank during 1996-2000

Destination	Samples distributed
Domestic users	97 595
Foreign institutes	4 828
Total	**102 423**

To use the germplasm effectively, more research, human resources and budgets should be allocated so that the breeders can better access to the characterization and evaluation data, along with the germplasm for much needed crop improvement. Detailed evaluation (physiological, ecological, genetic and quantitative traits) and documentation should be carried out through further projects.

International cooperation

RDA is looking forward to enhance international cooperation through joint collecting missions, research and germplasm exchange under the appropriate Memoranda of Understanding (MOU). RDA has dispatched their permanently stationed senior researchers to IPGRI, IRRI, CYMMITY and AVRDC to undertake collaborative research activities on agricultural sciences. Several research projects are being conducted to collect, conserve and characterize PGR jointly with a number of international organizations such as CIP, ICRISAT and ITTA under CGIAR and with foreign institutes in Mongolia, Russia, Germany, Uzbekistan, Philippines, Thailand, Canada, Japan, China, Israel and Ghana.

Future strategies

The RDA genebank has attempted to collect, conserve and utilize PGR for crop improvement and provided research materials to various users. Research infrastructure of PGR is very important to improve and utilize the collections. However, numerous problems are encountered in the conservation and utilization of PGR in Korea. Also, general public awareness and understanding the importance of plant genetic diversity or PGR needs to be urgently improved. For realizing further development of food and agriculture, the RDA genebank will continue to pursue the following:

1. Development of national and international networks to exchange germplasm and related information and carry out research on genetic resources.
2. Development of core collections of native PGR for better utilization.
3. Identification of duplicate accessions and rationalization of collections.
4. Effective utilization of PGR through further evaluation using genetic and biochemical tools.
5. Diversification of germplasm collections through international cooperation.

Plant genetic resources status and progress of activities in Mongolia

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Introduction

Mongolia is a land-locked country and located in Central Asia bordered with the People's Republic of China (PRC) in the South, East and West and Russia in the North. Mongolia covers a total area of 1 566 500 km^2 and is situated at an altitude ranging from 560-4565 m asl, with an average altitude of 1580 m asl. Total population is around 2.4 millions in 2000.

Mongolia is situated between 41.33°N and 52.06°N, has an average annual temperature of -5.3°C to +4.0°C with the lowest temperature recorded so far at –53°C and the highest at 41°C. The vegetation period is from 88-110 days.

The above extreme climatic conditions, including the short growing season, low precipitation and high evapotranspiration, impose overriding constraints on Mongolian agriculture. Particularly, the unseasonable frosts can cause a loss of 10-30% of crop production. Due to its topographic and climate extremes and the large area of vegetation, Mongolia possesses rich diversity of plants.

Integrated and systematic research work on crop genetic resources was started in 1979 when the Plant Genetic Resources Section was established at Plant Science and Agricultural Research Institute (PSARI). Recently the research efforts on plant genetic resources (PGR) in Mongolia were mainly made at PSARI, the East Regional Agricultural Research branch of the Mongolian State University of Agriculture (MSUA), the Altai Agricultural Research Branch of MSUA, the Ulaangom Regional Agricultural Research Branch of PSARI and the Research Institute of Animal Husbandry (RIAH). The overall status and progress of plant genetic resources activities can be observed from the indicators presented in Table 1. MSUA is in charge of overall coordination of nationwide crop germplasm research programmes. The Institute of Botany of Academy of Science (IBAS) has mainly the responsibility for performing national research project for wild species of grasses and berries. Since 1990, Mongolia has actively cooperated with IPGRI for strengthening PGR activities, establishing storage facilities and training personnel for national programme.

Table 1. Indicators of national programme on PGR

Indicators	1991-1995	1996-2000
National programme	-	Yes
Advisory body	Yes	Yes
Convention on Biological diversity	Yes	Yes
Quarantine Regulations	-	Yes
Plant Breeder's Rights	Yes	Yes
Seed Law	-	Yes
Environmental Protection Law	-	Yes
Germplasm Exchange Policy	-	Yes

Plant genetic resources and their distribution

In Mongolia, a total of 6334 species belonging to 1385 genera and 334 families have been found. The vascular plants rank first among different life forms and have 2823 species belonging to 662 genera and 128 families (Table 2).

Table 2. Composition of vascular and lower plants

Classification	Family	Genera	Species
Vascular plants	128	662	2 823
Moss	59	191	445
Lichen	53	175	930
Fungi	28	136	900
Algae	76	221	1 236
Total	**344**	**1 385**	**6 334**

The distribution of different Mongolian plant forms over different ecological zones is varied. While the big trees usually dominate the mountain taiga region, they lose their position in the transitional zones and gradually disappear towards the steppe, desert steppe and desert zones. Shrubs and dwarf shrubs form isolated communities or mixed communities, together with other plant species common in those regions.

Fig 1 shows the proportions of different plant species in Mongolia. Perennial herbaceous plants occupy 72.24% of total plant species, while climbers are only 0.25%.

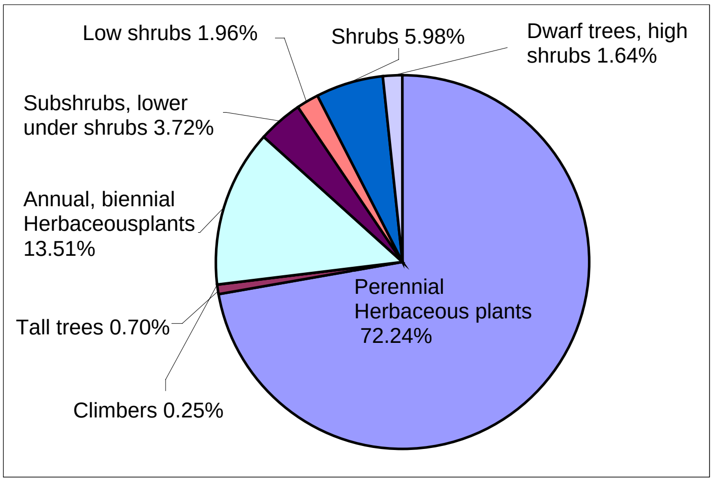

Fig. 1. Composition of plant species in Mongolia

Primitive plant relics and endemic species

More than 100 native plant species have been found in Mongolia including ***Ammopiptanthus mongolicus, Zygophyllum xanthoxylum***, ***Ephedra przewalskii, Reaumuria soongorica, Iljinia regelii, Sympegma regelii, Populus diversifolia, Halimodendron halodendron, Oxytropis grubovii, Caragana tibetica, Caragana jubata, Lancea*** spp**,** ***Abies sibirica, Nymphaea candida*** and ***Nuphar pumilum***.

There are relics from pre-historic deserts, forests, tertiary lakes, savannahs and the Ice Age, in particular. Many plant relics are endemic to Mongolia. There are about 150 endemic vascular and lower plants such as ***Stipa mongolorum, Adonis mongolica, Betula mongolica, Atraphaxis bracteata, Calligonum gobicum, Nanophyton mongolicum, Gymnocarpos przewalskii, Silene mongolica, Potaninia mongolica, Cheesneya mongolica, Astragalus gobicus, Oxytropis ulzij-chutagii*** and ***Artemisia gobica***. The Khangai, Gobi-Altai and Mongolian Altai regions are the most abundant regions in such species.

Useful plants

Mongolia has 845 species of plants used for medicine, over 1000 species for fodder, 173 for food, 64 for industry, 489 for decoration and 195 for other purposes. Also, there are 1150 species rich in vitamins, over 200 useful in fermentation, 281 with high alkaloid content, 231 with flavonoids, 65 with rumarin and 68 with soil restoration properties (Fig 2).

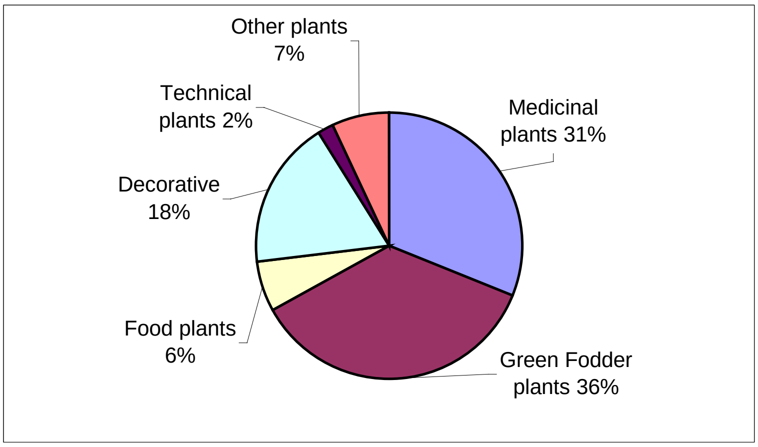

Fig. 2. Species used for different purposes in Mongolia

In this country, 547 species of plants belonging to 190 genera and 53 families are commonly used by bees. Of these species, 23 are woody plants, 72 shrub-like species and 452 grass species.

Endangered and threatened plant species

The subject of conservation, sustainable use and restoration of Mongolian plant species should be considered in the context of plant ecology and biology.

Eighty-six plant species were registered as endangered and threatened in the first edition of the Mongolian Red Book; the number increased to 128 in the second edition (1997). These endangered plants include 75 species used for medicine, 11 for food, 16 for industry, 55 for decoration and 15 species used in the soil erosion control and pest control. Examples are ***Nitraria sibirica, Amygdalus mongolica, Populus diversifolia, Caragana bungei, Artemisia involucrata, Agriophyllum pungens, Elaeagnus moorcroptii, Aves siberica, Gemnocarpus przewalskii, Rhodiola rosea*** and ***Allium oliquum***.

Weeds

There are 438 weedy species belonging to 212 genera and 49 families of which 369 (84.3%) are local species (apophit) and 69 (15.7%) are “newcomers” (antro-pophit). Examples of these species are ***Amaranthus retroflexus, Polygonum convolvulus, Polygonum aviculare, Fagopyrum tataricum, Avena fatua, Brassica campestris, Brassica juncea, Setaria viridis, Setaria glauca*** and ***Xanthium siberica*** that have colonized and damaged crop land. Mongolian weedy species are characterized by adaptation to severe climatic conditions and strong resistance against drought and strong winds.

Conservation of plant diversity

Activities on conservation of plant diversity are being carried out under the "Mongolian Law on Natural Plants", the "Mongolian Law on Forests", and National Biodiversity Action Plan, National Action Plan for Special Protected Areas, Governmental Guidelines on Ecology, National Security and other relevant documents with aim to conserve, restore and sustainable use of plant species in Mongolia.

More than 20 projects are currently under implementation dealing with the population structure, life form, distribution, diversity, breeding, anatomy, physiology, embryology, palaeontology, ecology and biology. These projects have identified the distribution of 130 plant species.

The same studies show that there were wild berry species growing in the Khentii, Khangai and Khubsgul mountains. These wild berry species include, for example, ***Ribes nigrum, Ribes altissimum, Grossularia acicularis, Rosa acicularis, Vaccunium myrtillus, Vaccinium uliginosum*** and ***Rhodococcum vitis-idaea***. In addition, field tests demonstrated that the mean yield of these berries could be around 223.6 kg ha^{-1}. In Mongolia, 85 species in 54 genera belonging to 26 families of ornamental plants have been grown on trial basis and 45 species belonging to 35 genera and 17 families were noted to be popularly grown.

Germplasm collecting

Mongolia is located near the Chinese and central Asian centres of origin of principal cultivated plants. It is well known that Mongolia has remained as an agricultural society for several hundreds of years. The latest collecting missions were undertaken jointly by Mongolia and Republic of Korea, USA and China. International cooperation between Republic of Korea and Mongolia in collecting and evaluating of crops and medicinal plants was undertaken during 1996-1998 (Bayarsukh, 1998; Bayarsukh ***et al***., 1998).

USA sponsored 3 international missions for collecting fodder grasses and legumes in Altai, Khangai and Gobi desert regions. From 1990 - 2000, nine collecting missions were carried out in all the regions of Mongolia with different collecting targets (Tsogoo and Batsukh, 2000) (Table 3).

Conservation of germplasm collections

The National Genebank was established in 2000 at PSARI with technical assistance of FAO, IPGRI and Republic of Korea. The total number of accessions preserved at PSARI and related institutes is increasing rapidly due to several collecting missions carried out during the last three years as well as due to introduction activities. Up to now, PSARI has held 18 765 accessions of 50 crops and 400 accessions of local wheat in medium-term storage (Table 4). A total of 192 accessions of 113 species in 52 genera are maintained in field genebanks.

The conservation facilities were also improved at RIAH in 2000 under the USA-Mongolian collaborative project. Now RIAH has 1923 accessions of 319 species, 180 genera, 46 families for grasses and legumes.

Table 3. International collecting missions carried out in Mongolia during 1990-2000

Year	Area	Participants	Collected materials
1990	Western Mongolia and Selenge province	Mongolia, Russia, Czech Republic	Cereals, vegetables, legumes, wild relatives 200 accessions
1993	Central and eastern Mongolia, 4 provinces	Mongolia, China	Fodder grasses and legumes 24 species 100 accessions
1994	Central and Eastern Mongolia, 6 provinces	Mongolia, USA	Fodder grasses and legumes 200 accessions
1996	High mountains and Gobi desert region, 7 provinces	Mongolia, Korea	Grasses, wild relatives 170 species 387 accessions
1996	Eastern and Central Mongolia, 6 provinces	Mongolia, Korea	Cereals, legumes, vegetables, onion, grasses, wild relatives 74 species
1997	Western Mongolia and Central regions, 4 provinces	Mongolia, Korea	Medical plants, wild relatives, food crops 110 genus 220 species
1998	Central, High mountain regions 8 provinces 3000 km	Mongolia, Korea	Food crops, medicinal plants and wild relatives 24 Genus 72 species
1998	Central, High mountain region, 8 provinces	Mongolia, USA	Fodder crops, grasses legumes
2000	Gobi, desert region, 4 provinces	Mongolia, Korea	***Allium*** species, grass legumes

Table 4. Present status of PGR preservation in Mongolia

Institute name	No. of accessions	Crop category	Location	Type of preservation
Plant Science and Agricultural Research Institute	18 765	Cereals, vegetables, industrial, oil crops, wild relatives, fruit tree	Darkhan	Short-term Medium-term
Research Institute of Animal Husbandry	1 923	Fodder grasses. Legume crops	Ulaanbaatar	Short-term
Altai Regional Research Branch (ARRB) of MSUA	289	Vegetables, cereals	Khovd	Short-term
Eastern Regional Research Branch (ERRB) of MSUA	273	Oil crops, industrial crops	Choilbalsan	Short-term
Ulaangom Research Branch (URB) of MSUA	513	Cereals	Ulaangom	Short-term
High Mountain Regional Research Branch (HMRRB) of RIAH	126	Grasses, legumes	Arkhangai	Short-term

Evaluation activities

PGR evaluation has two major purposes:

1. Essential characterization by the descriptors for each crop species.
2. Special characterization by germplasm users, breeders, which is very detailed or limited according to the needs of specific breeding programmes.

There are 4 research institutions involved in germplasm characterization and evaluation with focus on morphological characters, agronomic traits, disease and drought resistance, etc. (Table 5). Through the evaluation, PSARI has selected and introduced to farmers 9 varieties of 8 crops, and RIAH screened out 18 lines of 8 species and associated improved seed multiplication technology.

Table 5. Germplasm accessions characterized during 1996-2000

Institutions	No. of samples	Traits
PSARI	6 233	Morphological characters, agronomic traits, disease and drought resistance
RIAH	621	Botanical evaluation, morphological characters
ERRB	90	Quality analysis, agronomic traits
ARRB	152	Agronomic traits, morphological characters

Germplasm exchange and documentation

With the support of IPGRI, PSARI started to develop crop characterization and evaluation database management system in 1998. At present the relevant data of over 7200 accessions stored in Genebank has been stored in Genebank Management System (GMS).

During 1996-2000, the passport data of 8765 accessions stored in PSARI genebank were re-consolidated and computerized (Table 6).

Table 6. Accessions with new passport data

Crop	1996	1997	1998	1999	2000	Total
Wheat	1 949	631	-	1 611	2 328	6 519
Barley	-	1 355	-	3 861	-	5 216
Oats	1 187	-	-	-	149	1 336
Other cereals	360	256	581	-	86	1 283
Oil technical	-	78	325	-	-	403
Annual legumes	-	-	496	127	83	706
Fodder	-	-	-	357	-	357
Vegetables and potato	-	337	2 608	-	-	2 945
Total	**3 496**	**2 657**	**4 010**	**5 956**	**2 646**	**18 765**

From 1996-2000, 2712 accessions of various crops were introduced from Korea, Czech Rep., Russia, USA, Japan, China, India, Germany, Canada, Italy, Norway and other countries (Table 7).

Table 7. Number of introduced accessions

Crop	1996	1997	1998	1999	2000	Total
Cereals	30	64	394	1 334	6	1 828
Vegetables	108	112	42	112	12	386
Others	95	6	32	354	11	498
Total	**233**	**182**	**468**	**1 800**	**29**	**2 712**

During 1996-2000, 5775 accessions were distributed to foreign countries (Table 8) and 2278 accessions to national institutions for breeding programmes of cereals, vegetables, potato and other crops.

Table 8. Number of distributed accessions

Crop	1996	1997	1998	1999	2000	Total
Cereals	1 748	1 800	684	200	40	4 472
Vegetables	77	120	438	100	20	755
Other	86	356	16	90	-	548
Total	**1 911**	**2 276**	**1 138**	**390**	**60**	**5 775**

International collaboration

Mongolia has active collaboration with countries in East Asian and Russia, USA, Germany, and Canada. During 1996-2000, 5 collection missions carried out jointly with Republic of Korea and 3 with USA under bilateral agreements. During 1996-2000, 2712 accessions introduced from several countries, of which 60% from Republic of Korea.

In collaboration with IPGRI, we have computerized data generated from 7200 accessions from plant exploration and field evaluation by using GMS software.

During 1998-2000, 6 Mongolian scientists have received short-term training in different disciplines of PGR in Malaysia, Netherlands, USA and Germany through either IPGRI or bilateral support. An international conference was organized jointly with China and Russia on biodiversity and plant genetic resources. For developing the science on genetic resources in Mongolia there is a need for more personnel training on specific skills.

Mongolian strategy on conservation and use of PGR

During 1996-2000, progress has been made in strengthening the research capability. With technical assistance of FAO and IPGRI, the National Genebank was established at PSARI, Darkhan. With support of USA, the PGR conservation facilities were established at RIAH, Ulaanbaatar. Herbarium specimens collected for wild species are kept in the Institute of Botany, which holds 100 000 floristic samples. But Mongolia still lacks technical capability in many areas and facilities for PGR activities are poor. The main objectives of the future PGR activity for Mongolia will be:

- Enhanced characterization and evaluation of economically useful plants, including medicinal, essential oil, fodder and aromatic plants.
- Introduction of new varieties of cereals, fodder and less utilized crops for crop improvement programmes and sustainable livestock development.
- Development of documentation system and database of PGR at regional research organizations.

- Establishment of sub-genebank at RIAH and ARRB of MSUA under fully functional genebank at PSARI, Darkhan.
- Development of collaborative activities with regional countries on germplasm exchange, training of national research staff and collecting of PGR.
- Development and implementation of national research projects, based on better coordination and agreements between local institutions.

Capacity analysis

Strengths and opportunities

- Plant diversity protection measures have been guaranteed under the "Mongolian land on National Plants", the "Mongolian law on Forests, the Mongolia land on Seeds and varieties, and National biodiversity Action Plan for special protected areas.
- In 2001, the state started the new National Research Projects on crop genetic resources (PSARI, Darkhan, Altai Regional Branch, MSUA, Agrobiological School of MSUA), on PGR of fodder crops and grasses (RIAH) and on PGR of medicinal and technical plants (MSUA) in 2001.
- MSUA offers BSc degree programme on PGR for two semesters.
- Increasing involvement of international, nongovernmental agencies in activities related to PGR for food security and sustainable agriculture.

Weaknesses and threats

- Increasing number of species which were registered as endangered and threatened.
- Increasing number of weeds which colonize and damage cropland in central and northern agricultural areas.
- Inadequate laboratory facilities for research on PGR.
- Insufficient trained staff in regional institutions and stations due to economical situation.
- Lack of sufficient documentation and cataloguing capacity and facilities.
- Lack of components of basic researches on PGR.
- Inadequate exchange of germplasm between countries in the region (either through bilateral agreements and mutually agreed terms).
- Need for more regional cooperative collecting missions, for example, in bordering area between Mongolia and China, where special germplasm might exist due to its status of desertification.

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Regional network for conservation and use of plant genetic resources in East Asia

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Introduction

East Asia is an important source of genetic diversity of many of the world's major crops. The region encompasses the East Asia Centre of origin as identified by Vavilov, and more or less with Zeven and Zhukovsky's Chinese-Japanese area which is one of the mega centres of cultivated plant diversity (Zeven and Zhukovsky, 1975). This centre is origin/diversity for following crops: proso millet, foxtail millet, naked oat, buckwheat, japanica rice, Chinese cabbage, radish, Chinese yam, soybean, adzuki bean, rhubarb; orange, litchi, apricot, peach, jujube, kiwi fruit; and ginseng, bamboo, camphor, mulberry, tea and tung (***Aleurites*** sp.). In addition, the Chinese-Japanese region is also an important secondary centre of diversity for some other crops: barley, sorghum, maize, wheat, taro, sesame, melon, cucumber, eggplant and ***Brassica juncea*** (vegetable, oilseeds and forage). Therefore, many crop progenitor species and great number of landraces can be found in the East Asia region. Also, rich variability occurs in wild relatives of crop diversity in East Asia.

IPGRI Office for East Asia coordinates plant genetic resources (PGR) activities in five countries, namely China, Japan, DPR Korea, R. Korea and Mongolia. These countries greatly vary in size, climate, agroecosystems and crop diversity. China has diverse geomorphologic and climatic types. It is located mostly in the North Temperate Zone and Subtropical Zone. However, the climate in the highest mountain area is very frigid. Climate in Mongolia is typical continental and frigid. One-third of the land is the Gobi Desert. Japan is an island country with temperate and humid climate. Korean Peninsula is mountainous and hilly. Distribution and extent of crop diversity varies accordingly through the length and breadth of the whole terrain in East Asia. Agriculture plays an important role in national economies in this region. Although East Asia has long history of crop cultivation, it faces the problem of high population pressure. This region only encompasses five countries, however, it has the largest population in the world. It also faces problems of rapid genetic erosion due to deforestation, changing land use and climate factors. Thus, East Asia faces great challenges and opportunities for natural resource management to meet human needs. Different CG Centres are working in this context with the mandate to provide food security, alleviate poverty and protect environment.

In order to achieve these objectives with focus on conservation and effective use of PGR, the IPGRI Office has been collaborating with national programmes in the countries of East Asia to promote PGR activities in the region in the form of Regional Network for Conservation and Utilization of Plant Genetic Resources in East Asia (EA-PGR).

Establishment of EA-PGR

Regional Network for Conservation and Utilization of Plant Genetic Resources in East Asia (EA-PGR) was established in 1991. The members include China, Japan, Republic of Korea, Democratic People's Republic of Korea and Mongolia. The purpose of the network is to improve conservation and use of PGR through promoting documentation in national programmes, sharing PGR information and germplasm, training and advice to strengthening national programmes and implementing collaborative activities. As agreed by the member countries IPGRI Office for East Asia is acting as the interim Secretariat.

Goal

To improve conservation and use of the region's plant genetic resources through information exchange and collaborative activities that are of common interest to member countries.

Objectives

- Promote documentation systems in national PGR programmes
- Share PGR and information among member countries
- Strengthen national programmes on PGR by providing advice and training opportunities
- Coordinate research activities and avoid duplication efforts
- Implement a cooperative programme with common interests
- Improve conservation and use on PGR in the region

History

The first meeting

The first meeting, IBPGR Workshop on Underutilized Crop Genetic Resources of East Asia, held in 1991 in Beijing, China with special project funding from the government of Japan to IBPGR. Information on national programmes for PGR in member countries was exchanged. Common priority on underutilized crops were identified, e.g. buckwheat, small fruit trees and millets (Zhou, 1992).

The second meeting

The second meeting was held in the Chinese Academy of Agricultural Science (CAAS), Beijing, China on 23-25 September 1994. The recommendations of the meeting stressed on safe conservation and effective use of plant genetic resources in the region. At this meeting, participants strongly suggested forming a network for East Asia named the Regional Network for Conservation and Utilization of Plant Genetic Resources in East Asia (EA-PGR) (Zhou ***et al.***, 1995).

The third meeting

The third meeting was held in Suwon, Republic of Korea in 1998 to assess the progress of activities of the Network and to identify priority areas and species for developing cooperation among the member countries. The outcome of the meeting recommended priorities in networking and information exchange, ***in situ*** management and genetic diversity study (Zhou ***et al.,*** 1999).

Significant progress has been made between the last meeting and the present one, which will be reviewed and plans will be made for the future. The progress made during the last 2-3 years is presented here briefly.

IPGRI's response: programmes and activities

National programmes are the foundation of plant genetic resources work worldwide. IPGRI's work with national programmes takes a variety of forms, IPGRI-APO-based project activity on national programme support aims to strengthen national capabilities through a number of activities: staff visits and correspondence to assess status and provide advice; organizing national workshop; stronger regional collaboration; sub-regional meetings and networking for sustained collaboration among neighbouring countries; and emergency collecting when warranted.

Emergency collecting and evaluation

In its first decade, IPGRI (then IBPGR) focused on collecting threatened germplasm. The priorities for action on PGR have been expanded and activities on conservation and utilization have been initiated on a very broad range. Now IPGRI does not support germplasm collecting unless it has been given to high priority by national programme due to serious threat of genetic erosion or it is part of a genetic diversity study. During the past ten years IPGRI has supported collecting missions in China, Japan, Mongolia, DPR Korea and R. Korea, that were related to either genetic erosion or genetic diversity studies (Table 1). As a result, new germplasm have been added to the national genebanks. During 1986-1994, Chinese collecting missions with support from IPGRI collected 4321 samples in the country, including genetic resource in triticae, safflower, lotus and fewflower wildrice (***Zizania caduciflora***) and ***Malus*** spp. (Zhou, 1995). A collecting mission in Pakistan, sponsored by Japan, in collaboration with Plant Genetic Resources Programme of the Pakistan Agricultural Research Council, collected 1119 samples (> 50 species) during 1989-1991. Rice, pearl millet, sorghum, minor millet, mungbean constituted a major part of the collection (NIAR, 1992). Crop Experimental Station and Genebank in Rural Development Administration carried out collecting food legume genetic resources in R. Korea. A total of 260 samples of ***Glycine max, Glycine soja, Vigna unguiculata, V. vexillata, V. radiata*** and ***V. angularis*** were collected (Zhou, 1995). IPGRI also supported Mongolian collecting mission in 1993-1994. A total of 300 samples of food legumes, forage crops were collected. In 1995, IPGRI supported the Pyongyang Crop Genetic Resources Institute to collect genetic resource of food crops and legumes, which were eroding fast and 251 accessions of 24 crops were collected. All these collecting missions have resulted in securing valuable germplasm.

Table 1. Collecting crop genetic resources in East Asia

Crop	Year	Samples collected	Institute
Triticae	1986	2 764	ICGR and SWRI, China
Safflower	1990	48	BBG-CAS, China
Lotus	1992-1994	43	AVRC, China
Wild rice	1992-1994	26	AVRC, China
Malus	1993-1994	650	SAU, China
Food crop	1989-1991	1 119	NIAR, Japan
Food legume	1992	260	CES and Genebank, R. Korea
Forage crops	1993-1994	300	PSARI and AHI, Mongolia
Food crops and legumes	1995	251	PCGRI, DPR Korea

Characterization, evaluation and documentation

Table 2 shows the results of germplasm characterization and evaluation carried out in East Asia countries. Characterization and evaluation of safflower germplasm collections was supported by IPGRI and implemented by the Beijing Botanical Garden, Institute of Botany, Chinese Academy of Sciences. About 1545 accessions from 49 countries and 465 from China were characterized for 50 characters in 1990. In 1991, 300 accessions of Chinese buckwheat were characterized for 16 agronomic characters. Safflower characterization data were analysed and results were published in a book “Characterization and Evaluation of Safflower Germplasm” (Li ***et al.,*** 1993). Evaluation and identification of soybean germplasm for N_2 fixation in south China by the Oil Crop Research Institute, CAAS was supported. Total of 200 accessions were evaluated for agronomic, phonological and symbiotic characters.

Collecting and characterization of millets is being carried out in Mongolia and DPR Korea this year. IPGRI designated Rural Development Administration (RDA) genebank as sesame world collection centre in 1991, which at present holds about 7530 accessions (including 4540 landraces) of sesame germplasm for long-term conservation. IPGRI-supported project on multiplication and evaluation of world sesame accessions was implemented by RDA genebank during 1994-1996 in which 1000 accessions were multiplied and 577 accessions were evaluated at Suwon, Korea. The characterization data of sesame world collection in RDA are available at RDA genebank and IPGRI Office for East Asia. Adaptability of some genetic resources of sesame in South and East Asia was conducted in R. Korea, in connection with India, in 1994-1996.

Development of core collection is in line with priority actions noted by the Global Plan of Action (GPA) to enhance the utilization of PGR (FAO, 1996). In order to link conservation and use of genetic resources, IPGRI supported work on developing core collection in China during 1995-1997 and R. Korea during 2000-2001. The sesame collections in China were characterized by the Oil Crops Research Institute (OCRI) of CAAS, based on multivariate analysis of 14 characters. Using Ward's analysis minimum variance technique within each group, a preliminary pre-core consisting of 884 accessions was selected on the basis of proportional representation from each cluster. By growing out the pre-core materials in the field to confirm their representativeness, a final core of 453 accessions was established. The verification and validation of pre-selected and final core collection were conducted. Analysis of five isozymes, esterase (EST), amylase (AMY), peroxidase (PER), malate dehydrogenates (MDH) and 6-phosphogluconate dehydrogenates (6-PGDH) was also used. The results showed esterase is suitable isozyme for analyzing sesame genetic diversity. The esterase zymogram characteristics of pre-selected core significantly reflected that of the reserve collection (Zhang ***et al.,*** 1998; Zhang ***et al.,*** 2000). The development of core collection of sesame by the Crop Experiment Station R. Korea is being supported.

IPGRI facilitated a Japanese complementary-funded programme on joint characterization and evaluation of Nepalese plant germplasm. Joint evaluation of Nepalese rice germplasm by scientists from Nepal and Japan was carried out at the National Institute of Agrobiological Resources (NIAR), Tsukuba during 1996-1997. Through analyses of seed storage and wax proteins, rice landraces of Nepal were classified. In addition, RAPD analysis was used to study genetic diversity of rice germplasm of Nepal.

Table 2. Characterization and evaluation of germplasm in East Asia

Crop	Year	Activity	Accessions	Characters/ Descriptors	Institutes
Safflower	1990	Agronomic characterization	2010	50	BBG, China
Buckwheat	1991	Agronomic characterization	300	16	ICGR-CAAS, China
Soybean	1991	Identification	200	32	OCRI-CAAS, China
Sesame	1995	Multiplication/ Characterization	1000/577		Genebank, RDA, R. Korea
Sesame	1994-1996	Sesame core collection	884	14	OCRI-CAAS, China
Sesame	1995-1997	Sesame core collection	3		Genebank RDA, R. Korea
Safflower	2001	Agronomic characterization	30		XAAS, China

IPGRI supported the preparation and publication of bibliography and directory of buckwheat germplasm collections in 1996 (Zhou and Arora, 1996; Zhou and Zhang, 1996). Monographs on mango and citrus have been prepared and are under the process of editing and publication. The status of buckwheat genetic resource in Asia was surveyed in East Asia with emphasis on China. The complied status report of buckwheat genetic resource in Asia including Nepal and India was distributed. IPGRI published Safflower germplasm collection directory in 1999 (Zhang and Johnson, 1999). Electronic catalogue of 2010 accessions of safflower are available both in web site and electronic format.

Information documentation and management

A data interchange protocol (DIP) was proposed at the East Asia Coordinator Meeting held in Beijing, 1994. IPGRI-APO developed DIP for use in setting up national network information system that could lead to regional and international information exchange. With IPGRI support, the DIPVIEW software was developed and tested at CAAS, China, 1995 and necessary changes to format. In 1996, IPGRI held a DIP consultation meeting in Beijing, where documentation staff from national programmes of China, Japan, DPR Korea, R. Korea, Mongolia and other countries in the APO region as well as IPGRI staff attended the meeting. At the meeting, the DIP format was finalized. Documentation training course was held in Mongolia and DPR Korea to improve the information management.

Conservation

IPGRI supports activities relating to the development of complementary conservation strategies involving ***in situ*** and ***ex situ*** approaches. The major activities include ***ex situ*** conservation of assessed material in the genebank, base/active collections, field genebanks and ***in vitro*** conservation and cryopreservation. IPGRI also provides guidelines for seed conservation aspects and technical/scientific advice and assistance. IPGRI also provided facilities for improving conservation conditions. IPGRI supported groundbreaking research to improve conservation technology in the region. These include ultradry seed storage (Chen ***et al***., 1990; Chen ***et al***., 1997), development of ***in*** vitro conservation of citrus species, and cryopreservation of temperate fruits like apple, pear, grape and kiwi (Zhao ***et al***., 1999a; Zhao ***et al***., 1999b; Wu ***et al***., 1998; Wu ***et al.,*** 1999) and cryopreservation of mango. Feasibility study on buckwheat ***in situ*** conservation on farm was carried out in China (Zhao ***et al***., 1998). Participatory approaches to PGR conservation and use in China are being carried out by the Institute of Crop Germplasm Resources, Yunnan Academy of Agricultural Sciences. This project is providing information on farmer decision-making process that influences ***in situ*** conservation of agro-biodiversity and helping to strengthen capacity of national agricultural research centres for planning and implementation of on-farm management of agro-biodiversity.

Human resources development

Training is a key component of IPGRI's efforts to assist national programmes. IPGRI has organized short training course in documentation, conservation of vegetatively propagated crops, seed genebank management and tropical fruits. National programme staff from each country of East Asia attended these training courses held in the APO region (Table 3).

IPGRI-China Training Course on conservation, characterization and documentation of soybean genetic resources was held at Gong Zhu Ling in September 1990, in collaboration with Soybean Institute of Jilin Academy of Agricultural Sciences. Forty young scientists and technicians from China benefited from the course. IPGRI-Pyongyang training course on conservation and utilization of PGR was held in Pyongyang, DPR Korea in September 1992 in collaboration with Pyongyang Crop Genetic Resources Institute, DPR Korea. Forty Korean and three Mongolian scientists and technicians attended the course.

National training course on GMS software in documenting and managing PGR was taken place in Ulaanbaatar, Mongolia, 25-30 June 1997 and 17 participants attended the course. The GMS development has enabled Mongolian genebank to concentrate on documenting PGR conservation activities. National training course on documentation in DPR Korea was also run in Pyongyang in 1999.

A training course cum workshop on bamboo genetic resources was held under INBAR-IPGRI collaboration programme in Kunming and Xishuangbanna, Yunnan, China, May 10-17, 1998. The main reason for organizing this meeting in Yunnan was to explore the different bamboo species that occurred in Yunnan and to benefit from studying the large number of bamboo species maintained as ***ex situ*** conservation in the well-known Xishuangbanna botanical garden. Participants form 12 Asia countries, including both junior and senior scientists and some recognized experts in the field of bamboo research attended the course and workshop. Suggestions for priority of research on bamboo were summarized at the workshop, including 3-level-biodiversity conservation of bamboo, genetic enhancement, ethnobotany and ethnobiology studies and documentation of indigenous knowledge, assessing rare and threatened taxa and emphasis on ***ex situ*** conservation and promoting ***in situ*** conservation.

Table 3. Training course organized in East Asia

Course	Dates	Location	Participants
IBPGR-China training course on conservation, characterization and documentation of soybean genetic resources	Sept. 1990	Gong Zhuling, China	40
IBPGR-Pyongyang training course on conservation and use in DPR Korea	2-14 Sept. 1992	Pyongyang, DPR Korea	30
National training course on GMS software in Mongolia	25-30 Jul. 1997	Ulaanbaatar, Mongolia	17
Regional training course on Bamboo	10-17 May 1998	Kunming and Xishuangbanna, China	15
Regional training course on diversity study	14-17 Nov. 1998	Hainan, China	19
National training course on documentation in DPR Korea	20-27 Aug. 1999	Pyongyang, DPR Korea	23

Promoting PGR awareness

Various workshops and conferences were organized in East Asia to promote the public awareness on conservation and use of plant genetic resources (Table 4). National PGR Workshops were organized in Mongolia and China to assess national PGR needs and perspectives and to develop national conservation strategies. IPGRI supported the first Mongolian National PGR Workshop, 26-29 September 1995, Ulaanbaatar, Mongolia. Thirty scientists and technicians from different institutes, ministries and universities attended the workshop. Through this workshop, information of collecting, conservation and use of various crops in Mongolia was exchanged; needs and priorities for Mongolian national programme were discussed; recommendations on collecting indigenous materials, selecting materials collected for different agroecological conditions of Mongolia were put forward. The need for institutional enhancements was emphasized, resulting in the change of National Board for Plant Genetic Resources into Mongolian National Coordinating Centre on PGR. The national PGR work now is coordinated by the Centre (IPGRI and Mongolian National Board of PGR, 1995). In 1999, a China national workshop was supported by IPGRI. It was the first time to bring scientists working in agricultural, forestry and medicinal sectors together to discuss a medium term strategy on conservation and use of national PGR, made a suggestion for immediate development strategy and approaches of national PGR programmes in the future according to the key problems. Recommendations on different aspects of PGR (collecting, conservation, utilization, basic and strategic research, capacity building, polices and management as well as financial support) were developed and submitted to the related authorities for consideration (Gao ***et al***., 2001). The proceedings of these workshops were published and distributed to the participants and other users. National workshop of DPR Korea, supported by IPGRI, will be held in Pyongyang, 20-22 August 2001.

Crop specific regional and international workshops on buckwheat, safflower, horticultural crops, and seed sciences and technology were organized (IBPGR, 1992; Fu and Khan, 1992; Lin ***et al***., 1992; Li ***et al***., 1993). The details of the workshops/conferences organized in the region are given in Table 4. The deliberations during these workshops helped in creating PGR awareness amongst the policy makers and planners. During these workshops, priorities at national level got crystallized better and scientifically/technically sound proposals emerged for future implementation.

Table 4. Workshop and conferences organized/supported by IPGRI

Dates	Workshop/Conference	Location	Status
11-15 Mar. 1990	International conference on seed science and technology	Hangzhou, Ching	International
25-26 Apr. 1991	IBPGR workshop on less utilized crop genetic resources of East Asia	Beijing, China	Regional
26 Feb.-1 Mar. 1991	Asian sweet potato germplasm network meeting	Guangzhou, China	Regional
18-20 Sept. 1991	IBPGR workshop on buckwheat genetic resources in East Asia	Tsukuba, Japan	Regional
20-26 Aug. 1992	Fifth international symposium on buckwheat	Taiyuan, China	International
14-18 Jul. 1993	The third international conference on safflower	Beijing, China	International
26-29 Sept. 1995	Mongolian national workshop	Ulaanbaatar, Mongolia	National
12-16 May 1997	2nd international conference on seed science and technology	Guangzhou, China	International
10-14 Aug. 1998	18th international congress of genetics	Beijing, China	International
25-28 Oct. 1999	National workshop on conservation and use of PGR in China	Beijing, China	National
20-22 Aug. 2001	National workshop on conservation and use of PGR in DPR Korea	Pyongyang, DPR Korea	National

Developing improved technologies and information dissemination

Improved technologies

Developing and promoting improved strategies and technologies for PGR conservation and use is one of the important objectives of IPGRI. The following important studies are currently going on with IPGRI support in East Asian countries:

- Genetic diversity and feasibility study of on-farm conservation in buckwheat in China.
- Studies on the ecological adaptability of safflower germplasm in China.
- Collecting and characterization of millet genetic resource in Mongolia.
- Collecting, characterization and conservation of millet germplasm in DPR Korea.
- Studies on regeneration methods for germplasm seeds in genebank.
- Ultradry seed storage research and optimizing seed water contents to improve longevity in ***ex situ*** genebank in China in collaboration with USA and ICRISAT.
- Developing cryopreservation techniques for vegetatively propagated (temperate fruit trees) and recalcitrant seed species (Mango) in China.
- Indigenous classification of bamboos in China.
- Establishment of sesame core collection in R. Korea.
- Joint research on genetic diversity in ***Vigna angularis*** complex and related species in Japan, R. Korea, China and DPR Korea.
- Study on dehydration damage and repair mechanisms in axes of recalcitrant and imbibed orthodox seeds in China.
- Research on freeze-drying of seeds in China.
- Study of biodiversity of indigenous vegetables in China.
- Participatory approaches to PGR conservation and use in Yunnan of China.

Information dissemination

The East Asia office distributes IPGRI publications in the region which include: IPGRI-FAO Plant Genetic Resources Newsletter; Annual Report; Geneflow; Workshop/Working group proceedings; crop networks proceedings; crop descriptors; and PGR special publications/Policy issue papers. The IPGRI-APO Regional Newsletter in Chinese version is regularly brought out from East Asia office (3 issues in a year) and has a mailing list of over 700. On the whole, the office also provides and coordinates information service on all aspects of PGR as per queries received.

Forest genetic resources (FGR) programme

All the work done by IPGRI is not just on crops; it has a strong programme on forest genetic resources as well and is working with national programmes to develop and refine technologies that are needed for sustainable conservation and use of FGR. During 1994-1995, IPGRI collaborated with and supported the Research Institute of Tropical Forestry, Chinese Academy of Forestry (CAF), Guangzhou and Subtropical Forestry Research Institute, Fuyang, Zhejiang in carrying out the herbarium survey to determine the distribution of certain rattan and bamboo species in China. This collaboration has helped to obtain benchmark information on the distribution of bamboo and rattan in China, on which further ecogeographic work currently under way is based. During 1996-1997, IPGRI/INBAR supported the Subtropical Research Institute of Forestry, CAF, Guangzhou in the evaluation of ***ex situ*** conservation and ***in situ*** conservation of rattan germplasm in China. In 1996, IPGRI supported a training course on bamboo conducted by Professor Fu Mao Yi and sponsored five participants from China. In 1998, an international training course on bamboo genetic resources conservation and use was conducted in Kunming, China. These efforts will further enhance the human resources available to carry out work on bamboo and rattan conservation improvement and use.

Future concerns

Among the objectives set up for this current meeting the important ones are to identify new areas for possible collaboration, and to discuss and develop an action plan for next 2-3 years. In order to achieve this goal and strengthen EA-PGR network some future concerns are:

EA-PGR network development

Enhancement in the operation of the EA-PGR network is needed so that it can truly function as a means of promoting cooperation among member countries in enhancing PGR conservation and use on a sustainable basis. Based on analysis of current EA-PGR network operation in East Asia region with focus on PGR management several areas need to be looked at in the future.

Resource generation

Develop more effective resource generation strategies for subregional networks so that sufficient resources will be available for pursuing agreed joint activities. This could be in the form of proposal development with the collaboration of members and coordinated by the secretariat, encouraging resource commitments by members and effective networking with funding agencies.

Policy initiatives

National and international developments and debates increasingly affect PGR work. A number of recent developments have taken place that requires countries to take a fresh look at conservation and use of PGR. These include the Convention on Biological Diversity, Agenda 21, World Food Summit, and Global Plan of Action for PGR conservation. Therefore, at national level, governments are placing growing emphasis on sovereignty over the resources within their borders. At the international level, the major new agreements are being negotiated or have come into force covering access to germplasm and the sharing of benefit resulting from their use. Access to PGR and benefit sharing are two important issues and would be important topics for EA-PGR. Regulations and rules of germplasm management including exchange of germplasm need to be developed including the institutional framework required for these exchanges.

Challenges beyond the International Undertaking

The Food and Agriculture Organization’s (FAO) undertaking on plant genetic resources has been the most influential inter-governmental mechanism influencing the direction of agricultural plant genetic resources flow and access at the global level. It has originally considered PGR for agriculture and food uses as “common heritage for human kind” with unrestricted access to germplasm as one of its principles, in contrast to the Convention’s national sovereign rights. Efforts on harmonization of the Undertaking with Convention has been led by FAO’s Commission on Plant Genetic Resources. There will be a ministerial meeting to finally decide on the International Undertaking in November of this year. Whatever happens on the major issues of farmer’s rights, access and benefit sharing, multilateral or bilateral systems, EA-PGR should be ready to discuss what to do in the context of the approved International Undertaking.

Other concerns

Strategic issues in PGR conservation and use in East Asia should be considered when we set up priorities for the region. These include rapidly declining PGR due to destruction of habitat (deforestation, monoculture, land use change), loss of indigenous knowledge related to PGR conservation and use, increasing constraints in exchange and sharing of PGR, as well as low institutional capacity for PGR conservation and use. Strategies for these issues should be developed at national and regional level.

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Plant genetic resources exchange and use and Intellectual Property Rights: implications to EA-PGR network

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"What is important is not to clog the channels of cooperation, but to keep alive the vary principle of evolution of agriculture over the last 10 000 years. Agriculture has evolved through materials taken by human beings, birds, waves and currents."

-- Dr. M. Swaminathan

Rationale for germplasm exchange

The continued evolution of plants for food, medicine, aesthetic and general well being of human society will be dependent on the process of germplasm exchange and use in support of sustainable development. There are strong reasons for enhancing the exchange and use of plant germplasm (Sajise and Batugal, 2000). The strongest rationale for this is that no one country possesses sufficient plant genetic resources (PGR) within its borders to meet all its present and future needs and species of plants do not respect country boundaries and centres of biodiversity often span across the entire region. For example, in 1993, taro blight destroyed 95 percent of the taro crop in Western Samoa where it is a staple food. The only reason for the recovery of Western Samoa of its production of this staple crop is the availability of leaf blight resistant taro varieties from the Philippines and Palau, which they were able to use for their crop production. The historical records are replete with similar examples that befall on important crop plants to illustrate this important rationale and to emphasize that PGR is a common heritage of humankind (Granett ***et al.,*** 1991). Another reason for plant germplasm exchange is that many of humankind's' agricultural crops are already distributed worldwide and has gone beyond its biodiversity centres or centres of origin prior to the Convention on Biological Diversity (CBD), which recognized sovereign rights of countries over their PGR (Crucible II Group, 2000). Currently, there is a prevailing notion that CBD applies more to the wild crop relatives or natural biodiversity while the FAO sponsored International Undertaking (IU) applies more to agricultural crops instead of a continuous spectrum of wild species from natural ecosystems to crop species in agricultural ecosystems.

Exchange of PGR will allow for enhancement of genetic diversity, which is a natural defence mechanism against genetic vulnerability and even environmental risk (Anon, 1973; Brown, 1983; Lebot, 1992). Countries which still have a significant amount of genetic diversity and species diversity have a responsibility unto themselves as well as the world at large to conserve it and make it available for use (Ramanatha Rao and Riley, 1994).

Constraints and opportunities for promoting germplasm exchange and use

Before the 1980s, PGR were considered as a common good and heritage of mankind and were exchanged freely. This was the essence of the FAO IU adopted in 1983 (Hawtin, 1999).

During the last two decades, various forces have changed the existing paradigm on PGR as a common heritage. Advances in science, especially molecular genetics, resulted in growing interest and investment of private organizations in coming up with new varieties and materials with intellectual property rights protection (IPP) primarily through patenting. There was also pressure for national governments to strengthen their IPP legislation with the World Trade Organization (WTO) through the provisions in Trade Related Intellectual Property Rights (TRIPS) thus eroding rapidly the concept of PGR as a common heritage of humankind (Hawtin, 1999). While this was taking place in the agricultural sector, there was also the growing movement and concern for protecting the environment and biodiversity recognizing the need for a fair and equitable sharing of benefits. This concept, arising from the perception of developing but biologically rich countries, argues that the gene-rich countries are not fairly compensated for the use and exploitation of these biological resources. These concerns led to governments negotiating the Convention on Biological Diversity (CBD), which came into force in December 1993. The CBD is a legally binding and aims to promote the conservation of biodiversity, its sustainable use and the fair and equitable sharing of the benefits arising from their use. It also recognizes biodiversity as a resource that is subject to national sovereignty.

Since the plant varieties and other biological products could now be patented and has become a major material to be traded internationally, WTO has been calling on the member countries to adhere to TRIPS agreement. TRIPS agreement has also an impact on germplasm exchange and needs to be considered in developing plans for PGR conservation and use. Under this agreement, the countries are required to have some sort of IPP (patent, ***sui generis*** or other forms) to plant materials and its products and processes.

These developments during the last two decades has caused a distinct paradigm shift with regards to the status of PGR from a common heritage of humankind and therefore is free to be exchanged to one that has been subject to more IPP due to commercialisation. Therefore exchanges of germplasm could not take place freely unless there is mutual consent or mutually agreeable basis from parties concerned which include the sharing of benefits and responsibilities for its sustainable use. The FAO Commission on Genetic Resources for Food and Agriculture decided to negotiate the IU to bring it in line with the CBD and the new paradigm. This has taken a long time to renegotiate and in the meantime, these international protocols have caused some ambivalence in the position of countries with respect to exchange of PGR, resulting in a slowdown in the building up of biodiversity buffers for sustainability. While all this is happening, poor farmers are not able to access freely good materials to alleviate food insecurity, poverty and environmental risks. However, the opportunities for sharing and exchanging PGR still exist as indicated in the CBD as long as the Contracting Party shall do it on mutually agreed terms.

The summary of the chronological developments of the global agreements, which have affected access to and exchange of PGR and technology, is given in Table 1.

Options for enhancing the sharing of PGR

Exchanges of plant genetic materials have taken place both on a multilateral and on a bilateral and mutually acceptable terms and conditions between parties involved in the exchanges. There are two options, which can be considered to enhance plant germplasm exchange and use. These options have their own advantages and disadvantages.

Table 1. Chronology of policy events on global protocols influencing access and exchange of PGR (Crucible II Group, 2000)

Year	Global policy events on germplasm exchange
1983	FAO IU-non binding, considers PGR as "common human heritage", generated against a background of rising concern that while developing countries provide plant genetic materials of agricultural crops on the basis of common human heritage, developed countries tend to appropriate proprietary rights to these resources.
1993	The Convention on Biological Diversity came into force, legally binding recognized sovereign rights over these PGR.
1994	The CGIAR's International Centres signed agreements placing most of their germplasm collections "in trust" under FAO auspices; policy on the in trust collections under the Commission on PGR for Food and Agriculture; Material Transfer Agreements are used for access and exchanges to these materials; prohibits granting of IPRs to these materials by users but allows for Plant Breeders Rights for new varieties developed.
1995	The World Trade Organization came into being with its Chapter on Trade Related Aspects of Intellectual Property Rights (TRIPS) requiring protection of plant varieties by patents or ***sui generis***, conflicting in some aspects with provisions of CBD.
1996	The Leipzig Global Plan of Action for PGRFA was adopted though not fully implemented.
1998	The 1991 Act of the Union for the Protection of New Varieties of Plants (UPOV) Convention entered into force closing the door for new parties to join the 1978 accord.
1999	The FAO Commission on PGRFA continues to re-negotiate its IU and as part of this, Farmer's right; Ministerial Deliberations will take place November 2001 to finalize harmonization with CBD.

Option 1: Bilateral exchange

This involves the exchange of germplasm between two countries, which is decided by researchers of both governments. It is the present exchange system used by some countries guided by a mutually agreeable Material Transfer Agreement in some cases. However, negotiating with even one country is often difficult and it is much more difficult with several countries which own germplasm of interest. Access could be improved if both countries have mutual interest to exchange germplasm but not if only one country is interested and they do not have as much valuable germplasm to exchange Success depends on knowledge of the performance of specific germplasm in national collections. Most of the time this information is inadequate and often not accessible. Access to germplasm is often weak and country requests are often difficult to service due to economic technical, quarantine and political reasons. Also, the range of germplasm that can be exchanged with one country is often limited.

Option 2: Establishment of regional collection for evaluation and exchange (multilateral exchange)

This involves the conservation and evaluation of valuable germplasm in a designated regional host country and the germplasm collected are conserved, evaluated and exchanged on mutually agreed terms. Once countries agree to contribute germplasm and share these germplasm conserved in the regional collection, requests for germplasm will only be made to host country of the regional collection. It requires documentation of available information at national level on the performance of specific germplasm and generation of additional data by all member countries; development and use of standard methods of characterization and evaluation by all members of the network and development and sharing of database which will serve as working basis of selecting germplasm of interest for conservation and exchange. It is a system that needs to be established through networking.

The proposal for East Asia Plant Genetic Resources Network (EA-PGR)

It is proposed that member countries of the EA-PGR Network discuss the possibility of initiating a mutually agreeable process of enhancing germplasm exchange by specific species of interest. The steps involved could cover some of the following:

1. Group together determine the species of interest after joint discussion. Then one country exchanges a list of varieties of interest held by other member countries. At the same time each country lists own varieties and materials that have been indicated as of interest to some of the member countries.
2. Discuss mutually agreeable terms for the exchange, which could be covered by a Material Transfer Agreement (MTA) and selecting the best and appropriate options or arrangements. Basic to this second step is the agreement of and a willingness to put out a list of the varieties identified for exchange as indicated by the members in exchange of germplasm materials that you are interested in from the other members of the network.
3. Agree on the safe procedure for transfer of these materials, following necessary phytosanitary procedures, regardless of whether you will adopt Option 1 or 2.
4. Provide a mutually agreeable time frame for these processes to take place.

The EA-PGR Network must also be prepared to meet the final scenario, which will be shaped by the IU after November of this year with regards to the status of PGR access and exchange. Whatever the case maybe, it is important that ways must be found to continue with PGR access and exchanges to enhance the attainment of food security and environmental protection for the survival of our peoples in this region and throughout the world. IPGRI is committed to collaborate with all countries of the world to promote these exchanges and attain the goal of food security of all.

Conclusion

The world we are living in is rapidly changing but society’s need for food, clothing, shelter, medicine and cultural values will remain basic that could be supplied by utilizing plant and animal diversity. Therefore, representative genetic resources have to be collected, studied, conserved, exchanged and used for present and future generation before they disappear forever.

There had been rapid advancement in technology, the political environment and global agreements and protocols which have shifted the paradigm of PGR as “a common heritage of mankind” to that of a proprietary commodity influencing conditions of its exchange and utilization for alleviating poverty and improving the welfare of human society in general. This scenario is not promoting food security and social equity at the detriment of human society in general. We must find a way of reversing these trends, while recognizing innovation and providing the right incentives for such innovations provide an effective cutting edge for science and development. In order to bring this about, there is a need for a spirit of understanding and sharing of ideas and technologies and there is a need for developing a strong culture of global stewardship. Only in the globalisation of these spirits can we truly realize that genetic resources from plant, animals, fungi, microorganisms and other living things will truly humankind’s instrument and means of attaining sustainable development.

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Thematic reports

Conservation and use of common millet germplasm

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Introduction

The existence of several geographical zones such as high land, taiga, steppe and desert and prevalence of extreme climatic conditions all contribute to forming exclusively unique natural conditions, which are quite different from those prevailing in other regions situated at the same latitude. With the undulating grassland, Mongolia is rich in genetic diversity of pasture grasses, herbs, onions as well as valuable landraces of cereal crops.

In recent years, increased urban population has raised the demand for cereals and vegetables. In order to meet increasing demand for agricultural production, systematic activities such as developing new and productive varieties, improving cultivation practices and introducing advanced technologies in collaboration with international agencies are being carried out. One of the significant activities in crop production improvement programmes is to expand crop diversity through introducing more new productive crops into the production system.

Although the common millet is not a new crop in Mongolia, there is an increasing demand for this crop in recent years. The common millet, locally called “khar budaa”, is one of the widely used crops from ancient times in Mongolia. Mongolia was considered as one of the secondary centre of origin of common millet. This crop is characterized by the lowest water requirement than any other cereals and can be grown on the poorest of soils.

From the ancient times, common millet had been widely used as a food crop in the central, northern and western parts of Mongolia. Common millet is usually used for food with a raw grain, roasted grain so called “changaamal” and as powder for bakeries. In addition, millet grain and straw are considered to be valuable feed for chicken, swine and other animals. Traditionally, herdsman used the common millet as a treatment for strengthening weak animals. The millet straw contains 59% crude protein, 2% oil and 27% fibre. The green mass of millet plant contains much more vitamin A and grain yield comparing to other cereal crops (Baast ***et al***., 1985).

Collecting and conservation of common millet genetic resources

Collecting

The first common millet landraces were collected by Russian Researcher V.E.Pisarev and his team in 1921 as a part of expeditions of great Russian scientist N. I. Vavilov. The major domestic collecting missions throughout the country were carried out between 1950-1960 and 1990-1998. At the moment about 30 accessions of common millet landraces are stored in the National Genebank at Plant Science and Agricultural Research Institute (PSARI) (PSARI, 2000).

There are two main species of millet distributed in Mongolia. These are common millet (***Panicum miliaceum***) and the weedy type ***Panicum segetale***. Common millet mainly grows in the central northern and western parts of Mongolia at an altitude 1300 m or below and matures much earlier than any other crops.

The landraces were divided into two different ecogeographical groups and most millet landraces belong to the Buriat-Mongolian group and others belong to Sayan-Altai mounting group.

Diversity in common millet landraces had been observed. Some populations of the common millet even consisted of two to six different forms. Much diverse materials were found from Khovd aimag in Altai mountainous area of Mongolia.

A number of millet accessions were also collected through the international germplasm exchange programme. From 1970 to 1990, about 300 millet accessions, originated mostly from east European countries, were introduced from Vavilov Institute of Plant Industry (VIR), Russia. Since 1990, 51 accessions from Korea, India as well as Russia have been introduced.

Conservation

Totally 402 accessions of common millet are stored in the National genebank at PSARI. They include 314 accessions from VIR Russia, 42 from Republic of Korea, 27 local landraces and 19 varieties from other sources (PSARI, 2001). The millet collection at PSARI includes two main species ***Panicum miliaceum*** (95.3%) and ***Setaria italica*** (4.7%).

The millet accessions stored under the short-term storage condition were packed in paper and aluminium foil packets. Only 10% of them were regenerated and placed under the long-term storage in past three years. According to the viability tests in last three years, 218 millet accessions stored under the short-term condition had a viability of 30-40%. Therefore, most of millet accessions need to be regenerated, multiplied and placed into the long-term storage.

Utilization of genetic resources

All the collected landraces were characterized and evaluated for their agronomic performance. The research activities conducted on common millet mainly focus on selection and introduction of high yielding varieties suitable to grow in our condition for commercial production.

During 1966 - 1972, the first improved local variety of common millet “Burgaltai” was developed by mass selection. Another variety named “Saratovskaya-853”, originating from Russia, was released for fodder production in Mongolia. The commercial yields of these varieties were 1.78 - 2.29 t ha^{-1}. The local variety “Burgaltai” had higher grain yield, 1000-seed weight, oil content (6.4%) and starch content (48.2%) and was more tolerant to shattering.

Between 1980 and 1990, the comparative studies of new varieties of common millet from Russia were carried out at the state variety testing branches located in different ecological regions. Based on the results of these tests, “Omskaya-9” and “Orlovskoe carlikovoe” were selected as the suitable varieties for the central agricultural region in Mongolia. Average grain yield of these varieties was 1.49 - 2.0 t ha^{-1} and growth duration was 74 days. On the basis of the studies on agronomic performance, cultivation methods of common millet varieties were developed. In the central agricultural region, it was found that the most suitable sowing time for common millet was on May 20 - 30 and the seed rate was 20-25 kg ha^{-1}.

Genetic improvement in high yield, large grain, shattering resistance, low pericarp: endosperm ratio, high aroma and high protein content are required. Therefore, more germplasm with desirable characters are necessarily introduced for the common millet.

Current problems

Many diverse forms of local common millet landraces are disappearing because of limited cultivation by farmers. Thus it's necessary to strengthen research activities on collecting and conservation in areas where the threat of erosion is high.

As the existing common millet accessions have been conserved in an unsuitable condition for a long time, many accessions are losing their viability and urgently need to be regenerated and multiplied for long-term storage.

There are many specific areas not covered by previous collecting missions in Mongolia. The international germplasm exchange was also not sufficient.

Future plans

- Carry out collecting missions for millet landraces in the areas with specific environmental conditions
- Take immediate action for regeneration of millet accessions with low viability and place them in long-term storage
- Promote international cooperation for germplasm exchange and evaluation

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Characterization and classification of spring barley

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Introduction

Barley is an annual crop, belonging to ***Hordeum*** genus, Poaceae family. There are 29-30 species in ***Hordeum***, of which ***Hordeum sativum*** is the only cultivated species. In our country, the following classification for cultivated barley is generally accepted. Cultivated barley varieties are grouped into 3 categories: multi-row barley, two-row barley and intermediate according to characteristics of spikelet attached to node, and also can be divided into spring, winter and facultative barley according to growth habit (Table 1).

Table 1. Classification of barley varieties

Types	Main characteristics
Multi-row, two-row	Number of spikelets
Spring, Winter, Facultative	Response to temperature
Hull-less	Presence or absence of hull
For beer industry	Low protein content
Early, medium, late	Maturity

Barley is a crop with great economic significance. Barley grain contains 64-70% of carbohydrate, 8-10% of protein, 2.5% of oil, 2-4% of fibre and 2.2% of ash. Barley is widely used as raw material for making bread, cake, sugar and beer. Green leaves and stem, with considerable amounts of carbohydrate, protein, oil and fibre, are important sources of feed. Barley germplasm activity in our country has made a considerable improvement during the last few decades.

Out of 2500 accessions of barley germplasm that were collected, evaluated and conserved so far, 20 varieties have been released to farmers, which account for the majority of national commercial varieties. CIMMYT and ICARDA are main donors for barley germplasm.

This presentation gives a brief description of the results of the evaluation and use of spring barley germplasm in DPR Korea.

Diversity in heading time

Earliness is an important character for developing early varieties suitable for double-crop farming system and variation to be found in barely germplasm is important. Barley grain normally ripens 25-35 days after heading. So varieties heading before May 20 can mature between June 20 and June 25. As shown in Table 2, accessions that head before May 20 account for 6.4%, whereas the percentage of germplasm with heading time from May 26 to May 31 is 76%. Earliness in barley varieties is normally accompanied by low yield and yield components, however, early maturing accessions could be used as parents for developing early varieties.

Table 2. Variation for heading time

Category	No. of accessions	*Percentage (%) of accessions*			
		Before 21 May	**21-25 May**	**26-30 May**	**After 30 May**
Two-row	667	6.4	20.1	44.5	29.0
Multi-row	1 391	6.4	32.5	47.0	13.7
Hull-less	490	5.1	29.6	51.8	14.5
Total	2 548	6.4	28.7	47.3	17.6

Diversity in stem height

The stem height of barley is closely correlated with its tolerance to lodging. In the windy double-cropping areas of our country, it is very important to develop short-stature, early-maturing barley varieties. To this end, the genetic resources available should be classified by their stem height. The variation for stem height for barley germplasm conserved in our country is shown in Table 3.

Table 3. Diversity for stem height (cm)

Category	Total accessions	Percentage (%) of accessions					
		< 50	**50.1-60.0**	**60.1-70.0**	**70.1-80.0**	**80.1-90.0**	**> 90.1**
Two-row	667	3.6	16.9	47.7	26.8	4.4	0.5
Multi-row	1 391	7.7	43.1	34.7	9.6	3.6	1.1
Hull-less	490	8.0	25.7	44.1	19.6	2.4	0.2
Total	2 548	6.8	32.9	39.9	16.0	3.6	0.8

As shown in the Table 3, the spring barley germplasm accessions with a stem height less than 70 cm account for 79.6% of the total accessions conserved in our country. The percentages are 68.3%, 85.7% and 77.8%, respectively, for the 3 categories: two- row hulled, multi- row hulled and hull-less barley varieties. Dwarf accessions with stem height shorter than 60 cm have been used as parent for the development of barley varieties with a strong tolerance to lodging.

Classification by grain number per spike

The grain number per spike is one of the quantitative characters that is highly sensitive to the cropping areas, conditions, types and methods, and variation for grain number can be high.

The grain number and 1000-grain weight of barley are closely correlated with the productivity. Therefore, to increase the grain number per spike is an important objective for increasing productivity in barley. The diversity of grain number per spike for the accessions of spring barley germplasm conserved in our country is shown in Table 4. The accessions with grain number more than 30 per spike are desired by barley breeders.

Table 4. Diversity for grain number per spike (range)

Category	Total accessions	Percentage (%) of accessions				
		< 15	15.1-20.0	20.1-30.0	30.1-40.0	> 40.1
Two-row	667	22.3	58.0	19.5	0.2	0
Multi-row	391	0.3	3.2	48.7	44.4	3.2
Hull-less	490	9.4	8.6	28.6	41.8	11.6
Total	2 548	7.8	18.6	37.3	32.3	4.0

As shown in Table 4, the grain number per spike of multi-row and hull-less barley is generally greater than that of two-row hulled one. The accessions with 20-40 grains per spike account for 69.6% of the total accessions conserved in our country and 93.1% for multi-row hulled and 70.4% for hull-less barley.

However, for the two-row hulled barley, the accessions with 20-40 grains per spike account for only 19.7%, while those with 15-20 grains per spike occupy as much as 58.0%.

Diversity in 1000-grain weight

The 1000-grain weight, along with the grain number per spike, is closely associated with the productivity of barley. Hence the 1000-grain weight is regarded as one of the important parameters. The percentages of the spring barley accessions conserved in our country by 1000-grain weight are shown in Table 5.

Table 5. Distribution for 1000-grain weight (g)

Category	Total No. of varieties	Percentage (%) of accessions				
		≤ 20.0	20.1-30.0	30.1 -40.0	40.1-50.0	≥50.1
Two-row	667	0	0.2	18.3	63.4	18.1
Multi-row	1 391	0	3.6	55.8	39.1	1.5
Hull-less	490	2.0	53.3	39.2	4.5	1.0
Total	2 548	0.4	12.2	42.8	38.8	5.8

As shown in Table 5, of the total spring barley accessions conserved in our country, there are 81.6% accessions having 1000-grain weight ranging from 30 to 50g.

Of the total number of hull-less barley accessions, there were 5.5% accessions with a 1000-grain weight greater than 40g (heavy-grain type), while the majority with 20-40 g. For the two-row hulled barley, on the contrary, accessions with a 1000-grain weight greater than 40g account for 81.5% of the total, indicating that the heavy-grain type occupies a comparatively high percentage. The heavy grain-bearing barley germplasm accessions, along with those with a high grain number per spike, are used as source materials in the development of barley varieties with a high productivity.

Diversity in number of spike-bearing tillers

The number of spike-bearing tillers in barley is an important characteristic of barley varieties, which affects the productivity per unit area as well as the grain weight and grain number per plant. Therefore, more attention should be given to increasing the numbers of spike-bearing tillers per plant and per unit area in the breeding and cultivation of barley. The diversity of the number of spike-bearing tillers per plant for the spring barley accessions conserved in our country is summarized in Table 6.

Table 6. Distribution for the number of spike-bearing tillers

Category	Total No. of varieties	Percentage (%) of accessions					
		≤0.2	0.3-0.5	0.6-0.8	0.9-1.1	1.2-1.4	≥1.5
Two-row	667	3.5	19.8	3.3	24.4	13.0	9.1
Multi-row	1 391	37.5	26.4	15.8	11.0	4.5	4.8
Hull-less	490	24.5	51.4	15.3	5.9	2.9	0
Total	2 548	26.1	29.5	17.5	13.5	6.4	5.0

As shown in Table 6, most of the accessions had a numbers of spike-bearing tillers per plant less than 1. In particular, as for the multi-row hulled and the hull-less barley, the accessions with a low number of spike-bearing tillers account for a high percentage. On the contrary, as for the two-row hulled barley, the accessions with a high number of spike-bearing tillers account for a high percentage.

Based on the results of the classification of principal characters, more than 20 high-yielding, early-maturing varieties suitable for the double-cropping system in our country had been screened out and introduced to production practice. Some of those varieties were characterized as shown in Table 7.

Table 7. Characteristics of several released varieties

Variety	Seeding Date (mm/dd)	Date of emergence (mm/dd)	Tillering time (mm/dd)	Heading time (mm/dd)	Time of maturity (mm/dd)	1000-grain weight (g)	Yield (kg ha^{-1})
Pungnyon No.2	3.14	4.60	4.20	5.22	6.22	45.4	2 919
Spring barley No.14	3.15	4.10	4.14	5.14	6.15	35.5	3 550
Ryonggang No.21	3.20	4.10	4.25	5.17	6.18	33.6	3 563
Hull-less barley No.7	3.21	4.10	4.24	5.21	6.21	39.6	3 676

As shown in Table 7, the 4 varieties reached maturity at around mid-June, producing good yield (3000-3700 kg ha^{-1}). Therefore, these varieties can be grown prior to rice on paddy fields and to maize and other crops on non-paddy fields.

Conclusion

Barley is an economically important crop in DPR Korea. A total of 2500 accession of barley were collected and conserved in the genebank of DPR Korea. These germplasm were evaluated for the characters of heading time, stem height, grain number per spike, 1000-grain weight and number of spike-bearing tiller. Considerable variation was observed on various characters among the accessions. The ranges of the variation of different characters and the proportions of accessions to different ranges of the variation were presented and discussed. These information will be useful to barley breeders for determining parent materials for breeding purpose. However, more effort is needed to identify individual accessions with desirable characteristics which could meet the breeders' requirements for the variety improvement of barley in DPR Korea.

The *Vigna angularis* complex and related species in East Asia

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Introduction

For the last three years a collaborative project on “Analysis of genetic diversity in the ***Vigna angularis*** complex and related species” has been carried out. Much progress has been made and it is being reported here. The objectives of this report are:

1. To provide information on ***Vigna angularis*** complex and related species in East Asia.
2. To present progress on the collaborative activities of on-going IPGRI supported collaborative project.

Vigna diversity in East Asia

Importance of Vigna

In East Asia, the cultivated ***Vigna*** species are generally considered as minor legumes. However, cultivated ***Vigna*** species are not minor legumes in a global context. In South and Southeast Asia, the green and black grams (***V. radiata*** and ***V. mungo***) are important sources of dietary protein. The cowpea (***V. unguiculata***) is a major legume in Africa and has become an important crop in many other parts of the world. ***V. unguiculata*** is widely cultivated in East Asia. It is also found in wild environment, having escaped from cultivation in some parts of Asia. The most closely related genus of ***Vigna*** is ***Phaseolus,*** which also includes some important legume cultigens.

The ***Vigna*** cultigen that is most closely associated with traditional East Asian cuisine is ***V. angularis***, the adzuki bean. If we take this species as a focus for genetic resources studies, the results may have implications for the conservation of an array of related species cultivated in the world (Fig.1).

In situ *conservation research - Genetic and pollination studies of the* Vigna angularis *complex*

The adzuki bean complex has a wide distribution from Nepal through China and Korea to Japan. However, it has only been studied in detail in Japan. The results of research on the adzuki bean complex presented here provide information relevant to genetic diversity and conservation studies.

The ***Vigna angularis*** complex consists of two taxonomically recognized varieties var. ***angularis*** and its close wild relative and presumed progenitor var. ***nipponensis***. In addition, an intermediate type has been recognized and called a weedy type (Yamaguchi, 1992). The weedy type of adzuki is variable in its morphological characters, of which some are similar to wild adzuki and others to cultivated adzuki. Typical weedy adzuki is recognized in the field by its bushy habit and often greenish-yellow leaves. A table comparing the characteristics of wild, weedy and cultivated adzuki bean is shown in Table 1.

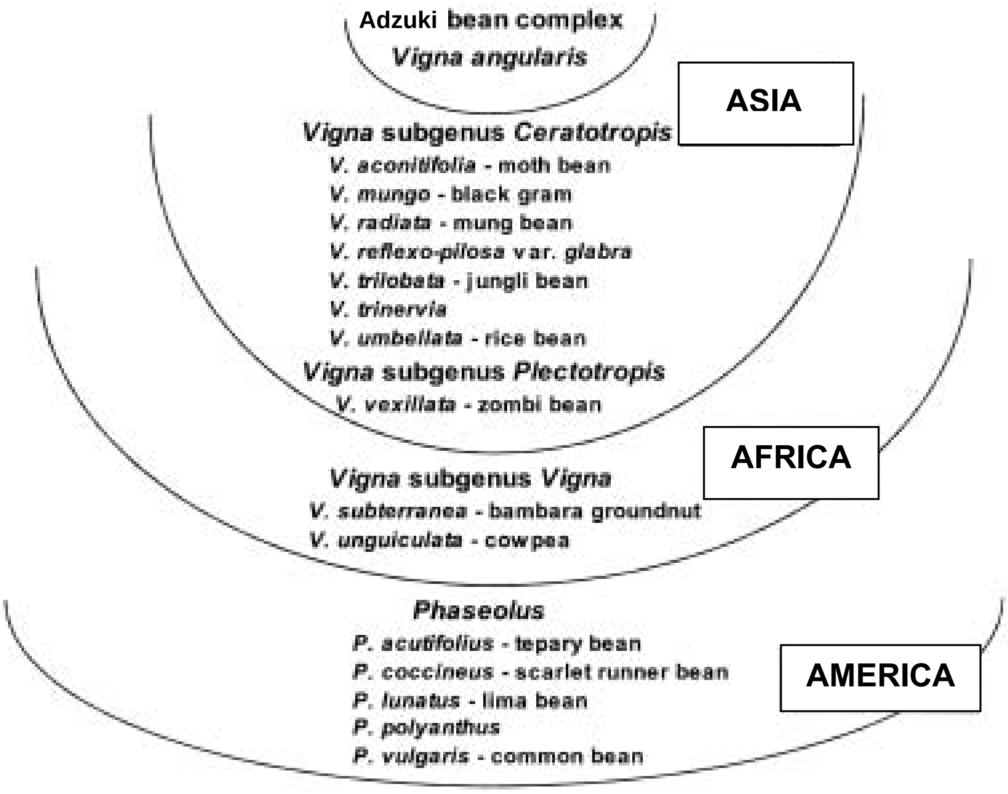

Fig. 1. The cultivated legumes of the *Vigna-Phaseolus* group

Genetic changes of wild populations

Genetic resources workers usually observe the populations at the time when seeds are near maturity. Thus, the impact of disturbance is not apparent. Monthly observations of wild and weedy adzuki populations on Tsushima Island, western Japan were made by Yasuda and Yamaguchi (1998). These observations revealed that the 12 populations of wild, weedy or mixed wild/weedy populations observed monthly between early June and late October all were disturbed at least once by either human activity or natural events. Six populations were disturbed once, 4 were disturbed twice and 2 were disturbed 3 times. The disturbances in order of frequency were by herbicides (10), cutting (7), construction (1), farming (1) and flooding (1).

Studies of several ***in situ*** conservation sites being monitored over several years in various parts of Japan have revealed the impact of disturbance and gene flow (Tomooka ***et al.,*** 2001a). Hybrid swarms are uncommon and transient because of barriers to gene exchange. In addition, selection pressures for either the weed or the crop were apparently strong (Harlan, 1965a). In 1999, an adzuki hybrid swarm was found at Tatebe, Okayama. However, during the second year of observations, half the population was found to be covered with soil.

There are complex populations, which had variable compositions including wild and weedy plants scattered over a wide area and commonly in the fields in the vicinity the adzuki beans are grown. A population at Koge village, Tottori, Japan was a good example (Fig. 2). This population has been studied for over 5 years. Cultivated adzuki beans were planted in different fields annually and the weedy plants had been found in new locations each year.

Table 1. Comparison of characteristics of wild, weedy and cultivated adzuki

Traits	**Wild adzuki**	**Weedy adzuki**	**Cultivated adzuki**
Life cycle	Annual	Annual	Annual
Plant stature	Slender twining	Bushy to slightly climbing	Bushy
Pod dehiscence	Dehiscent	Dehiscent	Indehiscent
Pod colour	Black	Black/straw	Red/straw/black
Pod length [c]	29-91	29-97	84-111
Pod wall	Striated coriaceous	Striated coriaceous	Papyraceous, moniliforme
Inflorescence[a]	Racemous, exerted from plant canopy	Racemous, not exerted from plant canopy	Racemous, not exerted from plant canopy
Branching[a]	2-4 lateral branches and many branchlets over one meter	Lacks lateral branches from lower axils	Lacks lateral branches from lower axils
Seedling[a]	Expands first leaf from dark purple (rarely green) main stem, and extends lateral branches horizontally in close contact with the soil from axils of the first leaves and subsequent cauline leaves	Expands first leaves from green (rarely purple) main stem at 6-10cm above ground level and extends its first long branch from the fourth or fifth node.	Expands first leaves from green (rarely purple) main stem well above ground level and extends its first long branch from the fourth or fifth node
First leaf height (cm) [b]	2.05-3.74	6.19-13.1	8.05-15.4
First leaf length (cm) [b]	2.68-4.25	3.26-4.21	4.13-6.26
Seeds/pod [c]	3-13	4-11.8	6.4-9.8
Seed length (mm)[c]	3.65-4.59	4.26-5.78	5.2-8.39
Seed width (mm)	2.76-3.69	3.24-4.55	3.54-6.17
Seed thickness (mm)	2.37-3.3	2.79-4.3	3.03-5.76
100 seed wt. (g)[c]	0.9-4.9	1.2-9.3	12.2-21.7
Seed coat colours[c]	Black mottled on grey or green	Variable: Yellow/brown, grey, yellow/green, brown mottled on light brown	Usually red, also black, black on red, red/straw, or rarely same colours as the weedy form

a. Yamaguchi (1992); b. Yamaguchi and Nikuma (1996); c. Vaughan ***et al.*** (2000).

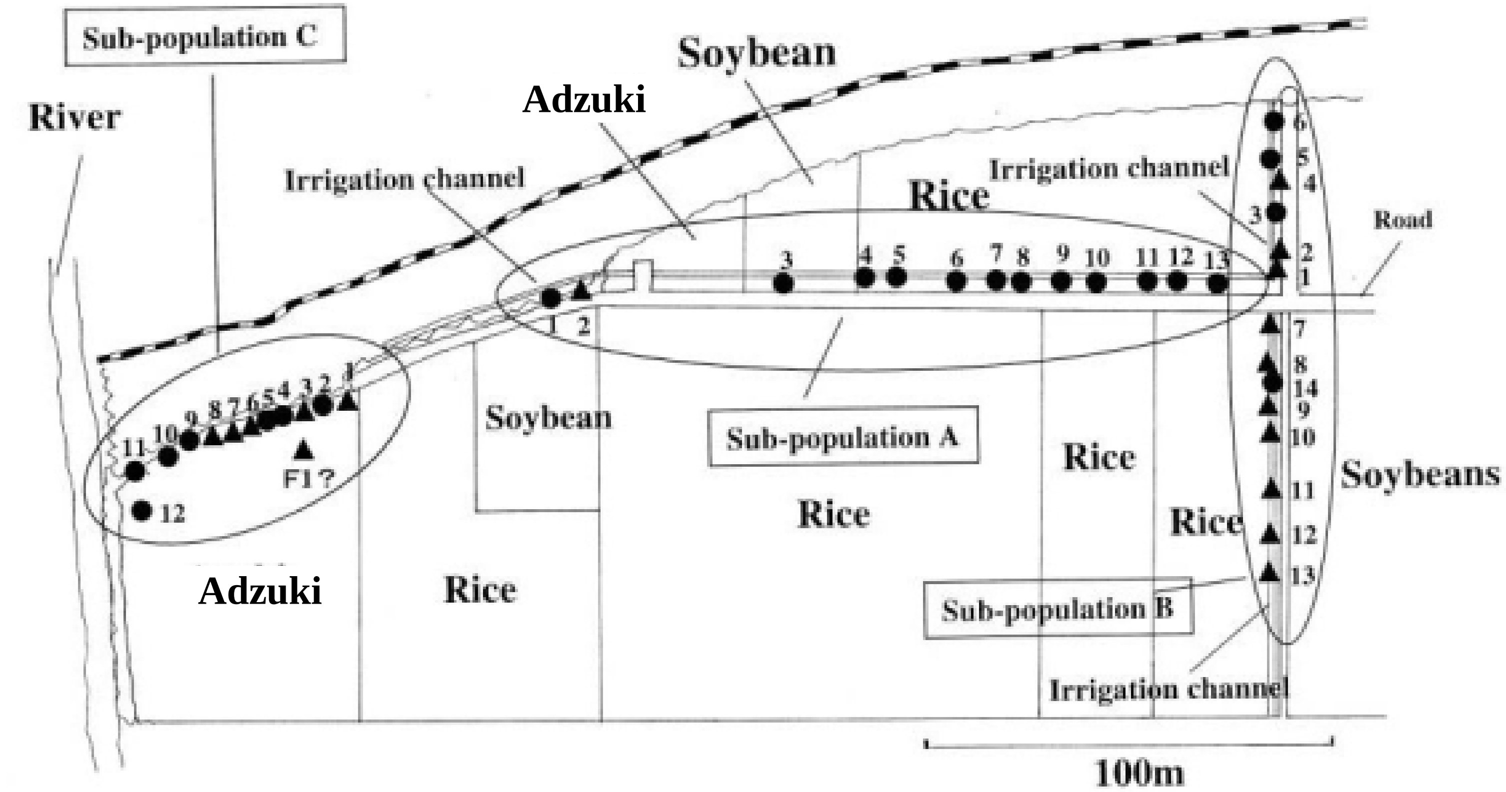

Fig. 2. Distribution of wild (●) and weedy (▲) adzuki bean plants in a complex population at Koge village, Tottori prefecture, Japan

The extent and role of gene flow among different populations in the adzuki bean complex is not known. However, insect visitors with pollens on their bodies were observed on different populations. The study showed that bumblebees in the genera ***Megachile*** and ***Xylocapa*** are the most frequent visitors to adzuki flowers (Table 2). The complex flower structure, nectaries, large and bright coloured flowers were important characters affecting the gene flow facilitated by insects. Since insects of the same genera visited the flowers of both wild and cultivated adzuki bean it is possible that gene flow was happening among populations of the adzuki bean complex. However, the differences of flower size may decrease the rate of successful cross-pollination among the populations in the complex and result in the geneflow happening more likely in one direction. This would help explain, at least, what was segregating sub-populations within a complex population. The variation in some plant traits in the population at Koge revealed this pattern (Table 3).

Field observations over several years revealed that populations of the adzuki bean complex were changing constantly. Each population had its own particular characteristics resistant to disturbance and genetic make-up. From a biosystematics the perspective wild, weedy and cultivated types of adzuki bean could be recognized in the field for the moment. However, observations over time might reveal a more dynamic picture.

Table 2. Insect visitors to adzuki bean populations (Tomooka *et al.*, 2001a)[1]

Flower visitor		Wild	Cultivated
Family	Genus		
Megachilidae	***Megachile***	11	15
Anthophridae	***Xylocapa***	14	3
Aphidae	***Bombus***	1	1
Halictidae	***Halictus***		1
Vespidae	***Polisters***		1
Vespidae	***Anterhynchium***		1
Syrphidae		1	1

[1] Based on observations on 4 populations from 7 AM to noon.

Genetics of different population types

An analysis of genetic variation in adzuki bean complex accessions showed that wild ***V. angularis*** had a high level of genetic diversity in the sub-tropical highlands of southwest China and the Himalayas (Mimura ***et al.,*** 2000). However, Mimura ***et al.*** (2000) hypothesized that cultivated adzuki was probably domesticated from wild adzuki bean in East Asia, Korea or Japan, probably through a stage like weedy adzuki because wild and weedy adzuki beans from East Asia show a high genetic similarity to cultivated adzuki. At archaeological sites in Japan, beans had often been unearthed and these were presumed to be adzuki bean (Yoshizaki, 1995, 1997). Others speculated that adzuki bean had its centre of origin and centre of domestication in China based on diversity of Chinese landraces of adzuki bean compared to other regions (Yee ***et al.,*** 1999). As lack of analysis on many other areas with the distribution of wild and cultivated adzuki bean, the questions related to centres of diversity and origin of the adzuki bean complex remains to be answered.

Table 3. Characteristics of the sampled individuals of adzuki bean populations at Koge, Tottori prefecture, Japan (modified from Tomooka *et al*., 2001a)

Population	No.	Growth	Seed colour	Pod colour	100-seed wt. (g)	Pod length (cm)	Seeds per pod	Remarks
Koge A	1-13	Twining	Black mottled	Dark grey	2.0	5.1	9	
Koge B	1	Semi erect	Black mottled	Dark grey	2.2	6.0	11	
	2	Semi erect	Black mottled	Dark grey	2.8	6.2	11	
	3	Twining	Black mottled	Dark grey	1.9	6.0	10	
	4	Twining	Black mottled	Dark grey	2.1	5.7	10	
	5	Twining	Black mottled	Dark grey	1.9	5.0	9	
	6	Semi erect	Black mottled	Dark grey	8.8	7.5	9	Very big seed
	7	Semi erect	Black mottled	Dark grey	3.1	7.0	10	
	8	Semi erect	Black mottled	Dark grey	2.9	5.7	10	
	9	Semi erect	Black mottled	Dark grey	3.3	6.0	10	
	10	Semi erect	Black mottled	Dark grey	2.7	6.5	10	
	11	Semi erect	Black mottled	Dark grey	2.9	5.5	9	
	12	Semi erect	Black mottled	Dark grey	2.8	6.0	10	
	13	Semi erect	Black mottled	Dark grey	1.9	5.5	9	Semi erect, small seed
	14	Twining	Black mottled	Dark grey	2.4	5.5	10	
Koge C	1	Semi twining	Black mottled	Dark grey	2.5	5.0	8	
	2	Twining	Black mottled	Dark grey	1.8	6.2	10	
	3	Semi twining	Black mottled	Dark grey	2.5			Long pod
	4	Twining	Black mottled	Dark grey	1.8	5.5	9	
	5	Twining	Black mottled	Dark grey	2.7	4.5	8	
	6	Semi twining	Black	Dark grey	3.3	5.5	9	
	7	Semi twining	Black mottled	Dark grey	4.2	8.5	13	Long pod, big seed
	8	Semi twining	Black mottled	Dark grey	5.2	6.7	12	Big seed
	9	Twining	Black mottled	Dark grey	1.3	4.7	9	
	10	Twining	Black mottled	Dark grey	1.8	6.0	10	
	11	Twining	Black mottled	Dark grey	3.0	6.2	11	
	12	Twining	Black mottled	Dark grey	1.5	4.0	6	
	F_1	Erect	Sparsely black mottled	Dark grey	7.3	7.3	10	Cultivar/ wild adzuki
	Cult	Erect	Red	White	19.5	11.0	9	

In Japan, there has been extensive exploration and genetic analysis of the adzuki bean complex (Vaughan et al., 2000; Yamaguchi, 1992; Xu et al., 2000a, b). These studies give a clear insight into the relative genetic diversity of different components of the adzuki bean complex. Maps of population types of adzuki bean complex across Japan revealed that the most abundant area with all complex populations types was situated between 134°E and 137°E (Fig. 3). This may reflect the area where the environment is best suited for wild and weedy adzuki in Japan. It may also reflect the history of Japan since this area encompasses the ancient capitals of Japan, Nara and Kyoto. This was one of the early urban areas in Japan and might have a long history of adzuki bean cultivation compared to other parts of Japan. The consequent human disturbance to wild populations and possibly gene flow might have had an impact on the genetic variation of the adzuki bean complex in this region of Japan today.

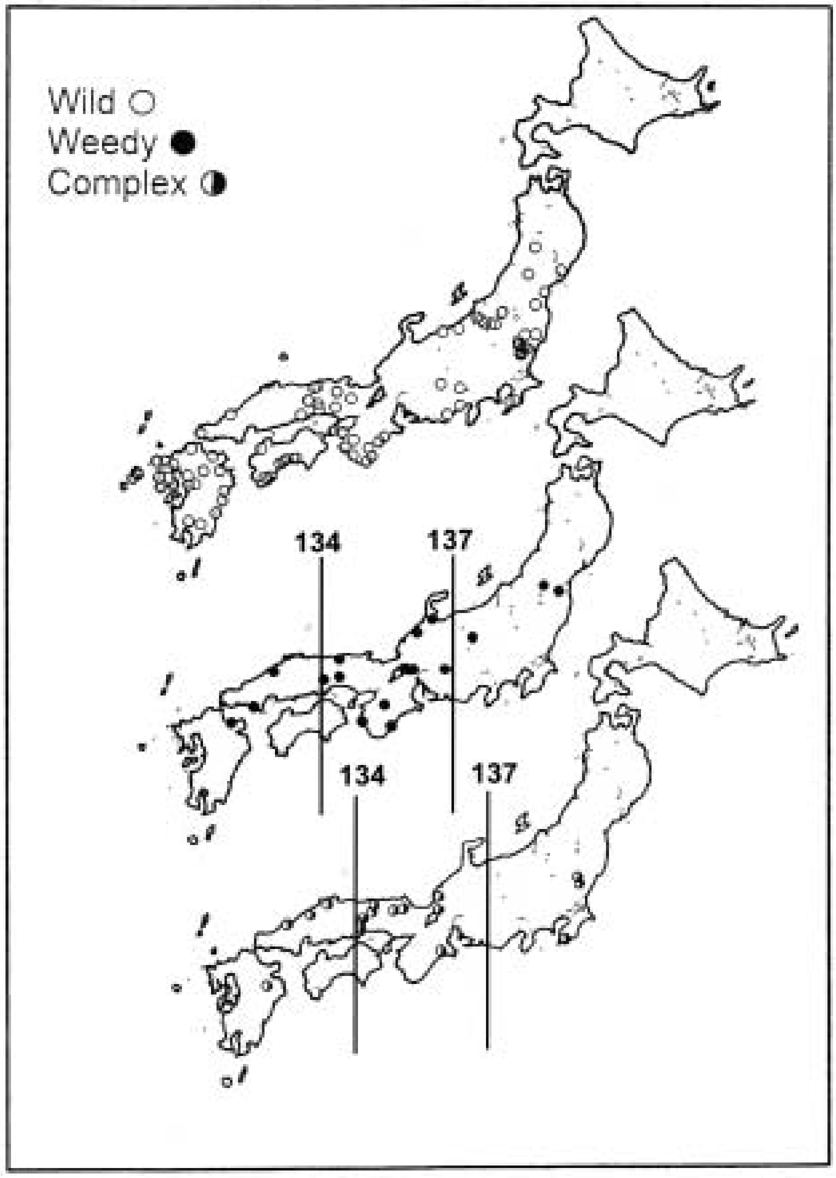

Fig.3. Distribution of *Vigna angularis* complex population types in Japan based on direct collection (modified from Vaughan *et al.,* 2000)

Using the AFLP technique Xu ***et al.*** (2000a) examined genetic diversity in populations of ***V. angularis*** complex in Japan. Wild populations showed clinal variation from west to east suggesting that wild populations are locally adapted. The local adaptation of weedy and wild adzuki beans was also revealed by the relative inter and intra population genetic variation. About two thirds of the genetic variation was found between populations and one third within populations. Thus for ***ex situ*** conservation of the adzuki bean complex, sampling more populations will capture greater genetic diversity than sampling more individuals in a few populations. Considering ***in situ*** conservation, selection of widely scattered sites in more areas may be preferable to more sites in the same area.

The different molecular analyses showed that wild adzuki bean had greater population variation than weedy and cultivated adzuki bean (Table 4). However, the greatest population diversity was found in complex populations. Molecular analyses help in understanding the genetic diversity of weedy and complex populations and they are discussed below.

Table 4. Intra population variation based on RAPD and AFLP polymorphism detected in population groups of *Vigna*

Population groups	RAPD polymorphism[1]	AFLP polymorphism[1]
Cultigen	0.079	0.353
Weedy	0.124	0.561
Wild	0.132	1.191
Complex	0.152	-

[1] Based on Shannon’s diversity index.

a. Weed populations

Three hypotheses had been proposed for the evolution of weedy races (DeWet and Harlan, 1975), i.e. weedy races are:

(a) Escapes from cultigen; (b) Hybrids between the wild type and the cultigen and (c) Directly evolved from the wild type.

DNA analysis results suggested that weedy populations might be the result of hybridization or have evolved directly from the wild type. Cluster analysis of RAPD data suggested that weedy populations might result from both processes (Fig. 4). Two weedy populations were clustered with cultivated adzuki and three clustered with two groups of wild adzuki. Evidences that support the weedy type resulting from hybridization between wild and cultivated adzuki includes:

(a) Seed coat colour variation in some weedy populations resembles that of artificial hybrid populations; and

(b) Populations that appear to be hybrid swarms have been observed (Vaughan and Kaga, 2000; Yamaguchi, 1992).

Evidences that support weedy adzuki evolved directly from wild adzuki includes:

(a) RAPD bands found in the wild and weedy types but not in the cultigen, and no specific weedy RAPD bands (Xu ***et al.,*** 2000b);

(b) Higher genetic diversity in wild populations than weedy populations (Table 4); and

(c) Field observations suggesting, in some locations, that weedy adzuki was adapted to wetter habitats than nearby wild populations. For example, weedy adzuki could be found in such habitats as the sides of streams that are particularly disturbed due to seasonal flooding.

Therefore, it may be specifically adapted to more highly disturbed ecological niches than the wild type. Larger seeds may have advantage to support seedling growth through high level of silt cover and the bushy habit of the population may have advantage resistant to flooding which usually removes plants with twining growth habit.

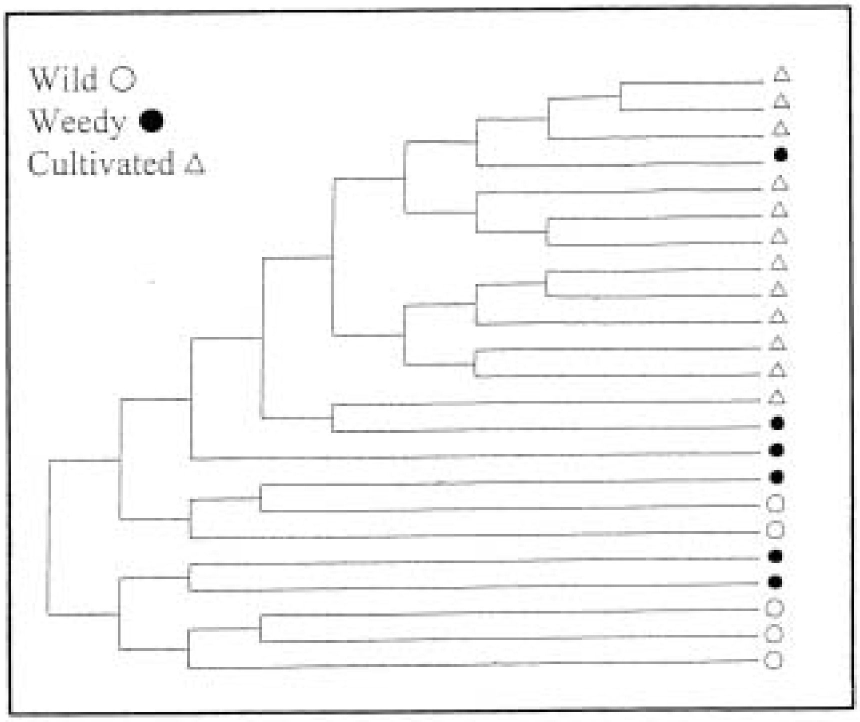

Fig. 4. Neighbour-joining tree based on Jaccard's dissimilarity coefficient of different population types in Japan based on RAPD analysis (cultivated △; weedy ● ; wild O) (Modified from Xu. *et al.*, 2000b)

b. Complex populations

Field data and molecular analyses were used to assess the genetic characteristics of complex populations. Complex populations had been reported for other crop, in the case of ***Phaseolus vulgaris*** they were called inter-breeding complexes (Beebe ***et al.,*** 1997). AFLP methodology was used to analyze individual plants from three populations, wild, weedy and complex, growing within 6 km of each other in Tottori prefecture, Japan. All three populations analysed were adjacent to farmland where small fields of cultivated adzuki beans were grown. A dendrogram resulting from this analysis showed that the complex population had similar plants to those of both wild and weedy populations (Fig. 5). In addition, the wild-like plants in the complex population had greater genetic diversity than the wild population and these plants formed two groups. The high level of genetic diversity in complex population suggested that complex population should be the focus for both ***in situ*** and ***ex situ*** conservation of adzuki beans.

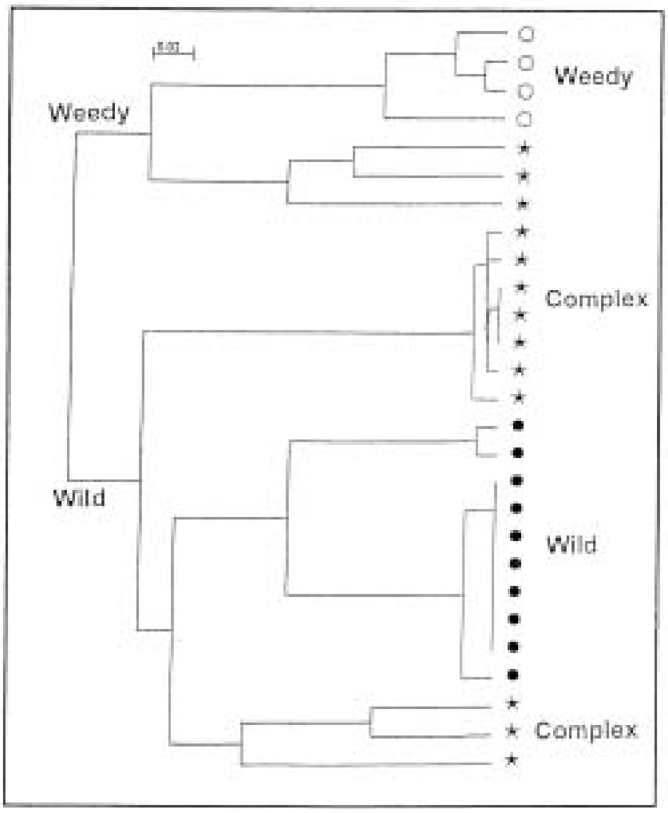

Fig. 5. UPGMA dendrogram, based on matrix generated from AFLP data, representing the association among individual plants from three different types of natural populations (wild •; weedy o; complex ♣) belonging to the adzuki bean species complex from Tottori prefecture, Japan (Modified from Xu *et al*., 2000a)

c. Domestication

Domestication of adzuki beans occurred a long time ago but the process of domestication is continuing in breeding stations and farmers fields today. In common with other crops, character changes by domestication are non- or reduced seed dispersal and increase in size of edible parts. For example, seed size of cultivated adzuki is about 6 times that of wild adzuki. Unlike some crop wild relatives, the level of dormancy in wild adzuki in Japan is low. However, loss of dormancy usually associated with domestication is not important in Japan.

To answer the question whether adzuki would have been a likely plant to domesticate in ancient times, the yields of pods and seeds from wild and weedy populations in Japan were determined by Yasuda and Yamaguchi (1998) (Table 5). The results were compared with the similar studies of wild plants in the Middle East. One pod of wild adzuki could yield as three times high as that of wild soybeans (Vaughan ***et al.,*** 2000). Thus, wild adzuki might have been an attractive plant to harvest and then domesticate.

Considering strategies for ***in situ*** conservation of crop complex genepools, the study of the adzuki bean complex showed that three factors appear to be critical:

(a) ***Disturbance,*** which is mainly imposed by farmers. Their knowledge on the importance of the disturbance is critical to preventing succession. In several regions in Japan it had been reported that in earlier times when food was in short supply the presumed weedy types of adzuki bean were gathered and eaten (Yamaguchi, 1992). Indigenous knowledge on the value of wild and weedy forms of adzuki might be useful in protecting populations of these plants.

(b) ***Pollinators and their protection***. How do the numbers and species of pollinators fluctuate from year to year? Bumblebees, particularly the species ***Xylocopa appendiculata*** Smith, frequently visit flowers of ***V. angularis*** for nectar. Therefore, these bees might be instrumental in pollen transfer between different members of the adzuki bean complex growing in close proximity. There still have many unanswered questions on the topic of gene flow within and between sympatric wild, weedy and cultivated adzuki. However, the floral features and activity of insects on the flower suggested that cross-pollination would be possible even if only occasional.

(c) ***Monitoring.*** To understand the changes occurring in populations the scientific monitoring both at different times during the year and from year to year is necessary. It is important to monitor both the immediate environment of the population and its general vicinity.

Table 5. Yields of collected wild plants

Species	Yield g ha^{-1}	Reference
Diploid wild wheat	1 000	Harlan, 1965b
Tetraploid wheat	500	Ladizinsky, 1975
Lentil (wild)	10*	Ladizinsky 1987
Lentil (wild in tilled field)	110*	Zohary, 1989
Adzuki (pod) wild weedy cultivated	735 1 762 1 980 (control)	Yasuda and Yamaguchi, 1998
Adzuki (seed) wild weedy cultivated	187 170 723 (control)	Yasuda and Yamaguchi, 1998

* Estimated assuming seeds from 100 plants can be collected in one hour from scattered wild populations and 200 plants in one tilled field.

Potential new uses of East Asian Vigna *species*

The wild and weedy relatives of ***Vigna*** in East Asia have a potential value for agriculture. ***V. marina*** grows on sandy beaches and may be a source of salt tolerance. ***Vigna riukiuensis*** is being investigated as a source of heat tolerance for growing adzuki beans in the tropics and subtropics (Egawa ***et al.,*** 1999). ***V. riukiuensis*** is also a useful bridging species between cross-incompatible species related to adzuki bean (Siriwardhane ***et al.,*** 1991; Takeya and Tomooka, 1997). ***Vigna nakashimae*** is confined in its distribution to North Eastern Asia and it is thus likely to be a source of cold tolerance in the early and late of growing season.

One of the major constraints to legume production is the destruction of seeds by pests in storage. Bean weevils are the most prevalent and serious storage pests. Recent evaluation of wild and cultivated ***Vigna*** genetic resources from Japan has revealed the new sources of resistance (Table 6) (Tomooka ***et al.,*** 2001b). Resistance found in the variety Menaga of ***V. umbellata*** from Tsushima Island, Nagasaki Prefecture is currently being investigated in detail since the mechanism of the resistance in this variety is new (Kashiwaba ***et al.,*** 2000). In addition, this source of resistance to bean weevil may be better than that currently available because it was found in a cultigen and thus safe for human consumption. ***V. riukiuensis*** and ***V. nakashimae*** are being used as bridging species to introduce the resistance to bean weevils, ***Callosobruchus chinensis*** and ***C. maculatus,*** from cultivated rice bean (***V. umbellata***) to adzuki bean.

Table 6. Levels of resistance in Japanese *Vigna* species against *C. chinensis* and *C. maculatus* (modified from Tomooka *et al*., 2001b)

Species	**Accession**	**100-seed weight (g)**	***C. chinensis***				***C. maculatus***			
			Eggs/rep. (No.)	**Emerg. (%)**	**Damaged seeds (%)**	**Developmental duration ♀ (days)**	**Eggs/rep. (No.)**	**Emerg. (%)**	**Damaged seeds (%)**	**Developmental duration♀ (days)**
V. angularis var. ***angularis*** (Adzuki bean)	102	14.0	47.7	75.0	100.0	25.3	143.3	43.1	100.0	27.3
	Average	14.0	47.7	75.0	100.0	25.3	143.3	43.1	100.0	27.3
V. angularis var. ***nipponensis*** (wild ancestor of adzuki bean)	96101204	2.7	79.5	17.6	100.0	25.4	50.0	20.9	93.3	26.8
	96101602	3.8	102.0	16.1	100.0	25.3	72.3	18.5	96.7	27.9
	96111108	2.8	119.7	10.5	100.0	25.8	53.3	22.6	96.7	27.2
	Average	3.1	100.4	14.7	100.0	25.5	58.6	20.7	95.6	27.3
V. nakashimae	Ukushima	2.0	23.0	43.9	90.0	27.9	51.3	14.0	63.3	27.2
	Average	2.0	23.0	43.9	90.0	27.9	51.3	14.0	63.3	27.2
V. riukiuensis	Yona4-1	1.1	28.0	24.5	56.7	30.4	30.7	5.7	16.7	43.0
	Ri89018	1.3	15.0	5.7	10.0	31.0	31.3	2.0	6.7	29.0
	Average	1.2	21.5	15.1	33.3	30.5	31.0	3.8	11.7	36.0
V. reflexo-pilosa var. ***reflexo-pilosa*** (ancestor of ***V. reflexo-pilosa*** var. ***glabra)***	Irio 4	1.5	21.0	6.9	13.3	32.0	37.0	22.1	83.3	27.4
	Ref 1	1.8	28.0	26.5	63.3	28.7	42.3	24.5	80.0	26.3
	Average	1.6	24.5	16.7	38.3	30.4	39.7	23.3	81.7	26.9
V. umbellata (cultivated) (Rice bean)	Bakaso	6.0	33.0	5.1	16.6	32.0	44.0	0.0	0.0	
	Kagoshima	6.1	33.0	2.9	10.0	28.5	52.3	0.0	0.0	
	Menaga	6.2	30.0	0.0	0.0		45.0	0.0	0.0	
	Miyazaki	5.9	32.3	0.0	0.0		50.0	0.0	0.0	
	Average	6.1	31.2	2.0	6.7	30.3	47.8	0.0	0.0	0.0

Apart from the potential for agriculture, the wild and weedy ***Vigna*** species may have a potential to contribute to agriculturally related industries. Legumes are a particularly diverse source of secondary compounds, many of which are not found in other plant groups (Gomes ***et al.,*** 1981; Harborne ***et al.,*** 1999). These secondary compounds may enable the development of new environmentally safe chemicals. For example, ***V. angularis*** is known to show allelopathic activity and could be a source of allelochemicals (Fujii, 2000). Recently, ***V. trinervia*** was found to be a cover crop under rubber trees in Thailand and seeds of this species commanded a price ten times higher than that of rice in a local market (Tomooka ***et al.,*** 1999). Thai farmers also reported that they grow ***V. umbellata*** as a cover crop. A phytoalexin detected in the leaves of ***V. unguiculata***, vignafuran, is fungitoxic and the flavonoid robinin found in ***Vigna*** species shows antibacterial activity (Harborne ***et al.,*** 1999).

The major cultivated legumes in the world can be classified into two main phylogenetically related groups (Chappill, 1995). The first group consists of the predominantly temperate, forage legumes that include genera such as ***Trifolium*** and ***Vicia***. The second group includes the cultivated grain legumes that thrive in hot weather conditions and grow in tropical regions or temperate areas with hot summer. This second group includes the genera ***Vigna***, ***Phaseolus***, ***Glycine*** and ***Cajanus*** that all have cultivated species. The peanut (***Arachis hypogaea***) is not phylogenetically closely related to other cultivated legumes. In the second group, ***Vigna*** has the smallest genome that is only about 30% larger than that of rice, which has one of the smallest genomes among major cultigens (Arumuganathan and Earle, 1991). Among the ***Vigna*** species, a basic transformation system has been developed for ***V. angularis*** (Yamada ***et al.,*** 2001), making ***Vigna*** species in general and ***V. angularis*** in particular, a useful model within the hot weather legume group for genetic and genome studies.

Analysis of genetic diversity in the *Vigna angularis* complex and related species in East Asia

During the last East Asia PGR Coordinators Meeting, Dr. Shoji Miyazaki, Genebank Director, Japan, proposed joint study on ***Vigna angularis*** and related species by members of the East Asia Network for Conservation and Use of Plant Genetic Resources (EA-PGR) (Zhou ***et al.,*** 1999). This was followed up by a specific project proposal submitted by the National Institute for Agrobiological Resources (now National Institute of Agrobiological Sciences-NIAS) to IPGRI in July 1999 with the agreement of the collaborating genebanks in China, Democratic People's Republic of Korea and Republic of Korea. This collaboration was facilitated by IPGRI Office for East Asia in Beijing. In August 1999, the proposed three-year project was approved by IPGRI and the activities commenced.

The project has two components:

a. To train one scientist working on legumes for each of the participating countries in the genebank of Japan for collecting and ***in situ*** conservation research on the ***Vigna angularis*** complex and related species; and

b. To develop a joint database related to the ***Vigna angularis*** complex and related species in East Asia.

Diversity collecting and analysis

In October 1999, Dr. Mun Sup Yoon from the Genetic Resources Division, National Seed Management Office, Rural Development Administration worked for 5 months at NIAS. During this period, Dr. Yoon joined a collecting trip to the islands of southern Okinawa where different species of wild ***Vigna*** were collected, including ***V. riukiuensis***, ***V. reflexo-pilosa***, ***V. luteola*** and ***V. marina***.

Dr. Yoon used the material collected in Japan and materials from Korea to study the eco-genetic differentiation of two ***Vigna*** species, i.e. ***V. riukiuensis*** and ***V. nakashimae*** that have main centres of diversity in Japan and Korea. The AFLP results were the first detailed analyses of these two species. It was possible to use newly developed software analyze the genetic parameters not just phenotypic parameters.

Vigna riukiuensis and ***V. nakashimae*** are closely related to ***V. minima*** that grows in tropical East and Southeast Asia and these three species have been called the ***V. minima*** complex. The objectives of our study were to estimate the genetic relationships among the species of the ***V. minima*** complex and analyse intra-specific diversity for ***V. riukiuensis*** and ***V. nakashimae*** (Yoon ***et al.,*** 2000).

Relationships among species

Analyses revealed a clear separation of each species and supported the view that ***Vigna minima***, ***V. nakashimae*** and ***V. riukiuensis*** were distinct taxa. ***Vigna minima*** had an average genetic distance of 0.0256 from ***V. nakashimae*** and 0.0252 from ***V. riukiuensis*** (Table 7)**.** ***Vigna nakashimae*** and ***V. riukiuensis*** had a genetic distance of 0.0117 from each other. The high degree of divergence between ***V. minima*** and ***V. nakashimae*** and ***V. riukiuensis*** might be a reflection of the origin of samples analysed and/or length of time these species have been isolated. Thus it seems reasonable to consider ***V. nakashimae*** and ***V. riukiuensis*** as separate species within the ***V. minima*** complex since morphological differences between these taxa had been elaborated (Tateishi, 1985).

Table 7. Phenetic and genetic distances and Shannon's diversity index (H_a) among species of subgenus *Ceratotropis.* Phenetic and genetic distances and Shannon's diversity index (H_a) among *V. minima* accessions from different regions (From Yoon *et al.,* 2000)

	Phenetic distance[1] (Genetic distance[2])				H_a[3]
	V. nakashimae	***V. riukiuensis***		***V. minima***	
	Kyushu, Japan	**Yonaguni-Ishigaki-Iriomote**	**Hateruma-Miyako**		
V. nakashimae					
Korea	0.107(0.0036)	0.275(0.0114)	0.282(0.0117)	0.480(0.0256)	0.027
Kyushu, Japan		0.271(0.0112)	0.279(0.0117)	0.475(0.0252)	0.014
V. riukiuensis					
Yonaguni-Ishigaki-Iriomote			0.108(0.0039)	0.486(0.0265)	0.032
Hateruma-Miyako				0.492(0.0271)	0.021

[1] Phenetic distances are calculated as 1 – Jaccard's similarity coefficient

[2] Genetic distance is based on nucleotide diversity (B), which is estimated from the proportion of shared AFLP bands following the method of Innan ***et al.*** (1999).

[3] Similarity indexes are mean values for each population included in the comparisons.

Variation within species

Vigna riukiuensis has a restricted distribution in Taiwan, China, and Okinawa prefecture, Japan, and the 16 populations analyzed cover much of the species range (Fig. 6). Clear genetic differences between ***V. riukiuensis*** populations from the Miyako and Yaeyama archipelagos (Iriomote, Ishigaki and Yonaguni) had been revealed by PCA (Fig. 7). One population from Hateruma was intermediate. The genetic distance between Miyako and Hateruma populations and those of Iriomote, Ishigaki and Yonaguni was 0.0039 (Table 7).

This suggests that there would be a floristic barrier between Ishigaki and Miyako islands. The distance between the Yaeyama archipelago island of Ishigaki and both Miyako (Miyako archipelago) and Yonaguni (Yaeyama archipelago) was the same, about 120 km, but these two island groups have a different geological history. This may explain, in part, the genetic variation observed between ***V. riukiuensis*** populations from these two neighbouring archipelago.

The 18 populations of ***V. nakashimae*** analysed came mainly from the eastern part of distribution areas of this species (Fig. 6). The similarity coefficient among ***V. nakashimae*** populations was almost identical to that among populations of ***V. riukiuensis*** (0.89). In addition, the genetic distance between Korean and Japanese populations of ***V. nakashimae*** (0.0036) was similar to that of between Yaeyama and Miyako archipelago populations of ***V. riukiuensis*** (0.0039) (Table 7). This may reflect the fact that these two species have evolved over a similar time span in the areas studied. The difference between Korean and Japanese populations of ***V. nakashimae*** is illustrated by a PCA plot (Fig. 8). No relationship was found between the place where populations were collected in Korea and genetic diversity. In conclusion, this study has shown that the two endemic species of the ***V. minima*** complex in East Asia, ***V. nakashimae*** and ***V. riukiuensis***, have distinct intra-specific genetic variation related to their geographic distribution.

Fig. 6. Collecting sites of populations of *Vigna nakashimae* and *V. riukiuensis* analysed

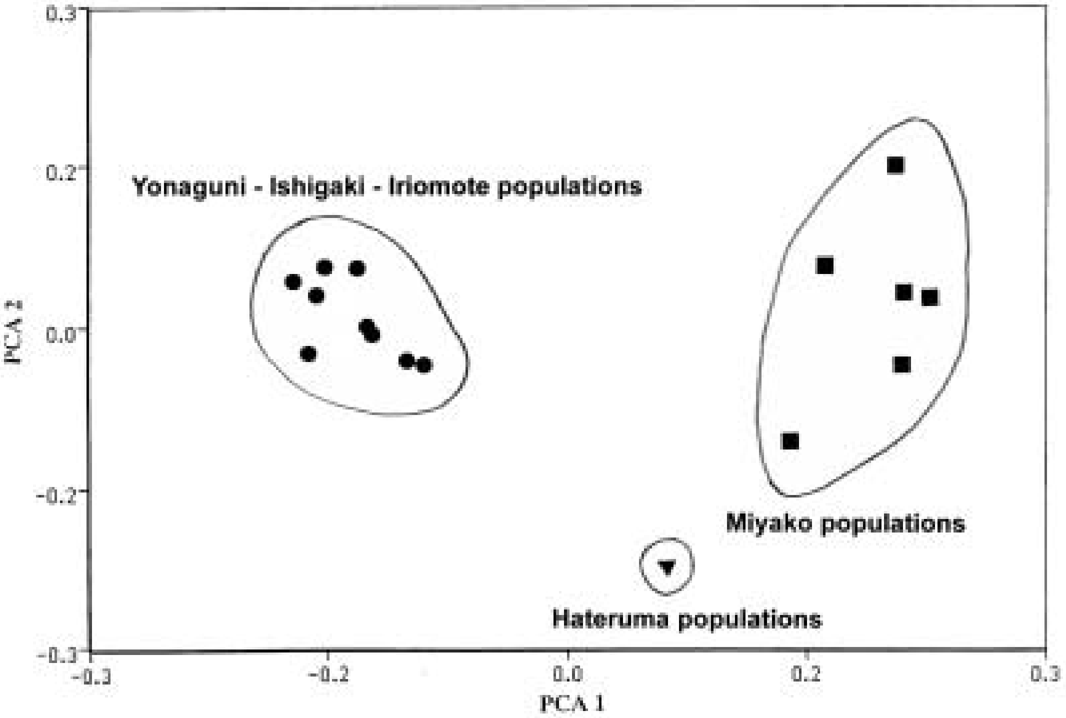

Fig. 7. Association among *Vigna riukiuensis* populations. PC1 accounts for38.0% of the total variation and PC2 9.9% (modified from Yoon *et al*., 2000)

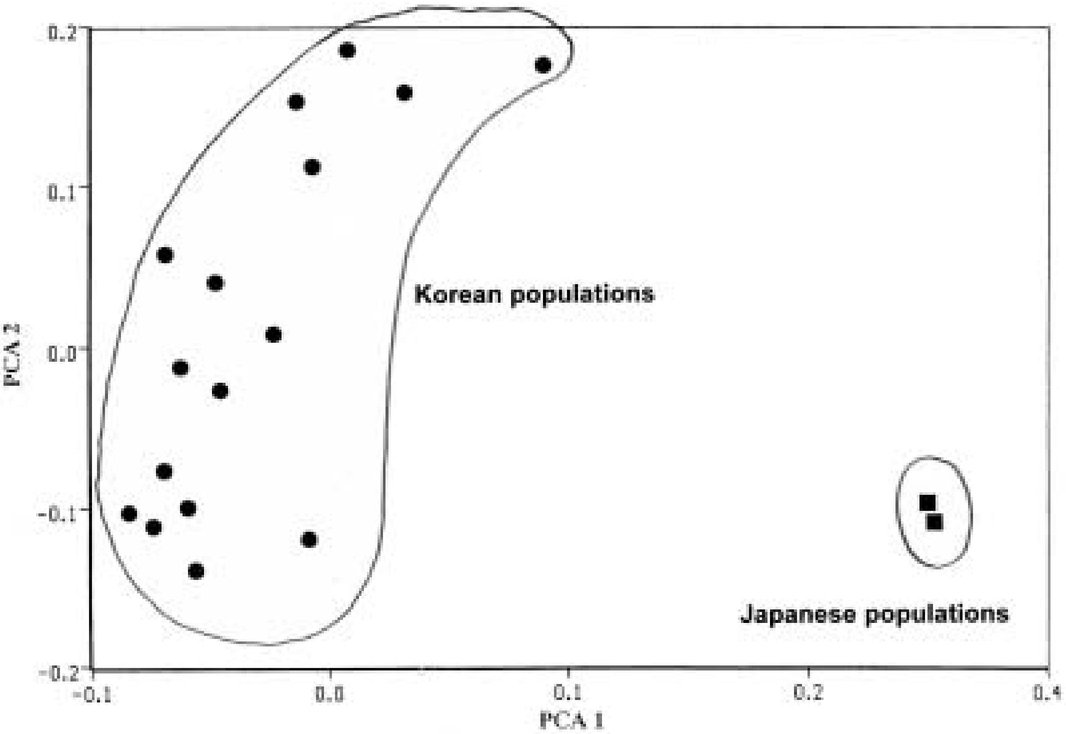

Fig. 8. Association among *Vigna nakashimae* populations. PC1 accounts for 21.7% of the total variation and PC2 12.8% (modified from Yoon *et al*., 2000)

The studies of East Asian ***Vigna*** species will continue and Mr. Zong Xuxiao from the Institute of Crop Germplasm Resources, CAAS, China will visit NIAS, Tsukuba. During his visit, the research will focus on comparing ***Vigna angularis*** complex germplasm from China and Japan.

Development of adzuki bean database

Database development is a major component of the cooperative project on adzuki bean in East Asia. It aimed to integrate the passport and characterization data of adzuki bean germplasm collections from each participating country and establish a comprehensive database on adzuki bean in East Asia.

Identification of descriptor list for data collection

It is important to provide standard format for data collection in order to set up a central database. Based on a list provided by NIAS, a minimum list of descriptors for adzuki bean was identified and agreed among partners and IPGRI. The list was formatted in IPGRI style with help of the specialist at IPGRI HQ. The list is composed of descriptors including 15 passport descriptors and 32 characterisation descriptors. It was agreed that the minimum list would be further developed into a full list of descriptors for adzuki bean as an international standard list.

Database development

The data on adzuki bean germplasm were collected by all partners according to the minimum descriptor list and submitted to IPGRI Office for East Asia for compilation. A database was set up with MS Excel and included the data on 308 accessions of adzuki bean collections in collaborative countries, including 71 accessions on 36 descriptors from china, 87 accessions on 40 descriptors from Japan, 100 accessions on 41 descriptors from Peoples Democratic Republic of Korea and 50 accessions on 27 descriptors from Republic of Korea. The database has been made available to all partners of the project.

Acknowledgements

The support of IPGRI, particularly the IPGRI Office for East Asia, for the project “Analysis of genetic diversity in the ***Vigna angularis*** complex and related species” is much appreciated. We would like to thank the postdoctoral scientists that have worked with us over the last several years, some of their results are presented in this report, and they are Koji Doi, Koichi Kashiwaba, Ru Qiang Xu and Mun Sup Yoon.

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Cryopreservation of temperate fruit tree germplasm

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Introduction

Cryopreservation of temperate fruit tree germplasm in China

The cryopreservation of temperate fruit tree germplasm was first studied on mulberry stems with dormant buds in 1988. Since then different materials like dormant buds, pollen, callus, or ***in vitro*** shoot tips of about 9 species have been successfully cryopreserved (Table 1).

Table 1. Primary summary on the cryopreservation of temperature fruit tree germplasm in China

Species	Material	Results
Mulberry (Wang, 1988)	Dormant buds	PR
Kiwifruit (Jian and Sun,1989)	Stem with dormant buds	PR
(Li, 1996)	Callus	Callus formation and PR
(Wu, 2000)	***In vitro*** shoot tips	PR
Apple (Wang, 1992)	Dormant buds	PR
(Chang Y.J., 1992)	Pollen	Survival
(Zhao and Wu, 1994)	***In vitro*** shoot tips	PR
Apricot (Wang, 1992)	Dormant buds	PR
(Chang Y.J., 1992)	Pollen	Survival
Plum (Wang, 1992)	Dormant buds	PR
(Chang Y.J., 1992)	Pollen	Survival
Grape (Wang, 1992)	Dormant buds	PR
(Zhao and Wu, 1994)	***In vitro*** shoot tips	PR
(Chang Y.J., 1992)	Pollen	Survival
Pear (Chang Y.J., 1992)	Pollen	Survival
(Zhao and Wu, 1996)	***In vitro*** shoot tips	PR
Peach (Jian, 1989)	Pollen	Seed setting after pollination
Sweetcherry (Wu and Zhao, 1994)	***In vitro*** shoot tips	PR

Conservation of fruit tree germplasm at Changli Institute of Pomology

The Changli Institute of Pomology (CIP) is the main centre in China for the conservation of temperate fruit tree germplasm. The field genebank includes 1232 accessions (cultivars or strains) of 12 species.

As a complementary strategy for germplasm conservation, research on ***in vitro*** conservation and cryopreservation of temperate fruits was initiated in 1989 at CIP. As a result, a total of 240 cultivars or strains of 9 species are now being stored ***in vitro*** under slow growth (with subcultural interval from 6 to 8 months), and 50 cultivars of 5 species have been cryopreserved (Table 2).

Table 2. Fruit tree germplasm conserved at Changli Institute of Pomology

Species	Field genebank (accessions)	*In vitro* (cultivars)	Cryopreserved (cultivars)
Apple	700	180	37
Grape	106	29	3
Pear	57	15	4
Peach	121	2	-
Plum	42	1	-
Apricot	30	-	-
Cherry	42	5	4
Strawberry	-	3	-
Kiwi	-	4	2
Walnut	24		
Chestnut	45		
Jujube	24		
Persimmon	26		
Maytree	15		

Cryopreservation of *in vitro* apple shoot tips

The aims of this work was to study the effect of various parameters on the cryopreservation of temperate fruits, compare the availability of different techniques and select the optimal cryopreservation protocols of ***in vitro*** shoot tips of temperate fruits.

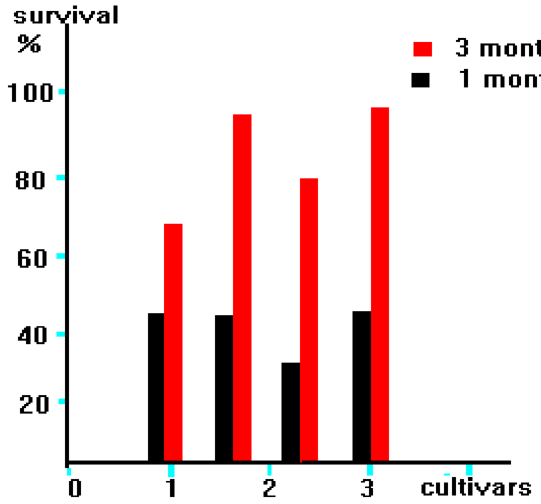
Materials and methods

In vitro apple shoot tips (about 0.5-1.5 mm) were excised from explants (cultured for 1 to 8 months since their last subculture and with or without 3 weeks cold hardening at 5°C with 8h light/16h dark) and cryopreserved with different methods. Three methods were tested on the cryopreservation of ***in vitro*** shoot tips: a) two step freezing, b) vitrification and c) encapsulation dehydration. Factors like a) subculture interval and cold hardening of mother plants, b) cryoprotectant and c) pre-treatment, that affect the cryopreservation of ***in vitro*** shoot tips were tested using different methods.

Main results

Two-step freezing method

The survivals of four cultivars after cryopreservation was significantly increased by using the mother-plant subcultured for 3 months instead of 1 month (Fig. 1).



Cultivars: 1. Fuji 2. Golden Delicious 3. Shengli 4. Jincui

Fig. 1. Effect of subculture interval on the survival rate of cryopreserved apple shoot tips

Cold hardening could improve the survival of two cultivars from 15% or 35% (without cold hardening) to 72% or 90% (after 3 weeks cold hardening), while extending the hardening time could not increase the survival further (Fig. 2).

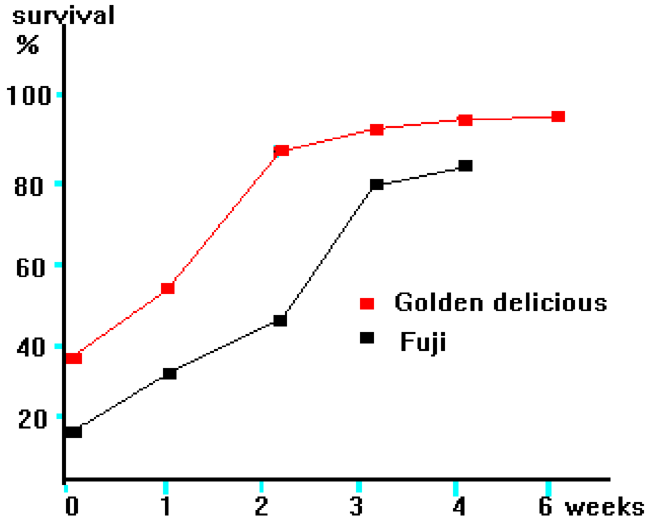
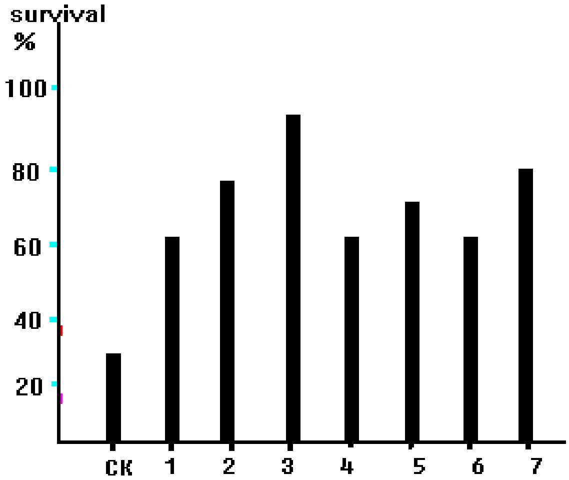


Fig. 2. Effect of cold-hardening on the survival rate of apple shoot tips after cryopreservation

Besides the control, all tested cryoprotectants gave high survival rates. The highest survival 96% was obtained with cryoprotectant 5% dimethylsulfoxide (DMSO)+5% glycerol (Fig. 3).



1. MS liquid medium(CK), 2. 5% DMSO, 3. 10% DMSO, 4. 5% DMSO+ 5% glycerol,
5. 5% glycerol, 6. 10% glycerol, 7. 5% DMSO+5% Propylene glycol,
8. 10% Propylene glycol.

Fig. 3. Effect of cryoprotectant on the survival rate of apple shoot tips after cryopreservation

With the increase of freezing rate, the survival decreased. At 0.1 or 0.2°C / min, the best survival rate 92% (Golden delicious) and 70% (Fuji) were obtained.

The optimal protocols were selected for apices sampled on plantlets subcultured for 3 months and cold hardened for 3 weeks, precultured with 5% DMSO+5% glycerol at 0°C for 30 min, then frozen to -40°C at 0.2°C / min in same cryoprotectant before immersion in LN (Fig. 4).

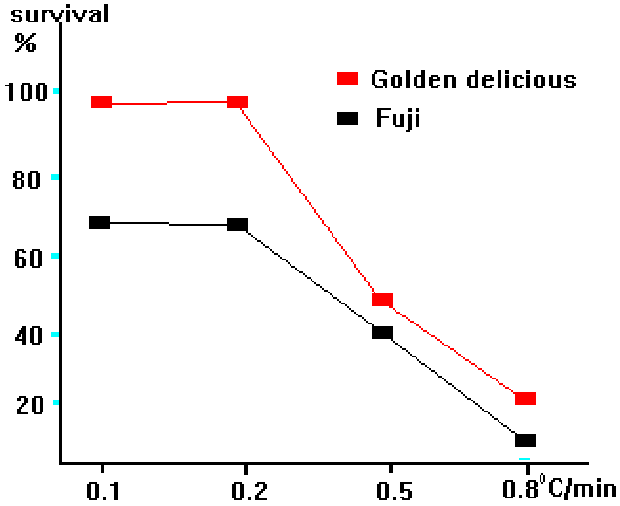


Fig. 4. Effect of freezing on the survial rate apple schoot tips after cryopreservation

Vitrification methods

For all the tested vitrification solutions, only with PVS3 got survived shoot tips. The result demonstrated that selection of vitrification solution is very important for vitrification method (Table 3).

Table 3. Effect of vitrification solution on the survival rate of apple shoot tips after cryopreservation

Cultivars	Survival rate (%)				
	PVS1	PVS2	PVS3	PVS4	PVS5
Golden delcious	0	0	65	0	0
Wanglin	0	0	71	0	0
Jonagold	0	0	75	0	0

PVS1: 22% Glycerol+13% propylene glycol+13% ethylene glycol+6% DMSO(w/v)

PVS2: 30% glycerol+15% ethylene glycol+15%DMSO(w/v)

PVS3: 50% glycerol+50% sucrose PVS4: 5% glycerol+5%DMSO; PVS5: 10%ethylene glycol(w/v)

Non apices survived after cryopreservation when they are excised from plantlets subcultured for 1 month with or without cold-hardening. While 65% (Golden delicious) or 75% (Jonagold) survival rates were observed when apices excised from 3 month old explants and cold hardened for 3 weeks (Table 4).

Table 4. Effect of subculture interval and cold hardening on the survival rate of apple shoot tips after cryopreservation

Cultivar	Survival rate (%)			
	Cold hardening		Non cold hardening	
	1 month	3 month	1 month	3 month
Golden delicious	0	65	0	0
Jonagold	0	75	0	0

Increased survival was observed when treatment time was extended. At 80 min, the survival reached the peak on all the tested cultivars.

For vitrification, the highest survival was obtained for apices sampled on plantlets subcultured for 3 months and cold hardened for 3 weeks, precultured for 24h at 5°C on MS solid medium with 0.7M sucrose, treated with PVS3 vitrification solution for 80 min before immersion in LN (Fig. 5).

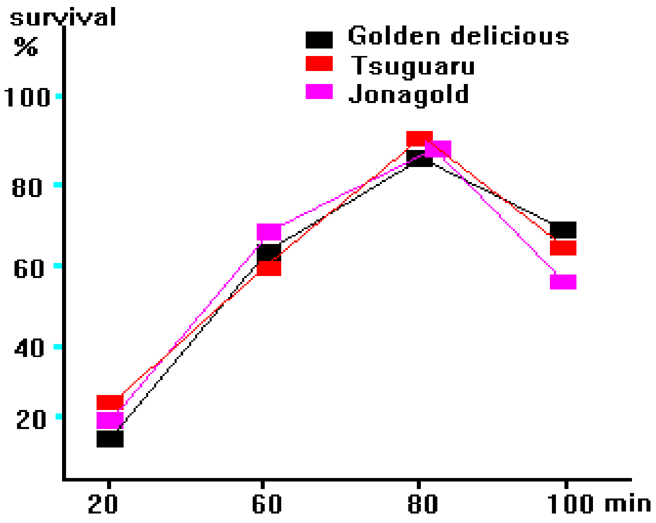


Fig. 5. Effect of vitrification solution treatment time on the survival rate of apple shoot tips after cryopreservation

Encapsulation-dehydration method

The water content of shoot tips decreased from 85% to 66% when mother plants were kept without transfer to new medium for 6 months. With the shoot tips of 66% water content, the survival rates were drastically improved (Fig. 6).

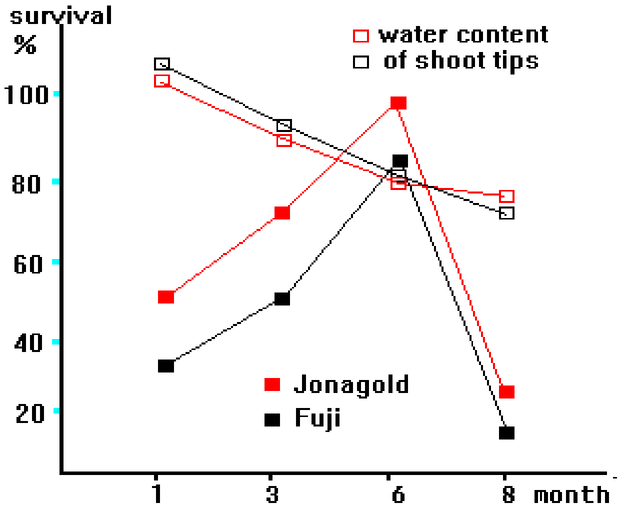
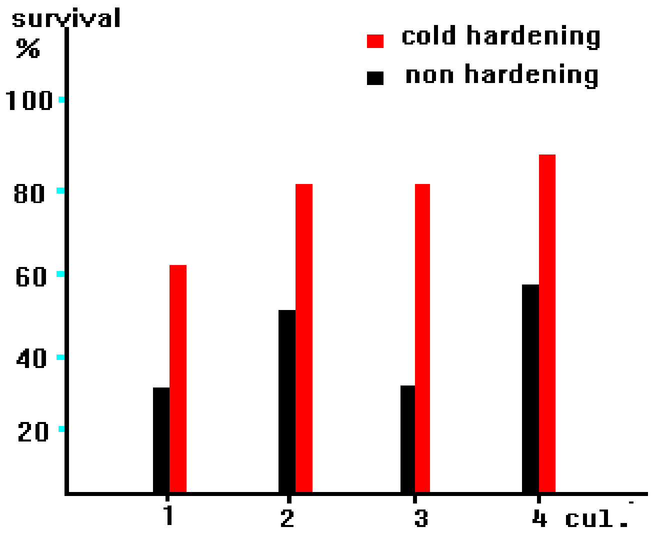


Fig. 6. Effect of subculture interval on the survival rate of cryopreserved apple shoot tips

Without cold-hardening, limited survival (25-50%) of cryopreserved apices was achieved. While survival of apices were drastically increased when apices were excised from mother plants cold hardened for 3 weeks (Fig. 7).



Cultivars: 1. Fuji 2. Golden Delicious 3. Shengli 4. Jincui

Fig. 7. Effect of cold-hardening on the survival rate of cryopreserved apple shoot tips

From 0.1M to 1.0M sucrose concentrations, the survival of apices increased in line with the increasing sucrose concentrations employed during preculture, from 0 or 35% to 65% or 75%. While the 1.2 M sucrose concentration decreased the survival to 50% or 70% (Fig. 8).

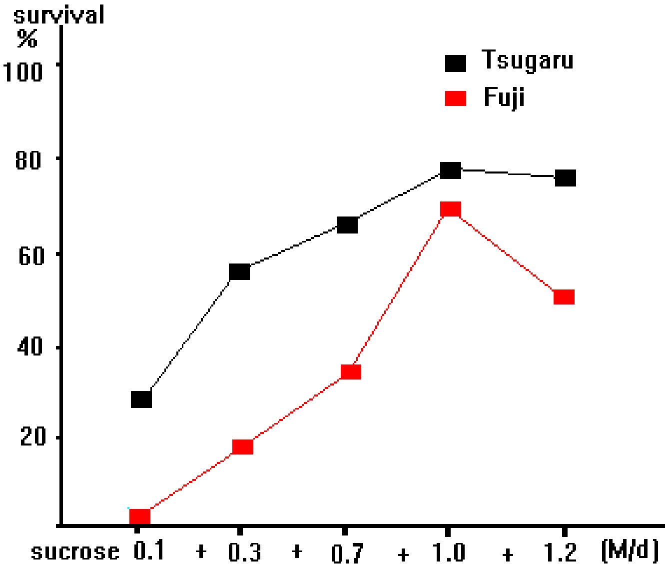


Fig. 8. Effect of sucrose pretreatment on the survival rate of cryopreserved apple shoot tips

Without dehydration, the survival rate of cryopreserved apices was 10% only. Survival increased progressively up to 77.8% when beads were desiccated to 4 hours and reached a MC of 30%, then decreased for lower MCs.

For encapsulation dehydration, apices sampled on plantlets subcultured for 3 months and cold hardened for 3 weeks, were successfully cryopreserved after encapsulation, daily transfers on media with progressively increased sucrose concentration from 0.1M to 1.0M, followed by desiccation to about 30% MC and rapid freezing (Fig. 9).

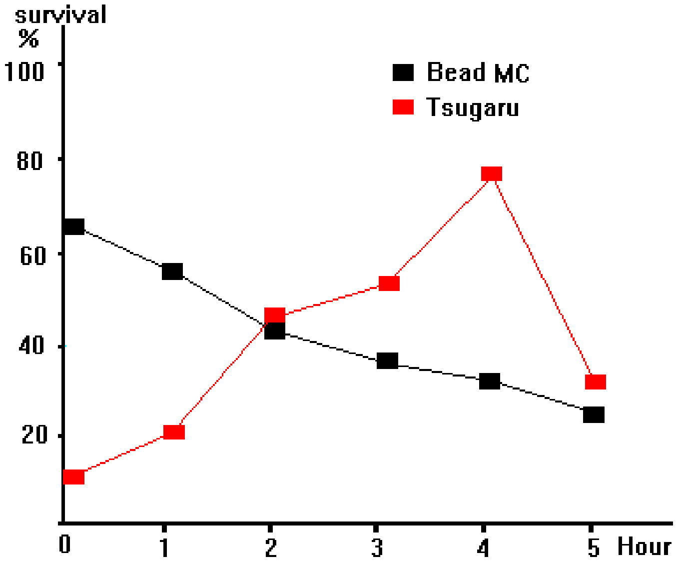


Fig. 9. Effect of desiccation period on the bead moisture content (%, fresh weight basis) and survival rate of cryopreserved apple shoot tips

Discussion

1) This study developed three techniques on the cryopreservation of ***in vitro*** apple shoot tips.
2) The results confirm that to develop one cryopreservation protocol it is necessary to test the different parameters including the subculture interval of mother plants, cold hardening, cryoprotectant pretreatment and dehydration treatment.
3) This work underlined the critical importance of subculture interval and cold-acclimation of mother-plants to achieve successful regrowth of apices after cryopreservation.

Selection of cryopreservation technique

As several efficient techniques are available on the cryopreservation of apple shoot tips, additional work undertaken to study the effects of techniques on the survival rate, regrowth pattern and speed of shoot tips and to select an applicable technique.

Based on the total regrowth rate measurement, vitrification was more efficient than encapsulation dehydration and two step freezing, with an average regrowth rate of 81% against 66% and 62% for encapsulation dehydration and two step freezing method (Fig. 10).

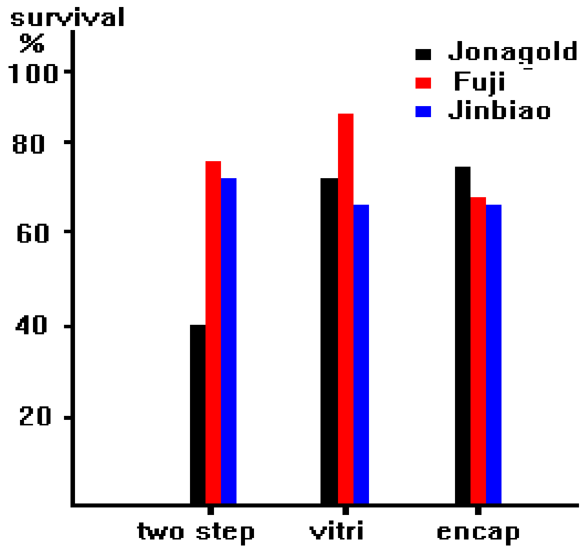


Fig. 10. Effect of cryopreservation technique on survival rate of cryopreserved shoot tips of three apple cultivars

However, this difference changed when callus regrowth was considered, since no callus formation was observed with encapsulation-dehydration method (Fig. 11).

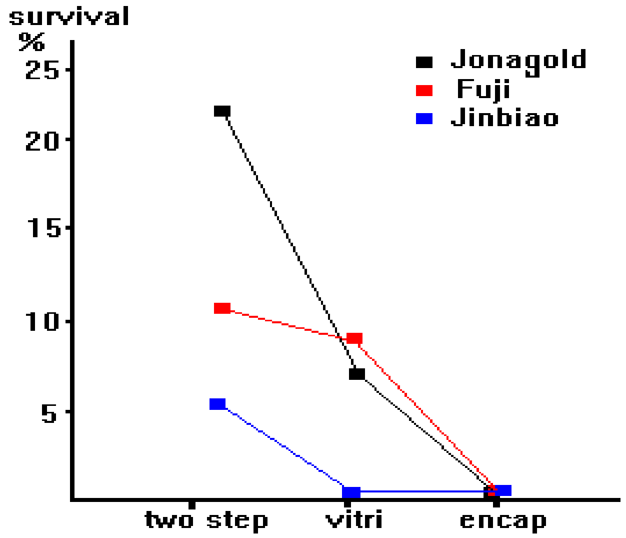


Fig. 11. Effect of cryopreservation technique on the regrowth pattern (callus formation rate) of cryopreserved shoot tips of three apple cultivars

With cultivars tested, the first sign of regrowth was observed slightly more rapidly for apices cryopreserved using vitrification and encapsulation dehydration method (Fig. 12).

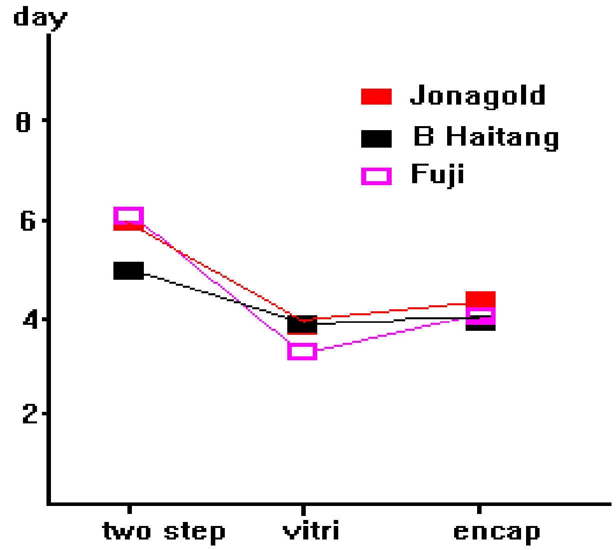


Fig. 12. Effect of cryopreservation techniques on the time requested to observe survival of cryopreserved apple shoot tips

Discussion

1) The choice of a cryopreservation technique for routine application to the conservation of a germplasm collection should be based on quantitative and qualitative results such as the regrowth rate and the regrowth pattern of cryopreserved explants.
2) In the present work, vitrification and encapsulation-dehydration was selected as the method of choice for cryopreserving apple germplasm, mainly based on quantitative and qualitative observations.
3) Under the optimal conditions determined, encapsulation-dehydration produced high regrowth rates, and, most importantly, regrowth of cryopreserved apices was always direct, without callusing.

Applicability of selected technique on the cryopreservation of temperate fruit shoot tips

The choice of a cryopreservation technique for routine application should also be based on the applicability of the technique to the broad genetic diversity possible. So the developed protocols here were tested with a large number of genotypes to evaluate their applicability and operational practicality (Table 5).

Apices of apple (eleven cultivars), pear (2 cultivars), sweet cherry (1 cultivars), grape (4 cultivars), kiwi (3 cultivars) and the dormant buds of one apple cultivar employed could withstand cryopreservation, with direct regrowth rates ranging between 22 and 80%.

Table 5. Cryopreservation of different genotypes using vitrification(*) and encapsulation dehydration methods

Cultivars	Regrowth rate (%)	Cultivars	Regrowth rate (%)
Apple			
278	42	*Pear**	
Fuji-12	57	Ya	78
GQ Fuji	59	Xuhua	80
Yatac	75	Sweetcherry *	
CG-80	73	Mahali	85
Fuji-1	33	Grape	
Fuji-2	54	Cabernet franc	25
Tsugaru	41	Chardnnary	35
Jonagold	79	LN33	40
Xianghong	45	FH-51	51
Red Star	80	Kiwi	
Golden delicious		Tomvi.F	22
Dormant buds	70	Tomvi.M	56
		Chinesis	49

* Apices of apple (eleven cultivars), pear (2 cultivars), sweet cherry (1 cultivars), grape (4 cultivars), kiwi (3 cultivars) and the dormant buds of one apple cultivar employed could withstand cryopreservation, with direct regrowth rates ranging between 22 and 80%.

Genetic stability of regenerated plantlets

Though the optimal technique selected here is convenient for the cryopreservation of temperate fruit shoot tips, it is essential, in establishing the procedures, that the genetic stability of the regenerated plantlets be identical to the initial starting materials. Therefore, plant morphology studies and molecular analysis were performed to identify the genetic stability of regenerated plantlets. Preliminary studies on the plant morphology ***in vitro*** and peroxidase enzyme mapping showed there was no significant variation in regrown plantlets. Other studies on field morphology and molecular analysis with Random Amplified Polymorphic DNA (RAPD) analysis are being performed.

Tissue culture and plant morphology in vitro

Though the plant regrowth recovered from cryopreservation was slower than the control, this difference disappeared when plantlets were subcultured second time.

No significant variation was found on the plant height, leaf colour, leaf type, subculture rate and rooting rate among plantlets cryopreserved or non cryopreserved.

Enzyme mapping of peroxidase of plantlets in vitro

No considerable variation was found on the enzyme mapping of peroxidase among the regrown plantlets and the control.

Conclusion

1. This study developed three cryopreservation techniques and selected the optimal protocols for the cryopreservation of temperate fruit shoot tips through quantitative and qualitative results, such as the survival and regrowth pattern of cryopreserved explants, but also confirms the applicability of the cryopreservation on the broadest genetic diversity possible, and on its operational practicality.

2. The results here also demonstrated the critical importance of the subculture interval and a cold-acclimation period of the mother-plants for the successful cryopreservation of most temperate species. It is possible that modifications in these parameters such as duration, temperature and photoperiod cold could further improve the applicability of the cryopreservation technique on wider fruit tree germplasm.

Acknowledgement

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Characterization and evaluation of plant genetic resources

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Introduction

The role of plant genetic resources (PGR) in the improvement of cultivated plants and thus in sustainable agricultural development is generally well understood. The main justification for the conservation of PGR is their use in improvements of plants. For proper utilization of PGR, characterization and evaluation is the key. Thus, expanding characterization, evaluation, and the number of core collections to facilitate use were listed among the 20 priority activities in the Global Plan of Action (GPA) of the Food and Agriculture Organization (FAO). Development of characterization and evaluation programmes to identify useful accessions and for detecting valuable genes has been accorded high priority.

The key to successful use of variability from broad gene pools requires the knowledge of desirable traits available in the germplasm and this requires a systematic evaluation of germplasm (Rao, 1980). Such information about a germplasm accession has to be catalogued and retrieved from genebanks for use of specific accessions with desirable traits. Therefore, characterization and evaluation of germplasm accessions are essential both to conservation and use of PGR (Riley ***et al***., 1996). The International Plant Genetic Resources Institute (IPGRI) has been according high priority for characterization and evaluation of both existing and new germplasm collections. IPGRI has been assisting the development of descriptor lists, germplasm directories, core collection concepts and methods, as well as occasional direct support to countries to assist in characterization and evaluation.

Characterization and evaluation may serve two functions. Firstly, many of the characters that are recorded on individual accessions serve as diagnostic descriptors for the accessions. Such diagnostic characters will help genebank curators to keep track of an accession and check for the genetic integrity over a number of years of conservation. Second function is related with use of the material. Both characterization and evaluation result in recording of a number of agronomic traits and this helps the user to identify accessions with desirable traits for use in crop improvement.

Appropriate descriptors and their use

For evaluation of PGR it has now become a routine to develop a list of characters and their states (in terms of measures or qualities, such as colour and shape), which are formally known as descriptors. There are different types of descriptors and these are:

A. ***Passport descriptors***: These provide the basic information used for the general management of the accession (including registration at the genebank and other identification information) and describe the parameters that should be observed when the accession is originally collected.

B. ***Management descriptors***: Provide the basis for the management of accessions on the genebanks and assist with their multiplication and regeneration.

C. ***Environmental and site descriptors***: These describe the environmental and site-specific parameters that are important when characterization and evaluation trials are held. They can be important for the interpretation of the results of those trials. Germplasm collecting site descriptors are also included in this type.

D. ***Characterization descriptors***: These enable a quick and easy discrimination between phenotypes. They are generally highly heritable, can be seen easily by the eye and are equally expressed in all environments. In addition, these may include a limited number of additional traits thought desirable by a consensus of users of the particular crop.

E. ***Evaluation descriptors***: Many of the descriptors in this category are susceptible to environmental difference but are generally useful to crop improvement and others may involve complex biochemical or molecular characterization. They include yield, agronomic performance, stress susceptibilities and biochemical and cytological traits.

With increasing use of information on traditional knowledge and molecular markers for PGR characterization, additional descriptors have been added to characterization and evaluation descriptors. All these descriptors are important for the management and recording of the sample during regeneration, multiplication and storage, and finally for use, either by breeders and other scientists, or directly by farmers. However, the number of descriptors used by different genebanks and for different crops will vary significant. It must be noted that these lists are only for guidance and the actual number and type of descriptors selected would depend on the individual researchers and genebanks and their objectives.

Characterization is primarily the responsibility of genebank curators using easily observable, highly heritable traits that are stable across environments. Characterization should be therefore be carried out based on the needs of the curators and other users to identify and manage the diversity in the collections. Many of the characterization descriptors are botanical characters. In many crops, simple and useful systems of classification have been developed that rely on only a few simply inherited and easily observed traits (Harlan and de Wet, 1972; Prasada Rao ***et al***., 1992). There is need for continued work on systematics and taxonomy in other crops to develop and promote simple classification systems based on a few key descriptors. This would allow curators to focus on characterizing a greater portion of their collections for these key traits.

In contrast, evaluation descriptors are more often are agronomically useful traits and probably more important in terms of use of PGR in crop improvement. Many of these can be complex and would require particular techniques, facilities and should be carried out by multidisciplinary teams to get best results.

In addition to the above or included in the above categories, ethnobotanical descriptors, farmers' preferences, molecular markers are being added to further expand the scope of descriptors that are being developed in recent years.

Description of heterogeneous accessions

Most accessions in any genebank are genetically heterogeneous. This is so not only true with out-breeders, but this can also be true in inbreeding landraces and wild populations. Such variation could be for one or more characteristics in an accession. It is important that this intra-accession variation be recorded, but the presently available descriptor lists do not satisfactorily meet this need. There are various ways in which the problem is dealt with: (1) to divide the accession into uniform subsamples and identify each subsample by a separate accession number, (2) to record the mean on the most common state, ignoring the rarer (that may be of interest) states, (3) to record mean and variance for quantitative traits or the frequency of all qualitative states, and (4) to record variable traits as variable without any particular score (Riley ***at al***., 1996). Sapra and Bhag Singh (1992) and Hintum (1993) suggested methods for curators to record within-accession variability. Recent descriptor lists also refer these to.

The suggestion 1, which has been gaining some attention in different genebanks as cost-cutting genebank management tool (Hintum ***et al***., 2001), needs some elaboration. Splitting of an accession means dividing it into different accessions based on easily identifiable intra-accession variation such as seed colour or plant height. Before deciding to split an accession one has to consider several issues. Since our major concern is genetic conservation, I focus here on genetic issues only. Splitting tends to change the distribution of the genetic variation for a character. In most cases, the change will be small, however, the trait selected should be simple and highly heritable. Since we know that most of the characteristics are correlated, splitting can result in some loss of variance in traits that are actually not selected for the purpose of splitting. This will probably increase in genetic drift during regeneration process. We should also consider the role that a selected trait may be playing in fitness (reproduction). Since in genebanks we are dealing with small populations, splitting the original collection might further reduce the population size and can increase the genetic drift further. Another overriding practical consideration is the fact that most of the collections that we are interested (and that show heterogeneity) are the landraces. Since it will be almost impossible (though some argue conversely) to reconstitute original population, one has to careful about the consequences of bringing landraces to the genebanks and changing them (either through splitting or combining similar accessions) for ease characterization, evaluation and other management needs and then failing to restore them to farmers as and when such a need arises. Such linking of genebanks with farmers is an essential step in countries that plan to integrate ***in situ*** (on-farm) conservation efforts with ***ex situ*** efforts and implement complementary conservation strategy.

From the above discussion, it is clear that there is no rapid, inexpensive, or precise method to describe heterogeneous accessions.

Descriptors and breeding objectives

As noted earlier, evaluation descriptors are generally useful from crop improvement perspective and thus these are often determined by the needs of crop improvement scientists interacting with any genebank. Breeders' needs would depend on the breeding objectives and these could be (Riley ***et al***., 1996):

1. Improvement of agronomic performance
    - Yield and yield related characters
    - Response to fertilizers
    - Resistance to lodging, shattering, etc.

2. Tolerances/resistances to biotic stresses such as
    - Disease resistance (fungal, viral, microbial, nematode)
    - Insect resistance

3. Tolerances or resistances to abiotic stresses such as
    - Drought/heat resistance
    - Photoperiod sensitivity/insensitivity
    - Resistance to water logging
    - Resistance to adverse soil conditions

4. Quality characters
    - Improved nutrition
    - Improved cooking quality
    - Improved flavour

Most of these traits are discipline-specific such as plant breeding, physiology, pathology, microbiology, biochemistry and a multidisciplinary effort would be necessary to systematically evaluate the germplasm. The process of evaluation would be greatly assisted if the objectives of breeders and curators were somewhat similar. Specialized, and in some cases sophisticated facilities may be needed; screening techniques will have to be developed/adopted and used. The fact that a large percentage of germplasm collected has yet to be evaluated can partly be explained by the technical and infrastructural difficulties in effectively evaluating large collections for a number of characters. The efficacy of evaluation depends on the optimum and uniform prevalence of a stress factor in the area of evaluation or on the efficiency with which such epiphytotic conditions could be created artificially (Riley ***et al.***, 1996). Effective screening techniques would be imperative for evaluating large collections and the objectives of breeding in a region would dictate the emphasis placed for developing such techniques.

Farmers' traits

With the increasing interest in ***in situ*** conservation (see page 102-109 in this volume) and traditional knowledge, generating information on traits that farmers use on their farms has gained importance. Additionally, direct use of germplasm by farmers is now well recognized by IPGRI and many other genetic resource workers as a valid and potentially important mechanism for use (Riley ***et al.***, 1996). New methods for participatory selection and breeding that include farmers in choosing what traits and germplasm they need has gained acceptance (Hardon, 1995) and have been endorsed in the Global Plan of Action (FAO, 1996a). The close involvement of farmers and scientists can result in effective evaluation of germplasm using descriptors and descriptor states that reflect farmers' priorities. Most of such traits may be location specific and in the case of taste preferences for example, characteristics may be conditioned by many genes.

The following ethnobotanical data are now becoming part of many descriptors list and most of these are collected at the time of germplasm collecting.

- Associated folklore
- Frequency of use of the plant
- Main cooking methods
- Time to cooking [min]
- Processing (Fermentation, etc.)
- History of plant use
- Parts of plant used
- Plant uses
- Local vernacular name and Translation/Transliteration
- Ethnic group
- Palatability (taste quality, if different plant parts depending on their use as food)
- Special uses
- Growing conditions
- Preferred growing conditions
- Associated flora
- Popularity of the crop
- Market information
- Seasonality of availability

While evaluating PGR, a number of above can be combined with other farmer-preferred traits (e.g. plant height, shape, etc.) and information generated would be very useful in selecting appropriate material for farmers' conditions. Acceptance of such material will be much greater than those that are developed solely based on researchers' criteria.

It is also now well recognized in some areas, farmers have developed distinct systems of classification and description. In the case of classification of cassava by the Aguaruna people (Boster, 1985), distinctions could be made among landraces using easily recognizable traits, which were not connected with use. However, the majority of studies of farmers' classification and description have found a utilitarian-based taxonomy using traditional knowledge (Berg ***et al.,*** 1991). Renewed attempts are now being made to incorporate such traditional knowledge with scientific knowledge. IPGRI is presently including traditional knowledge into standard collecting descriptors. A key question is to understand the relationship between farmers or folk taxonomies, and formal classifications including botanists' taxonomies and genetic diversity analysis (Riley ***et al***., 1996).

Use of Molecular techniques for characterization and evaluation

Much of the characterization and evaluation of PGR that has been done so far in many genebanks is based on recording of qualitative and quantitative characters. Developments during the last 10-15 years in the filed of biochemistry and biotechnology as permitted emphasising their use in characterization of PGR. The use of morphological phenotype for genotype characterization has advantages and disadvantages (Ramanatha Rao and Riley, 1994a,b). The multilocus nature of most of these characters provides information that is highly useful to breeders. However, the complex inheritable and interactions with the environment makes breeding difficult. The use of gene products (proteins, peptides) or metabolites (terpenes, flavonoids, etc.) partly solved this problem. Mendelian inheritance of isozymes makes genetic analysis still easier. However, variation in isozymes is often low. Molecular genetic characterization has several advantages: 1) no environmental influence, 2) any plant part from any growth stage can be used, 3) there is no limit on numbers for analysis, 4) requires only small amounts of material and 5) DNA is highly stable, even dry samples can be used. The major practical disadvantage is that it is not very suitable for large-scale screening. Experimental data on nucleotide sequence variation usually characterize only small parts of whole genome, often not related to economically interesting traits (Ramanatha Rao and Riley, 1994a,b).

Four areas of PGR characterization in which biotechnology can be used are: a) identification of genotypes, including duplicate accessions; b) "fingerprinting" of genotypes; c) analysing genetic diversity in collections or in natural stands and d) assembling a core collection (Dodds and Watanabe, 1990). Many genebanks receive significant number of accessions without any relevant passport data. Hence most genebanks carry an overload of duplicate accessions resulting in increased costs of management of collections. DNA fingerprinting with molecular markers can be very useful in this case (Watanabe ***et al***., 1995). However, identification of accessions, especially commercial cultivars, though is possible, is yet to be used on a large scale for identification of duplicates in collections. Thus, it appears that the value of fingerprinting is more in the area of varietal identification.

There are several examples of identification of genotypes, fingerprinting and study of genetic diversity using isozyme markers (Jarret and Litz, 1986; Glaszmann, 1988; Nevo, 1990; Bhat ***et al***., 1992; Lebot ***et al***., 1993). However, many of such studies involved relatively few loci and alleles in the analysis. Since any method would look at a small part of the genome, there is a need to use a variety of methods (Anderson and Fairbanks, 1990) and some of the drawbacks with isozyme analysis may be overcome with the use of molecular techniques. A combination of morphological and agronomic evaluation with biochemical and molecular analysis would give a more complete picture, as these studies provide complementary information. For detailed reviews see the related references (Peacock, 1989; Anderson and Fairbanks, 1990; Kennard ***et al.***, 1994; Ramanatha Rao and Riley, 1994a,b; Clegg, 1993; Watanabe ***et al.***, 1995; Virk ***et al.***, 1996).

In evaluating germplasm, multivariate analysis of isozyme data can be an additional set of criteria to identify a broad range of diversity that is needed for screening for resistances to stress factors or yield. If one needs to work on a narrow range of diversity then isozyme data and RFLPs can help identify similar or related germplasm collections. This is especially useful when the passport data on site of collection is not available.

At present, the cost of description of a germplasm sample using a molecular method is still higher than for conventional phenotypic description.

Table 1. Comparative assessment of different molecular genetic screening techniques

Characteristics	Isozyme*	RFLPs	RAPDs	Sequence-tagged SSRs	AFLPs	PCR sequencing
Development costs ($per probe)	Low (none)	Medium (100)	Low (none)	High (500)	Low (none)	High (500)
Level of polymorphism	Medium	Medium	Medium	High	Medium	Medium
Automation possible	No	No	Yes/No	Yes/No	Yes/No	Yes
Cost of automation	Low	Medium	Medium	High	High	High
Repeatability	Low	High	Low	High	Medium	High
Level of training required	Low	Low	Low	Low/ Medium	Medium	High
Cost ($ per assay)	High (2.00)	High (2.00)	Low (1.00)	Low (1.50)	Medium (1.50)	High (2.00)
Radioactivity used	No	Yes/No	No	Yes/No	Yes/No	Yes/No
Samples/day (without automation)	30-40	20	50	50	50	20

(Source: Karp ***et al.***, 1997)

However, with developments in this field are expected to make molecular methods powerful and economical tools for evaluating germplasm and locating useful genes and for routine characterization of germplasm. While selecting appropriate molecular tool for assessing genetic diversity one will require to consider type of information required; taxonomic levels to be measured; the expected level of polymorphism; reproducibility of the results; costs and automation and speed.

Improved evaluation and use

Germplasm conserved in the genebanks are not fully utilized, and in many genebanks, this problem is quite a significant one. Surveys done on distribution and use of conserved genetic resources have shown several reasons for such lack of utilization (Gao ***et al.***, 2000; 2001), most of important being lack of evaluation and limited access to information on evaluation. Among the one of the methods that can help in both improving the evaluation of germplasm and their use is development of a core collection. A core collection is a limited set of accessions of a crop species and its wild relatives, which would represent the larger collection, with a minimum of repetitiveness, the genetic diversity in the collection (Frankel and Brown, 1984). This subset would provide potential users with a large amount of the most of genetic diversity available in collection of a crop gene pool in a manageable number of accessions. It would therefore be useful to plant breeders seeking new characters which require screening techniques not possible with a large collection. In the late 1980s, IBPGR had worked on the development of a position paper on core collections, based on literature then available. It was clear from two meetings organized on core collections (Hodgkin ***et al***., 1995; Johnson and Hodgkin, 1999) that the core collections are not for conservation but for accessing and using large collections. IPGRI and several others have developed the methodology for establishing core collections (Hodgkin ***et al.,*** 1995; Kresovich ***et al***., 1995; Marita ***et al***., 2000; van Raamsdnon and Wijnker, 2000). Core collections may also have a role to play in genebank management from the point of view of distribution of representative samples. Several studies on the relevance as well as methodology for the development of core using different types of information, either singly or in combination, are going in many genebanks and universities. IPGRI supported the Oil Crops Research Institute of CAAS in China and National Bureau for Plant Genetic Resources of India to study on establishment of sesame core collections and is supporting similar study in South Korea.

Core collections can be developed using different kinds of information on the accessions of a collection including passport data, characterization data, evaluation data, biochemical and molecular marker data or a combination of one or more types of these data. In most cases characterization and evaluation data (this may include biochemical and/or molecular characterization), in combination with passport data provided most representative core subsets (Hodgkin ***et al***., 1995). Thus, whilst developing a core collection, complete evaluation of available collection and documentation of evaluation could become part of the objective.

While core collections may be useful for small breeding programmes, where fewer accessions and wide diversity are needed, or where initial exchange between countries of a representative sample of diversity is requested, core collections cannot replace evaluation for key traits of the entire collections as described in issue 3 above.

New information tools for better PGR management

All activities in PGR programme (exploration, collecting, characterization, evaluation, conservation and distribution) would generate significant amount of information that would be required at different stages of germplasm management, including is exchange and analysis. Thus, it is important that the genebanks develop appropriate information tools. A number of information tools are under development that can increase the exchange and re-use of germplasm data.

a) ***System Wide Information Network for Genetic Resources (SINGER)***. The Genetic Resources groups in the CGIAR centres scattered around the world, which hold large collections of the major food crops, were brought together under the System Wide Genetic Resources Programme (SGRP). A component of this programme, called SINGER, has linked the information on the germplasm holdings in different CG centres, allowing access to this information via Internet. The CGIAR has strengthened its activities in genetic resources, and through SINGER data and information on all centres, as well as other CGIAR genetic resources databases, will become fully available electronically to the world community. The data delivery mechanism preserves the autonomy of existing databases of different Centres and replicates the data at a central node that can be accessed through the Internet. Data could also be provided on CD-ROM, diskette or as printed output.

b) ***Data Interchange Protocol (DIP)***. Within a genebank, germplasm information on a given species is usually recorded in a standardised format. The Data Interchange Protocol is an initiative developed by the IPGRI APO Regional Group. The protocol seeks to provide information in a report format that enables a given genebank to export their descriptor lists and states in a form that allows recipients to re-use the data with their software. Using this format, germplasm information has been successfully interchanged between the genebanks in Beijing and Tsukuba. The Regional Information System for Bananas and Plantains, a part of INIBAP, uses DIP as a tool to facilitate setting up a network for information exchange among genebanks in Asia/Pacific and a user manual has been published (Yongsheng ***et al***., 1995 and is available on internet at http://www.ipgri.cgiar.org/system/page.asp?theme=3). Efforts are underway to make DIP to assist in the sharing and re-use of existing data in genebanks in information networking, statistical and visual analysis, and electronic publication.

c) ***Multimedia for easier access to PGR information***. With paradigm shift internationally, farmers who may not readily understand information recorded in conventional databases may increasingly access genebank information. The M S Swaminathan Research Foundation in Chennai, has been compiling genebank descriptor information on seed and plant characteristics using video clips that become part of the descriptor information stored in the computer. Video clips of farmers describing landrace characteristics using their own terms and language is also included so that indigenous knowledge is retained from the farmer as accurately as possible. Several other centres are also developing multimedia systems on computer, to provide precise and easy-to-visualise information on germplasm.

d) ***Geographic Information System (GIS)***. Another potential tool for better visualisation of descriptor data is GIS, in which different types of data that have a geographic reference can be plotted on a map using computers (Greene and Hart, 1999; Greene ***et al***., 2001). For example, the geographic distribution of existing ***ex situ*** collections might be viewed on a map, with the patterns of diversity expressed through various descriptors for which information is available. GIS may also have use in monitoring ***in situ*** diversity, using appropriate descriptor information including ethnobotanical data and indigenous knowledge in farmer-managed systems.

e) ***Expert system***. In developing descriptors, sufficient emphasis has been placed on descriptors to assist the curator to conserve the germplasm. However, most documentation systems attempt to provide germplasm users with information to enhance utilization of the germplasm. Thus there is an increasing tendency to ignore the importance of the use of descriptors for the purposes of accession-identification (diagnostic) and its management. If we ignore the curators’ needs for management of information to identify and maintain viable accession, one may be left with information but no accession. Similarly lack of information can also have the same effect. The long periods of storage for seeds have resulted in the perception that curators can maintain the germplasm with the current levels of information collected in genebanks. The need to emphasize the development of storage descriptors and genetic drift descriptor is being addressed in part by the Decision Support System for regeneration in genebanks, which is presently being developed by IPGRI.

In 1993, the idea of using Expert Systems (ES) for genebanks was discussed. ES are software that is developed to capture the options for decision-making. A genebank in a developing country may not have resources to maintain many experts in the genebank, especially if it were a multicrop genebank. Therefore, an ES for genebank management can be used to take over this task with the knowledge available. Software with “artificial intelligence" developed as ES can be used to compile the knowledge of expert curators for germplasm conservation and training of curators. A prototype ES developed in APO was readily accepted by participants of the regeneration meeting held in ICRISAT in 1995. Further work is in progress, jointly with NIAR, Japan and ICGR, China. The major impact of ES is seen as better utilization of knowledge on PGR conservation accumulated by IPGRI.

Conclusion

The importance of adequate characterization and evaluation data for both the effective management and use of PGR has been highlighted. There is need to establish priorities at the genebank level, with decisions made by curators and other users on the key descriptors that can be recorded on the accessions taking existing resources and needs into account. The descriptor lists developed by IPGRI serve as useful guides in standardising the way in which the information is collected and recorded. Actual users of descriptor lists may select and make necessary changes to the published lists for their use.

Improved evaluation is possible through the use of isozymes and molecular markers. Coupled with traditional morphological markers, the modern tools can help not only in better management of genetic resource collections, but also in better using the information. By generating more information on accessions and developing core collections using such information will greatly enhance the utilization of conserved germplasm.

With increased emphasis on on-farm conservation and involvement of farmers in plant breeding, gathering information on traditional knowledge and ethnobotanical information has to be promoted. Appropriate descriptors need to be developed for several crops to be included in the descriptor lists.

Recent developments in information and communication technologies offer possibilities to improved access and use of germplasm information. Use of computers is becoming more common and ability to handle multimedia data including indigenous knowledge about germplasm accessions and landraces, both ***in situ*** and ***ex situ*** is on the increase. Developing descriptor lists based on information received from breeders, curators, farmers and other users will help to include the most useful descriptors and descriptor states. Computerized information can be easily exchanged and analysed to be able to better management PGR collections and to derive greater benefits from use of conserved PGR.

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Towards *in situ* conservation of plant genetic resources

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Introduction

In situ conservation is dynamic in contrast to the semi-static nature of ***ex situ*** conservation, and these approaches complement each other help us maintain much more genetic diversity than it would be possible using only one method. Due recent awareness on biodiversity conservation, ***in situ*** conservation has been generally given higher priority over ***ex situ***. This is mainly because of its ability to maintain the evolutionary potential of species and populations (Altieri and Merrick, 1987; Ledig, 1988; Brush, 1989; Ledig, 1992; Brush, 1993; Hodgkin, 1993; IPGRI, 1994; Riley, 1995; IPGRI, 1996; Sthapit and Joshi, 1996; Jarvis, 1999; Sthapit and Jarvis, 1999; Jarvis ***et al***., 2000), and because it helps increase the access to and control of local communities over their genetic resources. However, given the fact that human activities can cause habitat destruction and loss of biodiversity in some cases, and the maintenance of biodiversity in other cases, it will be necessary to complement it with ***ex situ*** conservation. Any ***in situ*** conservation effort (wild or on-farm) must be composed of activities focusing on assessing, locating and monitoring. It is the information on genetic diversity - how much and where it is located and how it is changing over space and time – that is the most important for conservation and more so for utilization of that diversity.

The Convention on Biological Diversity (CBD) requires, under the Article 8, that the countries develop guidelines for selecting areas for ***in situ*** conservation, establish protected areas, regulate the use of resources so as to make a sustainable use and protect ecosystems and natural habitats. It also asks the countries promote environmentally sound development, rehabilitate degraded lands, ecosystems, and control or eradicate exotic species that may threaten the existence of native species, ecosystems, or habitats. It also wants the countries to ensure compatibility between conservation of biodiversity and sustainable use, respecting and preserving knowledge, innovations and practices of indigenous and local communities. Countries are required to provide regulatory mechanisms for the protection of threatened species and populations and, based on monitoring, regulate or manage relevant processes and categories of activities and provide financial and other support for ***in situ*** conservation. In the case of crop genetic resources, ***in situ*** conservation or on-farm conservation involves the maintenance of traditional crop cultivars (landraces) or farming systems by farmers within traditional agricultural systems. Many farmers use landraces, which they have developed over years of selection based on their preferences and are adapted to their environments. This approach to conservation has been gaining importance in recent years, though farmers have been using it for centuries.

In the case of agrobiodiversity, the effects of growers-practices and preferences are of paramount importance for conservation and utilization. IPGRI's current focus is on ***in situ*** conservation of forest species and wild relatives of crops and on-farm conservation of crop genetic diversity. The objectives of its study on on-farm conservation are to have information to know (Ramanatha Rao ***et al.,*** 2000):

1. The extent and distribution of diversity maintained on farm.
2. The processes used to maintain this diversity.
3. Who is maintaining this diversity?

4. The factors that influence these people to maintain diversity on farm.
5. Direct and indirect values of genetic diversity in terms of economic and socio-cultural benefits, ecological benefits and genetic benefits.

At this point of time, however, it must be noted that the genetic diversity conserved on-farm is subject to several influences, both natural and human made, and our understanding of the effects these influences on the genetic structure of the plant populations on farm is yet very much limited. This presentation, which is based on a presentation made last year (Ramanatha Rao ***et al***., 2000), on ***in situ*** conservation of agricultural biodiversity, emphasizes the process and not the scientific basis.

Role of *in situ* conservation

We know now that the ***in situ*** or on-farm conservation of agrobiodiversity helps not only to conserve the genetic diversity in target plant species, but also the evolutionary processes and the ecosystems that host the genetic diversity. In addition, on-farm conservation can play a role in other aspects of the ecosystem (such as ecosystem health, services and functions) and in socioeconomics of communities that are involved in such conservation efforts. Below is a list of some areas in which on-farm conservation has a role to play (Ramanatha Rao ***et al***., 2000):

1. Conservation of the processes of evolution and adaptation.
2. Conservation of diversity at all levels (ecosystems, species, intra-specific).
3. Integrating farmers/communities into national plant genetic resources (PGR) conservation systems.
4. Conservation of ecosystem services and ecosystem health.
5. Maintaining the process of local crop development by strengthening capacity of farming communities in landrace assessment, selection and exchange of crop germplasm.
6. Improving the livelihoods and quality of life of farmers.
7. Empowering farmers and communities over their crop genetic resources and improving access to them.
8. Providing information for national seed policy decisions regarding importance traditional seed supply system.
9. A component of complementary conservation strategy-linking farmers to genebank.

Establishing an *in situ* conservation programme

It is generally argued that farmers have been conserving PGR over centuries. However, from the increasing trend of integrating rural areas into national and global development efforts, some level of intervention will be required if the farmers have to continue practising on-farm conservation and benefit from it. There have been several suggestions as to how this could be achieved (Altieri and Merrick, 1987; Brush, 1993; Brush, 2000; Bellon ***et al***., 1997; Sthapit and Joshi, 1996). On-going research at IPGRI has shown that it is possible to conserve much of the genetic diversity on farm by assisting the farmers and communities in doing so while ensuring that they benefit from it at the same time. ***In situ*** (on-farm) conservation could play a significant role in supporting the local, indigenous, and rural communities to treasure their PGR, thereby putting the FAO's concept of Farmers' Rights in practice. IPGRI has developed a guide for establishing an ***in situ***/on-farm conservation research programme (Jarvis ***et al***., 2000). However, much of the discussion therein will be useful for establishing actual ***in situ*** conservation programmes as well.

To establish an ***in situ*** conservation programme for agricultural crops we will need to consider the following broad requirements:

Institutional framework

As indicated earlier, farmers have been practising ***in situ*** conservation informally for a long time. However, a focused programme on it would require some level of institutionalising the effort at local levels. Appropriate organizations that are committed to ***in situ*** conservation (similar to organizations that deal with ***ex situ*** conservation) need to be identified and guidelines for their interactions have to be developed and implemented. Roles of local and national institutions are central to enhance the local management decisions for agro biodiversity conservation and utilization. The role and responsibilities of individual organizations need to be clearly identified from the very beginning (though these could change during the period of the programme) and appropriate linkages for working together will be developed.

Sensitizing and strengthening local community

Identification of grassroot institutions that match the objectives of on-farm conservation is essential along with the strengthening their capacity to implement the programme. The rationale behind this is that the strategy for on-farm conservation will only succeed if indigenous communities and grassroot organisations are involved at different stages and their needs and problems are understood and addressed. This requires better understanding of what they do, how they do it and why they do it. Scientists working in this field often ignored this step when establishing framework for collaboration and partnership (Sthapit and Jarvis 1999).

Collaboration

In an effort like on-farm conservation several different organizations and people with different backgrounds will come to work together. In addition to teamwork, as the expertise that is required to carryout an ***in situ*** conservation programme is very diverse, there is a need for multidisciplinary and multi-institutional teams. To be effective, such teams would need to be well coordinated through effective communication, networking and participatory approaches. Any hurdles to collaboration should be identified ahead of time and remedial measures taken, so that the work goes on smoothly.

Framework for collaboration

In order to have institutional understandings for the people to work together in teams some sort of agreements such as Memorandum of Understanding (MOU) may need to be formalised at national level. Teams have to build close rapport with various rural people and in particular build up collaboration with farmers and farming communities. It is important to note that building rapport and making collaborative arrangements with farming communities are the most essential steps for the success of ***in situ*** conservation programme and time may be needed to develop a framework for collaboration. The participation of farmers is crucial in setting goal, as they knew better their needs in their local varieties. Biggs (1988) categorised farmer participation in agricultural research into four classes: contractual, consultative, collaborative and collegial. As the decision-making capacity of local institutions improved the quality of participation is enhanced from collaboration to collegial participation. It is essential to link on-farm conservation of PGR with various market outlets and incentives so that the farmers see the value of conservation.

Representative partnerships and equitable sharing of benefits

On-farm conservation initiatives should also promote equity at all project levels, from farmer participation to research to project management and decision-making. Equitable gender, ethnic and other minority involvement not only for data collection but also as members of research and management teams is the key for ensuring representative partnerships and benefit sharing. Increased women, minority, and farmer participation in decision-making is essential to ensure that diverse perspectives are incorporated into project objectives and that all stakeholders feel ownership in the project.

Process of on-farm conservation

Once understanding between institutions, collaborators and farming communities has been reached, the actual effort of on-farm conservation would start. This would include preparation, site selection, sampling and participatory approaches to on-farm management of agrobiodiversity. Ahead of site selection, the existing data such as descriptor lists, databases of e***x situ*** germplasm collections, herbarium collections, published literature in the natural and social sciences and other unpublished information shall be collected and used for eliminating inappropriate sites. Personal knowledge of experts, including personnel from NGOs, CBOs, and others existing local institutions would be most valuable. Simultaneously, the criteria for site and farmer selection have to be well defined. Broadly speaking, the criteria would be based on the genetic diversity, accessibility and interest of the farmers to continue to grow the varieties that are being targeted and these will have to be evaluated through a survey. Some generalized criteria that could be used for developing an on-farm conservation programme could include:

1. ***Ecosystems:*** It will be important to select sites in diverse agroecosystems preferably with different ecotypes. This will increase the chances of conserving genetic diversity, as this may be associated with agroecosystem diversity.
2. ***Intra-specific diversity within target species:*** It is important that the areas selected are grown to different landraces.
3. ***Specific adaptations:*** Efforts should be made while selecting different agroecosystems (see 1 above) to select sites with extreme environmental conditions (high soil salinity, cold temperatures, etc) and variation in pests. This will help to include types with specific adaptations.
4. ***Genetic erosion:*** It is better to select sites with less threat of genetic erosion to increase the life of conservation efforts.
5. ***Diverse use values:*** It is possible to ensure conservation of hidden genetic diversity by selecting sites with diverse use values of crops for food and other uses. It is important to note that for many farming communities, a crop is not just a matter of food production but also of investing and maintaining social relations and religious rituals.
6. ***Farmers and communities:*** Farmer's interest and willingness to participate are keys in site selection. This may require preliminary work in community sensitization on the benefits to farmers of conserving crop varieties. Site selection should also include sites with: socio-cultural and economic diversity; diversity of livelihoods, and importance of target crops for various ways of life; farmers' knowledge and skills in seed selection and exchange; and market opportunities.
7. ***Partners:*** Partners with interest in community and cooperation, experience in conservation interventions will be beneficial to the programme. Partners with distinct community participation expertise will have comparative advantage in dealing with community.

8. ***Logistics:*** These would include mainly the accessibility of the site throughout the year (in ***in situ*** conservation monitoring is essential) and availability of resources.

The existing data should be combined with an exploratory survey, using a Rapid Rural Appraisal (RRA), Participatory Rural Appraisal (PRA), or a similar approach. The Community needs to be sensitised to issues on hand and for this use of participatory approach is recommended (Ramanatha Rao ***et al***., 2000; Friis-Hansen and Sthapit, 2000).

Benefits to farmers

Farmers would grow a particular crop or crop cultivar only when they benefit from it. The benefit may be in the form of subsistence or livelihood, cash income, cultural uses, pride, adaptation to particular abiotic or biotic stresses. As noted earlier, the needs and preferences of farmers may change over time, leading to cessation of cultivation of particular crop species or a cultivar. So, if we aim to conserve a particular crop or cultivar, it is necessary to enhance the benefits for farmers from local crop diversity. This essentially means that the farmer would continue to cultivate the same crop or cultivar and, at the same time, benefit more from it either in terms of economics, socio-cultural or ecological value. In the changing scenario of APO region, ***in situ*** conservation of crops can be linked with eco-tourism, for example, agricultural habitat used as a resort or agro-tourism site, adding value and enhancing the sustainability of the effort. This could be achieved through some of the following means (Ramanatha Rao ***et al***., 2000).

1. Increasing crop genetic diversity's competitiveness for farmers.
2. Improving the crop itself through participatory plant breeding and/or through strengthening farmers' seed management and by improving the agroecosystem health.
3. Improved farmers' access to genetic materials. Attempts are underway to do this in other crops through maintaining Community Biodiversity Registers (CBR); seed exchange networks; linking farmers' seed/seedling supply systems to the formal sector; incorporating local crop resources into agricultural extension packages and by organizing diversity fairs.
4. Increasing consumer demand. This can be done by adding value through processing; diversifying the product base, respect for the environment and organic farming; public awareness, changes to policy, linking to eco-tourism and agro-tourism.

Identifying crop genetic diversity to conserve in situ

Genetic diversity is central to conservation and utilization of PGR. Through different means we are attempting to conserve and use plant genetic diversity. To do so effectively, it is important to have some understanding of the extent and distribution genetic diversity and its use value. Presently little information is available on the status of genetic diversity on farms. In this context, crop history can help to some extent. However, another source of information on genetic variation and uses of crop plants is the farmers' knowledge/traditional knowledge on propagation and exchange of germplasm within and between communities. There is a need for systematic documentation of IK on crop diversity and uses.

Conservation sites can first be established with the criteria mentioned above together with traditional knowledge of crop diversity and then genetic diversity determined within the sites. Based on the information on genetic diversity, it should be possible either to rationalize the number of sites or choose additional sites. It should, however, be noted that currently only morphometric methods are used to locate and characterize diversity. It is now possible to monitor and estimate genetic diversity using molecular markers, but actual use of these in countries where ***in situ*** conservation may be planned may take some more time. This may be further complicated as only limited resources are available for such work and thus it would be imperative to do the work in collaboration with other resource rich countries. Thus, we recommend that project leaders begin right away to systematically document traditional knowledge on crop diversity as a means to help guide them, together with historical and other information, to sites where they wish to invest resources in molecular measurements of genetic diversity. Experiences of IPGRI's global projects in Nepal and Vietnam suggest that community based organisations could be mobilized to locate and monitor crop plant diversity through participatory methods such as diversity fairs and biodiversity register. Based upon these information molecular markers can be used to estimate genetic diversity from diversity rich regions.

Other considerations

As ***in situ*** conservation of crop genetic resources is a long-term programme, it requires control of land rights in local communities, education, extension and development of environmental awareness. Once again it is reiterated that any ***in situ*** conservation programme should benefit the local communities. Management by local communities can often be developed to effectively link conservation and use. Thus, peoples' participation and cooperation between local people, researchers and conservationists and NGOs, is paramount for the success of on-farm conservation efforts. One should also consider the establishment of areas of intensive management or high yielding plantations within the areas where ***in situ*** sites are located. This would help in long term sustainability of ***in situ*** conservation programmes.

The essential elements of an ***in situ*** conservation programme for any crop genetic resources would be:

1. Identify sites with typical ecotypes/landraces of the countries concerned based on traditional knowledge and historical information and where available genetic diversity information.
2. Identify organizations that are stakeholders in such an effort, including community-based organizations.
3. Identify threats to continued maintenance of farms with unique and diverse crop cultivars.
4. Identify means to remove the threats in short term (to gain time to put in place the longer term efforts).
5. Ensure continued management of such farms by enhancing benefits to farmers, the custodians of genetic diversity.
6. Identify means to remove the threats in the long term (these could include a proper study to understand the basis for ***in situ*** conservation of crops, and other issues such as adding value, market incentives, improving the current cultivar for specific traits so that the maximum diversity is maintained).
7. Identify sustainable ways to monitor genetic erosion of crop genetic diversity using help of local institutions or organizing participatory approaches such as diversity fairs and CBR by the local community itself.

Next steps

The following general process of ***in situ*** conservation may be useful in moving forward in this area (Ramanatha Rao ***et al.,*** 2000).

1. Creating (or using existing) institutional framework and management.
2. Site selection (Training could be provided to national programme personnel how to do it in participatory manner).
3. Sensitizing and strengthening local community and institutions.
4. Locating diversity (e.g. crop diversity fair).
5. Measuring and assessing diversity.
6. Understanding value of genetic diversity.
7. Understanding and validating the processes that maintain diversity.
8. Monitoring diversity (e.g. Community biodiversity register).
9. Developing strategy for on-farm conservation.
10. Linking problems with new opportunities (capacity of local farming community enhanced using CBR and diversity fair, adding value through market and non-market incentives).
11. Institutionalising on-farm strategy integrating farmers into national PGR system.

There will be a need for national partners to spend some time to work out above processes in the context of specific target crop farming system. Community participation is central to ***in situ*** conservation, which needs substantial input from national partners and IPGRI to sensitize the national programmes and communities before a pilot scale ***in situ*** conservation strategy for any crop could be developed.

To set off in this new direction, we need:

- IPGRI can share ***in situ*** project information with EA-PGR partners
- Identify national partners who wish to integrate ***in situ*** conservation of crops
- Discuss and develop the process of ***in situ*** conservation with participation of grass roots stakeholders
- Identify resources.

Conclusion

In situ conservation or on-farm conservation of crop genetic diversity is feasible and a component of an integrated approach to conservation of germplasm. Efforts are underway to collect, conserve and use the crop genetic diversity in many countries in the region. Currently ***ex situ*** approach is the main focus of many national programmes. There is a need to focus on ***in situ*** approach, as together these two approaches would help us effectively conserve and access maximum crop genetic diversity. We need to understand how farmers value crop diversity, how they select and exchange the materials within and between communities so that sustainable crop genetic resources conservation ***in situ*** can be achieved. Another important aspect of on-farm conservation is the possibility of linking farmers and communities with national ***ex situ*** collections and to provide additional security for preserving locally adapted crop cultivars. In addition, on-farm conservation will assist the researchers to work towards the development goals of the conservation efforts, i.e. the well being of our main partners, the farmers.

Efforts are underway in different places to understand the genetic basis of on-farm conservation. Some assumptions have to be made, as the entire basis for ***in situ*** conservation is not clear yet. It is expected that any effort in this direction would only lead to a win-win situation, i.e. conserving and using crop genetic diversity for the benefit of those who depend on it, in addition to contributing to environmental health through its contribution to ecosystem functions in general.

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Conservation of forest genetic resources with special reference to endemic and endangered forest species in East Asia

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Introduction

There are two common approaches to genetic conservation that guide both crop and forest genetic resources conservation programmes (e.g. Namkoong, 1998). The ***ex situ*** approach relies on advanced agricultural technology, the use of rapid breeding techniques for specific traits and stored seed collections as the main form of gene conservation. These techniques are widely applicable for ***ex situ*** conservation of crops while they are less applicable for forest trees owing to much longer generation time and less-straightforward multiplication, for example. The second approach is that natural regeneration maintains plant populations in an optimum and stable state regarding their genetic resources and subsequently preservation of this natural endowment is the best form of conservation. Namkoong (1998) argued that either of these approaches alone would not help us to conserve all the forest genetic resources (FGR) for the following reasons. It is often assumed that the nature of the genetic resources is static while in fact the genetic resources are continuously in a dynamic state, whether they are in ***ex situ*** conditions or ***in situ.*** The rate of change is low under ***ex situ*** conservation such as genebank and faster in natural populations exposed to various factors affecting genetic processes. In addition, the genetic resources have changed in historically constrained ways and rarely, if ever, achieved an optimum 'adaptedness' to given environmental conditions. Thus it is important to realize the need for a complementary conservation strategy.

Long-term conservation of FGR in seed banks is problematic in many tree species and therefore the long-term conservation is mostly dependent on conserving living trees (e.g. Sigaud ***et al***., 2000). While conservation of crop genetic resources is mainly focused to individual species and actions are carried out for each species independently from other crops, conservation of FGR goes beyond that as forests consist of an array of species with complex interactions (Finkeldey, 1996). Thus conservation and management of FGR is much more complex task than management of crop genetic resources, except probably when one is dealing with ***in situ*** conservation (on-farm) of the later in which, along with agroecosystem considerations, the socioeconomic and anthropogenic factors can also make conservation very complex. While objectives and expected outputs of ***in situ*** conservation of FGR are in most cases species-specific, this approach also provides additional benefits, such as conserving multi-species ecosystems and the services they provide. Managing genes of various species in forest ecosystems requires information on various phenomena and processes, such as ecological interactions between species, genetic diversity within and between populations, gene flow and mating systems, for example. In addition, the task involves seeking common understanding between conservationists, managers, users and policy-makers who all have different expectations on how forests, not only genes, should be managed to obtain various benefits and services. However, some level of ***ex situ*** conservation will be in order, considering its role in making access to FGR diversity much easier.

In this paper, we summarise the different phases of the conservation of FGR in general and present some data on the state of endemic and endangered forest species in East Asia.

The Tree Conservation Database and the Plant Database of UNEP-WCMC[1] were used to derive information on these species in East Asia focusing on China, DPR of Korea, Japan, Mongolia and the Republic of Korea. In this presentation, the term 'forest genetic resources' mainly refers to genetic resources of forest trees but some information on bamboo and rattan species is also presented. Finally, we discuss how conservation of these endemic and endangered forest species could be improved in the future.

Forest resources in East Asia

In East Asia, like in many other regions, forests have been subjected to intense human use for centuries and in China for example, intercropping of forest trees and agricultural crops has a history of almost 1000 years (Huang ***et al.***, 1997; Huang, 1998). In 1995, the total forest area of East Asian countries totalled nearly 182 million ha, of which 74% were located in China (Table 1). Of the total land area of these countries, the forest cover is less than 16% (FAO, 1999) even though in some countries the coverage is considerably high (Table 1). The annual changes in forest cover were relatively small during the period of 1990-1995 indicating that the present state of forest is more or less stabilised after the long-term human exploitation. In case of China, the successful establishment of various protective forest systems since 1950s has significantly contributed to the present state of forests in the country (Li ***et al.***, 1999). However, vast areas of protective forests and tree plantations in China were established as monocultures using a few tree species and, in some cases, poor-quality planting material (e.g. Gu, 2001). This has caused problems in the plantations, such as pest and disease outbreaks, and some efforts have been initiated to diversify the monocultures towards multi-species plantations (Li and Zhou, 2000).

Table 1. Forest resources in East Asian countries (FAO, 1999)

Country	Total forest area in 1995 (1000 ha)	Percentage of land area (%)	Natural forest area (1000 ha)	Annual change in forest area, 1990-1995 (1000 ha)	Annual change rate, 1990-1995 (%)
China	133 323	14.3	99 523	-87	-0.1
DPR of Korea	6 170	51.2	4 700	0	0
Japan	25 146	66.8	-	-13	-0.1
Mongolia	9 406	6.0	9 406	0	0
Republic of Korea	7 626	77.2	6 226	-13	-0.2

According to the Tree Conservation Database, there is considerable a number of endangered tree species in East Asia (Table 2). Most of the tree species (127) are classified as vulnerable, i.e. they are facing a high risk of extinction in the wild in the medium-term future (for explanation of the IUCN red list classification see endnotes of Table 2). A total of 45 tree species have been categorised as endangered (a high risk of extinction in the wild in the near future) and 32 species as critically endangered (similar risk in the immediate future). So far, two tree species have been recorded as extinct in the wild and another two species have become extinct without reasonable doubt. In addition, a number of other tree species have been classified into the lower risk categories (Table 2).

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[1] United Nations Environmental Programme-World Conservation Monitoring Centre (www.unep-wcmc.org)

Habitat destruction and forest fragmentation are common causes a forest species to become endangered, whether it is rare or not, which reduce the size of reproductive population and disturb reproductive biology. In some cases, rare tree species are threatened with extinction due to hybridisation with their more abundant relatives. Selective and large-scale exploitation of a species for wood or non-wood products is also a common reason for endangerment. A notable example of the risks of hybridisation is ***Cercocarpus traskiae*** in Santa Catalina Island off the cost of California (see Carney ***et al***., 2000). This species is one of the rarest trees in North America and its population size has dwindled to a few adult individuals. Interspecific hybridisation with its more abundant congener, ***Cercocarpus betuloides*** ssp. ***blancheae***, has considerably contributed to the decline of ***C. traskiae*** in addition to grazing and rooting by introduced herbivores.

Table 2. Number of endangered tree species in East Asian countries (data source: UNEP-WCMC Tree Conservation Database, http:// www.unep-wcmc.org, July 2001)

Country	EX	EW	CR	EN	VU	LR/cd	LR/nt	LR/lc	DD	NE
China	2	2	32	44	114	7	48	41	17	28
DPR of Korea	-	-	-	-	3	-	1	-	2	2
Japan	-	-	-	1	10	-	5	2	5	3
Mongolia	-	-	-	-	-	-	-	1	-	-
Republic of Korea	-	-	-	-	-	-	2	1	2	1

1994 IUCN red list classification: EX extinct without reasonable doubt; EW extinct in the wild; CR critically endangered; EN endangered; VU vulnerable; LR/cd lower risk, conservation dependent; LR/nt lower risks, near threatened; LR/lc lower risk, least concern; DD data deficient, inadequate information available; NE not evaluated against the criteria.

Conservation of forest genetic resources

The aims of FGR conservation and management are to safeguard the evolutionary potential of forest ecosystems and to ensure sustainable use of the genetic resources to meet the present and future human needs. The general conservation strategies for FGR are basically similar to those ones applied to crop species and consist of consecutive phases. The existing forest resources and their genetic variation are a starting point for conservation activities. Subsequently, the identification of objectives and the selection of priority species for conservation are of utmost importance because future activities will be based on the objectives and priorities established during the planning phase. After the priority species have been identified, their genetic diversity needs to be assessed and located so that the following conservation activities and possible germplasm collecting can be focused on suitable areas. Selection of conservation methods depends on the objectives of a given conservation programme and provides a framework for the actual implementation of conservation activities in practise (see Ramanatha Rao and Koskela, 2001), including the regeneration of the conserved material. In the following chapters, we highlight some issues of these different phases (for more comprehensive presentation, see Koskela and Amaral, 2002).

Setting conservation priorities

As a general guideline, genetic conservation should focus on species with current or potential economic importance and/or under immediate threat of extinction (e.g. Finkeldey, 1996). It has been estimated that more than 50,000 tree species exist worldwide (see National Research Council, 1991) but less than 500 species have been systematically tested for their usefulness for man (see Palmberg-Lerche, 1999). Less than 140 tree species are being utilised in forestry and less than 40 are under active breeding programmes. However, if the direct utilisation by forest dwelling communities is taken into account, this figure may be much larger and very difficult to estimate. In addition to timber products, many more tree species are useful for man in terms of non-wood forest products and environmental services. Thus there is a need to strengthen long-term FGR conservation efforts (e.g. National Research Council, 1991; Palmberg-Lerche, 1999).

In theory, the aims of genetic conservation are rather simple, to ensure the survival of locally adapted populations and to prevent the loss of rare alleles (Mátyás, 1998). In practise, both human and financial resources are extremely scarce as compared to the conservation needs and relatively little is known even on the very basic biology of most trees or other forest species. Thus priority-setting for conservation is urgent for national programmes, which are trying to identify priority tree species and populations for inclusion in conservation programmes. The University of British Columbia in Canada has been developing a framework for prioritising species, populations and conservation methods within an IPGRI supported research project. The project attempts to rationally prioritise species or populations based on threats, potential or present values and the means that are available for conservation (see IPGRI, 2000).

The framework requires basic information on the status and dynamics of genetic diversity as well as its values, threats and potential for conservation management. This kind of information range is rarely available for most tree species but the framework can be used as a tool to compile the existing information and identify research needs. Using the framework, it is possible to produce a priority ranking of species into priority groups to be subsequently used by managers for selecting and implementing the necessary activities. Koshy ***et al***. (2002) stated that the framework, which is based on a decision tree approach, is as an effective tool for rational decision-making in genetic conservation, provided that the information needed can be estimated (if not available) and if the monetary values can be assigned with reasonable accuracy. Other benefits are that the collection costs of additional information can be directly compared against the expected returns and that the framework enables sensitivity analysis to improve our understanding what factors affect most in decision-making.

Locating genetic diversity

The decision-making process demonstrates the importance of information on the extent and distribution of genetic diversity. Conservation efforts cannot be effectively focused unless adequate information on genetic diversity in the target species is available. Currently, however, this information is lacking for many tree species and it cannot be made rapidly available. Thus, different layers of information, i.e. patterns of species and forest ecosystem distribution, threats, and the amount and spatial distribution of genetic diversity, needs to be combined to achieve an adequate assessment of the state of genetic diversity in a region or country.

The combination of information provides spatially explicit framework for conservation efforts by identifying areas to be ranked according to the level of threats and the genetic diversity they hold (Boffa ***et al***., 2000). As soon as species distribution has been identified, more efforts can be invested to evaluate genetic diversity within populations. Detailed information on genetic diversity and threats is essential in designing truly effective conservation areas, which can safeguard intraspecific diversity and maintain evolutionary processes.

Conservation methods

A wide range of methods, from protected nature reserves to intensive management of breeding populations for production systems, can be applied to conserve FGR. The choice of methods depends on the objectives of conservation, available genetic material and selected time scale. The choice of methods and subsequent implementation of the conservation strategy also depends on the availability of human and financial resources.

The two common approaches are ***in situ*** and ***ex situ*** conservation. The term '***in situ***' refers to the continued maintenance of tree populations in their natural sites under the environment to which they are adapted. ***Ex situ*** conservation takes place outside the natural habitat and may consists of activities such as the establishment of live collections or ***ex situ*** conservation stands and storing of seeds, pollen or tissue. To some extent, FGR can also be conserved and maintained by tree plantations or by other land-use practises such as agroforestry systems. However, it is likely that such management interventions reduce genetic variation in tree populations (e.g. Savolainen and Kärkkäinen, 1992) and thus these efforts can only support the more active conservation efforts.

No single conservation method is adequate alone and different methods should be applied in a complementary manner (Palmberg-Lerche, 1999; Boffa ***et al***., 2000). ***In situ*** conservation, however, has a number of benefits and thus it is often used as a basis for conservation programmes. The method allows the maintenance of evolutionary processes and subsequently continuing adaptation of tree populations to changing environmental conditions. This is particularly important for breeding programmes since the future human needs and environmental conditions are difficult to predict.

The establishment of protected areas has commonly been done on the basis of ecosystem or species conservation rather than genetic diversity conservation and therefore the design of ***in situ*** conservation programmes has been considered as primitive (National Research Council, 1991). In tropical forest especially, the complexity of interacting factors and a lack of scientific information have hampered the development of ***in situ*** conservation strategies. The uncertainties are related to an adequate size of ***in situ*** conservation area, number of individuals to be included, how to select conservation areas and how genetic variation is distributed within the selected areas (e.g. Palmberg-Lerche, 1999). Natural, pristine forest ecosystems are often considered as a starting point for ***in situ*** conservation. In reality, however, rural landscapes often form a mosaic of forest patches, ranging from seemingly natural to secondary forests and ending to seriously degraded forests and other wooded lands. The most obvious genetic effects of fragmentation are loss of genetic diversity both at the population and species levels, change in genetic structure of a population and increased inbreeding (Young and Boyle, 2000).

Ex situ conservation aims at capturing and maintaining a representative sample of the genetic diversity. The three major pitfalls in collecting germplasm samples for ***ex situ*** conservation are 1) limited coverage of genetic variation, 2) the collected plant material is biased in content, and 3) there is too much sampled germplasm to deal with (Brown and Hardner, 2000). To avoid these pitfalls, the sampling of populations and germplasm require special attention during the planning phase.

Traditionally, ***ex situ*** conservation of FGR is implemented by establishing conservation stands outside a native habitat of a given species for ease of management. However, long-term maintenance of the collected genetic diversity in these stands tends to be difficult owing to genetic drift and possible contamination by gene flow from outside. Another commonly used method for ***ex situ*** conservation is storing of seeds collected from a range of natural populations. In case of many tropical tree species, however, this method is not a straightforward or simple task due to recalcitrant seed behaviour (i.e. seeds are desiccation intolerant). Nevertheless, conservation stands and seed banks enhance the ability of researchers to readily access the material, evaluate it and use it.

In recent years, considerable amount of efforts have been put to the development of ***in vitro*** techniques to overcome these difficulties in ***ex situ*** conservation of recalcitrant tree species, cryopreservation being a notable example (Benson, 1998; Marzalina ***et al***., 1999). Cryopreservation provides great opportunities for a longer term ***ex situ*** gene preservation but problems in identifying proper protocols for a given species have limited its applicability. While it is likely that further research will ease these problems, the major potential of cryopreservation seems to be in supporting tree improvement programmes and conserving biotechnically-derived germplasm (Benson, 1998) rather than becoming a widely applied ***ex situ*** conservation method for FGR. Micropropagation, i.e. the use of tissue and organ cultures for organogenesis and somatic embryogenesis, can also be applied to maintain the genetic resources collected for ***ex situ*** conservation. Presently, however, the available technology for somatic embryogenesis is in most cases too expensive for cost-effective ***ex situ*** conservation.

Endemic and endangered tree species in East Asia

All endangered East Asian tree species in categories extinct in the wild (EW) and critically endangered (CR) are found in China (Table 3). Most of these tree species are endemic to certain locations or provinces in the country. The largest group of endangered tree species consists of the family Dipterocarpaceae despite the fact that these species only occur in southern parts of China. The six species in this family include ***Hopea*** spp., ***Shorea assamica*** ssp. ***assamica*** and ***Vatica*** spp., all having high-value timber properties. In the family Sterculiaceaea, there is one species listed in the EW category (***Firmiana major***) and other four in the CR category (***Pterospermum*** spp. and ***Reevesia rotundifolia***). The four critically endangered coniferous species consist of ***Abies*** spp. and ***Pinus squamata***. Other highly endangered families are Magnoliaceae and Cupressaceae with three and two tree species, respectively. The second species in the EW category is ***Thuja sutchuenensis*** (Cupressaceae).

Endangered tree species (category EN) in East Asia are listed in Table 4. Most of the species are found in China and only one is listed for Japan (***Picea koyamae***). In China, most of the species in this category belong to the family Magnoliaceae, including ***Magnolia*** spp. ***Manglietia ovoidea***, and ***Michelia*** spp. Eight out of the ten species in this family are endemic to China. The second largest group is the family Pinaceae with species like ***Abies fanjingshanensis***, ***Nothotsuga longibracteata***, ***Picea*** spp. and ***Pinus*** spp. Most of the species are also endemic to China. The species in the family Lauraceae include ***Alseodaphne rugosa***, ***Cinnamomum mairei***, ***Litsea*** spp. and ***Phoebe nanmu***, all endemic to China. In the families Taxaceae and Dipterocarpaceae, there are three (***Amenentotaxus yunnanensis***, ***Pseudotaxus chienii*** and ***Torrey jackii***) and two (***Parashorea chinensis***, ***Vatica mangachapsi***) species listed, respectively.

Based on the available information on the present or potential uses of the species listed in the categories EW, CR and EN, many of the tree species have potential to produce at least timber. Species like ***Hopea***, ***Shorea***, ***Vatica***, ***Erythrophleum***, ***Garcinia***, ***Abies***, ***Picea*** and ***Pinus*** spp. are all well-known for their timber qualities and sources for other wood-based products. Several species have also potential for other uses, such as fruits, oils and medicine, to name a few. Seeds of ***Horsfieldia pandurifolia*** are used to produce commercial oil while ***Cephalotaxus hainanensis*** and ***Cinnamum mairei*** have medicinal value. The most well known medicinal tree species of these is notably ***Ginkgo biloba***, which has an ancient geological record since the Jurassic period and which has been cultivated for centuries. It is also used as an ornamental species and has been introduced to many other regions like Europe, Africa, North and South

America and Oceania. ***Metasequoia glyptostroboides*** is another well known ornamental species, which has also been planted in many regions outside East Asia.

Many endemic and endangered tree species have proven and long-term use records but there is also a large number of species, which have not been studied in detail and relatively little documentation exists on the present or potential uses (e.g. ***Abies yuanbaoshanensis***, ***Cephalotaxus hainanensis***, ***Corylus chinensis***, ***Hopea mollissima***, ***Vatica xishuangbannaensis***). Some of these species have been described to science only recently while in case of other species, there seem to be differences concerning their taxonomic position between different databases. While analysing the reasons behind species becoming endangered (see Tree Conservation Database), it is seems that conversion of forest to agricultural lands and unsustainable logging have contributed in major part to habitat destruction of rare tree species or earlier more abundant species with specific site requirements. Concerning logging, it seems that large-scale, export-oriented commercial exploitation has directly caused the species to become endangered in families such as Dipterocarpaceae and Pinaceae while the indirect effects of logging (e.g. habitat destruction) have affected many other tree and plant species.

Table 3. Endangered tree species in China (data source: UNEP-WCMC Tree Conservation Database, http:// www.unep-wcmc.org, July 2001)

Category	Species / Genus	Family	Remarks
EW	***Firmiana major***	Sterculiaceae	endemic
	Thuja sutchuenensis	Cupressaceae	endemic
CR	***Abies spp.***	Pinaceae	3 species, all endemic
	Betula halophila	Betulaceae	endemic
	Bhesa sinica	Celastraceae	endemic
	Carpinus putoensis	Corylaceae	endemic
	Craigia kwangsiensis	Tiliaceae	endemic
	Cupressus chengiana var. ***jiangeesis***	Cupressaceae	endemic
	Diospyros vaccinioides	Ebenaceae	
	Euryodendron excelsum	Theaceae	
	Gleditsia vestita	Leguminosae	endemic
	Hopea spp.	Dipterocarpaceae	3 species
	Magnolia spp.	Magnoliaceae	2 species, both endemic
	Manglietia sinica	Magnoliaceae	endemic
	Metasequoia glyptostroboides	Taxodiaceae	endemic
	Myristica yunnanensis	Myristicaceae	endemic
	Nyssa yunnanensis	Cornaceae	endemic
	Ostrya rehderiana	Corylaceae	endemic
	Pinus squamata	Pinaceae	endemic
	Pterospermum spp.	Sterculiaceae	3 species, endemic
	Reevesia rotundifolia	Sterculiaceae	endemic
	Rhododendron protistum var. ***giganteum***	Ericaceae	endemic
	Shorea assamica spp. ***assamica***	Dipterocarpaceae	
	Sonneratia hainnensis	Lythraceae	endemic
	Ulmus gaussenii	Ulmaceae	endemic
	Vatica spp.	Dipterocarpaceae	2 species, both endemic

Table 4. Endangered tree species in China and Japan (data source: UNEP-WCMC Tree Conservation Database, http:// www.unep-wcmc.org, July 2001)

Country	Species / Genus	Family	Remarks
China	***Abies fanjingshanensis***	Pinaceae	endemic, relict species
	Alseodaphne rugosa	Lauraceae	endemic
	Amnentotaxus yunnanensis	Taxaceae	
	Annamocarya sinensis	Juglandaceae	relict species
	Bretschneidera sinensis	Bretschneideraceae	
	Burretiodendron tonkinense	Tiliaceae	
	Cephalotaxus hainanensis	Cephalotaxaceae	endemic, medicinal value
	Cinnamomum mairei	Lauraceae	endemic
	Corylus chinensis	Corylaceae	endemic
	Craigia yunnanensis	Tiliaceae	
	Dipteronia dyeriana	Aceraceae	endemic
	Erythrophleum fordii	Leguminosae	timber species
	Garcinia paucinervis	Guttiferae	timber species
	Ginkgo biloba	Gingkgoaceae	endemic
	Helicia shweliensis	Proteaceae	endemic
	Horsfieldia pandurifolia	Myristicaceae	endemic, oil from seeds
	Laportea urentissima	Urticaceae	
	Litsea spp.	Lauraceae	2 species, both endemic
	Magnolia spp.	Magnoliaceae	4 species, all endemic
	Manglietia ovoidea	Magnoliaceae	endemic
	Michelia spp.	Magnoliaceae	5 species, 4 endemic
	Nothotsuga longibracteata	Pinaceae	endemic
	Paranephelium hainanensis	Sapindaceae	endemic
	Parashorea chinensis	Dipterocarpaceae	
	Pellacalyx yunnanensis	Rhizophoraceae	endemic
	Phoebe nanmu	Lauraceae	endemic, timber species
	Picea spp.	Pinaceae	4 species, 3 endemic
	Pinus spp.	Pinaceae	2 species, 1 endemic
	Pseudotaxus chienii	Taxaceae	endemic
	Torreya jackii	Taxaceae	endemic
	Ulmus chanmoui	Ulmaceae	endemic
	Vatica mangachapsi	Dipterocarpaceae	timber species
Japan	***Picea koyamae***	Pinaceae	

As economic or other values always affect genetic conservation through priority setting, it is interesting to analyse what is the status of endangerment among the priority tree species listed by the FAO Panel of Experts on Forest Gene Resources. Table 5 lists selected indigenous priority tree species for East Asia based on FAO (2000). Only those species having their main distribution area within the East Asian countries were included and in some cases, the IUCN classification may indicate the status of a subspecies.

Table 5. Indigenous East Asian priority tree species, their conservation activities and level of endangerment (FAO, 2000; UNEP-WCMC Tree Conservation Database; CAB International, 2000)

Species	Conservation activities[1]		End uses[2]	IUCN classification[3]	Natural distribution in East Asia
	In situ	*Ex situ*			
Alnus cremastogyne	1	1	1-4		China
A. formosana	2	2	1-4		endemic to China
A. japonica	1	1	1-4		China, Japan, Korea
A. mandshurica	1	1	1-4		
Camellia oleifeira	2	1	4		endemic to China
Castanea mollissima	3	3	1-4		China, Korea
Chamaecyparis obtusa	1	1	1-4		China, Japan
Cinnamomum camphora	2	2	1-4		China, Japan, Korea
Cryptomeria japonica	1	1	1-4		China, Japan
Cupressus duclouxiana	2	2	1-4	DD	endemic to China
C. funebris	2	2	1-4		endemic to China
Cunninghamia lanceolata	1	1	1-4		China
Eucommia ulmoides	1	1	1-4	LR/nt	endemic to China
Fokienia hodginsii	1	1	1-4	LR/nt	endemic to China
Fraxinus mandshurica	1	1	1,3,4		China, Japan, Korea
Ginkgo biloba	1	1	1-4	EN B1+2c	China
Haloxylon ammondendron	2	2	2-4		China, Mongolia
Juglans mandshurica	2	2	1-4	NE	China, Japan, Korea
Ketaleeria pubescens	3	3	1-4		
Larix gmelini	2	2	1-4		China, Korea, Mongolia
L. potaninii	2	2	1-4	VU D2	China
L. sibirica	2	2	1-4		China, Mongolia
Paulownia elongata	2	2	1,3,4		endemic to China
P. fortunei	2	2	1,3,4		China
P. tomentosa	3	3	1,3,4		China, Japan, Korea
Phellodendron amurense	1	1	1-4	DD	China, Japan, Korea
Picea asperata	2	2	1-4		endemic to China
P. jezoensis	1	1	1-4		China, Japan, Korea
P. koraiensis	1	1	1-4	VU D2	China, Korea
P. meyeri	2	2	1-4		
Pinus densiflora	1	1	1-4	DD	China, Japan, Korea
P. koraiensis	1	-	1-4		China, Japan, Korea
P. massoniana	1	1	1-4	EN B1+B2	China
P. sylvestris var. mongolica	2	2	1-4		China, Mongolia
P. tabuliformis	1	1	1-4	LR/nt	endemic to China
P. yunnanensis	1	1	1,3,4		endemic to China
Populus euphratica	1	1	1,3,4		China, Mongolia
P. simonii	2	2	1,3,4		endemic to China
P. tomentosa	2	2	1,3,4		endemic to China
Quercus mongolica	1	1	1-4		China, Japan, Korea
Salix matsudana	2	2	1-4		China, Korea
Sapium sebiferum	2	2	1-4		China, Japan
Taiwania cryptomerioides	1	1	1-4	VU A1d	endemic to China
Tilia amurensis	2	2	1-4		China, Korea
Toona sinensis	2	2	1-4		China
Tsuga chinensis	2	2	1-4		endemic to China
Ulmus parviflora	1	1	1-4		China, Japan, Korea
Zelkova schneideriana	2	2	1-4		Japan

[1] Highest priority=1, prompt action recommended=2, important but less urgent than (1) and (2)=3.

[2] Industrial wood=1, industrial non-wood products=2, fuelwood, posts, poles=3, other uses=4

[3] 1994 IUCN classification: EW extinct in the wild; CR critically endangered; EN endangered; VU vulnerable; LR/cd lower risk, conservation dependent; LR/nt lower risks, near threatened; LR/lc lower risk, least concern

All of the listed priority tree species have more than one end use (except ***Camellia oleifera***, which is mainly used for producing high-quality edible oil in addition to its ornamental use). In many of these priority species, ***in situ*** or ***ex situ*** conservation activities have been recommended as high priority. However, only relatively a few of the species are included as endangered in the IUCN red list and none in the high-level endangerment categories (EW and CR). ***Gingko biloba*** and ***Pinus massoniana*** are listed in the EN category while priority species in the VU category include ***Larix potanii***, ***Pinus koraensis*** and ***Taiwania cryptomerioides***. The lower risk (LR) category includes three priority tree species, i.e. ***Eucommia ulmoides***, ***Fokienia hodginsii*** and ***Pinus tabuliformis***. In addition, ***Cupressus duclouxiana***, ***Phellodendron amurensis*** and ***Pinus densiflora*** are classified as data deficient (DD) and ***Juglans mandshurica*** as not evaluated (NE).

Endangered bamboo and rattan species in East Asia

There are more than 500 bamboo species in East Asia and of these about 450 are found in China (Li, 2000). Some 155 species is said to be endemic, endangered and rare (Hui, 2000). Presently southern and southwestern parts of China have more than 4 million ha of bamboo forests and their utilisation began 4000–5000 yeas ago (Yang and Xue, 2000). Some of the major priority bamboo species in this region include ***Bambusa bambos***, ***B. textilis***, ***B. vulgaris***, ***Cephalostachyum pergracile***, ***Dendrocalamus giganteus***, ***D. latiflorus*** and ***Phyllostachys pubescens*** (Rao ***et al***., 1998).

Apart from the more popular and economic bamboo species, the conservation status of many species is uncertain. Along with human exploitation and rapid conversion of forested areas to other land uses, the natural habitats of numerous bamboo species have been destroyed and the species threatened by extinction – a similar situation as in many tree species. The number of endangered bamboo species is not yet fully assessed in China but several species have been listed, namely ***Acidosasa chinensis***, ***Ampelocalamus actinotrichus***, ***Bashania spanostachya***, ***Chimonobambusa marmorea***, ***C. quadrangularis***, ***Ferrocalamus strictus***, ***Leptocanna chinensis***, ***Monocladus amplexicaulis***, ***M. saxtilis***, ***Qiongzhuea tumidinoda***, ***Sasa qingyuanensis*** and ***Yushania baishanzuensis*** (Fu Jinhe (INBAR), pers. comm.). Of these, only ***Q. tumidinoda*** is listed in the IUCN red list as rare (www.unep-wcmc.org). In addition, Hui (2000) listed a number of important endangered bamboo species, i.e. ***Cephalostachyum scandens***, ***Gaoligongshania megathyrsa***, ***Gigantochloa felix***, ***Dendrocalamus sinicus***, ***Ampelocalamus yongpingensis***, ***Teinostachyum yunnanensis*** and ***Melocalamus errectus***.

As many of the bamboo species flower only once in several years and the whole clump dies after flowering, long-term conservation and management of some of these species is more complex than in tree species. Comparing the few priority species listed above and the endangered species, it can be seen that there is no overlap, i.e. no endangered species have been identified as important which obvious make their long-term conservation a challenging task. However, as bamboos are highly valued species in general, their conservation has received some level of attention. In Yunnan for example, a total of 108 nature reserves exist hosting most of the bamboo species native to the area and about ten bamboo gardens have been set up for ***ex situ*** conservation (Hui, 2000).

The distribution of rattan resources in East Asia is mainly limited to the humid tropical forests of southern China, forming the northern most range of their distribution in Asia. Globally, there are some 600 rattan species of which 40 species and 21 varieties are native to China and 29 species and 15 varieties are endemic, respectively (Xu ***et al***., 2000). These include one species in the genus ***Daemonorops***, 35 species and 21 varieties in the genus ***Calamus***, and four species in the genus ***Plectocomia***. Some 21 priority rattan species (***Calamus*** spp.) have been identified and only two are found in China, i.e. ***Calamus palustris***(italics) (and two of its close relatives) and ***Calamus tetradactylus***(italics), which are endemic to China

(Rao ***et al***., 1998). Two rattan species in China are listed as vulnerable in the IUCN red list, i.e. ***Calamus erectus*** var. ***birmanicus*** and ***Plectocomia microstachys***. Like bamboos, also rattans have been intensively studied in China, especially their utilisation and cultivation. However, ***in situ*** conservation of rattans mainly relies on ***in situ*** conservation of forest trees as active efforts on rattans in this respect seem to be scarce (Xu ***et al***., 2000). Like in bamboos, botanical gardens are important for e***x situ*** conservation of rattans in China although intensive efforts have also been done applying in vitro techniques (Zeng ***et al***., 2000). An additional obstacle for the conservation of rattans is that their taxonomy is relative poorly studied, limiting our understanding on the number of endangered rattan species.

Discussion

The lists of endangered tree, bamboo and rattan species we have presented are not comprehensive but provide an overview on the situation in East Asia. In Japan, for example, there are a total of about 130 woody species considered to be threatened and rare (Yamamoto, 1996). These include species like ***Pseudotsuga japonica***, ***P. koraensis*** and ***Morus boninensis***, which are not included in the Tree Conservation Database but which are considered as endangered in Japan (Yamamoto, 1996). Similarly, a total of 345 tree species have been listed as endangered and rare in China (Gu, 2001). Also, the IUCN red list includes only few bamboo and rattan species in China. Obviously, the situation is similar in other East Asian countries and subsequently the actual number of endangered species is higher than we have now presented.

Typically the number of individuals of endangered species ranges from less than ten to several hundred, commonly distributed as isolated populations, and often the number of reproducing individuals is even less. In small populations, it is important to understand the difference between ecological or demographic processes and genetic processes, such as genetic drift (see Savolainen and Kuittinen, 2000). Without immediate conservation activities, small populations can be destroyed practically over-night as a result of habitat destruction making concerns about the effects of genetic processes irrelevant. In case we can assume that immediate extinction is not the main concern, it is relevant to analyse the effects of genetic drift and inbreeding. Small population size does not necessary indicate low levels of genetic variability although species with narrow distributions have often less variability than widely distributed species (Savolainen and Kuittinen, 2000). In small populations, genetic drift can considerably change allele frequency already over a few generations but usually the genetic effects take place slowly. Inbreeding, on the other hand, can result in deleterious alleles, which further reduce survival and reproduction potential even in relatively large populations but the level of inbreeding depression varies between species. In case of endangered species, the major genetic concern is to increase population sizes large enough so that mutation and recombination can generate enough variability within populations to respond to current selection pressures (Savolainen and Kuittinen, 2000).

Habitat destruction and genetic deterioration may not be the only threats to endangered and rare species. Under certain circumstances, hybridisation with congeners may become an additional threat and accelerate the rate of extinction. Recently, Carney ***et al***. (2000) highlighted the role hybridisation as an extinction factor and concluded that it is a real threat to the survival of many rare plant species. Hybridisation can decrease the fitness of rare species by outbreeding depression or by a cascade effect producing more and more hybrids and ultimately causing ‘genetic assimilation’. Ironically, controlled hybridisation with a common congener can also enhance genetic conservation in extremely rare species and save considerable amount of genetic material from inbreeding depression and a total loss (Carney ***et al***., 2000).

For critically endangered species, urgent ***ex situ*** conservation is the only reasonable short or medium term management alternative instead of passive protection of habitats or the remaining individuals. Many tree species are already so called ‘living dead’, i.e. they still exist but no regeneration takes place. For this kind of species, it is necessary to give high priority for immediate ***ex situ*** conservation, coupled with active efforts to promote reproduction and regeneration. As viable seeds are difficult or impossible to obtain, their reproduction have to rely on other means, such as vegetative propagation. Recently, the development of micropropagation techniques, such as shoot tissue culture and somatic embryogenesis, has opened new opportunities for conserving rare species and presently these applications are available for several tree species (e.g. Park and Son, 1996). In the future, it is also likely that the further development of ***in vitro*** techniques provides practical tools to apply controlled DNA modifications to increase mutation rates (Park and Son, 1996). This would be especially useful for increasing genetic variability in critically endangered species while it would also allow faster diversification than natural mutation or hybridisation.

As an active conservation measure, locally isolated gene pools of critically endangered species could be combined into new ***ex situ*** and ***in situ*** conservation stands, or into so called ‘forest gene banks’ in which large range of gene sources are purposely put together (e.g. Uma Shaanker and Ganeshaiah, 1997). These conservation stands could be established with micropropagated seedlings originating from as many individuals as possible. If available, seedlings propagated from seeds and wildings collected from natural stands could also be used to establish the conservation stands. Combining the remaining gene pools would reduce inbreeding rate and enhance outcrossing and mutation rates subsequently increasing the level of heterozygosity. The conservation stand should be established in areas where the threats by hybridisation to endangered gene pools can be eliminated.

Conclusion

Conservation of forest genetic resources is not an independent activity from forest management and utilisation for human needs (e.g. Finkeldey, 1996). Subsequently, conservation of endangered and endemic forest species is neither an independent effort from FGR conservation in general. The fundamental question in conservation of endemic and endangered forest species is related to financial and human resources. As both are scarce, it is obvious that conservation of economically more attractive species have received and will continue receive more attention as compared to rare species. Endangered species will be conserved if their economic values are recognised. ***Pinus koraensis*** is a good example of this. Although classified as endangered, it is a relative well-conserved species as it is important for plantation forestry (Wang and Hong, 2002). Inevitable fact is that many endangered species are already ‘living dead’ on their way to extinction unless immediate conservation efforts are carried out. Changing this situation would require high-cost ***ex situ*** conservation measures and obviously this is a task that many national conservation programmes are unable to do.

One cannot deny the importance of conserving rare and endangered species and thus alternative ways to increase awareness on the importance of these species should be developed. One way to do this is to obtain more basic information not only on the biological and ecological features of the species but also their present and potential uses. Often especially the uses are poorly documented and increasing the collection of traditional knowledge from local people could fill this gap. Once it is better known what can be lost, it is easier to justify urgent and possibly high-cost conservation measures while setting priorities.

Also, we should not only focus on analysing what species are endangered at the moment but also focus on how to prevent more species of becoming endangered, whether they are currently rare or abundant. Forest management practises can significantly contribute to this task. Recent development in the ‘sustainable forest management’-concept has also paid a lot of attention on management of FGR, which is ultimately a corner stone for applying this concept in practise. A number of criteria and indicators for sustainable forest management have been established and tested in the field (e.g. ITTO, 1990, 1992,1993; Prabhu ***et al***., 1999). Specific criteria and indicators to conserve genetic diversity in forest ecosystems have also been developed (Boyle, 2000). Thus it is expected that FGR management and conservation in general will be improved in the future but as this takes place slowly in the field, it cannot replace the need for immediate action to conserve endangered forest species and their habitats.

Since 1991, China has implemented its new FGR conservation strategy, which also pays special attention to endangered species and rescue conservation efforts have already been started for a number of species (Gu, 2001). What is noteworthy is that these efforts are an integral part of a national FGR conservation strategy with clearly defined short-term, mid-term and long-term objectives, and not an independent conservation activity as such. The conservation task in China is still enormous but the national FGR conservation strategy is the first step to tackle this challenge and other East Asian countries should follow this example. While doing so, it is also important to link FGR conservation strategies to national programmes for forestry and biodiversity to ensure overall coordination of natural resources management and conservation.

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Plant genetic resources data and information management and public awareness

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Introduction

Documentation is critical to the management of plant genetic resources (PGR). The data and information are derived from the activities on germplasm collecting, characterization, evaluation, conservation and utilization. The effective information management will help to promote the successful conservation and use of PGR (Zhang and Quek, 1999). Development of information network system and early warning system have been suggested by the Global Plan of Action (GPA) which will contribute to the successful implementation of other activities on conservation and use of PGR (FAO, 1996). Public awareness on conservation and use of PGR has become essential in the national, regional or international programmes.

The data and information are documented in many ways including publishing catalogues and directories, setting up computer databases, and developing information networks. The rapid development of information technologies has provided challenges and opportunities for effective documentation activities. With the accurate information, the relevant analyses could be carried out to identify gaps in germplasm research and collecting, and monitor genetic erosion, manage collections, and make decisions on relevant activities (Quek, 1999; Zhang and Quek, 1999).

PGR documentation

PGR documentation is to record, store, manage and use the data associated with germplasm collections with suitable information technologies. IPGRI is assisting national programmes to enhance the documentation and analysis of their own PGR data and information (IPGRI, 1999). The efforts are made to facilitate their access to and use of the information provided by others. Attention is also given to the use of computerized documentation systems and development of descriptor lists for different crops. Germplasm directories are considered as an important source of information on germplasm collections, conservation facilities, and status of characterization, documentation and distribution.

Standardize descriptors

Accurate data and information recorded on PGR is essential for effective management of the resources. Development of standards for recording data and information will help genebank managers and germplasm evaluators to record, manage, analyse, share, compare and use the information from different genebanks. IPGRI has collaborated with national programme partners and other crop research institutes in developing lists of standardized descriptors for crop species since 1977. As a result, descriptors for more than 85 crops have been published in the past 24 years. These descriptor lists provide uniform guidelines for documenting germplasm collections throughout the world. It has played an important role in facilitating characterization and evaluation, stimulating data and information sharing and exchange, and promoting the use of PGR (Alercia, 2001).

It is important that descriptors are comprehensive in their coverage and consistent across crop species. IPGRI coordinates and manages the development and production of the descriptor lists, and provides scientific and technical guidelines on developing crop descriptor lists. Generally, a descriptor list will cover passport data, environmental and site data, management data, characterization and evaluation data. However, some special descriptor lists were developed according to the requests from different users:

Multicrop passport descriptors: it was developed jointly with FAO. This list can be used for all kinds of crops.

Minimum descriptors: it only includes essential descriptors in which most of germplasm researchers and users would be interested.

According to a study conducted in 1997-98, the IPGRI descriptor lists were widely recognized as international standards for describing crop genetic resources and used by a majority of germplasm collection managers (Alercia, 2001). In order to meet the enormous demand for new descriptor lists, IPGRI is developing guidelines for producing them, which will help national programme staff to develop crop descriptors themselves. This will promote a wider adoption of the germplasm descriptor methodology in a larger number of crops, which need standard descriptor lists.

Develop documentation system

A well-organized set of interrelated databases is called a computerized documentation system (Painting ***et al.,*** 1993). It is characterized by the capabilities of entering, searching, printing and managing the data of germplasm collections in a genebank. Computerized documentation system is essential in any medium and large-sized genebanks. The available commercial hardware and software have provided the options for genebanks to manage their genetic resources data.

As most of genebanks have recognized the importance of documentation, efforts have been made to develop different kinds of documentation systems to manage and use the data obtained from different activities. These systems are usually designed particularly for a single purpose i.e. managing PGR data. In case of East Asia, some countries have developed their own documentation systems, for example, the Chinese Plant Genetic Resources System (CPGRIS) in the National Genebank of China (Wang and Liu, 1999), the Genebank Management System developed at the MAFF Genebank of Japan (Miyazaki, 1999) and the Germplasm Conservation Information System in Republic of Korea (Jun and Park, 1999).

Many commercial software such as MS Excel, MS Access, FoxPro are optional systems used to document germplasm accession data in some genebanks. For example, the Pyongyang Crop Genetic Resources Institute of DPR Korea uses MS Access to manage its passport and characterization data.

IPGRI has also made efforts to develop and promote computerized documentation systems. The Genebank Management System (GMS) was developed and provided to different genebanks for testing and uses. IPGRI also provided training on using this software. Mongolian National Genebank in Darkhan is using GMS to document its germplasm collections. At the same time, IPGRI is also promoting use of pcGRIN, a system developed in USA, through IPGRI-America Office.

Develop germplasm directories and catalogues

Germplasm directories provide useful information on germplasm collections, conservation conditions, status of characterization, documentation and exchange. They play a linking role among national programmes and sources of germplasm that can be accessed and the associated information. IPGRI has made efforts to gather relevant information and publish the germplasm directories on different crops. The crop network plays an important role in gathering information for such directories. For example, the safflower germplasm directory (Zhang and Johnson, 2000) and buckwheat germplasm directory (Zhou and Zhang, 1996) were published through the activities of underutilized crop networks.

A germplasm catalogue provides passport as well as characterization and evaluation information and helps breeders and other researchers' identify and access desired germplasm. IPGRI-APO is helping the national programmes in China and India to produce electronic catalogues of various crops that they conserved in their genebanks. For this purpose, software called DIPVIEW has been developed, which can directly import the file in DIP format, and is capable of incorporating the data of different crops from different genebanks. It has functions of browsing, searching and analysing the data and is a unique tool for distributing and using PGR data (Quek ***et al.,*** 1998).

Development of cooperative project database is an effective way to promote sharing information among partners. An example of this kind of database is the adzuki bean database developed under the cooperative project on adzuki bean in East Asia countries. The database has incorporated the passport and characterization data of 300 accessions of adzuki bean germplasm and made available to all partners for their uses.

Information networking

Information network is an approach to improve the information sharing among partners in the region. The concept of information network will be a virtual system, which will use all information technologies available for data and information management and sharing.

Information dissemination and sharing

Access to the data maintained by different genebanks is not easy. This is usually caused by the incompatible systems and languages used by different genebanks. IPGRI-APO has developed methods for data exchange and information sharing among partners in the region. To solve the problem of incompatible systems, the Data Interchange Protocol (DIP) was developed, which is a simple tool and enables linking different systems and developing information network in the region (IPGRI-APO, 2000; Zhang and Quek, 1999).

Internet

Improved access to Internet has provided opportunities for partners to share and access information related to PGR worldwide. Therefore, developing web pages and making the information available on Internet has become an important activity for IPGRI. IPGRI has launched a new institutional website at http://www.ipgri.cgiar.org. The website is designed to be a portal to information on PGR. It also reflects the vision, programmes and activities of IPGRI (Neate, 2001). The website includes the following information:

- Institutional information
- Genetic resources themes
- Regions
- Networks
- Information resources
- Crop/species
- Events
- Training
- Countries

For partners in East Asia countries, the following web pages are available:

http://icgr.caas.net.cn (Website for Institute of Crop Germplasm Resources of CAAS, China)
http://www.gene.affrc.go.jp (Website for the Genebank of MAFF, Japan)
http://www.niast.go.kr (Website for the National Institute of Agricultural Science and Technology, Republic of Korea)

Other useful sites are: http://safflower.wsu.edu (Website for safflower genetic resources), and http://www.ipgri.cgiar.org/nus/home.htm (Website for underutilized crop species).

Distance learning and virtual library

Web-based learning (either fully or partly) for training and human resource development and setting up virtual library are rapidly expanding areas of the information and communication technologies. These are addressing the cost-benefit issues of implementing relevant programmes and providing more channels to share and disseminate the information to more people concerned.

The web-based virtual library system is searchable system, covering a broad range of topics including directories, gateways and search facilities. Most of the sites for virtual library available on Internet are cost-free, high-quality information and analysis online. Many are gateway sites or have internal search engines. Each site may be changing rapidly in details of content. The directories in site usually contain the indexes of thousands of online libraries and library-related Web sites over the world. Gateways are linked to different on-line service of different libraries throughout the world. The search facilities are important for finding the particular information interested by different users, for example, www.vlib.org for biosciences.

Geographical Information System (GIS)

Geographic information system (GIS) is a useful tool to locate the diversity. In recent years, GIS is widely used in mapping biodiversity and managing natural resources. GIS is a database management system with specific function to handle spatial data, i.e. latitude and longitude (Guarino, 1995). Many applications on GIS have been developed for commercial purpose or for specific management purpose. IPGRI has been involved in developing two GIS software, i.e. FloraMap and DIVA for specific purpose of mapping biodiversity. These two systems are available almost free of charge and suitable for mapping and analysing plant diversity with geographic reference data.

Knowledge based management system

A knowledge-based system, also called an Expert System (ES), is usually a computer programme designed to simulate the problem-solving process of an expert in particular discipline. In agriculture, expert systems unite the accumulated expertise of individual disciplines, e.g., plant pathology, entomology, horticulture and agricultural meteorology, into a framework that best addresses the specific, on-site needs of researchers or farmers. Expert systems combine the experiential knowledge with the intuitive reasoning skills of a number of specialists to aid users in making the best decisions for their work.

Regeneration of germplasm conserved in genebanks has evolved into a complex process requiring the accumulation and integration of knowledge and information on many crops and species and from different experts. For determining the plant species, number of accessions, locations and budget estimation for regeneration activities, the genebank curators often rely on the monitoring data and experiences for decision-making. However, such experiences are not always available if the experienced curators left genebank. In order to reduce this problem, expert systems were identified as a useful tool with extensive potential in assistance to regeneration activities in genebanks.

IPGRI-APO is developing such an expert system called Regeneration Expert System (RES). It provides a platform to analyse and manage the monitoring data on viability of accessions and predict the overall viability situation of germplasm conserved in a genebank, and help curators to make decisions on which accessions need regeneration and to plan for regeneration work on annual basis. It also automatically creates a formula presenting relations between seed viability and storage conditions for particular crop or species. The prototype of this tool is under test and can be made available for others to test it further.

Documenting indigenous knowledge

Indigenous Knowledge (IK) is the knowledge of the people who are regarded as the original inhabitants of an area. It is therefore unique to the community and the basis of decision-making in their daily activities. The PGR IK is the results of long-term interaction between human activities for selection, conservation and use of various plant species for food, medicine and other purposes. It is closely associated with the on-farm management of PGR by farmers and related to the environment in which the people live. It is a living knowledge that changes over time as crops adapt to their changing environment (Quek and Zhang, 1997).

The introduction of modern technologies has resulted in the erosion of genetic materials and associated IK. The documentation of IK is important to ensure that the younger generations can learn and build on (Dai ***et al***., 1998). For documenting IK, IPGRI in cooperation with relevant national programme in Yunnan, China, a concept of “IK Journal” was developed and tested. In 1998, Yunnan Academy of Agricultural Sciences (YAAS) published four issues on the Journal of Yunnan Agricultural Science and Technology in cooperation with Yunnan Farmers’ Speciality Technical Association (YFSTA). All sources of articles were farmers provided through story telling and recorded with audiotapes or videotapes. Farmers are the first authors and scientists involved to further refine the article are co-authors. The journal has been translated into English and the concept is being tested in other regions.

Public awareness

The public awareness on conservation and use of PGR has become a very important activity. The activities on public awareness aim to obtain the support for conservation and use of PGR from different sources and people. The target audiences include policy-makers, donors, school children, etc. For short term, policy-makers and donors should be focused in order to gain support for suitable national policies and action plan for conservation of PGR threaten by human activities, climatic changes and natural disasters.

IPGRI has made efforts to raise public awareness through various ways including producing public awareness products, for example, magazine Geneflow, web pages, posters, postcards, calendars, etc. The magazine Geneflow has a broad range of readers, while the postcards, calendars and posters provided relevant information to selected people, particularly policy-makers and donors. For long term, IPGRI-APO has produced an Education Kit with focus on next generation of policy makers, genetic resources researchers and users. The Education Kit is a web-based training tool for 1-5 levels of school children. It provides basic knowledge and importance for conservation and use of PGR to school children. The English version was first launched in Malaysia in 2000. It is being translated into different languages and Chinese version will be launched in September 2001 in China.

Future concerns

Following areas could be priority activities on documentation, information management and public awareness in the future:

- Development of the gateway to plant genetic diversity would be an important for national programmes. The gateway could help users to access to and search for relevant information located in different sites.

- Bioinformatics is important for the analysis and documentation of molecular data. The effort should be given to studying the bioinformatics and its role in interpreting the molecular data.
- There is a need for a documentation system for ***in situ*** conservation activities. Development of such a documentation system will facilitate the relevant activities in national programmes.
- Multi-media documentation system with image processing facilities would help to manage and use available images for different research purposes in the national programmes. There is a need for developing such image tools.
- There is a need for developing the genebank early warning system which can assist the curators to manage the genebank effectively through providing warning signals on factors threatening germplasm conserved in genebanks.

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Recommendations on action plan for future activities

Action 1: Develop and implement *in vitro* conservation of vegetatively propagated crops

Proposed activities

1. Provide related technologies to the institute of the participating countries for technical assistance.
2. ***In vitro*** conservation of sweet potato (DPR Korea) and ***Allium*** (Mongolia) using slow growth methods for medium conservation in DPR Korea and Mongolia.
3. ***In vitro*** conservation of sweet potato (China), chrysanthemum (Japan) and garlic (R. Korea) using cryopreservation technologies in China, Japan and R. Korea.

Lead institute/country

Genetic resources Division, National Institute of Agricultural Science and Technology, RDA, Republic of Korea (develop proposal in cooperation with other partners)

Partners

Japan, China, R. Korea, DPR Korea and Mongolia

Action 2: Adzuki bean germplasm exchange

Proposed activity

Exchange 50 accessions from each country

Lead institute/country

National Institute of Agrobiological Sciences, Japan

Partners

China, Japan, DPR Korea and R. Korea

Action 3: Joint germplasm collecting

Proposed activities

During the discussions, each country identified crops in which they were interested in, as given below:

Japan: Wild species of ***Vigna*** and rice
Mongolia: Fodder, grass and legume
R. Korea: Wild soybean, wild rice
DPR Korea: Wild soybean
China: Forage and ***Vigna*** species

1. Develop proposal for joint collecting activities for crops, which are common to more than one country.
2. Each country should send the georeference data (latitude and longitude) on existing collections of above identified species to IPGRI Office for East Asia for assistance in mapping the diversity and identify gaps for collecting.

Lead institute/country

Mongolian State University of Agriculture, Mongolia.

Partners

Japan, China, DPR Korea, R. Korea and Mongolia.

Action 4: Black-box storage in Japan and China national genebanks

Proposed activities

1. Japan and China national genebanks to issue the formal offer for black-box storage for other countries.
2. Mongolia and DPR Korea will contact the national genebanks in China and Japan for black-box storage.

Lead institute/country

Pyongyang Crop Genetic Resources Institute, DPR Korea

Partners

Mongolia, DPR Korea, China and Japan

Action 5: Documentation and public awareness

Proposed activities

1. All country coordinators will send contributions to IPGRI newsletter, including news about PGR activities and short scientific papers, including forest and medicinal plants.
2. All countries make information on PGR publications available as soon as they are published.
3. National coordinators agreed to be proactive to obtain and supply relevant information to IPGRI Office for East Asia for updating PGR directory.
4. IPGRI will develop the prototype of EA-PGR web pages and circulate to national coordinators for comments and follow-up.

Lead institute/country

IPGRI Office for East Asia

Partners

All member countries

Action 6: Forest genetic resources activities

Proposed activity

Assist to identify national partners for forest genetic resources activities and send the information to IPGRI-APO.

Leading institute/country

All member countries

Partners

All member countries

Appendix I. Programme of the meeting

12 Aug. Sun.	Participants arrival	
13 Aug. Mon.	9.30 – 10.30	Inauguration (***Chair: N. Altansukh***) Welcome address by ***MSUA*** Welcome address by ***Zhou Ming-De***, IPGRI-Beijing Keynote speech by ***Percy Sajise,*** IPGRI-APO Keynote speech by ***D. Mishigjav***, State Secretary, Ministry of Education, Culture and Science Keynote speech by ***T. Galbaatar***, Vice-president, Mongolian Academy of Science.
	10.30 –11.00	Coffee break

Country Reports (20 min. for presentation and 10 min. for questions and discussion)

Chair: Jarkko Koskela

11.00 – 11.30	The status and progress of activities on plant genetic resources in China ***Liu Xu***
11.30 –12.00	Plant genetic resources status and progress of activities in Japan ***Tsukasa Nagamine***
12.00 –12.30	Current status of conservation and use of plant genetic resources in the Republic of Korea ***Nam-Kyu Park***
12.30 – 13.30	Lunch

Chair: Tsukasa Nagamine,

13.30 – 14.00	Plant genetic resources in the Democratic Peoples Republic of Korea ***Ju Yong Bong***
14.00 – 14.30	Plant genetic resources status and progress of activities in Mongolia ***N. Altansukh***
14.30– 15.00	Regional network for conservation and use of plant genetic resources in East Asia ***Zhou Ming-De***
15.00 – 15.30	Plant genetic resources exchange and use and Intellectual Property Rights: implications to EA-PGR network ***Percy E. Sajise***
15.30 - 16.00	Coffee break

Chair: Zhou Ming-De

16.00 – 17.00	Discussion on country reports and regional cooperation 1. Challenge and needs of national PGR programmes

2. Opportunities and activities for possible collaboration
3. Germplasm exchange and IPR issue
4. International Undertaking and GPA implementation

17.00-19.00 Visit to fodder crops experimental field RIAH

Thematic reports (20 min. for presentation and 10 min. for questions and discussion)

19.00-21.00 Dinner by NBPGR/MSUA

Chair: Liu Xu

14 Aug. Tue.

09.00 – 09.30 Conservation and use of common millet germplasm
N. Bayarsukh

09.30 – 10.00 Classification and use of spring barley
Ri Jin Yong

10.00–10.30 Conservation and utilization of soybean germplasm
Kang Jung-Hoon

10.30 –11.00 Coffee break

Chair: Ju Yong Bong

11.00 –11.30 The ***Vigna angularis*** complex and related species in East Asia
Norihiko Tomooka

11.30 – 12.00 Cryopreservation of temperate fruit tree species
Wu Yongjie

12.00 – 12.30 Towards ***in situ*** conservation of plant genetic resources
V. Ramanatha Rao

12.30 – 13.00 Conservation of forest genetic resources with special reference to endemic and endangered forest species in East Asia
Jarkko Koskela

13.00 – 14.00 Lunch break

Chair: Nam-Kyu Park

14.00 – 14.30 Characterization and evaluation of plant genetic resources
V. Ramanatha Rao

14.30 – 15.00 Plant genetic resources data and information management and public awareness
Zhang Zongwen

15.00 – 16.30 Visit to MSUA

Chair: N. Altansukh

16.30 – 18.00 Discussion on thematic topics

1. Complementary conservation strategy
2. Forestry genetic resources
3. Medicinal genetic resources
4. Documentation, information management and public awareness

	19.00-21.0	Dinner by IPGRI (Avtai Khan Mongolian Ger restaurant)

Chair: V. Ramanatha Rao

15 Aug. Wed.	09.00 – 10.30	Developing workplan for the activities on EA-PGR based on the earlier discussion
	10.30 – 11.00	Coffee break
	11.00 – 12.00	Presenting and finalizing workplan
	12.00 – 12.30	Closing remarks
	12.30 – 13.30	Lunch break
	13.30 – 16.30	Free time
	16.30	Leave for field trip to Darkhan

Chair: N. Altansukh/N. Bayarsukh

16 Aug. Thu.	09.00	Visit PSARI (Programme to be provided separately)
	13.00 – 14.00	Lunch break
	15.00	Leave for Ulaanbaatar
17 Aug. Fri.		Departure of participants

Appendix II. Participants of the meeting

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