

Rice Germplasm

Collecting, Preservation, Use

IRRI

INTERNATIONAL RICE RESEARCH INSTITUTE

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Collecting, Preservation, Use

PROCEEDINGS OF
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IRRI

INTERNATIONAL RICE RESEARCH INSTITUTE
P.O. Box 933, Manila 1099, Philippines

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Foreword

The collection in the International Rice Germplasm Center at IRRI is not the Institute's sole property: it belongs to the world. International cooperation in collecting, preserving, and using plant genetic resources without limitations must continue. Controversies that involve intellectual property rights and political systems need to be resolved. This will require broad-based discussions among scientists, lawyers, breeders, and the private and public sectors.

IRRI and IBPGR are working together to facilitate dialogue on this issue, and collaborated in hosting the third international workshop on rice germplasm. A distinguished group of scientists from all over the world who are concerned with safeguarding the world's rice germplasm participated. They vigorously discussed ideas and activities to foster the continuing exchange of germplasm. This is just part of their work to ensure that germplasm is always freely available, IRRI will continue to join forces in efforts to reach that common goal.

The third international workshop on rice germplasm was organized by Drs. T. T. Chang and D. A. Vaughan of IRRI in collaboration with Mr. P. M. Perret and Dr. J. M. M. Engels of IBPGR. Drs. Chang and Vaughan were the technical editors for the papers presented and discussion that took place during the workshop. Dr. L. Pollard edited this proceedings book, assisted by Ms. G. Argosino.

KLAUS LAMPE
Director General

Perspectives

International Rice Research Institute

K. J. Lampe, director general

IRRI purposely scheduled this Rice Germplasm Workshop simultaneously with the Rice Genetics Symposium and the Fourth Annual Meeting of the Rockefeller Foundation International Program on Rice Biotechnology. The interaction between those who are responsible for the collection, documentation, and conservation of germplasm and those who are committed to using those resources for the enhancement of crops is vital in achieving our common goal.

The world is changing rapidly, and so is IRRI. With a new structure based on its strategy *IRRI toward 2000 and beyond* and its *Work plan for 1990-94*, and with a drastically reduced work force, we are adjusting to a new situation. What we must retain, at all cost, are the highest quality standards needed to safeguard the germplasm already collected. We also will make all effort to minimize further losses in the genetic resource base, including field collecting in critical areas.

During the three decades since the founding of IRRI, many national research systems have gained considerable strength. National germplasm centers have been developed and collaborative links established. This particular Rice Germplasm Workshop, jointly organized by IRRI and IBPGR, has been strongly influenced by the intellectual leadership of Dr. T. T. Chang, who developed IRRI's Germplasm Center and has headed it all these years.

IRRI will continue to play an active role in the conservation and use of plant genetic resources, especially in establishing and enhancing contacts among the different national and international genetic resources centers across boundaries of disciplines, languages, crops, and climatic regions. The plant germplasm of our globe must remain common property. The free flow of genetic materials among researchers working on food production must be safeguarded. We all can contribute to this objective. This workshop is a visible sign of our commitment.

Rice germplasm is a common heritage of mankind that has evolved through several millennia of cultivation and selection by our farming ancestors. IRRI shares with the national agricultural research systems of many rice-growing countries the responsibility for assembling and preserving this enormous and rich germplasm.

The tasks involved in conserving the world's rice germplasm for productive purposes are important, challenging, and difficult. Input is needed from every institution concerned. This workshop will help harmonize efforts in this collaborative venture.

Allow me to share with you a number of historical developments in international collaboration for rice germplasm conservation.

- 1970 Preliminary planning at Hyderabad involves Ford Foundation, USAID, USDA, AICRIP, and IRRI staff.
- 1971 The 100 rice breeders attending the Rice Breeding Symposium (IRRI 1972) urge IRRI to initiate and coordinate field collecting activities. USAID begins support of collecting in Nepal. The Rockefeller Foundation provides seed money for IRRI to start field collecting activities; the Ford Foundation, USDA, and USAID, provide logistical support in several countries. Field collecting activities involving IRRI staff continue to 1985.
- 1977 The first Genetic Conservation Workshop is held at IRRI (IRRI-IBPGR 1978), in conjunction with the dedication of the Rice Genetic Resources Laboratory building.
- 1978 IBPGR commits funds for field collecting in South and Southeast Asia.
- 1978-85 Fourteen Asian countries join the massive campaign. IITA, WARDA, FAO, IRAT, and ORSTOM also collaborate on field collecting, with IBPGR inputs in several African countries. Madagascar joins collecting efforts during 1984-85. About 43,000 samples are collected in tropical Asia and 7,000 more samples are collected in tropical Africa.
- 1983 The second Genetic Conservation Workshop is held at IRRI (IRRI-IBPGR 1983).
- 1987 Field collecting activities involving IRRI staff resume, with emphasis on the wild relatives of rice.

This history illustrates genuine international and interinstitutional collaboration, involving many concerned people on an unprecedented scale. In concurrent developments during the last decade, the Government of Japan helped several Asian countries establish modern genebanks. China and India built their national genebanks. IRRI repatriated entire national collections to five Asian countries, two states of India, and one African nation.

Now it is time to assess the gains and consolidate the collections. New talents are needed to manage the modern genebanks and to ensure the security of conserved seed. IRRI held two comprehensive genetic conservation and management training courses in 1985-86 and 1988-89 and one data base management course in 1988. More recently, IBPGR launched its crop germplasm network approach and entered into a cooperative venture with IRRI to sponsor this Rice Germplasm Workshop. The new focus is on enhancing germplasm evaluation and use (Chang 1991).

I have been advocating an expanded role for germplasm workers in evaluation and enhancement, rather than their functioning only in a service role. This will link conservation with use. This workshop will develop ways and means to improve the capabilities of germplasm workers and strengthen their linkages with workers in other disciplines involved in rice improvement, including biotechnology.

International Board for Plant Genetic Resources

D. H. van Sloten, acting director¹

Many participants at this workshop will draw attention to earlier meetings on rice genetic resources. I want to refer in particular to the IRRI/IBPGR workshops on genetic conservation of rice held at IRRI in 1977 and 1983 (IRRI-IBPGR 1978, 1983). This 1990 meeting should be seen as the third workshop in this series. One should be careful not to reinvent the wheel, and I therefore request that you study the recommendations of the 1977 and the 1983 workshops in detail. Assess what has already been done and what still remains to be done.

This 1990 workshop will emphasize the formation of a rice genetic resources network. In practice, there is already a collaborative program among rice genetic resources workers throughout the world. What we have in mind is to build on that infrastructure rather than to create something new.

Within the CGIAR system, we all recognize the leadership role of IRRI in terms of rice genetic resources. We would hope that this particular role will continue to be fulfilled by IRRI, with specific reference to the building up of a world data base on rice genetic resources. The other organizations within the CGIAR system with major roles in rice genetic resources are IITA and WARDA; eventually, WARDA may play a larger role. The role of CIAT in rice genetic resources in Latin America also should not be underestimated.

Noting that these commodity-oriented centers in the CGIAR system are already involved in rice genetic resources activities and provide leadership in this area, the question remains as to what IBPGR's role is in this context. IBPGR's major role in rice genetic resources can be summarized in three parts:

- Stimulation of national genetic resources development. This is achieved through the support of IBPGR regional offices and the scientific support provided by both headquarters-based and outposted staff.
- Identification of funding sources. Although in the past, we might have given a slightly different impression, it should be clearly understood that IBPGR is not a funding agency. In relation to national program development and to crop

¹Delivered by P. M. Perret

genetic resources networks development, IBPGR sees a major role for itself in working together with national programs and with crop networks in identifying sources of funds outside the CGIAR system. I would, therefore, welcome any suggestions from workshop participants on particular areas for which funds are required and where IBPGR can be instrumental in identifying sources of funds.

- **Catalytic role.** With the limited resources available to IBPGR, one cannot expect it to be able to effectively carry out genetic resources programs in all the crops of the world. The stimulation of others to assume responsibilities in particular areas of conservation and utilization of the genetic resources of a particular crop is therefore of utmost importance and is an important role of IBPGR. This catalytic role is expressed in bringing together researchers and managers in the area of genetic resources, such as by our support for this particular joint IRRI-IBPGR workshop on rice genetic resources.

I would like to close by paying tribute to the most well-known rice genetic resources worker in the world, Dr. T. T. Chang. We all recognize the extremely important role T. T. has played in the conservation and utilization of rice genetic resources, in the creation of awareness of the need for the conservation of plant genetic resources in general, and in the support he has provided numerous national programs. Although T. T. will be retiring in the not too distant future, we all hope that he will continue to make available to all of us his expertise on plant genetic resources.

The genepools
of rice: collecting
activities
1983-1990



IRRI-national program collaboration in collecting rice germplasm in Asia

D. A. Vaughan

The focus of collaboration between national agricultural research systems (NARS) and IRRI has changed since the last rice germplasm workshop (IRRI-IBPGR 1983). Between 1983 and 1985, land races of rice were still being collected from previously unexplored areas. Collecting efforts covered regions and countries where no systematic field collecting had been done, such as the Aceh and Nias regions in Sumatra, Indonesia, and in Bhutan and Madagascar. Since 1987, IRRI's involvement in field collecting has concentrated on the wild relatives of rice. This paper gives details of those collecting activities and thoughts on the need for future preservation of rice diversity in the Asian realm.

Collecting land races of rice

From 1983 to 1985, Ian Roy Denton, an IBPGR-supported field collector stationed at IRRI, undertook a series of collecting missions in tropical Asia and Madagascar (Table 1). Comprehensive and systematic collecting of land races in Bhutan and Madagascar was accomplished. In addition, visits to Bangladesh, Sri Lanka, and Sabah State of Malaysia helped fill gaps left during earlier collecting trips.

The collection of rice accessions from Bhutan covers a range of almost 2,000 m in altitude, with the majority of the rices from the irrigated environment. The germplasm collected in Madagascar, primarily from two altitude ranges, near sea level and at about 1,000 m, includes varieties from irrigated, rainfed wetland, and upland environments (Table 2). More than 90% of the varieties collected from both countries are of the indica race.

Recent collecting of traditional varieties along the Kinabatangan River, Sabah State, Malaysia, revealed a rich cultural heritage associated with rice (Vaughan 1989a). Among the customs of this region is the planting of lemongrass (*Cymbopogon citratus*) among rice (this practice is said to promote tillering) and the imposition of fines (sogits) on people who break the strict rules of the ricefield. Two varieties collected in different villages were particularly unusual: both were called *Dinabur* (meaning mixture) and were deliberately maintained as mixtures of many morphotypes. In the village of Sukau, the lady farmer who shared *Dinabur* with the collectors said she was trying to conserve in the mixture the varieties handed down to her by her parents.

Table 1. National agricultural research systems-IRRI collaboration focused on collecting land races of rice since 1983.

Country	Collaborating NARS	NARS collectors	Date	Region	Samples ^a (no.) of land races and populations of wild species collected
Bangladesh	Bangladesh Rice Research Institute	Md. Nasiruddin M. K. Bashar M. K. Bashar	18 Aug-7 Sep 1983 2 Aug-27 Aug 1984	Mymensingh, Pabna Rajshahi Northeast and Southwest	95 103
Bhutan	Department of Agriculture	A. Baset Tek B. Ghaley Tek B. Ghaley B. K. Lepcha	21 Oct-1 Dec 1983 25 Sep-12 Nov 1984	Paro to Tashigang Punakha, Damphu, Shemgang	83 66
Indonesia	Bogor Research Institute for Food Crops/Central Research Institute for Food Crops FOFIFA	Soetjipto Kartowinoto	15 Mar-7 Apr 1984	Aceh and Nias, Sumatra	174 (4)
Madagascar		Rahinirina Jeanine Rakotonirainy Roland Noarisa Alfred Razakanary Velonaody Fabian Rahinirina Jeanine	9 May-6 Jun 1984 15 Apr-14 May 1985	Central plateau Southeast	98 123
Malaysia	Department of Agriculture Department of Agriculture and Malaysian Agricultural Research and Development Institute	Christopher Tseu Mary Siamun Mohd. Hatta Hadzim B. Khalid Ismail B. Mohd. Nor.	4 Jan-3 Feb 1985 15-29 Dec 1989	Sabah Kinabatangan, Sabah	227 121 (6)
Sri Lanka	Central Agricultural Research Institute	S. Balendira	3 Feb-5 Mar 1984	Central and south	108(14)

^aNumbers collected in the field prior to comparison for duplicates at IRGC. Populations of wild species are in parentheses.

Table 2. Distribution of IRGC accessions of traditional rices collected in Madagascar and Bhutan, by altitude and by cultural type.^a

	Accessions (no.) from Madagascar	Accessions (no.) from Bhutan
Altitude range(m)		
0 - 250	63	-
251 - 500	5	-
501 - 750	-	-
751-1000	9	8
1001-1250	22	10
1251-1500	3	24
1501-1750	7	27
1751-2000	-	12
2001-2250	-	9
2251-2500	-	9
> 2500	-	1
Cultural type		
Irrigated	56	91
Rainfed wetland	16	2
Upland	37	7

^aFrom passport data gathered by I. R. Denton and collaborators.

Collecting wild relatives of rice

In 1987, IRRI embarked on an intensive collaborative effort to collect the wild relatives of rice. The focus on this rice type was a consequence of

- Deficiency in sampling wild rices during earlier missions when the focus was on old land races. Also, the approach in collecting wild rice is different from that used in collecting cultivars (IBPGR-IRRI Rice Advisory Committee 1982).
- Increasing realization of the great genetic diversity in wild relatives of rice, as is indicated, for example, at the molecular level (Cordesse et al 1990).
- Knowledge that wild rices are a rich source of useful genes, particularly in respect to resistance to or tolerance for pests and diseases that have recently gained prominence (cf. Chang et al 1977, Chang 1984, 1989; Heinrichs et al 1985; Ikeda et al 1990).
- Ease in utilizing this germplasm now, because of improved wide hybridization techniques and new technology (Vaughan and Sitch 1991).
- Desire to find new sources of genetic variability for rice improvement and to reinstate genetic diversity in major commercial cultivars (Chang 1984, Hargrove et al 1988).
- Realization that, in some rapidly developing parts of Asia, many populations of wild rice are threatened with extinction (as was recorded for Taiwan by Kiang et al [1979]).

A summary of NARS-IRRI missions for collecting the wild relatives of rice undertaken to date is given in Table 3; materials collected are listed in Table 4. The collecting missions have revealed how much we still are unaware of the extent of the geographic spread of wild rices and their diversity (Vaughan 1991). A list of notable discoveries is given in Table 5. This list indicates how little attention had been paid

Table 3. National agricultural research systems-IRRI collaboration focused on collecting the land races and wild relatives of rice, 1987-1990.

Country	NARS organization	NARS collectors	Date	Region	Samples ^a of land races and populations of wild species collected
Bangladesh	BIRRI	Zarina Zeenat Sayad Md. Ibrahim M. Enamul Haque	4-24 Dec 1988	Kushtia, Jessore Khulna Habiganj and Sylhet	25 (62)
Cambodia	Ministry of Agriculture	Leng Sothath	26 Oct-3 Nov 1988	Phnom Penh/ Takeo	(29)
	Ministry of Agriculture	Leng Sothath	12-22 Jan 1989	Phnom Penh/ Kompong Chhnang	(45)
India	NBPGR NBPGR/CRI	V. K. Muralidharan V. K. Muralidharan S. D. Sharma	17-30 Nov 1987 6-21 Nov 1988	Kerala Tamil Nadu	(65) 22 (8)
Indonesia	NBPGR BORIF/CRI BORIF/CRI	S. S. Malik Soewito Tjokrowidjojo Soetjpto Kartowinoto	8-23 Nov 1989 29 May-14 Jun 1988 5-20 Jun 1989	Eastern India Java Southern Sumatra	2 (128) (55) 4 (39)
Laos	Ministry of Agriculture	Viengsavanh Manivong	26 Nov-7 Dec 1989	Vientiane plain, Luang Prabang	11 (28)
Malaysia	MARDI Department of Agriculture MARDI	Abdullah Bin Md. Zain Jamilah Idris Hadzim Khalid	29 Jan-4 Feb 1989 15-29 Dec. 1989	Kelantan Sabah	16 (9) 121 (6)
Nepal	National Rice improvement Programme, National Agricultural Research and Services Center PhirRice NPGRL	G. L. Shrestha Ismail B. Mohd. Nor	30 Sep-18 Oct 1988	Terai and Kathmandu Valley	4 (40)
Philippines		L. Engle E. Quintana Nestor Altoveros	25 Feb-3 Mar 1990	Bicol, Samar, Leyte	(20)

Table 3 continued

Country	NARS organization	NARS collectors	Date	Region	Samples ^a of land races and populations of wild species collected
Sri Lanka	CARI	S. Balendra	1-14 Feb 1988	Central and South	(68)
Thailand	Pathum Thani Rice Research Institute	A. S. U. Liyanage Songkran Chitrakon	1-12 Dec 1987 3-13 Jan 1988	Central and North Southern	(74) (36)
Vietnam	National Institute of Agricultural Sciences	Songkran Chitrakon Luu Ngoc Trinh Nguyen Vu Trong	23 Nov-2 Dec 1988 21 Oct-5 Nov 1989	Northeast Northwest	(135) 33 (10)

^a Populations of wild species are in parentheses.

Table 4. Representation of *Oryza* species complexes in recent collecting of wild rices under NARS-IRRI collaboration.

Species complex	Representation (%)
<i>O. sativa</i> complex	83.0
<i>O. officinalis</i> complex	
Diploid species	8.5
Tetraploid species	1.6
<i>O. ridleyi</i> complex	0.8
<i>O. meyeriana</i> complex	3.7
Related genera (<i>Leersia</i> , <i>Hygroryza</i>)	2.1

previously to the more distant relatives of rice. Less accessible areas or habitats far from ricefields need to be explored. Although the distant relatives seem at present to have little practical value, in years to come they could be the precise germplasm needed to solve particular problems.

Training for collectors

Since 1983, IRRI has assisted in training field collectors in Indonesia, Myanmar, Thailand, and Vietnam, but the courses have been primarily on techniques and methodologies for collecting rice cultivars.

To learn how to collect wild rice, on-the-job training is necessary: habitat identification and becoming accustomed to the growth habits of wild rices require a practiced eye. Collaborative collecting missions have been followed up by participants, and additional populations of wild rice discovered. After a recent collecting mission in the Philippines, some participants later visited Zamboanga, Mindanao, and found *O. minuta*, thus greatly extending its earlier known distribution. Similarly, after a collecting mission in Nepal, one species of *O. officinalis* not found earlier was located by Dr. G. L. Shrestha when he was traveling in the western Terai.

Considerations for future prospecting

The capacity of genebanks to conserve collected materials is relevant to a collecting

Table 5. Some discoveries of *Oryza* species in Asia.

Country	Species
Indonesia	<i>O. ridleyi</i> germplasm collected at two sites in Sumatra
Laos	<i>O. granulata</i> collected in mountains around Luang Prabang
Malaysia	<i>O. meyeriana</i> found in upland ricefield near Gua Musang, Peninsular Malaysia
Philippines	<i>O. officinalis</i> found on Samar Island
	<i>O. meyeriana</i> germplasm collected in southern Luzon
Vietnam	<i>O. granulata</i> and <i>O. rufipogon</i> found near the Laos border in the northwest

strategy. Manpower, land, storage capacity, regeneration cycle, and financial resources limit the number of accessions a genebank can properly conserve. The resources needed to conserve wild germplasm *ex situ* are considerably greater than those needed to conserve a cultigen. For wild species that produce few seeds, permanent gardens may be needed. Screened areas, pots, panicle bags, and germinators are among the items needed to conserve such genetic resources.

For conserved germplasm to be used, evaluation and its associated inputs are necessary. If appropriate consultation, site identification, and preparations are complete, collecting samples is perhaps one of the less problematic aspects of conservation.

Traditional rice varieties

There are still a number of important areas where only cursory collecting or no collecting has been carried out. This, unfortunately, remains true for parts of the Asian region where rice is most diverse, from Nepal to northern Vietnam.

At this time, simple collecting of rice diversity is not enough. Collecting in the 1990s should take full account of advances made over the last few decades. Much more complete passport data need to be recorded. In some areas, joint expeditions with anthropologists in culturally diverse regions would provide a great deal of useful information about varieties and cultures, which are essentially interlinked. Both genetic erosion and cultural erosion are occurring as regions develop. For example, collecting and research in Muong Te district in Lai Chau Province of Vietnam would be of benefit. Such a multidisciplinary approach would also be of benefit in parts of Laos and Myanmar, among other areas.

A comprehensive discussion at this workshop of the types of passport data recorded for cultivated rice and wild rice, leading to agreement on essential and desirable passport data, would help future collecting missions. Although much has been accomplished, the need for collecting or re-collecting rice germplasm continues as new genebanks are completed.

Wild relatives of rice

In the past, most national programs gave collecting wild relatives of rice a lower priority than collecting cultivars. Wild rices are agronomically unattractive, relatively expensive to conserve, and, at least currently, difficult to use. Evaluators and breeders only turn to this germplasm as a last resort.

However, if present trends are an indication, demand for wild germplasm will increase markedly. Its utilization in breeding programs will become routine. There is now no doubt that this sector of germplasm contains a broad array of useful genes.

A dual approach to conserving this germplasm may be needed:

- For NARS to establish populations of wild species in reserve areas, if threatened populations fall outside such areas.
- For specific centers to take the lead, as in the past, in conserving these species *ex situ*. However, NARS could, at least for high seed-producing species, collect sufficient number of seeds from wild populations to permit immediate entry into long-term storage.

Because there are such rapid changes in the ability of scientists to use the wild relatives of crops, it is not wise to prioritize species within the genus *Oryza* for collecting. Prioritization of regions for collecting wild germplasm is appropriate.

A review of *Oryza* taxonomy was published recently (Vaughan 1989b). Now the question is, to what extent is further information needed to permit NARS scientists to identify the habitats of these species and to collect germplasm of all wild *Oryza* species?

New germplasm

New germplasm, such as bridging species, mutants, isolines, aneuploids, polyploids, tissue cultures, hybrids, and mapping populations, are being generated in many laboratories worldwide. The large number of scientists currently attending the rice biotech/genetics meetings at IRRI attests to the momentum of developments in rice genetics. These scientists are generating new germplasm, sometimes at considerable expense. In the future, genebanks may be required, and should be prepared, to conserve the new genetic materials.

The acquisition (rather than collecting) of this germplasm and its appropriate conservation will further stretch a genebank's resources. However, it would be a mistake for genebanks not to keep abreast of new developments and be ready to meet the challenges posed by judiciously conserving the new germplasm. At the same time, appropriate support for this job will be needed. Perhaps participants in this workshop could make recommendations concerning the role of genebanks in conserving newly generated germplasm and seek support for upgrading genebank personnel to handle such materials.

Field collecting of rice germplasm in tropical Asia by staff of the Ministry of Agriculture, Forestry and Fisheries of Japan and the National Institute of Genetics

K. Hayashi

Sufficient genetic resources is a fundamental basis for crop breeding programs. Except for a few crop species, Japan is deficient in plant genetic resources. The importance of collecting and conserving plant genetic resources is now widely recognized. The Ministry has been promoting genetic resources projects for many years. Since 1975, it has regularly sent missions to various countries to collect plant genetic resources. Four or five collecting teams have been organized annually. The activities are based on a long-term plan for collecting plant genetic resources outside Japan.

During the last decade, three rice collecting missions were undertaken in tropical Asia, in cooperation with the national governments concerned. In 1983, two Japanese researchers explored Bangladesh and collected 152 cultivars. In 1986, two Japanese scientists were sent to north and northeast Thailand, where they collected 99 cultivars and 17 populations of wild rices. In 1989, three Japanese scientists visited Sumatra Island of Indonesia and collected 363 cultivars, including deepwater rices.

A few Japanese researchers joined IBPGR collecting missions for many crop species in Nepal in 1984, 1985, and 1986. During those missions, the teams collected 273, 295, and 263 cultivated rice samples, respectively. In 1989, three Japanese researchers organized a collecting mission in Pakistan with funds from IBPGR. They collected 191 rice cultivars in cooperation with the Plant Genetic Resources Program of Pakistan.

In 1983-89, teams from the National Institute of Genetics visited Thailand, Indonesia, Bhutan, and Bangladesh and collected samples of 432 cultivars and 142 wild rices. Details of the earlier trips have been published (Morishima et al 1984, National Institute of Genetics 1987); details of the most recent trips are being prepared for publication.

Rice germplasm exploration and collecting in Africa since 1983

N. Q. Ng

Africa is rich in rice genetic resources. It contains representatives of four of the six known genomes in the genus *Oryza*: AA (*O. longistaminata*, *O. barthii*, *O. glaberrima*, and *O. sativa* introductions), BB and CC (*O. punctata* and *O. eichingeri*), and FF (*O. brachyantha*). When plant genetic resources collecting and conservation gained worldwide attention during the 1970s, IBPGR and IITA recognized the urgency for exploration and collecting of rice genetic resources in Africa (Sharma and Steele 1978). IRAT and ORSTOM in Ivory Coast started exploration and collecting of African rices in 1974 (Bezançon and Second 1984). IITA began an intensive search throughout Africa in 1976 (Ng et al 1983). IBPGR provided some financial and logistic support to strengthen IITA, IRAT, and ORSTOM collecting activities. WARDA also became involved. IRRI participated in some of the preliminary planning at WARDA in 1976 and through its liaison role in the IBPGR-IRRI Rice Advisory Committee 1976-85.

Exploration and collecting of rice germplasm since 1983

The review of Ng et al (1983) called for further exploration and collecting of rice in Africa. First priority areas were Angola, Burkina Faso, Niger, Madagascar, Mozambique, southern Sudan, Comoros Island, the islands of Tanzania, and Zaire. Second priority areas were the Central Republic of Africa, Mali, Togo, Mauritius, Ghana, Cameroon, and Congo. Third priority areas were Mauritania, Gabon, Gambia, Chad, Senegal, Guinea, Republic of Benin, and Sierra Leone.

A plan of action for field collecting in Africa by IBPGR, IITA, IRAT, ORSTOM, and WARDA in 1983-87 was recommended at the 1983 workshop (IRRI-IBPGR 1983). Although not all the plans have been realized, achievements have been substantial. Between 1985 and 1989, IITA fielded 14 plant exploration missions to 14 African countries; considerable new rice germplasm was collected (Goli and Ng 1985; Goli 1986, 1987a,b,c,d; Osunmakinwa 1986; Padulosi 1987a,b,c, 1988; Vodouhe et al 1990). These exploration trips netted a total of 679 germplasm specimens, consisting of 418 *O. sativa*, 115 *O. glaberrima*, 35 *O. barthii*, 93 *O. longistaminata*, 18 *O. punctata*, and 1 *O. brachyantha*. In addition, IITA supported the national programs in Ghana and the Republic of Benin in collecting *Oryza* germplasm in 1988-89 and 1989, respectively.

IBPGR supported the national programs of Burkina Faso (1983 and 1984), Madagascar (1984 and 1987), and Kenya (1984) in in-country explorations (IBPGR 1984, 1985a, 1986, 1987, 1988). IRRI was involved in the exploration in Madagascar during 1984-85, with one scientist participating. In addition, IBPGR collaborated with IITA in an exploration in Mali during 1986. These explorations netted more than 1,463 samples of rice germplasm. Except for the materials from Kenya, most of the materials collected were received at IITA and shared with IRRI.

Need for further plant exploration

Rice germplasm collecting efforts in Africa have benefited from intensive international cooperation. An impressive array of germplasm of cultivated species of *Oryza* has been assembled. However, there is an urgent need to fill major gaps in the germplasm collection for *Oryza*.

Priorities include

1. Collecting cultivated rices and their wild relatives in Mozambique.
2. Collecting traditional varieties in isolated pockets of southern, central, and eastern Africa.
3. Collecting wild *Oryza* taxa in Uganda, Sudan, southeastern Chad, and central and eastern Africa.

In addition, there is a need to collect samples of related genera, particularly *Leersia*, *Maltebrunia*, and *Prosochloa* (Ng et al 1991).

National collecting activities

Bangladesh (Md. Enamul Haque)

About 650 cultivars and 75 populations of wild rices were sampled 1983-89 by scientists from the Bangladesh Rice Research Institute.

Brazil (A. C. de Souza Medeiros)

Rice production in Brazil is concentrated in the southern region (43%) of the country; the state of Rio Grande do Sul is the leading producer. Irrigated cultivation predominates in this region. The second most important area for rice production is in the central-west region, where upland rice predominates (Table 6).

During 1979-89, 37 expeditions involving the staffs of CENARGEN and CNPAF collected rice cultivars in 13 states and territories (Table 7). The 1,649 rice accessions that resulted from these collection trips are conserved. In 1987, a collaborative trip to collect wild rice in the Amazon Basin involved scientists from Louisiana State University, USA, and EMBRAPA. They collected 29 samples of wild rice species *O. alta*, *O. grandiglumis*, and *O. rufipogon*.

Cambodia (R. C. Chaudhary)

Members of the Cambodia-IRRI team carried out a program to collect local varieties Oct-Dec 1989. Many collectors gathered 574 land races from the districts of Takeo, Kandal, Kampong Speu, and Svay Rieng. About 200 of the varieties have been processed. Basic passport data recorded for each sample include district, cultivar name, cultural type, season, and days to maturity.

Table 6. Brazilian rice production by cultural type (Teixeira 1988, 1989).

	Irrigated rice	Upland rice
Production	4.8 million t	6.3 million t
	43%	57%
Area	1.06 million ha	4.27 million ha
	20%	80%
Grain yield	4.5 t/ha	1.3 t/ha

Table 7. Rice samples collected in Brazil, May 1979-December 1989 (Fonseca 1989).

State and territory	Accessions (no.)
Mato Grosso	103
Maranhao	429
Minas Gerais	176
Roraima	59
Amazonas	75
Acre	73
Rondonia	127
Piaui	165
Goias	282
Espirito Santo	56
Santa Catarina	4
Mato Grosso do Sul	78
Ceara	22
Total	1649

Collecting rice germplasm in China (*Cunshan Ying*)

Rice is the most important crop in China. The area planted to rice (about 33 million ha) is 28% of the country’s total crop area and 23% of the world’s rice area. Rice production in 1987 (about 177 million t) was 44% of China’s total grain production and 37% of the world’s rice production (IRRI 1988b). The history of rice cultivation in China dates back at least 7,000 years. Natural and human selection of rices adapted to varying ecological conditions and cropping systems have resulted in a broad array of cultivars. The diversity of both indigenous cultivars and wild rices is very rich (CAAS 1986).

Field survey and collecting of rice germplasm have been the focus of conservation efforts in China. Three periods of exploration to assemble the nationwide diversity of rice occurred: the 1930s, the mid-1950s, and 1978-82. From 1978 to 1983, an extensive exploration for wild relatives of rice in Yunnan, Guangxi, Guangdong, Fujian, Hunan, and Jiangsi Provinces yielded 3,200 seed or plant samples. Consequently, much rice germplasm, including traditional cultivars and wild rices, has been collected and is conserved (CAAS 1986, Chang et al 1987).

Table 8. Summary of the collecting trips.

Date	Collectors	Place visited	Material collected
1981-84	Shuping Zhen Huoshang Xiao	Tibet	30 samples of cultivated rice
1986-89	Maocai Yang Diansheng Zheng	Shen Nong Jia San Xia	Samples of 300 cultivated rice and wild rice
1986-89	Guanyuan Huang	Hainan	Samples of 500 cultivated rice and wild rice

Since 1983, additional collecting has been undertaken by the Institute of Crop Germplasm Resources of the Chinese Academy of Agricultural Sciences, in collaboration with the Hubei and Guangdong Academies of Agricultural Sciences.

The areas explored were Tibet, Shen-nong-jia, the three gorges on the upper reaches of the Yangtze River bordering the western part of Hubei Province (19 counties), the eastern part of Sichuan Province (3 counties), and Hainan Island (19 counties) (Table 8).

Discussion

H.I. Oka: Could you tell us the scope of genetic erosion in the past decades?

C. Ying: China did not have a modern genebank until 1980. Seed stocks were scattered over different provinces, with some sets kept at cool and semiarid sites. Over three decades, about 10,000 samples were lost. Most of the nonviable varieties have been re-collected during recent missions.

India (*R. S. Rana and S. D. Sharma*)

Collecting the variability observed in indigenous rice cultivars began in India around the turn of this century. The work received special attention following establishment of the Agricultural Research Station at Dacca (eastern India) in 1911 and the Paddy Breeding Station at Coimbatore (southern India) in 1912. Setting up the Indian Council of Agricultural Research (ICAR) at New Delhi in 1929 and the Central Rice Research Institute (CRRI) at Cuttack in 1946 further strengthened these efforts. That led to recommendations for general cultivation of 394 varieties developed from pureline selections among collected germplasm.

During the second phase of systematic explorations, the Jeypore Botanical Survey explored South Orissa and adjoining areas of Madhya Pradesh during 1955-60, which led to the collection of 1,745 cultivars. During 1965-67, 900 traditional cultivars of Manipur in far eastern India were collected. The Assam Rice Collection of 6,630 cultivars was made by staff of the Indian Agricultural Research Institute during 1967-72. The Raipur collection of 19,116 rice cultivars grown locally in Madhya Pradesh region was made 1971-76. Additional collection of 1,938 cultivars was made through a special drive for upland varieties under cultivation in Andhra Pradesh, Karnataka, Maharashtra, Madhya Pradesh, Uttar Pradesh, Orissa, and West Bengal. Collaborative explorations by NBPGR, and state agricultural universities added nearly 7,000 cultivars during 1978-80. The Vigyan Parishad Kendra Agricultural Station at Almora collected 1,247 cultivars from hilly regions of Uttar Pradesh. NBPGR and CRRI jointly explored Sikkim, South Bihar, and parts of Orissa in 1985 and collected 447 local types. Explorations by NBPGR during 1983-89 led to further addition of 4,862 cultivars to the national germplasm collection.

In addition to spectacular variability in its traditional cultivars, India is also rich in genetic diversity of wild *Oryza* species, particularly *O. nivara*, *O. rufipogon*, *O. officinalis*, and *O. granulata*. Collecting these materials began with the pioneering work of S. Sampath at CRRI during 1948-55. He focused attention on *O. perennis*. Subsequently, S. V. S. Shastri and his associates in IARI made extensive collections

of wild species of *Oryza* from western, northern, central, and eastern India and assembled striking variability, including *O. nivara* and *O. officinalis*. More recently, variability in *Porteresia coarctata* has been collected from the coastal areas of eastern India.

The national genebank at NBPGR has only 6,478 of these indigenous collections in long-term storage. Active collections maintained by CRRI in Cuttack amount to nearly 18,000 accessions; those by Indira Gandhi Krishi Vishva Vidyalaya in Raipur, about 20,000. A large number of collections are scattered over nearly 30 rice research centers across the country. There are bound to be duplicates among the different holdings. An all-out effort is needed to link these collections and enable the institutes, stations, and centers to upgrade their holdings.

NBPGR will hold the national base collection in long-term storage, with an enlarged duplicate set kept by CRRI under medium-term storage as the national active rice collection. The 15,000 Indian cultivars in IRRI's germplasm bank will serve as a backup collection. A national data base on all crop genetic resources, including rice, will be assembled at NBPGR. A Crop Advisory Committee on Rice has been set up to review the status of current collections, to identify gaps, and to recommend priorities.

In addition, several other countries have joined the effort to collect wild rices in India. Japanese exploration teams led by H. Kihara in the early 1960s and T. Watabe in the late 1960s and early 1970s made systematic collections in western Uttar Pradesh, Bihar, Andhra Pradesh, and parts of Maharashtra. H. I. Oka traveled extensively on collecting trips in different parts of India. French scientists from IRAT and ORSTOM collaborated with ICAR teams in collecting *O. officinalis*, *O. nivara*, and *O. rufipogon* from Goa, Karnataka, Maharashtra, and Gujarat in 1986. During 1987-89, ICAR and IRRI scientists undertook more intensive collecting for wild rices in South India and West Bengal.

Madagascar (*S. Ravaonoro* and *X. R. Kakotonjavahary*)

Apart from collaborative collecting with IRRI in 1984 and 1985, FOFIFA scientists collected cultivars and the wild rices *O. longistaminata* and *O. punctata* in the east, northwest, and north of Madagascar in 1986. Complete passport data for collections were taken during these trips.

Malaysia (*A. Md. Zain, Hj. A. Boerhannoedin, and O. Omar*)

Eight collecting trips to different parts of Malaysia 1983-90 involved staff of MARDI. A total of 628 land races and 43 populations of wild rices were collected and complete passport data recorded. Collecting trips by staff of the Department of Agriculture in Sabah and Sarawak States also took place during this period.

Myanmar (*Myo Nyunt*)

Myanmar's genebank at Yezin was completed in February 1990. ARI needs to train more of its staff to operate the new facilities. The services of a short-term consultant would be helpful.

Nepal (*M. P. Upadhyay and S. R. Gupta*)

Nepalese collecting teams, joined by scientists from USAID and Shinshu University of Japan, undertook exploration 1983-88. Passport data were taken, but full details of these trips have not been received.

Sri Lanka (*A. S. U. Liyanage and S. Balendira*)

Apart from collecting trips involving IRRI, efforts in Sri Lanka in 1985 and 1990 led to the collecting of 201 land races and 8 samples from populations of wild rices. Complete passport data were taken on samples collected.

Thailand (*Songkran Chitrakon and Chawewan Vutiyo*)

About 90% of the Thai traditional varieties, mostly lowland rices, have been collected. The remainder consists of hill rices (upland type), rainfed lowland rices in remote areas, and wild rices. Thai researchers in regional centers are trying to collect these genetic resources before they disappear from natural habitats.

Between 1983 and 1989, comprehensive collecting of cultivated (12,232 samples) and wild rices (733 samples) was undertaken in all parts of Thailand, sometimes with participation from Japanese and IRRI scientists. Complete passport data have been recorded.

The National Rice Seed Storage Laboratory for Genetic Resources at Pathum Thani supplies approximately 2,000-3,000 seed samples to scientists annually. Some wild rice seeds often cannot be supplied because seed stock is limited, although regeneration is done every year.

At present, all passport data of cultivated and wild rices are kept in notebooks. These data should be standardized and computerized for use in breeding programs. Many potentially useful agronomic characters in the national collection have not been fully utilized because data are inaccessible. To facilitate the use of rice germplasm, a microcomputer with hard disk is needed for data processing.

Vietnam (*Nguyen Dang Khoi, Bui Chi Buu, and Luu Ngoc Trinh*)

Rice germplasm conservation activities in Vietnam began in the early 1930s. The resulting rice collection was incomplete, and many accessions were lost during the long war years, especially in southern Vietnam.

In 1983, the Vietnam rice collection held 2,500 accessions. They represented all rice groups of the country, but were predominantly from irrigated areas. From 1983 to 1989, the Cuulong Rice Research Institute in Haugiang and INSA in Hanoi conducted exploration activities. The Cuulong Institute collected traditional varieties from the Mekong Delta region. Exploration activities concentrated on collecting varieties adapted to deepwater conditions and/or tolerant of acid and saline soils. Wild species were included. About 500 cultivars and 4 samples of wild rice species *O. rufipogon*, *O. nivara*, *O. sativa* f. *spontanea*, and *O. officinalis* were gathered during this period.

Between 1984 and 1988, INSA collaborated with the Vavilov Institute of Research of the Soviet Union to collect about 300 cultivars in Lai Chau, Sonla, Quangninh, Ha Son Binh, and Binh Tri Thien Provinces.

Vietnam's rice germplasm collection currently consists of 3,410 traditional rice accessions and 6 wild species.

During the next 5 yr, field collecting will be directed toward replacement of nonviable accessions and collecting in the more remote areas of the central highlands, northwest region, Mekong Delta, and the mountain regions of central Vietnam. A national survey estimated that about 600-800 traditional rice varieties are still in cultivation, but genetic erosion is accelerating. High priority has been given to collecting wild species and traditional varieties adapted to adverse environmental conditions. The proposed field collecting plan for 1990-94 will be coordinated by INSA and the Cuulong Rice Research Institute.

Many of the target areas for collecting are in remote regions that are difficult and expensive to reach. Consequently, Vietnam requires substantial financial assistance from international agencies for effective implementation of the proposed 5-yr collecting program.

The network approach



A proposal for a network on rice genetic resources conservation

P. M. Perret

Since its creation, IBPGR has benefited from the expertise of hundreds of scientists worldwide. The informal network of specialists has allowed this organization, at least during its first 10 yr, to play its coordinating role in the conservation of plant genetic diversity successfully. Furthermore, five crop advisory committees for wheat, rice, maize, sorghum, and millet, and the genus *Phaseolus* were implemented in close collaboration with the CGIAR centers responsible for these crops (CIMMYT and ICARDA, IRRI, CIMMYT, ICRISAT, and CIAT, respectively). Similarly, numerous working groups (eg, for *Hevea*, cotton, cacao, *Vitis*, tropical and subtropical forages, and forages for the Mediterranean and adjacent semiarid areas) provided guidance on further action. The latter consisted primarily of establishing priorities for collecting, but storage standards were also established under the expert advice of the crop advisory committees and working groups. Many institutes have agreed to store base collections or establish field genebanks for one or more crops. Crop descriptors published for a large number of crops are now widely used. Other activities in field collecting, training programs, and regional conferences were implemented.

Crop genetic resources networks

The notable increase of genetic resources collections throughout the world, especially at the level of national programs, is creating the need for a more systematic coordination of activities. The safety of existing germplasm needs to be ensured and its duplication guaranteed. Much of the accumulated materials have not yet been characterized and/or evaluated, thus widening the gap between conservation of germplasm per se and its use by breeders or researchers. Correct identification of samples, meaningful re-collection of remaining materials before their possible disappearance, application of adequate regeneration methods, and, above all, distribution of germplasm to users require intensification and coordination of research efforts in different fields (eg, ecogeographic studies, genetic diversity patterns, taxonomy, evolution, breeding systems, and cross compatibility).

This situation has led IBPGR to initiate a pilot program for the implementation of crop genetic resources networks. These networks should stimulate a collaborative approach to conserving the genetic resources of a particular crop, based on goodwill, sharing of responsibilities, and full participation in the decisionmaking process by all

interested parties. Specific objectives, allocation of responsibilities, and formulation of an integrated plan of action have to be defined for each network by its members. This approach will improve the coordination of activities on a global, regional, or national level, rationalize conservation and utilization efforts, and catalyze activities such as germplasm exchange and research.

The long-term objective is for the crop networks to attain self-sustainability. However, it is realized that, especially at the initial stage, resources in addition to those already existing may be necessary. IBPGR will help the coordinating body or bodies designated by the participants of an established crop network to approach national or multinational donor agencies to seek the funding required. IBPGR will also take advantage of the development of crop networks to focus its own scientific and financial support on specific needs within the networks.

In the first phase of the pilot program started in 1988, eight crops (barley, *Beta*, groundnut, maize, *Medicago*, *Musa*, okra, and sweet potato) were selected, with consideration for a reasonable spread between different crop groups (cereals, legumes, roots and tubers, fruits, vegetables, forages, and industrial crops), temperate and tropical crops, seed and vegetatively propagated crops, and crops within and outside the mandate of other centers in the CGIAR system.

Example of an existing crop network

The recommendations of a workshop for *Beta* illustrate the strategy for an existing crop network.

Participants in the *Beta* Workshop asked the Center for Genetic Resources of the Netherlands to act as the international *Beta* data base, for collating, analyzing, and disseminating information. They nominated a *Beta* Coordinating Committee (BCC) composed of three members (including the person responsible for the international *Beta* data base) to provide a central link between all members and to stimulate realization of the aims of the network. Activities during the next 2 yr until the next meeting of the network's participants will focus on exchange of data (passport and stock, characterization, and evaluation), plans for collaborative regeneration of accessions, and sharing in collecting activities.

The BCC met for the first time in June 1989 and, in line with the recommendations of the workshop, launched a project for widening the genetic diversity in sugar beet breeding programs. This project consists primarily of developing a number of biennial base populations, each with different breeding objectives, from crosses between biennial beets and bulked annual accessions.

A rice conservation network

Rice genetic resources amount to nearly a quarter of a million accessions, distributed in 50 collections established in 42 countries. The number of unique accessions is roughly estimated to be 100,000; the remaining accessions are materials duplicated through exchange, intentionally in most cases, for safety.

Indeed, the safety and duplication system for rice, which was established by the IBPGR-IRRI Rice Advisory Committee and by the first IRRI Workshop on Rice

Genetic Resources (IRRI-IBPGR 1978), is very effective. As is well known, this system is composed of four base collections. IRRI has a global mandate for Asian tropical rices (*indica* and *javanica* races); the National Institute of Agrobiological Resources in Tsukuba, Japan, has a global mandate for Asian temperate rices (*japonica*); IITA in Nigeria and the National Plant Germplasm System of USA act as regional base collections for Africa and the New World, respectively. Actually, IRRI's IRGC, which holds more than 80,000 accessions (about 80% of all existing unique accessions worldwide) is systematically duplicating its germplasm in other rice base collections for safety and storage. There is still a need to include the remaining unique accessions into the IRGC. Its rice safety and duplication system, however, is one of the most successful achievements for major crops because of goodwill and collaboration. Furthermore, all accessions held by the IRGC are systematically characterized for 45 morphoagronomic characters and evaluated for 39 traits. These data are available and specific data sets, as well as, of course, the germplasm itself, are distributed on request.

The International Network for Genetic Evaluation of Rice, formerly the International Rice Testing Program in operation since 1975, involves hundreds of rice researchers worldwide. It is a very successful network for the exchange of improved material from national programs and IRRI and for its testing. Most of the activities, which are downstream to the conservation of genetic resources, are already taken care of efficiently at the network level. National programs and IRRI also have numerous bilateral cooperative projects, some of them directly oriented to germplasm collecting or its conservation and utilization.

Strengthening and expanding national rice genetic resources programs should be given high priority in the conservation of rice genetic resources. The emphasis during the first two rice conservation workshops was on strengthening the international system for collecting germplasm and on ensuring duplication for safety of the germplasm kept in active collections. This international system is now well-established. It is known, for example, that IRGC has been able to repatriate national germplasm that had been lost or that was not held by active collections.

Our main concern now is that some national genetic resources programs for rice may be weakened or underfunded. To take an extreme example, some governments may consider that conservation of their national rice genetic resources is taken care of by IRGC or the international system of safety duplication, and thus not provide sufficient funds for proper operation of their national rice genetic programs. Active collections are the backbone of a network for conservation and utilization of crop genetic resources. In addition, if there is not a sufficient number of national partners with whom to dialogue and plan collaborative activities, an international center will, in the long term, be unable to properly operate and stimulate activities on genetic resources.

Important objectives of this network could be to

1. Define a strategy to favor direct exchange of information and germplasm between national programs. This could eventually take the form of a central data base, but other possibilities can be envisaged and the choice of an adequate strategy will have to be discussed.

2. Identify, at the national level, bottlenecks and constraints that impede good seed preservation and efficient genebank management.
3. Improve knowledge of the patterns of distribution of rice genetic diversity between and within ecoclimatic regions, species, and populations.
4. Develop approaches to in situ conservation.
5. Design new research techniques for screening for specific traits or for better knowledge of the genomes.
6. Define the interface between conservation or users and biotechnology,

In some instances, a rice conservation network will only be able to identify gaps or needs and draw these to the attention of appropriate organizations working on specific problems. In other cases, participants of a network may play a more active role, by linking directly with other networks or organizations and by providing advice or services (eg, subsets of germplasm needed for specific research). Finally, participants of a network may be able to undertake specific research by sharing activities according to expertise and location advantages. Donor agencies could be contacted by a representative body of network participants when additional funds to those already committed by national programs may appear necessary.

I anticipate this workshop will not be in a position to prepare all the plans of action that could be undertaken within a rice conservation network. However, I hope that participants interested in this concept will be able to lay down a basic framework and mode of operation for such a network. A Rice Conservation Committee composed of about four managers of national rice programs, each representing specific ecoclimatic conditions or specific conditions or interest and importance to national programs, plus a representative of IRGC, could be nominated by participants here. This committee could then follow up the minimal plan of action agreed upon and elaborate further proposals on the basis of the recommendations. IBPGR will be ready to support the next meeting of this committee.

Discussion

Enamul Haque: The approach of forming a germplasm network among the rice-growing countries is surely a positive step. As we think about such a network, this is also the appropriate time to overcome the problems common to several countries. By sharing materials, information, expertise, methodologies, ideas, etc., among participants, we will be in a better position to meet needs. However, we should first evaluate the current status of all participating germplasm conservation centers and set minimum criteria for joining the network, so that all members can actively participate. For those who lack minimum facilities, attempts should be made to provide such facilities and enable them to join the network. In this regard, we should also make ourselves acquainted with the national policies of each country so that free exchange of ideas and materials can take place without difficulty.

The International Network for Rice Germplasm Conservation

T. T. Chang

Participants in the 1977 Rice Germplasm Conservation Workshop held at IRRI developed a collaborative plan to preserve and rejuvenate conserved rice seed stocks (see IRRI-IBPGR 1978, p. 32-33). The plan has the following components:

1. As the base collection center, IRRI shall preserve a complete set. Other national and international centers shall help IRRI on rejuvenation. (The collaborative rejuvenation phase has not materialized.)
2. IRRI shall preserve, rejuvenate, and distribute the indica and javanica cultivars and breeding lines of *O. sativa* and other *Oryza* species, except those from Africa.
3. Japan shall preserve, rejuvenate, and distribute as many of the japonica (or sinica) varieties of East Asia as possible.
4. The United States shall preserve, rejuvenate, and distribute varieties from the U.S., temperate South America, and the Mediterranean area; the U.S. also shall continue to store duplicate samples of conserved IRRI stocks.
5. IITA shall preserve, rejuvenate, and distribute cultivars of *O. glaberrima* and wild species of Africa. IRAT plans to collaborate with IITA on seed multiplication. IRAT, ORSTOM, and WARDA plan to collaborate with IITA on medium-term storage.
6. The above centers shall exchange and carefully compare accession lists to minimize the maintenance of obviously duplicate accessions within single collections and to ensure that no distinct accession or ecostrain is overlooked in the inventory process. (This phase has been partly implemented.)

We now need multilevel (national vs state or lesser entities) and multisector (public vs private) collaboration in various conservation activities. The time has come for the international agricultural research centers and the national agricultural research systems to work more closely, not only on field collecting but also on documentation, consolidation of conserved stocks, research on germplasm, and systematic evaluation. Such important topics comprise the main focus of this workshop.

Discussion

N. Q. Ng: Enrolling a greater degree of participation by the NARS is an important approach. However, many NARS lack the resources and continued support that would enable them to make long-term commitments.

H. I. Oka: Personal working relationships are crucial to such collaborative efforts.

The International Network for Genetic Evaluation of Rice (INGER)

D. V. Seshu

INGER was established in 1975 (as the IRTP) to provide a mechanism for the exchange of elite rices among rice scientists in different countries, for evaluation and utilization in their respective environments. Promising breeding lines developed at the international centers in the CGIAR system are also evaluated through INGER. The program thus represents an intercountry cooperative effort toward genetic improvement of rice targeted to the many environments around the world in which the crop is grown. With such an access to a wide range of genetic materials, purchase of time is an important dividend for scientists in their efforts to develop improved varieties.

The main objectives of INGER are

- to provide rice scientists around the world access to a wide range of varietal diversity through the broad-based exchange and evaluation network
- to provide rice scientists channels to test their breeding materials under a wide range of agroclimatic conditions;
- to reduce the time and investment required to identify and develop superior rice varieties for different environments;
- to identify genetic donor varieties tolerant of major biological, soil, water, and climatic stresses;
- to identify genetic variation (biotypes, races, etc.) in major insects and pathogens;
- to serve as an information center on the interaction of varietal characteristics with diverse rice-growing environments; and
- to promote continued interaction and cooperation among the world's rice scientists.

INGER is organized and coordinated by IRRI and is currently funded by the United Nations Development Programme. About 800 rice scientists from more than 80 countries in Asia, Africa, Latin America, North America, Europe, and Oceania participate in the network. Representative scientists from some participating countries serve on an advisory committee to assist in program planning and implementation.

The more than 25 different types of nurseries composed and distributed each year fall into two broad categories:

- nurseries for identifying superior varieties for different rice cultural systems.
- nurseries for identifying genetic donors for individual biological, physical, and chemical stresses.

Approximately 65% of the entries are contributed by national programs, the remaining originate from the IARCS.

About 75% of the nurseries are tested in different regions of Asia, 10% each in Latin America and Africa, and the remaining 50% in Europe and Oceania. Nurseries are distributed and tested in Latin America in collaboration with CIAT; in Africa, in collaboration with IITA and WARDA.

Scientists from the national programs and from international centers participate periodically in INGER-sponsored international monitoring programs to review the performance of entries in the international nurseries, and in the national breeding trials of selected countries. The monitoring program provides a forum for interaction among rice scientists and for planning breeding strategies.

Multilocation trial results are analyzed and published as annual nursery reports. These are distributed to all concerned researchers in different countries for appropriate follow-up research. Observations and recommendations pertaining to different monitoring visits are also published and distributed.

Through INGER, 174 breeding lines originating from 18 national programs and from IRRI, CIAT, and IITA have been released to farmers in 50 countries in Asia, Africa, and Latin America. National breeding programs and IRRI also have utilized several hundred entries in hybridization programs to improve certain agronomic traits or resistance to specific stresses in current varieties. INGER trial results have helped identify several alternative sources of resistance to various stresses. Biotype differences in brown planthopper and gall midge, and pathogenic race differences in blast have been identified. Rice-weather relationships were elucidated.

Wild species and
land races



Distribution of genes in rice populations

H. I. Oka

The populations of wild plants and crop land races are, in general, genetically polymorphic. This is an important issue in deciding the strategy and system of germplasm conservation. This paper extends the paper presented at the 1983 Rice Germplasm Conservation Workshop (Oka 1983).

Average gene diversity is given as

$$H = \frac{1}{n} \sum_j (1 - \sum_i x_{ij}^2) \quad (1)$$

where x_{ij} is the frequency of allele i at locus j in a given population, and n is the number of loci observed in the data (Nei 1975). The H value differs between populations of wild and cultivated rices. The distributions of H values obtained from data for six polymorphic isozyme loci in different ecotypes of the Asian common wild rice *O. rufipogon* and land races *O. sativa* are presented in Table 9. Perennial wild rice populations are usually highly heterogeneous; some land race populations also carry large gene diversity.

When a population is divided into subpopulations or an assembly of samples is divided into groups, the H value for the whole can be partitioned into H values for subdivisions in the same manner as variances are analyzed. Differences among populations can be evaluated by the index of gene differentiation as

$$G_{ST} = (H_T - H_S)/H_T \quad (2)$$

where H_T is the average gene diversity for all populations and H_S is diversity within populations. Mean H_S , G_{ST} , and some other parameter values obtained in different ecotypes of the wild rice and land race populations are shown in Table 10.

In wild rice, perennial populations are more polymorphic than annual populations, but the annual populations are more divergent from one another, as was found for metric characters (Morishima and Oka 1970). This reflects their different breeding systems, as shown by their heterozygote frequencies and fixation indices. Some land race populations are polymorphic, although they are predominantly self-pollinating. They are also differentiated into varieties, as shown by a high value for G_{ST} .

Table 9. Distribution of within-population average gene diversity (H_S) in ecotypes of Asian common wild rice *O. rufipogon* and land races *O. sativa*.^a

Species and ecotype	Distribution of average gene diversity									Populations (no.)
	0	.05	.10	.15	.20	.25	.30	.35	.40	
<i>O. rufipogon</i>										
Perennial			1	1	3	2	2		1	10
Intermediate		1		1		2		1	1	6
Annual	4	5	3	1						13
Weedy					1	4	1	1		7
<i>O. sativa</i>	1	7	2	3	2					15

^aBased on data for 6 polymorphic isozyme loci (from H. Morishima): *Acp-1* (acid phosphatase), *Cat-1* (catalase), *Pgi-1* and 2 (phosphoglucose isomerase), *Pox-1* and -2 (peroxidase).

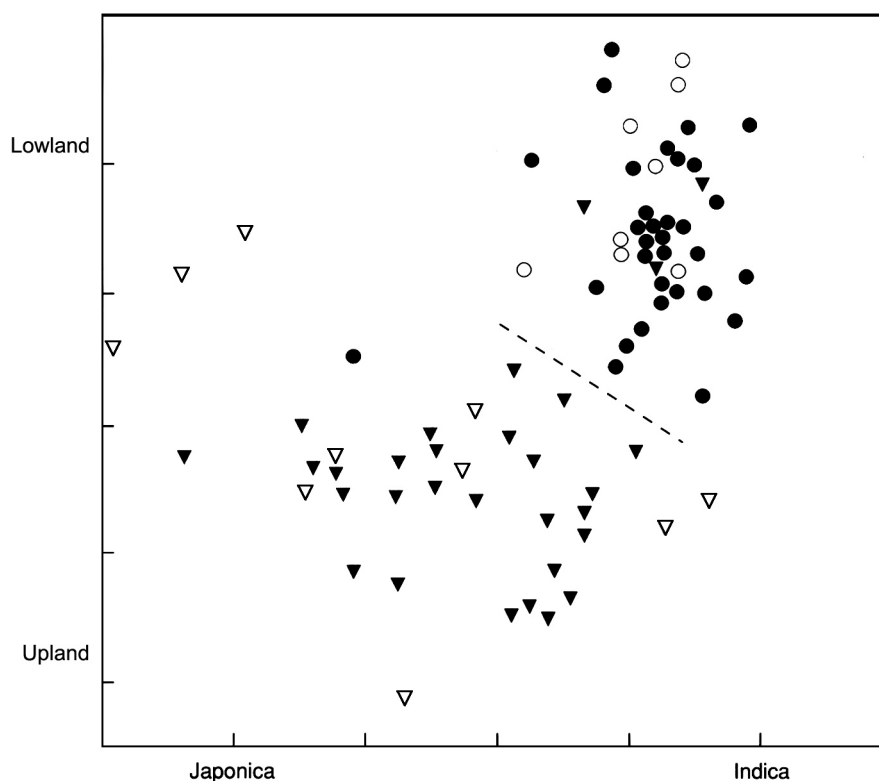
In this context, it is worth mentioning that upland rice populations are generally more polymorphic than lowland rice populations (cf. Oka 1988, p. 166). An example of this comparison is shown in Figure 1. Plants in the lowland populations were largely indica varieties; a tendency to indica-japonica differentiation was seen in the upland populations. We have evidence that suggests upland culture of incipient domesticates contributed to the origin of the japonica type.

In general, it is known that gene diversity based on isozymes is parallel to that based on genes for morphological traits. In rice, however, this relationship does not hold true when the wild population and indica and japonica varietal groups are compared (Table 11). Isozymes show greater gene diversity on the order of wild > indica > japonica; in coloration genes, the order is wild < indica < japonica. Why such opposite trends occur is unknown, but diversity among groups of genes differs, depending on whether they are neutral gene groups or gene groups subject to selection.

Although the H values between populations and kind of genes differ, wild, weed, and land race populations usually contain different genes for isozymes and for such characters as disease resistance. For example, a number of lines derived from two wild populations from Thailand and two land race populations from Yunnan, China, were observed for variations in reaction to four Japanese isolates of *Xanthomonas campestris* pv. *oryzae*, the causal organism of bacterial blight (BB) disease (C. Hamamatsu and H. Morishima, unpubl. data). The results showed the populations to be highly

Table 10. Within-population gene diversity (H_S), index of gene differentiation (G_{ST}) and other parameter values estimated for six isozyme loci in ecotypes of Asian common wild rice *O. rufipogon* and cultivated land races *O. sativa* (Oka 1988).

Species and ecotype	Populations (no.)	Gene diversity		G_{ST}	Poly-morphic loci	Hetero-zygote frequency	Fixation index (F)
		H_S	Range				
<i>O. rufipogon</i>							
Perennial	10	.235	.10-.40	.396	.58	.136	.437
Intermediate	6	.249	.05-.40	.289	.67	.120	.513
Annual	13	.056	.00-.15	.600	.21	.011	.877
Weedy	7	.276	.20-.35	.272	.64	.129	.596
<i>O. sativa</i>	15	.086	.00-.20	.772	.33	.0035	.991



1. Plants of an upland (triangles) and a lowland (circles) population from seeds harvested by the Yi tribe in Yunnan, China, scattered according to scores showing indica-japonica differentiation and upland vs lowland adaptability. Solid marks and open marks indicate positive and negative phenol reaction, respectively. To observe the roots, plants were grown with artificial soil granules (vermiculite) in baskets placed on culture solution in pots. Adaptability was evaluated by the sum of standardized values of the upper roots/lower roots ratio, shoot/root ratio, and days to heading. The intergrades between indica and japonica types were evaluated by the sum of standardized values of $KClO_3$ resistance, low-temperature tolerance, and apiculus hair length (from Oka 1988, p. 167).

polymorphic for resistance genes. The line-mean reaction to isolate T7133 is shown in Table 12. Analysis of variance showed that between-line differences were genetically controlled, although the genes involved have not yet been identified. The wild annual population NE4, with a lower gene diversity for isozymes, was as polymorphic for reaction to BB as the intermediate perennial-annual population CP20, with a greater diversity for isozymes. Reactions to the BB isolate in the upland land race population also had a wide range.

Harlan (1975) said that land races have low yielding capacity, but high yield stability. This is important to farmers who rely on subsistence agriculture. Such crop populations carry an array of resistance genes and are well buffered, so that no single race or biotypes of parasites can increase to an epidemic level (Harlan 1975). Agroecosystems molded by natural selection would thus be stable. The genes for BB

Table 11. Average gene diversity (*H*) estimated in different plant groups (from Oka 1988).

Species and race	Coloration gene ^a		Isozyme gene ^b	
	Strains	<i>H</i>	Strains	<i>H</i>
<i>O. rufipogon</i>	49	0.052	56	0.476
<i>O. sativa</i>				
indica	64	0.211	82	0.338
japonica	66	0.384	85	0.145

^a7 loci: *C A*, *P*, *Ps-1*, *Ps-2*, *Ps-3*, and *I-Ps-3*; total of 15 alleles. ^b11 loci: *Acp-1*, *Amp-3*, *Cat-1*, *Est-2*, *Est-9*, *Pgd-2*, *Pgi-1*, *Pgi-2*, *Pox-1*, *Pox-2*, and *Sdh-1*; total of 40 alleles.

resistance may serve as evidence supporting this view of land races. The rice plants in Thailand and China have probably not been exposed to the bacterial isolates collected in Japan, yet they seem to be preadapted to such unselected isolates of a parasite. The populations may be regarded as natural composite varieties containing an array of resistance genes or as a pool of gene resources.

Of the large collection maintained in the IRGC at IRRI, some 9,700 are already known to have such useful traits as tolerances for drought, cold, deep water, and various adverse soils and resistances to diseases, insect pests, and nematodes (Chang 1980). But when a particular trait is sought, the probability of finding a useful gene will be low (Table 13). Wild relatives and primitive land races are important objectives in germplasm collecting and conservation because they are expected to be treasure-houses of useful genes.

Table 12. Variations in resistance to a Japanese isolate (T7133) of *Xanthomonas campestris* observed in wild *O. rufipogon* and land race *O. sativa* populations.^a

Population	Lines (no.) with given resistance score									Total (no.)	H_s^b
	Resistant					Susceptible					
	1	2	3	4	5	6	7	8	9		
Wild (Thailand)											
W1933 (CP20, intermediate) ^c	1	3	6	5	5	5	2	2		29	0.360
W1866 (NE4, annual) ^d	3	4	3	4	1	4	2	4	2	27	0.193
Land race (Yunnan, China)											
Ch 54 (lowland) ^e						1		2	37	40	0.074
Ch 55 (upland) ^e	3	4		3		1	2	3	22	38	0.095
Cultivar (control)											
N8 (Japan)					2	4	6	6	8	26	0
130 (Taiwan)				1	3	4	5	4	4	21	0
419 (India)							2	3	24	29	0

^aTested by the injection method by C. Hamamatsu and H. Morishima, unpubl. data. ^bAverage gene diversity for 9 isozyme loci. ^cAn intermediate perennial-annual population, near Ayutthaya. ^dAn annual population, near Saraburi. ^eA lowland and an upland population grown by a Yi tribe farmer, near Shilin (cf. Oka 1988, p. 167).

Table 13. Frequency of finding resistance to the whitebacked planthopper *Sogatella furcifera* (from Chang 1989a).

Species	Accessions (no.)		Resistant (%)
	Tested	Selected	
<i>O. sativa</i>	48,554	401	0.8
<i>O. glaberrima</i>	681	309	45.4
Wild <i>Oryza</i> spp.	437	202	46.2

In conserving rice genetic resources, the unit of operation is an accession, which is considered to be and is handled as a fixed line. Because rice is predominantly self-pollinating, the practice of handling accessions in this way is unavoidable in managing a large collection. But a population cannot be represented by an accession. How many accessions are necessary to preserve a population depends on its genetic diversity. I once suggested 20 to 100 lines (Oka 1983). A more elaborate report on this problem in dealing with plant species with varying breeding systems has recently been published (Breese 1989). In the conservation of heterogeneous populations, an indexing system consisting of two series of numbers is recommended. An example is 12345-12, where 12345 represents a population and 12 stands for a given line derived from the population.

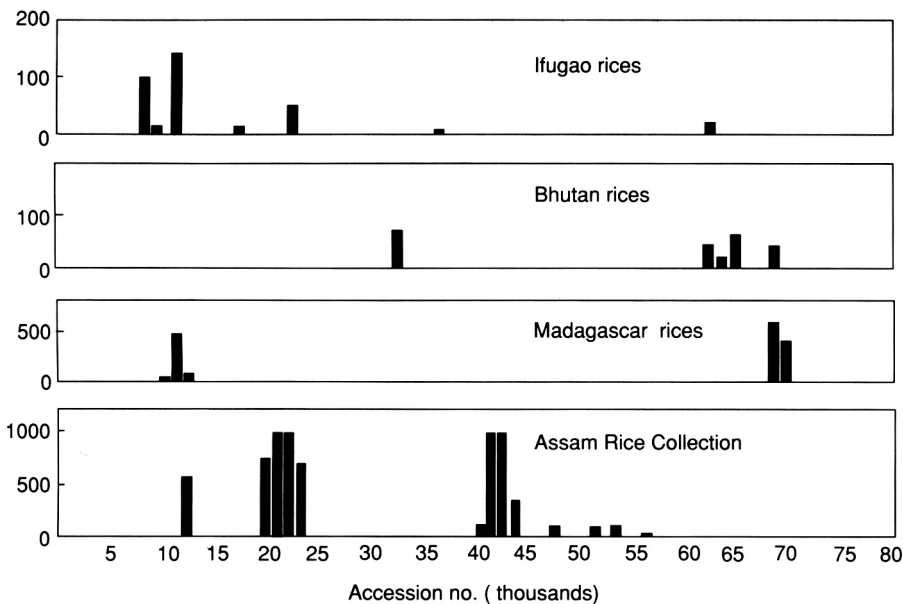
Gene distribution in germplasm collections

D. A. Vaughan

The number of rice accessions in germplasm collections is now very large. In India, two collections contain about 20,000 accessions. In China, about 60,000 accessions of rice are conserved. At IRRI, more than 80,000 accessions are conserved. Efficient evaluation of the germplasm, to find the genes needed for crop improvement, will help promote the use of conserved germplasm.

The accession numbers of conserved germplasm in the IRGC collection are assigned consecutively. Accessions from one region of a country or from one country are clustered (Fig. 2). If a trait is well understood, the choice of germplasm to screen might proceed in a logical, step-wise fashion. For example, in looking for cold-tolerant germplasm, it might be best to search accessions coming from high latitudes and high altitude, if that information is available. On the other hand, if evaluation is for a new

Number of accessions



2. Distribution of variety groups in RGC, by accession number.

trait, such as tolerance for changing quality of radiation, it may not be obvious which germplasm is most appropriate. There are, however, numerous examples of useful genes being found in germplasm that would not have *a priori* been expected to have the trait, such as the cold tolerance in variety Silewah (IRRI Acc. 25718) from 1,200-m elevation in Sumatra or the flood tolerance in variety Kurkaruppan (IRRI Acc. 15449) from Jaffna district in the dry zone of Sri Lanka.

Large numbers of accessions have been screened at IRRI for resistance to several traits. More than 40,000 accessions each have been screened for resistance to blast (Bl), bacterial blight (BB), green leafhopper (GLH), and brown planthopper (BPH). Analysis of the distribution of sources of resistance (Vaughan 1991) reveals two patterns.

- For Bl and GLH, sources of resistance are evenly distributed in the germplasm collection.
- For BPH and BB, sources of resistance are clustered by both geographic origin and accession number.

Different approaches to sampling germplasm for evaluation include sequential, stratified, biased (for example, by ecology or country), and random. An understanding of the factors involved in the trait being sought will help reduce the time spent seeking useful genes. For very rare traits, such as some virus resistances, searching among wild *Oryza* species and *O. glaberrima* might be most appropriate.

More refined techniques are now available to evaluate germplasm and to store the information derived. For many accessions of rice in the IRGC collection, gene(s) for BB or BPH resistance have been identified. Screening for tungro resistance now under way involves screening for resistance to both rice tungro spherical and bacilliform viruses.

Since, unlike breeding lines, germplasm accessions are not transient, all information gathered on an accession should be added to the overall germplasm data base. The standard descriptors for rice (IRTP 1988) are a first step in recording data on evaluated germplasm; they can be expanded as more information on an accession becomes available.

In situ conservation of wild relatives of rice

M. P. Upadhyay, S. Balendira, and D. A. Vaughan

Nepal

Nepal is rich in preservation areas, with about 1.3 million ha (10% of the country's area) set aside for this purpose (Updety 1988). There is a need to explore these preservation areas for wild relatives of rice, to help determine whether or not they are currently acting as sites for in situ conservation of species.

Four wild *Oryza* species are found across the Nepalese Terai: *O. nivara*, *O. rufipogon*, *O. officinalis*, and *O. granulata* (Shrestha and Vaughan 1989). The Terai is the most heavily populated part of Nepal, and populations of wild rice there are vulnerable to such human disturbance as draining of their habitats or conversion of their habitats into ricefields.

A heterogeneous population of *O. rufipogon* and *O. nivara* near the village of Ajigara covering about 50 ha was threatened by a drainage project. The area was therefore proposed as a site for in situ conservation of wild rices and associated flora and fauna to His Majesty's Government of Nepal. The proposal was accepted. Appropriate technical assistance is needed, however, for the reserve to function as an in situ conservation site (letters from G. L. Shrestha to D. A. Vaughan dated 21 Dec 1988, 19 Feb 1989).

Sri Lanka

Sri Lanka is well endowed with national parks and wildlife sanctuaries managed by the agency in charge of wildlife. Monitoring the wild crop genetic resources in these areas requires inputs from a number of disciplines.

Five wild *Oryza* species occur in Sri Lanka: *O. nivara*, *O. rufipogon*, *O. granulata*, *O. eichingeri*, and *O. rhizomatis*. Several of these species reportedly occur in Sri Lanka's national parks (Vaughan 1989b). Since 1988, some populations of wild *Oryza* in these parks, from which seeds have been collected for ex situ conservation, have been repeatedly observed. There is a desire in Sri Lanka to monitor the stability and dynamics of these populations. How to do this needs to be addressed, to help scientists in national research programs make a positive contribution to in situ conservation of these species. For national programs, monitoring of in situ conservation sites, rather than ex situ conservation, may be a more appropriate approach to conserving these genetic resources.

Discussion

Y. Sano: The degree of success in conserving wild species in their natural habitats varies greatly among different species. The weedy races are not easy to preserve because they frequently interact with human activities.

Dssocumentation and data management



Data management within a rice germplasm network

J. M. M. Engels

Networks link people and organizations involved in activities of common concern. Network members may be located within a country, within a larger geographic region (eg, a continent), or across continents (Seshu 1988). One of the basic principles of a network is the exchange of information on research, administrative, or managerial methodologies and results. This applies to the rice network under discussion at this workshop.

One of the objectives of the proposed International Rice Germplasm Conservation Network is the rationalization of conservation efforts. This would not necessarily mean that all accessions have to be kept in a single genebank or in every national rice germplasm collection. A prerequisite to sharing rice germplasm among all the countries participating in the network would be for each member to have ready access to all information on all accessions conserved by all members. That means each member should be able to retrieve information on the whereabouts of individual accessions; their origin; their agronomic, taxonomic, and other relevant characteristics; etc. For such a system to function, one institution within the network must assume a coordinating role in terms of collecting, updating, and disseminating the required information to network members.

In this paper, I present some thoughts on the type of information that might be required by an individual member and on the overall data management needed.

Rice genetic resources data

In the management of germplasm data, it has become a widely accepted practice to use standardized descriptors and descriptor-states for individual crops. In general, such descriptor lists have been developed by crop advisory committees for a given species or group of species, then published by IBPGR. The descriptors are classified into four groups.

1. *Passport descriptors* are accession numbers, collecting information, and other data reflecting the history of an accession. The collector of an accession is responsible for recording most of the passport data. The curator assigns the accession number and monitors other names or numbers given an accession by the donor, if the accession was acquired from a source other than the original collector.

2. *Characterization descriptors* are terms designating characters that are highly heritable, can be easily observed, and are stable in expression over environments. Because of these features, characterization descriptors are useful in identifying accessions.
3. *Evaluation descriptors* are terms designating other traits, usually influenced to a large extent by environmental factors.
4. *Management descriptors* are terms used internally by the curator to assist in managing the germplasm collection. They consist of information indispensable to the management of accessions in medium- and long-term storage, for the multiplication and regeneration of material, and for the exchange of accessions.

The difference between characterization descriptors and evaluation descriptors is not always clear. Evaluation data are collected by scientists in disciplines such as plant pathology, entomology, and plant breeding; the traits are those in which expression depends on the environment. Characterization descriptors are generally given by germplasm curators; the traits are those which do not, or only to a limited degree, vary with the environment.

Details of the rice descriptors for each category can be found in various publications (IBPGR-IRRI Rice Advisory Committee 1980, IRRI-IBPGR 1983, and IBPGR 1989).

A system that allows two members of a network communicating about a given accession to be sure they are talking about the same accession is necessary. One way to ensure that would be for a detailed description of each and every accession to be made at different locations, based on characters that do not vary significantly with environment. Another possibility could be to register and maintain all accessions existing in all the member countries of the network at a central place (ie, the base collection), along with a comprehensive description made at the same location. The institute with the central data base must ensure that a unique identification number is assigned to each accession within the entire network, and that all records are kept in the central databank.

A data base for the rice germplasm network

In view of the fact that IRGC maintains the global base collection of rice, and that IRRI is the world's lead institute in rice research and improvement, it is a logical proposition that IRRI assume the responsibilities for coordination and maintenance of a central rice germplasm databank. This bank could contain the following information for all the accessions in the entire network:

- passport data
- characterization data
- evaluation data (as required)
- management data

What would a central databank look like? The first step could be to assemble the respective data files of all network members and keep these in a central data file, without integrating them into a central data base. An integrated central data base would be the next step in the development of a network data base. The coordinating institute

would integrate, update, and distribute requested portions of data base to members of the network.

The most important prerequisite for the functioning of either the central data files or the central data base is the commitment of all network members to give the highest priority to documentation of their rice germplasm collections and to sharing those data files with the coordinating institute and, through it, with all other members. This commitment would include regular updating of the data files and, as could be the case in later stages of network development, of the national rice germplasm data base.

To function properly, the data management systems in the network will require that:

- A common format for the exchange of data be defined.
- A set of standard passport descriptors be agreed upon by all participating members.
- All other descriptors accepted for incorporation be standardized, or at least detailed information be provided on where, how, and on which parts of the plant the data have been collected (this would allow the central data base coordinator to interpret the data correctly).
- All participants of the network be fully committed to submit and update their data sets in a timely fashion.
- An ad hoc or standing committee functions as a body to provide scientific guidance to the network.

Documentation and data management for rice germplasm banks

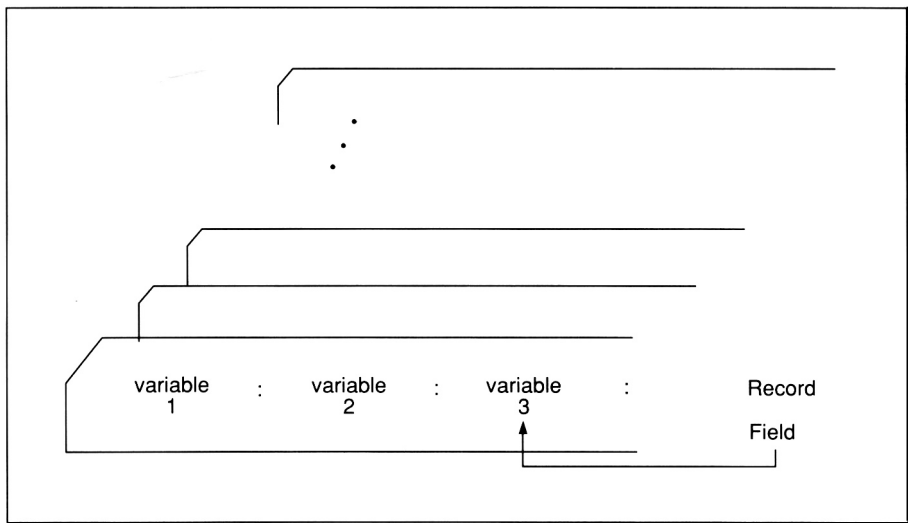
A. Gironella

The establishment of an electronic data base system starts with the identification of the variables about which data will be stored. The next step is to determine how the data will be stored. These steps require appropriate documentation. Such documentation will eventually serve as a guideline to users of the information stored. Documentation provides a picture of the data in terms of

- 1. Files: a collection of similar records,
- 2. Records: a collection of related fields, and
- 3. Fields: the elementary data items.

A collection of related data files is known as a *data base*. Figure 3 shows a diagrammatic representation of a one-file data base.

Data management's concern is to devise effective and efficient ways to catalog, store, and use information.



3. One-file data base.

As early as 1964, the IRGC had developed its rice germplasm databank. In 1990, the approximately 62,000 accessions of *O. sativa* had been completely characterized. Each record in the germplasm bank (GB) data file consists of

1. Accession number (ACCNO)
2. Accession name (ACCNM)
3. Former designation (DESIG)
4. Seed source (SS)
5. Country of origin (ORI)
6. 45 morphoagronomic traits (characterization data)
7. 37 GEU traits (evaluation data)

Today, the information retrieval system serves numerous users and researchers. The IRGC rice germplasm data base system could serve as a model for other germplasm databanks.

The vast information on rice germplasm stored in IRRI's computer system provides a rich source of statistical data on rice. Among the statistical tools that could be utilized in summarizing, describing, and analyzing data in rice germplasm banks are

1. Frequency distribution tables
2. Descriptive statistics (measures of central tendency; measures of dispersion, skewness, and kurtosis)
3. Multivariate techniques (correlation methods as a means for studying simultaneously how different plant characteristics co-vary)
4. Clustering techniques (a means of grouping accessions that are similar in some respects).

Recently, IRRI started using biometrical procedures to detect probable duplicates in the germplasm bank, utilizing the data on morphoagronomic characteristics of *O. sativa* accessions stored in its GB file (Gironella et al 1988).

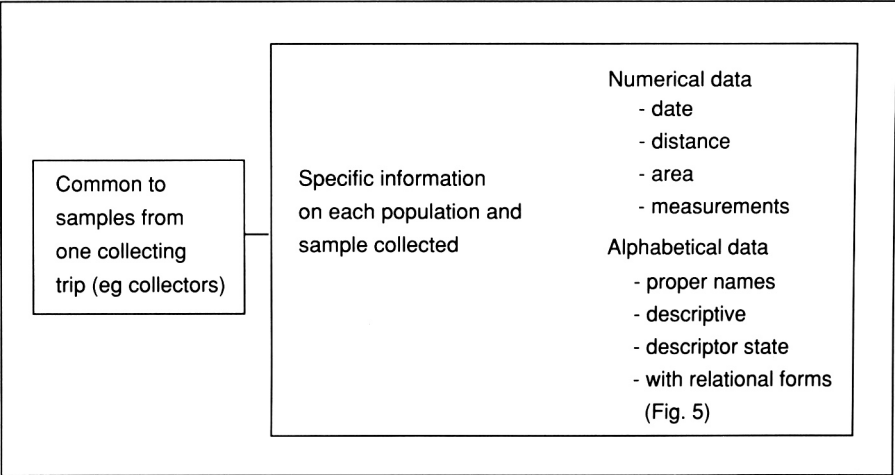
Passport data on rice and related species

D. A. Vaughan

The standardized descriptor list for characterization of rice cultivars was developed in the early 1960s (Chang and Bardenas 1965) and revised in 1978 (IBPGR-IRRI Rice Advisory Committee 1980). It did not, however, include passport data other than the country of origin and seed source, although the 1972 *Manual for field collectors of rice* (Chang et al 1972) included such items on the field record form. The importance of more detailed passport data is increasingly being recognized. Its value in helping accelerate evaluation and use of germplasm cannot be overestimated.

Passport data forms have been developed by many institutes involved in collecting germplasm of rice and related species. The forms differ, sometimes substantially. Recommendations for a set of passport data for rice germplasm that would also be as compatible as possible with passport data for other crops would be desirable.

This working paper was prepared by combining the main descriptors for passport data from different sources (including IRRI, IBPGR, IRAT-ORSTOM). Category headings are



4. Categorization of passport data.

Form/screen 1		Form/screen 2	
Herbarium sample	Yes No	Sent to - Kew Leiden - Paris Bangkok - Singapore Bogor - IRRI etc.	Date sent: _____
Soil sample	Yes No	<u>Soil analysis results</u> Analysis by: _____ Soil type: _____ Soil texture: _____ Soil color: _____ Soil pH: _____	

5. Descriptors and relational screens.

- Sample codes
- Collection trip parameters
- Location
- Site description
- Sample description—field
- Sample description—lab
- Conservation features
- Preservation/quarantine measures taken (Table 14)

The degree of detail that will be of value may need to be considered. Previously, descriptors needed to be closely defined to conserve computer space. As more advanced software and hardware become available, this limitation is less relevant. Relational data bases permit different sets of information on a sample or group of samples to be interlinked. The principle is illustrated in Figures 4 and 5.

Table 14. Passport descriptors - a maximum list.

Note: (C) after descriptor indicates applicability to cultigens; (W), applicability to wild species

(A) SAMPLE CODES

- | | |
|---------------------------------------|------------|
| 1 Collection number: | |
| 1a Accession number: | Institute: |
| 1b Accession number: | Institute: |
| 1c Accession number: | Institute: |
| 2 Collection date: day : month : year | |

(B) COLLECTION TRIP PARAMETERS

- | | |
|--------------------------------------|----|
| 3 Collectors: | |
| 3a Collectors' institute affiliation | |
| 4 Institute: | |
| 4a Acronym descriptions | |
| 5 Funding source: | |
| 5a Project code | |
| 6 Trip report(s): Yes | No |
| 6a Where deposited | |

(C) LOCATION

- 7 Map sheet:
- 8 Latitude: _____ N _____ S
- 9 Longitude: _____ E _____ W
- 10 Village (or distance and direction to nearest settlement):
- 11 Town/City:
- 12 District/Province:
- 13 Country:
- 14 Grower's name(C):

(D) SITE DESCRIPTION

- 15 Altitude (m):
- 16 Topography: _____
swamp (1), floodplain (2), plain level (3), plateau (4), undulating (5), hilly (6), mountainous (7), others (8)
- 16a Specify others:
- 17 Site position: _____ level (1), slope (2), summit (3), depression (4)
- 18 Aspect: _____ N, S, E, or W
- 19 Geological features:
- 20 Landform:
- 21 Natural vegetation of site:

(E) POPULATION DESCRIPTION

- 22 Cultural type (C) _____ – irrigated (1), rainfed-lowland (2), deepwater (3), upland (4), tidal wetland (5)
- 23a Cultural practices(C) shifting: Yes/No
- 23b Cultural practices(C) terraced: Yes/No
- 23c Cultural practices(C) direct seeded: Yes/No
- 23d Cultural practices(C): single (1), double (2), triple (3), transplanted (4)
- 23e Cultural practices(C) mixed stand: Yes/No
- 24 Sowing date(C): _____ day:month
- 25 Transplanting date(C): _____ day:month
- 26 Harvest date(C): _____ day:month
- 27 Ethnobotany/Usage:
- 28 Farmers' assessment (C): (a) yield under normal conditions:
- 29 Farmers' assessment (C): (b) cooking/eating quality:
- 30 Farmers' assessment (C): (c) main desirable characteristic:
- 31 Farmers' assessment (C): (d) main undesirable characteristic:
- 32 Origin (C): – local (1), exotic (2)
- 32a Specify from where -
- 33 Variety-group (C): _____ – indica (1), japonica/sinica (2), javanica (3), hybrid/intermediate (4)
- 34 Shading (W): —open (1), 1/2 shade (5), complete shade (9)
- 35 Population area (W): _____ m²
- 36 Population number (W): per m²
- 37 Water depth at time of collection: cm
- 38 Water depth maximum: cm
- 39 Distance to cultivated ricefield (W) (m):
- 40 Growth stage (W):*
(tillering) vegetative (2), flowering (6), mature (9), seed shed (10), mixed (x)
*Numbers correspond to those for rice
- 41 Fertility/seed production: sterile –0
to completely fertile –9
- 42 Period of seed set (W): day:month to day:month
- 43 Population vigor (W): expanding population –1
to almost extinct –9
- 44 Degree of introgression (W): –None–0
to 90% –9
- 45 Degree of grazing (W): None –0
Complete –9

- 46 % Cover (W): None —0
Complete -9
- 47 Associated species (W):
- 48 Dominant species (W):
- 49 Proximity to other populations (m):
- 50 Associated organisms-pests/beneficials:

(E1) SAMPLE DESCRIPTION — Field

- 51 Photo no.
- 51 a Where deposited:
- 52 Species name:
- 52a Taxonomic reference:
- 53 Vernacular/cultivar name:
- 54 Language/dialect:
- 55 Meaning of vernacular/cultivar name (English):
- 56 Collection source: —farmland (1), threshing floor (2), farm store (3), village market (4), commercial market (5), institute (6), field border (7), wild (8), others (9)
- 56a Specify others:
- 57 Sample status: wild (1), weedy (2), primitive cultivar (3), others (4)
- 57a Specify others:
- 58 Types of sample: seeds (1), panicles (2), vegetative (3)
- 59 Herbarium specimen: Yes No
- 59a Number
- 59b Where deposited
- 60 Sample composition: homogeneous (1), heterogeneous (deliberately) (2), heterogeneous (by accident) (3)
- 61 Sample method: random (1), non-random (specify) (2)
- 61 a: If non-random, specify:
- 62 Frequency: rare (1), occasional (3), frequent (7), abundant (9)
- 63 Soil sample: Yes No
- Soil analysis: 63a: soil parent material
- 63b: soil type
- 63c: soil texture
- 63d: soil color
- 63e: soil pH
- 63f: soil moisture
- 64 Duplicate sample distribution: Yes No
- 64a Institute(s):

(Note: This will be linked to accession number.)

(E2) SAMPLE DESCRIPTION — Lab

Note: This section is included for consideration, since it would permit regenerated samples to be compared with the original sample.

- 65 Panicle length (mm): _____
- 66 Awn length (mm): _____
- 67 Grain length (mm): _____
- 68 Grain width (mm): _____
- 69 Grain thickness (mm): _____
- 70 Lemma and palea color*
- 71 Seed coat color*

(F) CONSERVATION FEATURES

- 72 Status of species/variety: more common (1), less common (2), same (3)
- 73 Disturbance factors: Yes No
- 73a If yes, disturbance by: fire (1), grazing (2), soil erosion (3), human (4), others (specify) (5)
- 74 Protected area: Yes No
- 74a If yes, administrators:

(G) PRESERVATION AND QUARANTINE MEASURES TAKEN PRIOR TO REACHING GENE BANK

- 75 Drying: Yes No
if yes
- 75a: how: 75b: how long:

- 76 Fumigation/chemical application: Yes No
 if yes
 76a: what: 76b: how long:
- 77 Inspection in country of collection: Yes No
 if yes
 77a: who 77b: measures taken (if any)
 77c: certificate number
- 78 Inspection in any receiving country: Yes No
 if yes 78a: who
 78b: measures taken (if any) 78c: certificate number
-

*As for rice descriptors (IBPGR-IRRI Rice Advisory Committee 1980).

IRRI's germplasm data systems

IRGC (*M. Oliva and A. Alcantara*)

The computerized data management systems used at the International Rice Germplasm Center have been continuously improved since the IBM mainframe computer facilities were set up in 1976.

The ORACLE-based system, which runs on the VAX 8350, has the following features:

1. Data entry of the newly received seed samples.
2. Check of probable duplicates (based on accession name).
3. Printout of field books for initial seed increase.
4. Input of the 45 morphoagronomic traits.
(Screens consisting of the different traits gathered at different stages of growth were shown.)
5. Retrieval of identification and morphoagronomic and genetic evaluation and utilization data based on
 - a. Accession number: given a set (or range) of accession numbers, information on the accessions is retrieved and printed
 - b. Accession name: when a given variety name is attached to two or more accessions, or to accessions with similar names, all probable candidates are retrieved. The user can select the accessions on which he/she wants information to be retrieved and printed.
 - c. Specified conditions: accessions satisfying specified single or multiple criteria/conditions (specific observations on certain traits) are retrieved and printed.

The microcomputer-based IRRIGEN software was developed jointly by IRGC and Statistics staff members. It is designed to assist the staff of national genebanks to computerize such activities as

1. Processing newly received seed samples. This includes data entry, data editing, and retrieval of information accompanying newly received seed samples.
2. Selecting materials to be planted for initial seed increase, characterization, or rejuvenation.
3. Generating field plot and accession numbers and printing planting plans, field books, and data sheets for field operations.

4. Processing of the 45 morphoagronomic characteristics, including data entry, data editing, and information retrieval.
5. Keeping track of the amount of seed stocks in storage.

The IRRIGEN software and manual have been sent to germplasm workers in 12 national centers.

INGER (V. Lopez)

INGER (formerly IRTP) was established in 1975 to provide a mechanism for the exchange of improved varieties among rice scientists around the world for evaluation and utilization in their respective environments. About 2,000 INGER entries tested each year include entries received as nominations from participating national programs and international institutes. About 25 types of nurseries are composed and distributed to about 500 experimental sites in more than 80 countries. Multilocation trial results are compiled and analyzed by INGER and reports sent to participating scientists.

To facilitate processing the large amount of data involved, a data management system was developed for the IBM 4361 mainframe, using COBOL and FORTRAN programs. The system stores information on incoming seeds, generates seed increase and nursery field books, and processes nursery reports.

With the acquisition of the VAX 8350 and ORACLE (a relational data base management system), retrieval of INGER nursery data became easier. The seed inventory system monitors the flow of seeds to and from storage. The nursery data retrieval system facilitates retrieval of information on any INGER entry. To invoke this system, the user issues the command 'RUNFORM INGER.' The system accepts the INGER number or the designation of the entry of interest and displays the nurseries where the entry was tested. The user selects a particular nursery and year, and the trials or locations where the nursery was conducted appear on the screen. From among those trials, the user may choose one. The system will display the data for particular entries in that trial or the mean scores, as well as such general information as date of seeding, fertilizer, rainfall, or soil pH.

The INGER data system is linked to the IRRI Plant Breeding, Genetics, and Biotechnology Division files, allowing retrieval of the pedigree of an IR breeding line tested in INGER nurseries and its performance in replicated yield trials in Los Baños.

Data base management system for crop germplasm resources in China

Shuping Chen, Xianzhen Zhang, and Rongcheng Cao

The data base management system used at China's national crop germplasm center, the Institute of Crop Germplasm Resources (ICGR) in Beijing, has three parts.

1. The passport and viability data base for the national genebank. By the end of 1990, there will be 200,000 accessions stored in the national genebank. Passport data consist of national accession number, variety name, seed source, origin, seed harvest year, preservation unit, germplasm bank number, etc. Viability data consist of grain characteristics, seed germination percentage, seed moisture content, seed weight, etc.
2. The data base of crop germplasm characteristics evaluation. This data base contains data on 42 morphoagronomic characterization and evaluation characteristics.
3. The data base of germplasm exchanges. This data base contains information on crop germplasm exchange between national and foreign institutions.

The data base management system for crop germplasm resources is designed for an IBM PC-compatible computer. Hardware consists of a COMPAQ 386/33 micro-computer with 33-MHz Intel 80386 microprocessor, 4 megabytes system memory, 650 megabytes fixed disk drive. This system is suitable for managing all kinds of crop germplasm resources.

The three data bases were set up with different classes. The first is a management file in which crop data file is entered. The second is a format control file, which controls the data structure, the generation of Chinese or English reports, code exchange, the field selected by a user, etc. The third is a control file for code exchange. The three data files share the software that controls the system. The parameters in each data file are used as the common variable of the applied program. By judging different parameters, the system will go into the data base of each assigned crop to execute the generating, maintenance, retrieval, report printing, sorting, or statistical analysis requested. This results in independence of data files of each crop and reduces the work of program design. The system is convenient and flexible to use.

So far, we have incorporated 10,245,751 records into the three basic data bases. The data base of the national genebank has 2,734,590 records for 111 crops; that for crop germplasm characterization-evaluation has 5,552,413 records of 102 crops; and that for germplasm exchanges at home and abroad contains information on 160,000 accessions, 12 items each, for a total of 1,958,748 records.

The data base management system of the ICGR actively serves breeders. A data base has been set up for the genealogy of 3,566 wheat varieties. Through this system, breeders can not only seek specific characters of certain varieties, but also analyze their genealogy and learn the characters of the parents. The data base management system has become very important in managing the national genebank and Chinese crop germplasm resources overall.

The data base on characterization and evaluation consists of

1. Agronomic characterization: seeding date, heading date, maturity date, plant height, panicle numbers, panicle length, panicle fertility, 1,000-grain weight, grain shattering, etc.
2. Phytomorphological characterization: variety group, seasonality, awn length, cultural type, grain shape, grain length, apiculus color, glume color, etc.
3. Quality: percentage of brown rice, percentage of milled rice, protein content, lysine content, starch content, starch quality, amylose content, amylopectin content, gelatinization temperature, gel consistency, etc.
4. Disease and insect pest resistance and abiotic tolerance: seedling blast, leaf blast, neck blast, bacterial blight, cold tolerance, etc.

The data base on germplasm exchange consists of descriptors: variety name, name in Chinese characters, seed source, origin, accession number, distributing unit or exchange unit, preservation unit, family name, genus or subgenus name, species name, seed weight, seed import year, seed export details, etc. Altogether, 16 items are included.

Preservation of germplasm



National genebanks for rice germplasm

L. M. Engle and T. T. Chang

T. T. Chang and D. A. Vaughan surveyed participants in this workshop and their associates. A total of 21 national centers in 17 countries and 1 international center (IITA) completed questionnaires on their conservation programs related to rice. This discussion is confined to the responses on physical facilities and management practices related to seed preservation and documentation systems.

Most genebanks for rice and related crops were established in the 1980s. Although many of the countries built genebanks only recently, most started their rice conservation activities much earlier. The oldest rice genebank reported was established in Mahitsy, Madagascar, in 1932. The first modern genebank is the USDA-ARS National Seed Storage Laboratory in Fort Collins, Colorado, USA. This genebank, as is common to most of the others, does not deal exclusively with rice; it also serves as the central repository for seeds of many other crops. Recently constructed genebank facilities in Bangladesh, China (at CNRRI), Malaysia, Myanmar, Sri Lanka, and Thailand are primarily designed to serve rice conservation. Cambodia, through its IRRI-Cambodia Rice Project, has started conserving its rices in freezers. The PhilRice has a temporary storage facility, but plans to construct permanent storage in Maligaya, Nueva Ecija, with the help of the Japanese Government.

Type of collection

Most countries keep both base and active collections at the same location. Many genebanks also keep working collections in collaboration with rice breeders. PhilRice plans to keep its base collection at the National Plant Genetic Resources Laboratory in Los Baños. Indonesia keeps only active and working collections. Essential information related to base and active collections is summarized in Tables 15 and 16, respectively.

Physical capacity

Genebank floor space varies greatly among countries. The number of materials stored for base collections ranges from 1,300 accessions in Cambodia to more than 46,000 in China. Twelve of the 17 countries hold rice collections that range between 4,000 and 20,000 accessions. The storage capacity designed for active collections is usually larger than that for base collections: the figures provided range between 10,000 and

Table 15 continued

Country	Institution	Total accessions	Year built	Floor space/vol (m ²)	Capacity (accessions)	Temp (°C)	RH (%)	Drying method ^a	Seed moisture (%)	Seed container	Stock amount (g or seeds)
Myanmar	Myanmar Seed Bank	3,190	1990	112.5	43,200	5	40	B/C/D	6-8	Aluminum foil envelope	100
Nepal	Division of Agri- cultural Botany	-	-	-	-	-	-	A	-	-	-
Philippines	PhilRice	50	1985	45.0 m ³	-	-20	-	B/D	6	Aluminum foil envelope	60
Sri Lanka	PGRC	2,488	1989	32.0	25,000	1	35-40	B/C	5-8	Can with vacuum	180
Thailand	Pathum Thani Rice Res. Center	18,341	1981	75.0	20,000	-10	60	A/B	8	Vacuum zinc can	80
USA	NSSL	20,775	1958	93.0	16,008	-20 to -36	35-40	B	8-10	Aluminum foil envelope	200-300
Vietnam	INSA	4,307	1984 (each of 2 cold cabinets)	15.75 m ³	-	-10 to -15	45	A/B	-	-	-

^a A = sun drying, B = heat, C = with dehumidifier, D = desiccant. The drying method indicated for each institution applies to both base and active collections.

Table 16. Seed preservation facilities of active collections at different institutions.

Country	Institution	Total accessions	Year built	Floor space/vol (m ²)	Capacity (accessions)	Temp (°C)	RH (%)	Seed moisture (%)	Seed container	Stock amount (g or seeds)
Bangladesh	BTRI	-	-	90.0	15,000	20	55-60	10-12	Paper bag in glass jar	125
Brazil	CENARGEN	-	-	30.8	200,000	+5	30	-	Aluminum foil envelope; metal can	4000 seeds
China	ICGR	-	-	210.0	30,000	8	-	<7	Can	Varied
	CNRI	-	-	75.0	100,000	-1	35-45	6	Aluminum can; aluminum foil envelope	100-150
(Nigeria)	IITA	-	-	132.0	60,000	5	30±5	9	Screw cap plastic jar; paper envelope	500
India	CRRI	-	-	42.0	30,000	2±2	45	8-10	Laminated aluminum foil	6000 grains
Indonesia	BORIF	-	-	15.0 15.0	30,000	0 10	40 90	10	Glass jar	100
(Philippines)	IRRI/IRGC	80,000+	1978	178.0	130,000	2	40	6-8	Aluminum can or glass jars	250-500 ^a
Japan	NIAR	-	-	140.0	150,000	-1	30	5-7	Airtight plastic bottle	220
Korea (S) Madagascar Malaysia	NIG	-	-	5.0	10,000	5	-	7	Paper envelope	Varied
	RDA	-	-	176.0	200,000	4	40	8	PET-bottle	250
	FOFIFA	-	-	200.0	c.30	+20	65	10	Cloth bag	500
	MARDI	-	-	32.0	13,000	3-5	30-40	<9	Plastic bottle with screw top and a lid	180-200
Myanmar	Myanmar Seed Bank	-	-	56.25	1,824	15	40	6-8	Plastic bottle	100
Nepal	Division of Agricultural Botany	2,022	1984	-	-	5	45	-	Paper envelope in plastic jar	-

Table 16 continued

Country	Institution	Total accessions	Year built	Floor space/vol (m ²)	Capacity (accessions)	Temp (°C)	RH (%)	Seed moisture (%)	Seed container	Stock amount (g or seeds)
Philippines	PhilRice	2,375	1986	18.0	-	15-22	60-70	6-10	Paper envelope in glass jar	250
Sri Lanka Thailand	PGRC	-	1989	96.0	25,000	5	35-40	8	Foil envelope	320
	Pathum Thani Rice Res. Center	-	1981	100.0	25,000	5	60	8	Vacuum zinc can	80
USA Vietnam	NSGL	16,008	1958	880.0	16,008	-9	40	6-8	-	300-600
	INSA	-	1984	24.11 m ³ (each of 5 cabinets)		1-10	45	9-10	Metal can	100

^aVarying amounts of seed stocks (c. 40,000+ accessions per period) are kept in paper bags for 3-5 yr in the short-term storeroom for initial distribution.

150,000 accessions, but in most cases the current size of active collections was not indicated.

Storage conditions

For long-term storage of the base collection, temperature in the storerooms ranges from -30 to 20 °C with 30 to 65% relative humidity (RH). Cromarty et al (1982) of the IBPGR Seed Storage Committee recommended a range between -20 and -10 °C. Four genebanks use temperatures slightly above freezing only for the base collection.

Active collections are stored at temperatures that range from -1 to 22 °C with 30 to 90% RH.

Working collections are kept at temperatures ranging from 5 to 22 °C, or at room temperature, with 30 to 90% RH.

Seed moisture content (dry basis) for base collections is from 4 to 10%; that for active collections, from 5 to 12%.

Base collections are most frequently stored in aluminum foil envelopes. Four genebanks use metal cans. Active collections are kept in a variety of containers: glass jars, plastic bottles, metal cans, aluminum foil envelopes, paper bags, and cloth bags.

The quantity of rice seed stocks stored in the base collection ranges from 18 to 300 grams per accession. Given a 1,000-grain weight range between 20 to 40 grams, depending on seed size, this means 450 to 6,250 seeds are stored, per accession. For genetically uniform material, IBPGR recommends storage of 4,000 seeds, with a minimum of 3,000 (Hanson et al 1984). The recommended amount for heterogeneous material is 12,000, 4,000 minimum.

For the active collections, 80 to 500 grams per accession are stored. The mode is 100 to 200 grams. Working collection quantities are from 1 to 500 grams per accession. Materials for distribution are usually prepacked into subunits, although a few materials are stored in bulk.

Seed processing

Procedures used in processing seed prior to storage also vary markedly among rice genebanks. Sun-drying is used by 11 genebanks: 4 in Southeast Asia, 3 in South Asia, 2 in East Asia, 1 in Madagascar, and 1 at IITA. Nine genebanks use ovens with controlled temperature. At least one genebank indicated that heating temperatures may go beyond 40 °C. Five genebanks, all in the tropics, use silica gel in addition to other seed-drying devices.

Drying prior to storage is probably one area that needs to be improved. Sun-drying, if not properly handled, can be detrimental to seed quality and longevity, especially in the tropics (Cromarty et al 1982).

Only five genebanks fumigate seed prior to storage, usually with phostoxin or aluminum phosphide. Only one applies fungicide, and then only when needed.

Seed cleaning and selection are done by a combination of air blower and hand selection. Almost all the genebanks subject their seeds to such labor-intensive procedures.

BORIF in Indonesia complained of a lack of seed processing equipment. Workers in Madagascar find it difficult to lower seed moisture content in a very humid environment.

Seed longevity

Projected longevity for seed in base collections ranges from 2 yr to more than 200 yr. Genebanks in developed countries project longevity to be at least 25 yr. Genebanks in less developed countries are less optimistic, probably because of existing conditions in their genebanks and inadequate monitoring of seed viability in stored materials.

For active collections, projected longevity is from 1 to 30 yr. The genebank of NIAR in Tsukuba, Japan, projects longevity of the active collection to be more than 50 yr.

Viability in many genebanks of South and Southeast Asia is monitored at intervals of 1 to 3 yr, using random samples or selected samples. Genebanks in China, Japan, Korea, the US-NSSL, and Brazil's CENARGEN monitor viability at 5-yr intervals.

Regeneration standards vary from 30 to 85%. IBPGR recommends a rejuvenation standard of 85% (Hanson et al 1984).

Refrigeration and dehumidification

Most genebank storerooms have insulating materials in the walls, floors, and ceilings. In several newly constructed genebanks, polyurethane was used to insulate the walls and floors. BORIF in Indonesia and CENARGEN in Brazil used polystyrene. Insulation material in the older US-NSSL is cinder block and ridged concrete-foam.

Doors to subfreezing cold rooms are not heated along the edges, except at NBPGR in India, CNRRI in China, and RDA in Korea. Eleven genebanks have airlocks in front of the cold room.

Most genebanks have backup facilities in the form of extra compressors or emergency power generators.

Duplicate storage

The bulk of the collections for 10 of the national genebanks (or nearly the entire national collection) is duplicated at IRRI—six (Cambodia, Indonesia, Malaysia, Myanmar, Philippines, and Thailand) in Southeast Asia and three (Bangladesh, Nepal, and Sri Lanka) in South Asia. The wild species collection of the National Institute of Genetics, Japan, is duplicated at IRRI.

In addition to duplication at IRRI, the majority of the Asian countries have stored duplicate rice accessions in genebanks located in another region of the country. BORIF in Indonesia has duplicates stored at SURIF. Part of the CRRRI collection is stored at the NBPGR in New Delhi. PhilRice plans to keep its base collection at the National Plant Genetic Resources Laboratory at Los Baños. MARDI keeps duplicates of some accessions at Bumbong Lima. The national genebank of Vietnam only keeps duplicates in another cabinet at the same location.

In Nepal, duplicate sets are held by the National Rice Improvement Program and the Plant Genetic Resources Center. Sri Lanka has duplicates stored at ICRISAT in India. CAAS has some of its collection duplicated at CNRRI. The NIAR at Tsukuba has duplicates in several national agricultural experiment stations and in some other agricultural experiment stations. The cultivars stored in NIG, Japan, are partly duplicated in Hokkaido Green-Bio Institute of Hokkaido. RDA in Korea keeps duplicates at the Yeongnam Crop Experiment Station. CENARGEN has some wild rice duplicates at Louisiana State University. The US-NSSL keeps duplicates at the National Small Grains Laboratory in Aberdeen, Idaho.

Problems experienced by national genebanks

Seven genebanks consider loss of seed viability during storage one of their most serious problems, even though some of them have good storage facilities. On the basis of responses to the questionnaire, it appears improper prestorage processing may be the cause of such rapid loss of viability. In the case of the NIG, Japan, the problem of poor germination and low seed production is inherent in the wild rices they conserve.

Surprisingly, although the physical conditions of storage facilities appear adequate in most countries, 12 genebanks indicated some problems associated with the operation of their storage facilities. Among the problems listed are high running costs, repeated failure of air coolers, voltage fluctuation, and problems in maintaining low temperature and low relative humidity in the storeroom. The national genebank of Vietnam reported that its humidity control does not work properly when the temperature is higher than 33 °C and relative humidity more than 85%. MARDI in Malaysia reported breakdown of compressors due to gas leakage, belt snapping, and tripping of the electrical supply switch.

Another general problem is lack of funds and manpower.

Data management systems

Among the 19 institutions that responded to the survey, 14 have computer systems, mostly microbased. Seven plant genetic resources centers in China, India, Japan, Malaysia, Myanmar, and USA have their own computer systems. Six genebanks share their equipment and staff with other units in the national system. One contracts with a commercial firm to partly complete operations. The genebank in Sri Lanka did not provide details. Genebanks in China, Japan, Nigeria (IITA), and USA have computerized their seed inventory, seed multiplication, and seed distribution and exchange activities.

With regard to the scope of documentation, nine institutions have more than 50% of their passport, identification, and morphoagronomic information in data files or catalogs or data sheets.

Conclusions

Based on responses to the questionnaire, most countries have already built or have immediate plans to establish modern storage facilities for rice germplasm (the

exception is Cambodia). Construction work on Madagascar's facility has been temporarily suspended.

The respondents share several common problems in operation and maintenance of their facilities. Most genebanks attempt to meet the desired standards for seed preservation, but inadequate seed processing facilities or procedures sometimes pose bottlenecks. Emphasis on lowering seed moisture content to below 10% and the availability of free solar energy has prompted many to sun-dry their seeds or to use mechanical drying temperatures that exceed 40°C. It would be worth finding out if the rapid loss of viability reported in most genebanks is due to improper seed drying rather than to inadequate storage facilities. Unreliable seed containers may be another contributing factor.

About two-thirds of the responding genebanks now have varying degrees of computerized data management capability. In the less developed countries, the workers still have a long way to go in entering past records into computerized files and in using such information to aid genebank operations and to serve interested users.

Although there is still a need in some countries for fully operational rice genebanks, many existing genebanks need only modify and/or improve their operations to meet acceptable standards. A continuous supply of trained germplasm workers would be helpful in several aspects of genebank activities.

Seed storage in national centers

R. H. Ellis

Managers of genebanks in national centers aim to provide seed samples with high viability to plant breeders and researchers, promptly but without undue expense.

This service not only helps maximize the possibility of an adequate number of healthy, vigorous seedlings being established, but also minimizes the risk of genetic damage. Loss in viability is associated with damage to the genome (Roberts 1988). For example, seed storage conditions that result in a 50% loss in viability have the same effect on mutation rates in surviving seeds as an X-ray dose of 10,000 Roentgen (Roberts 1988). Even smaller losses in viability are associated with an increase in heritable damage (Dourado and Roberts 1984).

Seed longevity

For long-term seed storage, most rice genebanks rely on controlled conditions of low temperature and low moisture, with extremely infrequent regeneration (perhaps once a century).

We know that cooler and drier storage conditions will increase seed longevity. Refrigerated stores, however, are costly to construct, maintain, and operate. They also require a reliable supply of electricity. If we wish to increase longevity by altering seed storage environments, it would be useful to be able to quantify such effects, to determine the most cost-effective way of obtaining a given increase in seed longevity.

One attempt to do this is Harrington's rules-of-thumb: a 5 °C reduction in temperature doubles longevity; a 1% reduction in seed moisture content also doubles longevity (Harrington 1972). These rules are helpful in indicating the scale of the effect of seed storage environment on seed longevity, but are only accurate over limited ranges of temperature and moisture.

Viability equations

At Reading, we have developed two equations to quantify the relationship between seed storage environment and seed longevity, with a view to being able to quantify the effects of alternative storage conditions for genetic conservation (Ellis and Roberts 1980).

The first equation describes the shape of the seed survival curve under constant storage conditions. These curves are typically sigmoidal, and can be described as negative cumulative normal distributions.

$$v = K_i - p/\sigma \quad (1)$$

where v is probit percentage viability after p days in storage, K_i is a constant, and σ is the standard deviation of the frequency distribution of seed deaths in time, measured in days. The value of σ is a measure of seed longevity. For example, σ is the time taken in days for viability to fall from 97.7% to 84.1%, or from 84.1% to 50%.

The second equation relates the value of this measure of seed longevity to seed storage conditions.

$$\log_{10}\sigma = K_E - C_W \log_{10}m - C_H t - C_Q t^2 \quad (2)$$

where m is seed moisture content (% fresh wt), t is temperature ($^{\circ}\text{C}$), and K_E, C_W, C_H , and C_Q are constants. These viability equations have been shown to apply to a wide range of species (Dickie et al 1990).

Effect of moisture and temperature on seed longevity

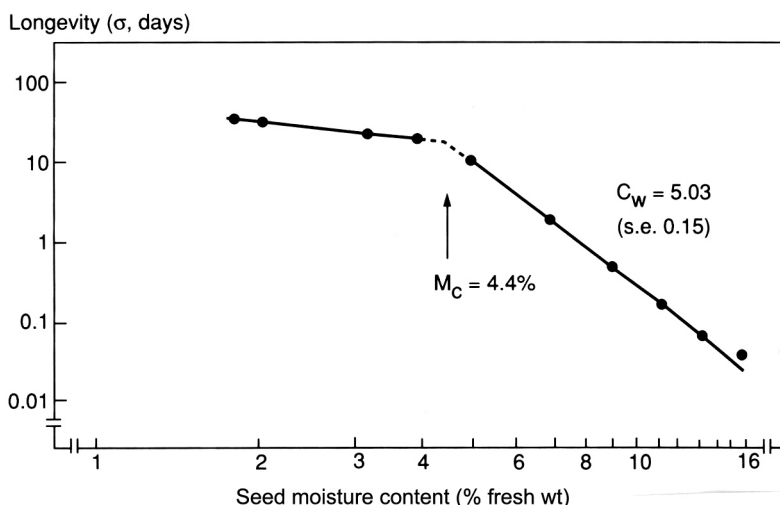
Although at first sight they may appear to be somewhat complicated, the equations have important consequences on decisions for genetic conservation by seed storage. The relationship described between longevity and moisture in equation (2) is logarithmic. One effect is that the benefit to longevity of a 1% reduction in moisture increases as moisture content is lowered. In contrast, the relationship between longevity and temperature is subject to the law of diminishing returns: although reducing temperature increases longevity, the relative effect of a 5 $^{\circ}\text{C}$ reduction in temperature diminishes as temperature is lowered.

Conditions preferred for long-term seed storage in the past were -18°C or lower with $5\pm 1\%$ moisture content (IBPGR 1976). We now know that reductions in seed moisture content are rather more beneficial to longevity than was previously thought, but reductions in temperature are not as beneficial.

Moisture content limits

The logarithmic relation between moisture and longevity is, however, subject to certain limits. At very high moisture content, a further increase in moisture increases longevity in aerobic storage, but has little further effect on longevity in anaerobic storage. We do not know the level of this upper critical moisture content in rice, but work on other species indicates it is likely to be in equilibrium with a relative humidity of 90% or higher (Roberts and Ellis 1989), say more than 18% moisture content.

We know rather more about the lower critical moisture content in rice. Figure 6 shows the relationship between seed storage moisture content and longevity for one seed lot of rice stored at a constant temperature. The logarithmic relation between longevity and moisture content of 5 to 16% is negative, but between 2 and 4% moisture



6. Relationship between seed moisture content (% fresh wt, logarithmic scale) and seed longevity (σ , days, logarithmic scale) for seeds of rice (BPI-76NS) in hermetic storage at 65 °C. The two lines intersect at 4.43% moisture content. At that moisture content, the seeds are in equilibrium with 10.2% relative humidity (from Ellis et al 1989).

content, a change in moisture content has very little effect on longevity. The lines intersect at about 4.4% moisture content (Ellis et al 1989).

Practical limit to seed desiccation for storage

It appears that 4.4% moisture content can be considered the practical limit to desiccation for seed storage: there is little advantage to longevity in reducing moisture content further. Variation among rice seed accessions in the level of this critical moisture content is likely to be small and limited to differences in seed composition. Work with a very wide range of species has shown that the critical values of seed moisture are close to those in equilibrium with 10% relative humidity.

Effect of low temperature on longevity

With regard to the effect of temperature on seed longevity, there is now considerable evidence that there are few differences among species in the values of the viability constants C_H and C_Q of equation (2) (Dickie et al 1990). Using the estimates of these constants provided by that study, we can quantify the diminishing benefit to seed longevity of reductions in temperature. Longevity is increased by a factor of almost 3 if storage temperature is reduced from 20°C to 10°C; by 2.4 if temperature is reduced from 10 °C to 0 °C; by 1.9 from 0°C to -10°C; and by 1.5 from -10°C to -20°C. These values contrast widely with the quadrupling of longevity per 10°C reduction in temperature implied by Harrington's rule-of-thumb.

Effect on longevity of a 1% reduction in moisture

One can use the viability equation in a similar way to demonstrate the effect of various reductions in seed storage moisture content on rice seed longevity. Ellis et al (1989) estimated the constant C_w of equation (2) for rice at 5.03. Longevity at 7.4% moisture content is 1.9 times longer than that at 8.4%; at 6.4%, it is 2.1 times that at 7.4%; at 5.4%, it is 2.4 times that at 6.4%; and at 4.4%, it is 2.8 times that at 5.4%. Thus, drying seeds to the low critical moisture content of around 4.4% is particularly beneficial.

Comparable combinations of moisture and temperature

Note that the final 1 % reduction to 4.4% moisture content is calculated to have the same effect as a 20 °C reduction in seed storage temperature, from 0 °C to -20 °C. Similar calculations show that the longevity of rice seeds with 4.4% moisture content stored at 10°C is expected to be similar to that of seeds with 6.4% moisture content stored at -20 °C.

Seed drying and packaging

It is fortunate that lowering the moisture content of seeds results in improved seed longevity. In resource-poor regions, it is generally cheaper to reduce and maintain seed moisture content at 4.4% than it is to maintain a seed storage temperature of -20 °C. Seed drying and packaging are, therefore, very important factors. Elsewhere, it has been suggested that seeds be dried at 15 °C with 10-15% relative humidity (Cromarty et al 1982). To dry rice seeds to 4.4% moisture content will probably require a further period of admixture with a desiccant such as silica gel. It is important that the desiccant be regenerated regularly. Where equipment is limited, silica gel can be used throughout for drying small quantities of the seeds of many accessions. With equal weights of seed and silica gel, it takes 2-3 wk at 20 °C to dry rice seeds from 11 % to 4.4% moisture content.

For packaging, it is essential to use a moisture-proof container (unless the humidity within the seed storage area is controlled). Controlling humidity is expensive, and usually occurs only in medium-term storage where accessions are subject to relatively rapid seed depletion through distribution. If controlled relative humidity seed storage areas are to be used, the decision on the relative humidity to be maintained depends on the costs and benefits from reducing relative humidity. Longevity is doubled for each 8.4% decrease in relative humidity between about 10 and 90% (Ellis et al 1989).

Suitable moisture-proof containers for hermetic seed storage include Kilner jars (glass), aluminum-foil packets, and metal cans. One of the cheapest solutions (in terms of materials, but not labor) is to seal seeds in vials formed from glass tubing.

The provision of large controlled-temperature storerooms is costly. It is worth remembering that small collections of rice seed accessions can be stored cheaply and conveniently at -18 °C in deep-freeze cabinets (Cromarty et al 1982, Ellis and Roberts 1982). For example, a 600-liter capacity deep-freeze cabinet could accommodate 160 accessions of 16,000 rice seeds each, or as many as 1,600 accessions if each lot was

restricted to 2,600 seeds. The provision of larger cold storage areas has been dealt with in detail by Cromarty et al (1982).

Seed dormancy and germination

If a seed fails to germinate in a germination test, then it is either dormant or dead. Compared to most other crops, rice has good seed storage characteristics but can show considerable dormancy.

One consequence of this is that very often the results of serial germination tests on stored rice seeds show an increase in germination with period of storage, before germination eventually begins to decline as a result of seed death. This can make it difficult to compare the longevity of different seed accessions.

A classic example has been provided by Roberts (1963). He stored seeds of six contrasting rice cultivars under the same storage conditions, testing germination at regular intervals. Initial germination ranged from zero to almost 90%. Germination rose to 100% in all but one cultivar. Subsequent loss in germination was identical in all six cultivars. This forms part of the evidence that there is no causal relation between seed dormancy and longevity in rice, but it also shows that many dormant rice seeds fail to germinate in standard laboratory tests.

Alternating temperatures

While many factors have been shown to promote the germination of dormant seeds, the most important in laboratory germination tests designed to estimate viability is temperature regime. For commercial testing of rice seed, the International Seed Testing Association (ISTA) prescribes an alternating temperature regime of 20/30 °C, the cooler temperature being applied for 16 h/d (ISTA 1985).

Alternating temperature regimes can be particularly useful in promoting the germination of dormant seeds of a wide range of species. The ISTA recommendation is probably adequate for many japonica cultivars, which show little dormancy, but it is better that the warmer temperature be applied for 16 h/d (Ellis et al 1983). From that comparison of a wide range of alternating temperature regimes, it has been concluded that 34/11 °C (higher temperature applied for 16 h, lower temperature applied for 8 h) is preferable for a wide range of rice accessions.

In the most dormant accessions of *O. glaberrima* and indica cultivars of *O. sativa*, the following combination of treatments may be required to promote germination: soak the seeds at 20 °C for 24 h in 0.1M HNO₃; soak for a further 24 h in 0.25M H₂O₂; test for germination at 34/11 °C with 0.01M 2-mercaptoethanol co-applied.

Further information

These notes are intended to supplement the information on genetic conservation by seed storage published by IBPGR in its series of handbooks (Cromarty et al 1982; Ellis et al 1985a, b). Although the notes are brief, they should be sufficient to demonstrate that, even with relatively limited resources, much can be done to maintain seed accessions for genetic conservation.

Regional base collection centers for rice

IITA's role (N. Q. Ng)

Scientists from IITA in Ibadan, Nigeria, began to assemble rice germplasm samples as early as 1972, for their work in the institute's cereal crop improvement programs (maize and rice). By the mid-1970s, they had several thousand rice samples, mainly of breeding lines from national and international sources. The collection was used primarily for adaptive selection and plant breeding.

The institute soon recognized the need for a program of genetic resources collecting and conservation. IITA established its Genetic Resources Unit in October 1975. Its role is to collect and conserve rice, food legumes, root and tuber crops, and the wild relatives of these crops in Africa. The unit has been actively involved in exploring and collecting rice in Africa since 1976 (Sharma 1980). The 1977 Workshop on Rice Genetic Conservation recommended that IITA preserve, rejuvenate, and distribute cultivars of *Oryza glaberrima* and wild species of *Oryza* from Africa (IRRI-IBPGR 1978). IBPGR also designated IITA as a regional base center for preserving *O. glaberrima* and the African form of *O. sativa* (IBPGR 1980).

At the 1983 Rice Germplasm Workshop, participating rice scientists recognized the central role of IITA, with its CGIAR mandate for the collecting, conservation, characterization, documentation, and distribution of rice germplasm from Africa. They recommended that samples of all collected materials from Africa be sent to IITA for preservation.

In its recent strategic plan, IITA reaffirmed its commitment to collect, characterize, document, and preserve rice germplasm for Africa (IITA 1988a, b), but announced it will phase out its rice breeding activities by the end of 1990. The rice germplasm collection will be made available to WARDA breeding programs.

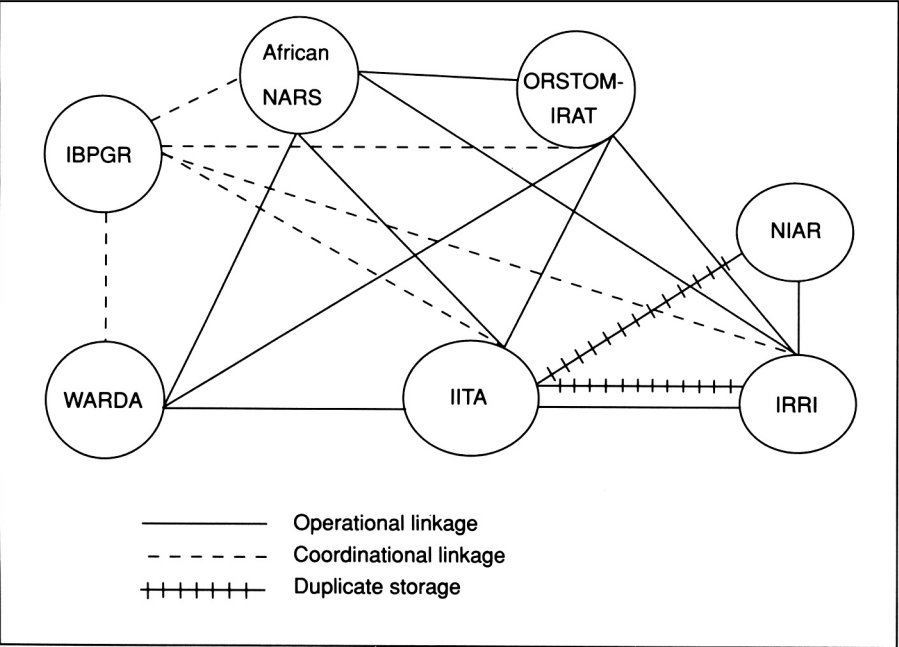
Operational linkage between IITA and other institutions

Given the size of the African continent and the very wide geographical distribution of rice species in Africa, it is impossible for any one institution to thoroughly collect the diversity in the gene pool. IITA has been collaborating with IBPGR, IRAT, ORSTOM, WARDA, IRRI, and national institutions in exploring and collecting rice germplasm (Ng et al 1983, IITA 1988c). Plant exploration carried out by IITA is always in collaboration with national scientists and agricultural authorities.

IITA has established a linkage with IRRI for the duplicate storage of rice germplasm collected in Africa. It has also sent part of its rice collection to NIAR in Japan, for research and conservation. IITA encourages national institutes in Africa to preserve a base collection of rice and is ready to repatriate any of its existing collection to national programs that are ready to preserve the rice germplasm of their countries. The operational linkage with respect to germplasm exploration and conservation between GRU/IITA and the various international, regional, and national programs is shown in Figure 7.

Collecting and distributing rice germplasm

IITA's genetic resources unit has been actively and systematically exploring and collecting germplasm of rice in Africa. Plant explorers of the unit have directly participated in 51 rice exploration missions to 26 countries in Africa so far (Ng et al 1983; Ng, this workshop) and have collected 4,621 rice germplasm samples. In addition to its own plant exploration missions, the unit has also acquired rice germplasm samples collected in Africa by other institutions, through exchange or donation. Most of the materials collected by IRAT-ORSTOM (except the wild species), WARDA, and national programs (with support by IBPGR) were received at IITA. Some of IRRI's African rice accessions from other sources were also given to IITA. Between mid-1984 and the end of 1989, IITA received 1,640 rice samples from IBPGR, IRRI, IRAT, and African national programs (Table 17).



7. IITA's rice germplasm collection and conservation linkages.

Table 17. *Oryza* accessions collected in Africa and received by the Genetic Resources Unit/ IITA through exchange or donation, 1984-89.

Country	Year	Donor	Accessions (no.)			Total
			<i>O. sativa</i>	<i>O. glaberrima</i>	Wild <i>Oryza</i> spp.	
Guinea	1984	IRAT	184	49	1	234
Zambia	1984	IRAT	2	-	-	2
Madagascar	1984	NARS/IBPGR	292	-	-	292
	1988	NARS/IBPGR	233	-	-	233
Zambia	1986	IBPGR	1	-	-	1
Togo	1986	NARS/IBPGR	4	12	-	16
Burkina Faso	1987	NARS/IBPGR	596	100	-	696
Mali	1987	IBPGR	1	1	2	4
	1989	IRRI	-	108	-	108
Ghana	1988	NARS	51	3	-	54
Total			1,364	266	3	1,640

The IITA rice germplasm collection has increased from 7,633 accessions in April 1983 to 12,360 in May 1990. The collection has 9,473 accessions of *O. sativa*, 2,503 of *O. glaberrima*, and 384 of wild species. This germplasm is freely available on request. Between January 1985 and April 1990, 16,020 rice germplasm samples were distributed: 9,708 samples to research programs within IITA and 6,312 samples to rice researchers or institutions all over the world.

Characterization, evaluation, and documentation

When IITA receives new samples, the usual practice is for the GRU to carry out initial seed multiplication and purification. The accessions are grown at IITA headquarters in Ibadan, Nigeria, during the main growing season June-November in rainfed upland plots supplied with sprinkler irrigation when necessary. Upland rice cultivation is predominant in Africa and a large proportion of the germplasm accessions at IITA were collected from upland ecological zones.

For each accession, 44 morphoagronomic characters are scored, using the standard descriptors (IBPGR-IRRI Advisory Committee 1980). Blast disease symptoms are noted. In some seasons, some plants of each accession are inoculated with rice yellow mottle virus to screen for resistance. Rice pathologists and entomologists also screen germplasm samples for resistance to rice blast and insect pests (such as the stalk-eyed fly and African rice gall midge).

IITA developed its computerized documentation system data base "OGRE" to store the following rice genetic resources information:

- Passport data (12 items).
- Agrobotanical characters (44 items).
- Information on seed storage management, including records of seed quantities, location of each sample, date of entering storage, and seed viability percentage when stored.

All germplasm information is routinely updated. Most accessions have complete passport data.

Seed storage and processing facilities

In 1982, GRU completed installation of a prefabricated 88-m³ cold storage unit that operates at -20 °C. By the end of that year, processing of the germplasm of rice and other crop species for long-term (base collection) storage began. Rice germplasm had been stored only in short-term seed storage at +20 °C and 40% RH.

In 1986, the unit renovated, reconstructed, modernized, and expanded its seed processing laboratory and storage facilities for germplasm of mandated crops, to meet recommended IBPGR standards (1985b). The new facilities provide three types of seed storage.

1. Withholding and drying seed storage conditioned at 15 °C \pm 1 °C and 15-20% RH, with a capacity of 68 m³.
2. Two active collection seed storage units maintained at 5 °C \pm 1 °C and 30% RH, units with a combined capacity of 410 m³.
3. A second base collection seed storage unit kept at -20 °C \pm 1 °C and less than 30% RH, with a capacity of 132 m³.

The processing facilities include a seed germination laboratory and a seed canning room with drying cabinets that can be conditioned to less than 10% RH at 20 °C, and that can dry seeds to less than 5% moisture content.

Procedure for preparing seeds for conservation

Soon after they are harvested, dried, and threshed, seeds in cloth or paper bags are placed in withholding seed storage, pending sorting and processing for banking in the active and base collections. This reduces the rate of seed deterioration, compared with seeds kept in ambient conditions. The withholding storeroom can also be used for drying.

For the active collection, seed containers are nonairtight plastic screw top jars, paper bags, or aluminum foil envelopes (after seed moisture has been reduced to less than 8%). Under these conditions, rice seeds in the active collection store (5 °C and 30% RH) equilibrate to around 8.5% moisture content. They can be preserved for 20 years or longer.

Initial viability of all germplasm accessions for the base collection is tested; only accessions that show 90% or higher seed germination are accepted for base collection conservation. Seed moisture content is reduced to 5% and the seeds sealed in airtight aluminum cans. Under storage at -20 °C, these rice seeds should remain viable for more than 100 years.

Regeneration standard and monitoring of seed viability

The regeneration standard for rice at IITA is 85% seed germination (Ng 1990). Viability is monitored by testing 1) a number of randomly selected accessions each year after 5 years of storage, 2) three test varieties every 2 years of storage, and 3) all accessions after 20 years storage. Additional tests on randomly selected accessions and

on test varieties will provide a double check and give better assurance of the safety of seeds in storage.

Japan's National Institute of Agrobiological Resources genebank (*K. Hayashi*)

Japan's NIAR constructed a new building at Tsukuba, Ibaraki, in 1988—the third generation of the National Gene Bank. This “Center Bank” for the genetic resources of plants, animals, and microorganisms functions in cooperation with 125 laboratories designated as “Sub-Banks” in local MAFF institutions. An expanded project on collecting, conservation, evaluation, and multiplication is now advancing through this network. The Departments of Genetic Resources I and II of NIAR and the Center Bank compose the Genetic Resources Center in the network.

Rice genetic resources are an important collection in the genebank. In accordance with the recommendation on the role of NIAR made by the 1977 IRRI-IBPGR Workshop, japonica varieties of East Asian origin provided by IRRI are conserved in the genebank. In addition, the Director General of NIAR agreed to store a subset of IRRI's collection for security purposes. The exchange of seed inventories between the MAFF genebank and IRRI has been completed.

The genebank is distributing rice genetic resources abroad in response to requests from various institutions in many countries. We fully recognize the significance of the international role of the NIAR genebank with regard to the conservation and rejuvenation of rice and other crop species.

Discussion

T. T. Chang: Most of the wild species and exotic cultivars assembled by National Institute of Genetics scientists have been deposited with the IRGC at IRRI. About 2,000 accessions came from collections in Japan. In turn, IRGC increases the seed and makes the materials available to rice researchers of the world. However, rejuvenation of the wild species is difficult and costly.

K. Hayashi: The National Institute of Agrobiological Resources has repatriated about 8,200 accessions from its stored seed to national centers that supplied the seed earlier.

Y. Sano: The National Institute of Genetics has also sent back 4,664 samples to different countries.

The USDA/ARS National Plant Germplasm System (*R. H. Dilday, C. F. Murphy, and H. L. Shands*)

Collecting and assembling genetic resources require international cooperation. In the United States, the preservation, evaluation, and distribution of germplasm to meet the needs of researchers for this germplasm rest with the National Plant Germplasm System (NPGS). NPGS is a coordinated network of scientists from the private, state,

and federal sectors of the agricultural research community. The U.S. Department of Agriculture/Agriculture Research Service (USDA/ARS) has the lead role in managing NPGS. To fulfill its responsibility to provide genetic diversity to increase crop productivity and reduce genetic vulnerability in future food and agriculture development, not only in the United States, but in the entire world, USDA/ARS developed the following mission statement:

"The mission of the U.S. National Plant Germplasm System (NPGS) is to effectively collect, document, preserve, evaluate, enhance, and distribute plant genetic resources for continued improvement in the quality and production of economic crops important to the U.S. and world agriculture. This is achieved through a coordinated effort by the U.S. Department of Agriculture in cooperation with other public and private agencies in the U.S. and international organizations. The NPGS's plant genetic resources are made freely available to all bonafide users for the benefit of mankind."

Four key objectives of the USDA/ARS National Plant Germplasm Systems Long-Range Plan (1983-1997) are germplasm acquisition, maintenance or preservation, evaluation, and enhancement. Here we discuss acquisition, maintenance, and preservation.

Acquisition

The focal point for rice germplasm acquisition in the U.S. is the Plant Introduction Office (PIO) of USDA/ARS. The PIO is administered through the National Germplasm Resources Laboratory, which is part of the Plant Sciences Institute in Beltsville, Maryland. The predominant source of foreign plant germplasm, including rice, enters NPGS through extensive worldwide contacts. The bulk of germplasm exchanges are handled by the PIO. Scientist-to-scientist contacts, however, also result in significant movement of plant germplasm. Specific foreign sources of plant acquisitions may also be obtained from scientists, research and germplasm organizations, and special research projects (such as Public Law 480, bilateral agreements). The IBPGR also sponsors germplasm explorations, usually in areas of high genetic erosion. The base collections are maintained in the U.S. at the National Seed Storage Laboratory (NSSL) of USDA/ARS, Fort Collins, Colorado (Murphy 1981).

Maintenance or preservation

The three major operational functions of maintenance or preservation in the NPGS are working (active) collections, the base collection, and germplasm services or information management. Most of the germplasm in the working collections are held in four Regional Plant Introduction Stations (RPIS), as authorized under the Research and Marketing Act of 1946. The stations are located at Griffin, Georgia; Ames, Iowa; Geneva, New York; and Pullman, Washington. Each RPIS is staffed with a curator; two to four scientists representing agronomy, horticulture, pathology, and entomology; research associates where feasible; and technicians. The regional stations increase and distribute seed to users, evaluate germplasm, and conduct other research activities

(National Program for Conservation of Crop Germplasm 1971). Duplicate samples in the working and commodity collections are held in a base collection at NSSL (Jones and Gillette 1982). Accessions also are grown at the regional stations to maintain adequate samples of accessions held in the base collections.

Working collections. Working collections (active collections) are composed of germplasm accessions maintained to meet the day-to-day research needs of geneticists, breeders, pathologists, entomologists, agronomists, and other users. Working collections of several important crops, including rice, are held in special commodity collections at several U.S. locations. Rice is part of the USDA/ARS National Small Grains Collection (NSGC) held at Aberdeen, Idaho. However, rice is unique in the NSGC: because it cannot be economically rejuvenated or evaluated at Aberdeen, the national responsibility for coordinating rice rejuvenation and evaluation was assigned in 1988 to the USDA/ARS staff at Stuttgart, Arkansas.

Base collection (NSSL). In 1944, the National Research Council of the National Academy of Science recommended that the USDA establish a national facility for the preservation of valuable plant germplasm. In 1949, a special subcommittee of the National Coordinating Committee for New Crops was appointed to prepare plans for a national seed storage facility. In 1956, Congress appropriated US\$450,000 for construction of the National Seed Storage Laboratory (NSSL) at Fort Collins, Colorado.

The laboratory has been in operation since 1958. It maintains plant germplasm at low (-20°C to -36°C) temperatures and in cryogenic storage (at -196°C), and serves as the base collection for the U.S. (Brooks and Barton 1977). Through formal and informal cooperation, NSSL is part of the global network of genetic resources centers (Plant Germplasm Preservation and Utilization in U.S. Agriculture 1985). Stocks in storage are categorized as basic plant introductions, recently released and obsolete varieties, open-pollinated parental lines and genetic stocks, differential host and virus indicator stocks, and type specimens for future reference.

The base collections in the U.S. are not intended to meet the day-to-day needs of geneticists, plant breeders, and other plant scientists. They act as reserve stocks to prevent loss of germplasm and erosion of genetic variability. NSSL seed is withdrawn only when all other sources of seed have been exhausted or when germination of stored seed declines to a level that indicates regeneration is necessary.

Accessions of all crops in the NSSL base collection total 396 genera and 1,848 species. The base collection of rice includes 20,775 accessions from 105 countries. Categories of rice seed stocks in storage include basic plant introductions, recently released and obsolete cultivars, parental lines, and genetic stocks. NSSL also serves as a duplicate storage site for IRRI.

Germplasm services or information management. The Germplasm Resources Information Network (GRIN) data base links germplasm sites and accumulates information about plant germplasm from a wide range of sources. Only curators and other authorized personnel are permitted to enter inventory and evaluation data into GRIN, but the data are accessible to any ARS scientist who has access to a computer and a modem. GRIN is also accessible to state and private germplasm workers as well

as to scientists in Canada, Mexico, and the IARCs. Descriptors common to both national and international collections are used to provide compatibility between systems and to enhance accessibility.

GRIN has become much more than a supporting element in the NPGS; it binds the NPGS operational units together. GRIN provides an automated retrieval capability for the collection and dissemination of plant germplasm information. Data processing expertise supports the production of data bases consisting of 450-500,000 discrete accessions. GRIN allows scientists in the U.S. and throughout the world to maintain communication. It aids in locating plant material needed for research or breeding and facilitates its rapid exchange. GRIN has the capability to manage germplasm information and programs in a manner not previously possible (National Program for Conservation of Crop Germplasm 1971).

Current issues in managing national genebanks

T. T. Chang

Managing a modern genebank is one of the main concerns of national rice germplasm programs in several Asian nations that have recently acquired such facilities, partly through the assistance of foreign agencies. Germplasm workers need to maximize their use of the capabilities offered by state-of-the-art preservation technology by interfacing sound biological practices, properly maintaining physical facilities, and efficiently deploying human resources. Because most rice genebanks will remain as service units in a national crop improvement program, germplasm workers must fully exercise their service spirit and maintain vigilance in safeguarding the germplasm collection while, at the same time, advancing their professional careers.

Time does not permit a detailed discussion of the management issues. The English version of a 1985 lecture on genebank management published in Chinese is included as appendix on pp. 163-167 (Chang 1986). Recent papers deal with the management of the germplasm of rice and other plants (Chang 1989b, 1991; Chang et al 1989). An earlier manual was written by Chang (1976).

A few salient points need brief mention. In a recent encounter with a TV talk show host, I used the metaphors of our complicated and difficult mission as being similar to that for a refugee camp—in sheltering threatened germplasm—and a hospital—in ensuring health and longevity. I keenly feel germplasm workers must love the materials under their charge; strive for continuous, even though small, improvements; and help fellow workers. While competency to carry out the necessary duties is crucial, much of the professionalism will come from on-the-job training and self-advancement. Conservation biology is not taught in universities; the practical innovations and skills must grow from hands-on experience. IRRI held two Genetic Resources Conservation and Management Training Courses of one-year length each in 1985-86 and 1988-89, but the number of workers who could receive the comprehensive training was limited to 23.

Continuity in personnel is vital to germplasm conservation programs, and germplasm workers should have opportunities to build rewarding careers. Even for seemingly routine operations, coworkers should share their knowledge and skills so they will be able to fill in for one another in times of need.

In the past, IBPGR has commissioned committees of experts to develop guidelines for the planning and design of modern seed storage facilities; these are both practical and helpful. Personally, I feel the time has come for IBPGR to provide additional much needed assistance, by dispatching its seed preservation officer and consulting engineer to provide on-the-spot advice in different countries.

Germplasm research and utilization



Improving utilization of plant genetic resources through core collections

T. Hodgkin

The large size of many collections of plant germplasm has led to increasing concern as to whether the full range of genetic diversity they contain can be effectively utilized. Worldwide totals for some of the major grain crops exceed two million accessions (Holden 1984). While this estimate includes a considerable number of duplicates, the number of truly unique accessions is now so large as to deter their extensive use except for a few, easily identified characters. As Holden (1984) pointed out, the management of such collections also poses major problems. Data on many accessions remain incomplete and inadequate.

One approach to resolving these problems has become the focus of increased attention over the last few years: development of the concept of a core collection. Here I outline the principal characteristics of a core collection and identify some of the more important issues that need to be investigated in developing such collections.

The concept of a core collection

Frankel (1984) proposed that a core collection should contain the genetic diversity of a crop species and its wild relatives, with a minimum of repetition. A proportion of the total germplasm collection of a crop and its wild relatives would be chosen to represent the major kinds of diversity present and to constitute a central core. This proportion would provide genebank managers, plant breeders, and research scientists with a manageable set of accessions on which to concentrate resources. Such a core collection would become the focus of the search for desirable new characters, detailed evaluation, and work on the application of new techniques.

Three points should be made at the outset. First, there is no suggestion that existing genebank collections should be reduced as a consequence of the development of a core collection. Indeed, one of the objectives of a core collection is to provide a way in which users can obtain more effective access to the total collection, guiding them to that fraction of the collection most likely to contain the character or combination of characters desired.

Second, the definition should be regarded as an ultimate objective. The data required to fulfill Frankel's definition do not yet exist, even for the most well-studied collections. Nonetheless, where collections have been characterized and evaluated in some detail, there seem to be good reasons to expect that core collections containing much of the genetic variation of a species can be developed.

Third, the selection by plant breeders and research workers of limited sets of accessions that meet their needs is not new. However, the adoption of the core collection concept will likely result in a more structured and efficient approach to identifying such limited sets and enable workers in different fields to compare results more effectively.

Development of a core collection

The successful identification of accessions in a collection that contain the genetic diversity of a crop species and its wild relatives raises a number of problems. In practice, limited data are available to resolve most of these problems for many germplasm collections. Brown (1989, 1990) has provided valuable overviews of some of the major issues involved: the distribution of allelic variation in the crop, the role of biological and ecological factors in determining allele variation, and the statistical aspects of selecting a limited sample of accessions with varying allele distributions.

Genetic diversity in plant populations does not occur at random but appears to be more or less structured, to an extent and in a way that reflects the biological characteristics, distribution, and ecology of the species examined (Hamrick and Godt 1990, Nevo et al 1988, Nevo and Beiles 1989). One of the most important factors affecting the genetic structure of diversity in a species appears to be its breeding system. Outbreeding species often possess higher diversity and less genetically differentiated populations than inbreeding ones (Hamrick and Godt 1990).

Geographic origin is also significant in determining the observed distribution of both yield-related characters and allozymes (Spagnoletti-Zeuli and Qualset 1987, Kahler and Allard 1981). Differences in allozyme frequency have also been found to occur over small distances as a result of environmental variation, such as degree of aridity (Nevo et al 1988). Such studies suggest that, in developing core collections, due attention should be paid to the biology of the crop species and its wild relatives. Passport data may be of considerable value in grouping similar accessions (Peeters and Martinelli 1989).

Sampling collections to assemble a core is bound to result in some loss of diversity, in comparison with that present in the whole collection. The amount of variation that might be lost and the sampling strategy that would minimize its loss are important for the development of successful core collections (Brown 1989).

Four types of alleles can be identified in collections: common and widespread, rare and widespread, common and localized, and rare and localized. Brown (1989) considered the probability that each of these types of alleles would be included in a core collection. He concluded that common widespread alleles would be included without difficulty. He also showed that a sample of 10% of an entire collection retained at least 75% of the rare-widespread group of alleles, at a probability of 0.95. On the basis of this study, Brown suggested that a core collection should contain approximately 10% of the accessions present in the whole collection or, for a very large collection, about 3,000 accessions.

The inclusion of common-localized alleles presents the most problems in developing a core collection. At the extreme, highly localized alleles might be omitted

because the particular accessions in which they occur are not included in the sample. In practice, such alleles are likely to have some selective advantage and would probably be included in a core collection that takes full account of edaphic and ecological factors.

The last group of alleles, rare and localized, also causes difficulties in developing a core collection. Examples of important alleles found at low frequencies in only one or two accessions have been cited. It is likely, however, that locating such alleles will always require a search of the whole collection; their exclusion from the core need not be a cause for concern. In fact, the major risk for such alleles is their loss during regeneration, as most regeneration procedures are not designed to ensure retention of alleles occurring at frequencies of less than 0.01.

To select accessions to be included in a core collection, it seems logical to first group accessions according to their similarity, given the information available. Various analytical techniques exist to accomplish this. Multivariate analysis is used when there are large amounts of data on different characters. Peeters and Martinelli (1989) recently showed that a hierarchical cluster analysis could be used to classify barley accessions. Within the groups identified, accessions may be chosen for pragmatic reasons (eg, seed or information availability and ease of handling) or at random. The number of accessions in each group will differ. It has been suggested that the number chosen from each group for a core collection should be in proportion to the logarithm of the number of accessions in each group (Brown 1990).

While sampling strategies derived from population genetic theory are an important basis for the development of core collections, most collections will be selected from the holdings of existing genebanks. Procedures used must take into account the nature of the material held. For many crop species, a large number of more or less uniform cultivars are held. Evidence suggests that the genetic diversity in cultivars is often limited, and that many are closely related. Their presence in the core collection may be required for utilization purposes and for the specific combinations of genes present, even though the genetic diversity they contain may well be present in land races of the same crop.

Land races themselves may cause some problems. In many genebanks, land races are divided into different accessions, based on variation for visible characters. Sampling procedures will have to take this into account.

Existing core collections

In late 1989, IBPGR initiated a survey of current work on core collections, soliciting information from scientists known or believed to be actively involved in the development of such collections. More than 20 projects were identified worldwide; current evidence suggests this number is increasing rapidly. To date, the number of core collections about which published information exists is limited. It is already clear, however, that many approaches have been chosen and different procedures adopted. Four examples illustrate this situation.

- One of the earliest core collections established was that for okra (Hamon and van Sloten 1989). Following characterization and evaluation of the 2,283 accessions in the ORSTOM/IBPGR okra collection based in Ivory Coast, a

core collection of 189 accessions was established in 1985. The accessions in the core were chosen on the basis of representative variability, as described by passport, characterization, and evaluation data, plus additional rare types that might not otherwise have been included.

- The core collection of perennial *Glycine* spp. developed in Australia (Brown et al 1987) was selected from over 1,400 accessions of 12 species. In this case, the major criteria were inclusion of at least a few accessions of each species, good geographic coverage with as broad a range of habitats as possible, and representation of any known cytological or isozyme variation.
- Mackay (1990) has developed a core collection approach for use with the Australian winter wheat collection. He believes that, with increasing computerization of passport, morphological, and agronomic data, it is possible to identify a specific core collection for further evaluation. In this case, the core identified depends to some extent on the characters in which the potential user is interested. The procedure adopted puts considerable emphasis on the use of ecogeographic data for selecting accessions that are likely to include all the diversity for a desired character.
- An international approach to develop a barley core collection is currently in progress. The Barley Working Group established by the European Cooperative Programme on Conservation and Exchange of Genetic Resources has suggested that a core collection, which should not exceed 2,000 accessions, be set up. It is envisaged that the accessions used for this collection will be maintained as homozygous lines, separately from existing collections. Accessions will be chosen to include a range of cultivars, land races, wild species, and genetic stocks. A hierarchical dendrogram using known morphological variation and ecogeographic data will be used to identify the groups from which accessions will be chosen.

Many of the factors that will affect the procedures for developing a core collection and the successful achievement of the objectives have yet to be clarified. The examples given illustrate the wide range of approaches already in use. Thus, core collections may be based on a single genebank or collection, as in okra, winter wheat, and *Glycine* spp., or may involve international collaboration, as in barley. The accessions identified may be physically separated, as in barley and okra, or merely marked on a genebank's data base, as in winter wheat. Other issues remain to be investigated. A different approach will be needed for clonally propagated crops for which field genebanks are maintained, for crops where genetic data are limited or absent, and when procedures to evaluate whether the selected core adequately represents the crop's variation still need to be developed.

Conclusion

Many studies, both theoretical and practical, will be needed to explore the full potential and major limitations of the core collection concept. IBPGR intends to continue collating information on the different core collection projects of which it is aware. This will permit continuous evaluation of progress made and identification of areas where

significant research or development work is needed. In this context, developments on core collections for rice at IRRI are to be welcomed, in view of the large size of the world collection of this crop and the extensive information available on it.

The crucial test for a core collection will be the use made of it. Collaboration between genebanks and between users of plant genetic resources and those concerned with collecting and maintenance, through appropriate crop networks, will be essential in developing and using core collections. It is unlikely that any single procedure will be appropriate for developing core collections of all crops; different crops, collections, and utilization priorities will require different approaches. International collaboration to devise appropriate strategies is likely to be of major importance in maximizing the benefits of investigations on establishing core collections and in ensuring their fullest use when established.

Acknowledgments

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Guidelines on developing core collections of rice cultigens

T. T. Chang

Rice workers began developing a collaborative plan to preserve, rejuvenate, and disseminate conserved rice seed stocks from four regionalized base collections in 1978.

- *IRRI*—as complete a base collection as possible of all rices preserved; duplicate storage of whole or partial sets of other base collections provided; and dissemination of indica and javanica cultivars, breeding lines of *O. sativa* and other *Oryza* species provided.
- *Japan*—preservation, rejuvenation, and distribution of the japonica/sinica varieties of East Asia provided, to the extent possible; partial duplicate set of IRRI's collection stored at NIAR.
- *USA*—preservation, rejuvenation, and distribution of the japonica/sinica varieties of the U.S., temperate South America, and the Mediterranean areas provided, to the extent possible; duplicate storage of IRRI's entire collection of *O. sativa* cultivars.
- *IITA*—preservation, rejuvenation, and distribution of *O. glaberrima* and wild species of Africa; duplicate set stored at IRRI.

Core collections can be set up within each of these regionalized base collections.

Pros and cons of core collections

Benefits

1. Setting up a core collection helps to elucidate the contents, diversity, and duplication within a large base collection—a learning process.
2. If truly representative, a core collection may help in deciding the quantity of conserved stocks that needs to be preserved (ie, smaller seed stocks for the base collection and larger seed stocks for the core collection).
3. A core collection facilitates preliminary research and evaluation, and information exchange.
4. The core collection approach helps in the formulation of subsets of the base collection for duplicate storage at other sites.

Drawbacks

1. Insufficient knowledge about the base collection may cause problems in setting up a useful core collection.
2. A core collection requires the increase of fresh seed and necessitates more storage space. It may require complicated data processing and probably statistical analyses.
3. Except for new workers, few researchers or breeders are willing to evaluate a core collection on its overall merit (ie, each worker has different and specific needs).
4. Breeders are only interested in using a small number of genes of economic significance; neutral alleles (or the earlier term, "favorable alleles") do not necessarily appeal to users who demand quick returns.
5. Rare or restricted alleles may be left out of a core collection.
6. Practicing the core collection approach does not materially help bulking, combining, or eliminating duplicate accessions.

Setting up a core collection

Guidelines (Brown 1989)

1. About 10% of the base collection.
2. Not less than 3,000 entries.

Complications in rice

1. Regionally oriented base collections—eg, IRRI (for tropical Asia), USDA (for America and the Mediterranean region), NIAR (for temperate East Asia), and IITA (for Africa)—differ greatly in contents and documentation.
2. Duplications exist between and within base collections.
3. Knowledge about most accessions is meager.

Hierarchical (stratified) sampling (in preference to random sampling)

1. Geographic classification, by continents or regions (see Vaughan, p. 109).
2. Species (*sativa*, *glaberrima*).
3. Ecogeographic race (*indica*, *sinica*, *javanica*, hybrid).
4. Geopolitical information (country of origin).
5. Cultural type and hydroedaphic regime (lowland, upland, deepwater, tidal wetlands, etc.).
6. Seasonal types (kharif vs rabi, aman vs aus and boro, yala vs maha, wet vs dry).
7. Maturity, plant stature, other morphoagronomic traits.
8. Grain type (dimensions and shape, pericarp color, endosperm type).
9. Known economic attributes (pest and stress tolerances); samples from special types with genetic information.
10. Isozymes, seed proteins, restriction fragment length polymorphism data, if available.

We are interested in trying out the core collection approach in *O. sativa*. The huge size of our collection (nearly 80,000 accessions of the Asian cultigen) may require

more than one core collection, to stay within a manageable size. Complete entry of passport and evaluation data into the base files, followed by appropriate editing, is needed before the sampling strategy is chosen. This also needs to be said: a core collection or subsets of a base collection will not replace the complete collection.

Core collections of wild relatives of rice

D. A. Vaughan

In recent years, the number of requests for samples of wild rice preserved in IRGC has increased severalfold. Evaluation of populations of wild rice is revealing useful sources of resistance and tolerance for pests and diseases. In addition, crossing many of the species in the genus with cultivated rice can now be done more efficiently than was previously possible.

Wild rice germplasm, however, is not easy to conserve. Seed multiplication is time-consuming and more costly than for cultivated rice. To reduce redundancy in the distribution of samples of wild rice for evaluation and research, the wild rices maintained by IRGC were sorted and organized into genetically representative subgroups of the entire collection, into core collections.

Three basic steps were taken:

1. Literature searches and herbarium studies were conducted to guide grouping of species and subspecies groups for the genus *Oryza*: 26 groups were recognized (Table 18).
2. The geographic range and variation within each species or subspecies group were assessed. Using these factors and the representation of each species in the IRGC collection as bases, the proportion of each species needed in the core collection was determined.
3. Accessions of conserved germplasm were assigned to one of five different, but approximately equally representative, core collections.

Good core collections can be developed if germplasm is well understood and well documented, particularly with respect to passport data.

Core collections are dynamic: as more information or new material is obtained, additional or different accessions can be assigned. For example, the chromosome number of a number of accessions of *Oryza punctata* conserved in IRGC was not known. As chromosome counts are undertaken, accessions of this species can be assigned to an appropriate core collection.

The process of sorting carefully through collections reveals duplication and deficiencies. For example, IRGC received samples directly from a collector who distributed seeds to several institutes. The same samples were sent to IRGC again by one or more of those institutes, with the accession number of the dispatching institute attached, but not the collection number. By tracing accessions back to the original collection number, previously unknown duplication within the germplasm collection is revealed.

Table 18. Representation (%) of wild *Oryza* species and subspecies in the core collection.

Species and subspecies (alternative name)	Distribution	Representation (%) in core collection
<i>B, C, D, E, F, and unknown genomes</i>		
<i>O. alta</i>	Latin America	2.4
<i>O. australiensis</i>	Australia	1.6
<i>O. brachyantha</i>	Africa	2.4
<i>O. eichingeri</i>	Africa	2.4
<i>O. eichingeri</i>	Sri Lanka	0.8
<i>O. grandiglumis</i>	South America	0.8
<i>O. granulata</i>	Asia	2.0
<i>O. indandamanica</i>	Andaman Islands	0.4
<i>O. latifolia</i>	Latin America	4.0
<i>O. longiglumis</i>	Papua New Guinea	0.8
<i>O. meyeriana</i>	Southeast Asia	1.6
<i>O. minuta</i>	Philippines	3.2
<i>O. officinalis</i> - 2x	Asia	9.6
<i>O. officinalis</i> - 4x (<i>O. malampuzhaensis</i>)	India	1.2
<i>O. punctata</i> - 2x	Africa	1.6
<i>O. punctata</i> - 4x (<i>O. schweinfurthiana</i>)	Africa	1.6
<i>O. rhizomatis</i>	Sri Lanka	1.6
<i>O. ridleyi</i>	Southeast Asia	2.4
<i>AA genome - diploid species</i>		
<i>O. barthii</i> (typical)	Africa	5.1
<i>O. barthii</i> (weedy)	Africa	6.0
<i>O. glumaepatula</i>	Latin America	2.7
<i>O. longistaminata</i>	Africa	7.5
<i>O. meridionalis</i>	Australia	2.7
<i>O. nivara</i>	Asia	13.0
<i>O. rufipogon</i>	Asia to Australia	11.0
<i>O. sativa</i> f. <i>spontanea</i> (weedy)	Asia	13.0

Deficiencies in the coverage of germplasm highlighted by the development of the wild rice core collection include inadequate representation of certain species, such as *O. alta*, *O. granulata*, *O. ridleyi*, and the perennial *O. rufipogon*. In addition, regions that have been poorly explored in the past, such as Indochina, Irian Jaya, Papua New Guinea, and parts of east and southern Africa, also were revealed.

Developing core collections helps a germplasm curator better understand the conserved collection, permits cost-efficient distribution and evaluation of germplasm, and can lead to useful sets of germplasm to better study germplasm diversity.

Evaluating germplasm for resistances and tolerances

Brown planthopper (*R. C. Saxena*)

Brown planthopper (BPH) *Nilaparvata lugens* (Stal.) has been a pest of rice in Korea since AD 18 and in Japan since AD 697. It destroyed all ricefields planted to cultivar Milfor in Calamba, Laguna, Philippines, in 1959. BPH became a particularly damaging pest in South and Southeast Asia following the introduction of high-yielding, semi-dwarf rices, such as IR8, grown with high levels of nitrogenous fertilizers. Expansion of irrigation systems that allow year-round rice cultivation exacerbated the problem.

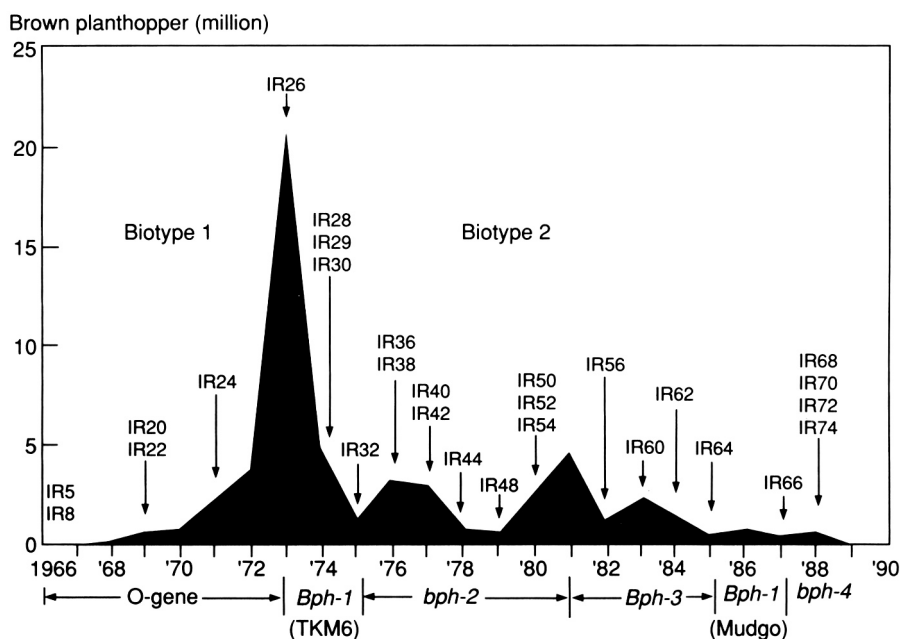
BPH sucks rice plant sap and causes the crop to wilt and dry (hopperburn). It also transmits grassy stunt and ragged stunt viral diseases. Losses caused by BPH exceeded US\$300 million in the 1970s.

Developing resistant varieties is the most practical solution to the BPH problem, and varietal resistance is the key component in integrated pest management programs. Breeding for BPH resistance started in 1965. Since then, more than 50,000 rice accessions and even more breeding lines have been evaluated. BPH thrives on susceptible varieties but not on resistant ones. However, varietal stability must be monitored, because new BPH biotypes can develop by natural selection.

The first resistant variety, IR26 (*Bph-1* gene), was released in 1973. It suppressed the original BPH population (biotype 1). After 2-3 yr of widespread and continuous cultivation, IR26 succumbed to biotype 2 in the Philippines, Indonesia, and Vietnam. IR36 (*bph-2* gene) replaced IR26 in 1976 and controlled biotype 2 for more than 6 yr. But in 1982, damage on IR36 reported in Mindanao (Philippines) and north Sumatra (Indonesia) indicated a new shift in the BPH population (biotype 3). Biotype 3 was also selected in the greenhouse from field populations reared successively on IR36 plants. By then, varieties and breeding lines with *Bph-3* (IR56) and *bph-4* genes had been developed (Fig. 8).

BPH is now under control in most countries where resistant varieties are grown and when appropriate pest management practices are used. IRRI has identified three more resistance genes (*bph-5*, *Bph-6*, and *bph-7*), which can be deployed if currently grown cultivars become susceptible to a new biotype.

We also have identified germplasm with tolerance or moderate resistance that would minimize biotype selection without loss of yield. Minor genes for BPH resistance that block biotype selection are being identified.



8. Release of IR rice varieties and their impact on catches of brown planthopper in 3 light traps on the IRRI farm, 1966-90.

Wide hybridization has provided new opportunities for incorporating pest resistances from wild rices. Using embryo rescue techniques, we have transferred resistance from *Oryza officinalis* to *O. sativa* while maintaining yield and grain quality.

Biotechnological advances on the horizon will provide broad opportunities to tap novel sources of resistance to BPH and other pests. Although the challenges are formidable, the genetic arsenal and understanding of host plant resistance to pests are being enriched every day. This will provide opportunities to stabilize production, a major goal of resistance breeding.

Bacterial blight (*R. Ikeda*)

More than 20,000 rice varieties from Asian countries have been tested for resistance to bacterial blight (BB) since 1986. From their reaction to six Philippine BB races, resistant varieties were broadly classified into five varietal groups: Java 14 (*Xa-3*), TKM6 (*Xa-4*), DZ192 (*xa-5*), CAS209 (*Xa-10*), and TN1 (*Xa-14*). Varieties belonging to the Java 14 group were found in almost all Asian countries, but the frequency of appearance ranged from 17.2% in Indonesia to 0.3% in India. Varieties with the *Xa-4* gene were found in all Asian countries. Distribution of the *xa-5* gene showed area specificity: frequencies of occurrence in rice germplasm from Bangladesh and Nepal were 25.9% and 13.3%, respectively, but in seven countries (for example, Thailand and Indonesia), the *xa-5* gene occurred in less than 1% of the accessions. Distribution of

the *Xa-10* and *Xa-14* genes was even lower; less than 5% of the accessions from any country.

Accessions of wild species were also screened for BB resistance, to compare the distribution of resistance genes in wild species with those in cultivated varieties. We tested 198 IRGC accessions comprising 10 wild species and 22 natural hybrids for BB resistance, using six races. Although only a few cases of resistance to six races in the Philippines were known in *O. sativa* varieties, more than half the tested accessions showed resistance to all six races (Ikeda et al 1990). On the other hand, *Xa-4*, one of the most common resistance genes in *O. sativa* varieties, was not found in any of the wild rices. Of the 198 accessions tested, 101 originated from Thailand; all were AA genome species. About 70% of the accessions from Thailand showed resistance to all six races; 10 showed a reaction pattern similar to that of germplasm having the *Xa-3* gene. The other known genes were not found in the wild species, but *Xa-3*, *Xa-4*, *xa-5*, *Xa-10*, and *Xa-14* have been found in cultivated varieties from Thailand.

The differences in distribution of BB resistance genes between cultivated varieties and wild species constitute an intriguing phenomenon.

Abiotic stresses (*B. S. Vergara*)

IRRI's Plant Physiology unit has screened 12,350 entries in the IRGC germplasm collection for submergence tolerance during the last 15 yr. Outstanding entries have been used in the breeding programs of IRRI and NARS. Most deepwater rices in the collection have been evaluated for internode elongation ability. Screening methods developed at IRRI for submergence tolerance and elongation ability are being used by national programs to evaluate their genetic materials.

Evaluation of the germplasm for cold tolerance is more complicated: tolerance may be needed at different growth stages, and these vary with cultivars. Screening under controlled temperature also is more difficult for national programs. Cold tolerance screening at different growth stages being conducted in collaboration with the Rural Development Administration in Chuncheon, Korea, involves entries from Korea, IRRI, and many national breeding programs.

Multilocation evaluation (*D. V. Seshu*)

INGER coordinated at IRRI is a mechanism for the exchange of elite genetic materials among the different rice-growing countries and international centers, and for their evaluation under different ecosystems in which rice is cultivated. The rice scientists participating in the network are given access to a wide range of genetic materials as well as test environments. INGER nurseries are designed for a) evaluation in different ecosystems, and b) screening for resistance to different stresses (biotic and abiotic).

The cooperative effort through INGER has led to the identification of more than 170 test entries as varieties for commercial production in 50 countries. Several lines have also been utilized as parents in the breeding programs of different countries as well as those of the international centers concerned with rice. Through differential varietal reactions in multilocation screening tests, various biotypes and races of major insects and pathogens that attack the rice crop have been identified.

Table 19. Examples of germplasm bank accessions found promising for tolerance for different stresses across locations and years.

Stress	Promising entries ^a
Low temperature	Jodo (55570), Ching Hsi 15 (36852), Akiyutaka (66973)
Salinity	Pokkali (8948), Nona Bokra (22710), Getu (17041)
Acid upland	Azucena (328), Mat Candu (33952), Djoweh (4125)
Blast	Ta-poo-cho-z (4285), Tetep (32576), Carreon (5993), Fukunishiki (40257)
Bacterial blight	Kuntlan (72936), Camor (17366), Kachamota Barisal (39567)
Tungro virus	ARC11554 (21473), Naria Bochi (26749), Utri Merah (16680)
Ufra nematode	Ba Tuc (10233), Sadapankaich (76250)
Brown planthopper	Suduru Samba (11671), Sinna Sivappu (15444), PTB33 (19325)
Whitebacked planthopper	Sinna Sivappu (15444), Chemparan Pandi (53422), Chemban (55070)
Stem borer	TKM6 (237), WC1263 (11057)
Thrips	Dahanala (15202)

^aIRRI accession no. in parentheses. Source: D. V. Seshu 1990.

Table 20. Examples of utilization of IRGC accessions^a by national programs.

IRGC accession	Country of origin	INGER nursery used in test	Country where utilized in crosses	Improved offspring entered in INGER	Country where improved offspring was released as variety
PTB33 (19325)	India	Brown plant-hopper	Sri Lanka	BG367-4 (08506)	India
Remadja (679, 3633, 5325)	Indonesia	Sheath blight	Sri Lanka	BG90-2 (26951)	Myanmar, China, India, Nepal, Kenya, Tanzania
Remadja (679, 3633, 5325)	Indonesia	Sheath blight	Colombia	P2217	Venezuela
Takaneshiki (2667)	Japan	Cold stress	-	-	Released directly in Bhutan
Tetep (32576)	Vietnam	Blast	Colombia	CICA8 (53078)	Belize, Brazil, Guatemala, Honduras, Panama, Paraguay
Sigadis (611, 5324)	Indonesia	Blast	Philippines	UPLRi-5 (50634)	Philippines
Palawan (353)	Philippines	Upland	Ivory Coast	RAT170 (64850)	Nigeria

^aIRRI accession numbers are in parentheses.

While INGER nurseries include predominantly improved germplasm, each year selected traditional varieties in the IRGC collection are entered in the screening nurseries for evaluation against different stresses. If germplasm bank entries are to be effectively utilized by rice scientists around the world, they should be characterized and evaluated appropriately, taking into consideration the genetic variation that exists among insects and pathogens as well as the variations in physical and chemical stresses. It is with this view that INGER and IRGC collaborate in using the INGER mechanism.

Nearly 500 germplasm accessions have been entered in various INGER nurseries over the last 15 yr: 58 were screened for tolerance for low temperature, 51 for adaptation to rainfed upland rice culture, and 44 for resistance to tungro virus. Other screening, involving fewer than 30 accessions each, included rainfed lowland, deep-water, salinity, blast, bacterial blight, sheath blight, ragged stunt virus, whitebacked planthopper, stem borer, gall midge, leafhopper, and thrips. Some accessions found promising for tolerance for different stresses across locations and years are listed in Table 19. Some of these have been utilized in various breeding programs, and the progenies of some released as varieties in different countries (Table 20).

These interactions and linkages between INGER and IRGC have enabled selected accessions from the germplasm bank to be evaluated in a more comprehensive manner. That has increased the use of these materials by rice scientists around the world.

Use of germplasm

Improving tolerance for abiotic stresses (*D. Senadhira*)

Adaptability to the abiotic stresses of a target environment is the main objective of national breeding programs. Breeders utilize traditional germplasm collected from their target environments and with improved germplasm obtained through international programs such as INGER. Although traditional varieties collected from the target area are considered to have good adaptability, this is not necessarily so. Indigenous varieties from similar areas may possess better or higher adaptation. This explains the need for concerted efforts to evaluate traditional germplasm for tolerance for abiotic stresses.

INGER concentrates on elite or improved germplasm, and may not be able to perform this task. Hot spots for screening against abiotic stresses are available, but it will be extremely difficult to convince breeders to undertake a uniform evaluation program: their objectives differ. A scheme of evaluation managed and conducted by germplasm conservation researchers, with cooperation from concerned breeders, is strongly recommended.

Deepwater rice breeding (*D. HilleRisLambers*)

Resistance to the ufra nematode

- 1974 Rayada selections collected in Bangladesh.
- 1985 Rayada varieties found resistant to the ufra nematode. Resistant varieties from this test and other entries compose the International Rice Ufra Screening Set (IRUSS). IRUSS results from Bangladesh, West Bengal (India), and the Mekong Delta (Vietnam) consistent in confirming varietal resistance in Rayada 16-011, Rayada 16-013, Rayada 16-05, Rayada 16-06, Rayada 16-07, Rayada 16-08, Bazail 65, and Ba Tuc.
- 1987 Hundreds of crosses made at IRRI, BRRI, and Vietnam (Cuu Long delta) with Rayada lines from the IRGC.
- 1988 Collectors return to site of original collection of Rayadas to obtain more accessions that might have resistance.

Cambodian floating rices

Between 1975 and 1978, Cambodia's national rice collection was lost to war and upheavals. Because farmers were not permitted to grow deepwater rices in some years,

this germplasm in particular was lost. A set of Cambodian varieties conserved by the IRGC was returned to the Cambodian rice researchers, but the identity of the floating rices among these accessions was not precisely known.

- 1987 All Cambodian entries in the IRGC planted in a flood-prone area in Iloilo, Philippines, and survivors noted.
- 1987 Literature search to identify the names of Cambodian floating rices. The list added to previous data in IRRI's germplasm bank on elongation ability of some Cambodian rices.
- 1988 All Cambodian entries in the IRGC planted in a controlled-water depth elongation test at Huntra, Thailand. The best elongators sent to Cambodia.
- 1989 Cambodian floating rices tested in natural deepwater situations in Cambodia.
- 1990 Seeds of the best-performing floating rices increased for future tests and redistribution.

Enhancement of rice germplasm

U.S.A. (*R. H. Dilday, C. F. Murphy, and H. L. Shands*)

Current technology for rice germplasm evaluation varies for each agronomic characteristic. For example, 10,100 of the 16,008 accessions in the U.S. World Rice Collection have been evaluated for 11 plant characteristics; the data are currently in the Germplasm Resources Information Network. In addition, 12,523 of the 16,008 accessions in the rice portion of the USDA/ARS National Small Grains Collection have been evaluated for at least one plant characteristic. There is technology to evaluate the remaining accessions for the 11 plant characteristics.

The National Small Grains Collection accessions also are being evaluated at Stuttgart, Arkansas, for ratooning ability, plant height, maturity, and straighthead; for sheath blight (*Rhizoctonia solani*) resistance; and for allelopathic activity to duck salad (*Heteranthera limosa*), purple ammannia (*Ammannia coccinea*), barnyard grass (*Echinochloa* spp.), and broadleaf signal grass (*Brachiaria platyphylla*). The same group of accessions is being evaluated for bacterial blight (*Xanthomonas campestris*) resistance at Manhattan, Kansas; for drought tolerance at Pine Bluff, Arkansas; and for salt tolerance at Fayetteville, Arkansas.

Current technology for the evaluation of most of these characteristics is adequate, although the allelopathy technology and methodology had to be developed at Stuttgart prior to their use in large-scale evaluations. Part of the U.S. rice collection also has been evaluated at Stuttgart for mesocotyl/coleoptile elongation potential (that character has an influence on stand establishment under dry seeding conditions).

Since the 1970 corn leaf blight epidemic, studies have been conducted to estimate the genetic base of major U.S. crop species and their potential vulnerability to a disaster caused by disease, insect, drought, physiological disorders, salinity, alkalinity, or numerous environmental factors (Cox et al 1985, Darrah and Zuber 1986, Smith 1988, Specht and Williams 1984, St. Martin 1982). Dilday (1990) demonstrated that only 141 germplasm accessions from the USDA/ARS rice collection (16,008 accessions) were present in the pedigrees of all rice cultivars released in the U.S.

These data demonstrate that the rice collection has not been thoroughly evaluated, and consequently has not been efficiently utilized in varietal development programs. For example, only 56 genotypes derived from 13 accessions have been utilized in developing cultivars in Arkansas, 49 genotypes derived from 12 accessions in Texas, 49 genotypes derived from 16 accessions in Louisiana, and 57 genotypes derived from 23 accessions in California. Furthermore, 10 of the 12 and 13 parental accessions in the Texas and Arkansas breeding programs, respectively, are identical, and so are 8 of the 13 and 16 accessions in the Arkansas and Louisiana breeding programs, respectively.

The U.S. rice collection needs to be thoroughly evaluated, characterized, and genetically analyzed. Germplasm possessing promising plant characteristics need to be enhanced so that diverse germplasm can be utilized more effectively in rice varietal development programs.

Table 21. Indonesian traditional germplasm found to exhibit resistance or tolerance for various desired traits.

Resistance or tolerance	Varieties
Brown planthopper resistance	Rambai Kuning, Gadis Ciamis, Ketan Paris, Pulu Parada, Ase Garis, Sari Dapet, Paedai Kalibungga, Paedai Nggulahi
Yellow stem borer (<i>Tryporyza incertulas</i>) resistance	Motang, Kuku Balam, Lalantik Ramben, Pandak Semarang, Siam Perupuk
Bacterial blight resistance	Pulu Mangkasa, Pulu Materi, Baka Kalenong, Ase Kapila, Pulu Baleng, Banda, Pulu Manurung, Ase Pulu Baddo, Ase Bogo Fatta, Ase Bulo, Ase Kado Kaun Ying
Tungro resistance (tested at Lanrang, South Sulawesi)	Kwatic Merah, Sitinik, Si Merah, Gambiri, Ingso Sambi, Ketan Gajih, Cingkrik, Genjah Betawi, Mayar, Sitopas, Cere Belut, Makatri, Rizal, Pare Tabang, Langkariri
Resistance to eight races of blast	Jabon, Sentral, Jongkok, Pulut Bango, PN2, PN4, Kuda, Kwatic Jamadi, Bojang, Loyang
Drought tolerance (tested at Mojosari, East Java)	Gedebung, Jenggut Hitam, Genjah Melati, Are Kuu, Are Bima, Si Udang Merah, Cere Melati, Ronggo Ketan Pote, Ane Noe, Ane Kolka, Ane Kao, Gogo Abang, Gogo Putih, Mambeng
Tolerance for aluminum toxicity (tested at Jasinga, West Java)	Seratus Malam

Indonesia (*T. S. Silitonga, S. Kartowinoto, and Z. Harahap*)

The Central Research Institute for Food Crops conserves more than 10,000 accessions of rice (Kartowinoto 1988, Siwi et al 1983, Siwi and Kartowinoto 1989). Many of these have been evaluated at different sites around Indonesia where stresses occur. Several local rice varieties have been found particularly useful in countering a number of pests, diseases, and environmental stresses (Table 21). Several of the best of these have been used in breeding programs (Table 22).

Philippines (*V. N. Villegas*)

The wild relatives of rice possess certain desirable genes which, when transferred to cultivated species, enhance the agronomic characters of cultivars. Some examples from IRRI's genetic evaluation and utilization program are

<i>Species</i>	<i>Useful traits</i>
<i>Oryza eichingeri</i>	Resistance to brown planthopper (BPH), whitebacked planthopper (WBPH), and green leafhopper (GLH)
<i>O. australiensis</i>	Resistance to BPH and tolerance for drought
<i>O. minuta</i>	Resistance to BPH, WBPH
<i>O. officinalis</i>	Resistance to BPH, WBPH
<i>O. punctata</i>	Resistance to BPH, GLH, bacterial blight, and bacterial leaf streak

In wide hybridization work, however, differences in genomic composition lead to problems of cross incompatibility and hybrid sterility. Plant breeders are now better equipped with techniques to circumvent these problems and increase the chance of successful gene transfer. Hybrid embryos that would otherwise abort prematurely can be rescued by culturing them in vitro. Sterility in the F₁ hybrid can be overcome by chromosome doubling through the use of colchicine. Using chemicals such as growth regulators and immuno-suppressants also increases the chance of getting hybrid plants. Advances in protoplast technology can lead to somatic hybridization.

In the new wide hybridization project of PhilRice, we have crossed several traditional Philippine varieties with *O. australiensis* (from Australia), *O. eichingeri* (from Uganda), *O. punctata* (from Tanzania), and *O. officinalis* (from the Philippines). Seeds of these wild species were obtained from IRGC.

The hybrid embryos were excised and cultured in vitro 7-11 d after pollination. Morphology of the F₁ hybrids is intermediate between the parents. Sterility problems are being overcome by chromosome doubling. After fertility restoration and a series of backcrosses, the new materials will be turned over to the PhilRice plant breeder.

Table 22. Several local Indonesian rice varieties used in hybridization programs.

Variety	Objective	Variety	Objective
Paedai Nggulahi	Brown planthopper	Jedah Jambe	Low temperature
Paedai Kalibungga	Brown planthopper	Ribon	Low temperature
Kencana Bali	Brown planthopper	Bayar putih	Tidal swamp
Mandi	Tungro	Kwatic	Tidal swamp
Baka Kebo	Tungro	Padi putih	Tidal swamp
Utri Rajapan	Tungro	Lemo	Tidal swamp
Utri Merah	Tungro	Ringgit	Tidal swamp
Hawara Bunar	Blast	Si Rumbia	Eating quality
Laka	Blast	Merdeka	Eating quality
Klemas	Blast	Ase Bako	Eating quality
Lagos	Blast	Ase Sawe Saleko	Eating quality
Genjah Lampung	Blast	Pulut Nangka	Eating quality
Leter	Blast	Utri Merah	Eating quality
Malio	Blast	Beak Ganggas	Eating quality
Napa	Blast	Hawara Batu	Eating quality
Jerak	Low temperature	Rajolele	Eating quality
Silewah	Low temperature	Utri Merah	Green leafhopper
Lumut	Low temperature	Utri Rajapan	Green leafhopper
Gadis Jambe	Low temperature	Mandai	Green leafhopper

IRRI started its wide hybridization work earlier, and has already obtained promising lines from crosses involving Asian cultivated species and *O. officinalis*, *O. minuta*, and *O. australiensis* (IRRI 1988a). The potential of using wild species as sources of genes capable of increasing the yield potential of cultivated rice is also being explored. *O. latifolia*, which has a high biomass and leaf area, is being tapped for this purpose. The introgression of genes from wild relatives to cultivated species will enhance the genetic variation essential to rice improvement.

Myanmar (*P. B. Escuro*)

The conservation efforts and seed dissemination service of IRGC have provided rice breeders worldwide a convenient and ready source of breeding materials for use in varietal improvement. In Myanmar, during my assignment as plant breeder 1979-85, I requested several hundred rice accessions from IRGC for use as parents in the rice hybridization program. The accessions included varieties with resistance to gall midge, yellow stem borers, leaf blast, sheath blight, and bacterial blight. We also requested accessions with desirable agronomic traits, such as short duration, lodging resistance, and good grain quality (to meet export requirements).

The accessions were screened for adaptability under local field conditions. A few vigorous selections were crossed with adapted Myanmar traditional varieties to obtain short-duration, high-yielding selections with the desired plant and grain qualities. By the end of 1985, a number of promising plants and lines had been identified for further observation and selection.

Many valuable exotic rice lines and varieties of different agroecotypes were provided through INGER; IRRI Plant Breeding, Genetics, and Biotechnology Divi-

sion; and the Thai-IRRI Collaborative Project on Deepwater Rice Breeding. Almost 2,000 of these lines were tested for adaptability in 1979-85. The best selections released directly as commercial varieties include IR42, IR50, and RD23 (lowland); C22 and LG240 (upland); and BKN6986-66-2, BKN6986-108-3, and RD19 (deepwater). Many other lines that excel in certain traits were identified for use in Myanmar plant breeding work.

New technologies and rice germplasm conservation research

D. Menancio-Hautea

Molecular biology, by generating new technologies and methods of analysis that either provide new approaches or supplement classical methods of analysis, has contributed significantly to increased understanding of many aspects of plant biology. In recent years, plant genetic resources scientists and other researchers have become increasingly aware of the potential applications and benefits of new technologies to plant germplasm conservation activities and researches. Promising areas of biotechnology that may serve plant genetic resources activities and research are shown in Table 23.

More comprehensive discussions on the technical aspects of these new technologies and their applications in plant germplasm conservation in general have been presented elsewhere (de Langhe 1983, Goodman et al 1987, Chang et al 1989, Withers 1989, Bernatzky and Tanksley 1989, Peacock 1989). This discussion attempts to outline the applications of these new technologies to rice germplasm activities and research.

Table 23. New biotechnologies and their potential applications in plant genetic resources activities.

Activities or research	Helpful new technologies
Collecting or acquisition	In vitro technology, recombinant DNA technology (gene/DNA library and cloned genes)
Characterization	
Biosystematics)	RFLP technology, protein/
Genetic diversity)	isozyme electrophoresis
Identifying duplicates)	
Genetic stability)	
Maintenance and preservation	In vitro technology and cryo-preservation, recombinant DNA technology (gene/DNA library)
Dissemination and exchange	In vitro technology, recombinant DNA technology (disease indexing, gene/DNA library, and cloned genes)

In vitro technology

- Seed and embryo culture techniques are currently being utilized by IRGC to rescue immature, damaged, or aged seeds of some accessions of *O. sativa* and wild rice species (IRRI 1985). Research to identify the most efficient media and culture conditions for a wide range of genotypes and species must continue.
- Meristem culture of wild rice species, particularly *O. longistaminata*, is being investigated in IRGC (D. Vaughan, pers. comm.), because of the failure of *O. longistaminata* to set seeds under greenhouse conditions. Its maintenance and preservation have been a serious problem. In vitro conservation using a technique combining meristem culture and slow growth culture may be a useful adjunct or alternative method to the current practice of maintaining the accessions as live plants in the greenhouse, and should be explored. In vitro flower induction and fertilization may also prove useful in seed production.
- Considering the difficulties of propagating and producing seeds of wild rice species, micropropagated plants may prove to be better materials for germplasm dissemination, particularly to fill requests from rice biotechnology workers, most of whose needs are for DNA samples from leaf materials. This alternative method will lessen the danger posed by frequent regeneration and the pressure on germplasm workers to grant more seeds per request.

Protein/isozyme and RFLP technologies

- The group of genetic markers generated by protein/isozyme and RFLP technologies has been used extensively in basic studies of taxonomy and population diversity. In the case of rice, protein and isozyme technology may be considered "old": it has been used extensively in studying racial differentiation within *O. sativa* (Morishima and Oka 1981, Sano et al 1986), in measuring genetic diversity among different ecotypes of Asian common wild rice and cultivated land races (Oka 1988), and in establishing the taxonomic relationships among the different species in the genus (Second 1982). More recently, RFLP technology has been used in taxonomic studies of rice (Tanksley et al 1990). RFLP probably will also be useful in studying genetic diversity in rice populations. Continuing research along these lines should use more accessions in the germplasm collections, taking into account new accessions acquired through continuing collecting activities.
- Setting up a core collection for rice may increase the efficiency of evaluation and increase the information on selected accessions. Isozymes and RFLPs can be used as molecular genetic markers to characterize the accessions, and in the process eliminate obvious redundancies as well as provide the data needed to implement effective hierarchical sampling.
- The use of in vitro conservation methods requires methodologies to monitor the genetic stability in these systems. Isozymes and RFLP markers may be used to monitor genetic changes in cultures of wild rice species during storage and subculturing, by measuring the amount of polymorphism shown by the markers used. In a similar manner, these technologies may provide a less

laborious alternative to the technique of checking for gross chromosomal aberrations found to be associated with loss in seed viability during prolonged storage of orthodox seeds.

Gene or DNA library and cloned gene sequences

- Peacock (1989) has extensively discussed the advantages of germplasm storage in the form of gene libraries; these advantages may very well apply in the case of rice. In setting up gene or DNA libraries in rice, however, high priority should be given to the wild species, since these are the materials most frequently requested by rice biotech workers.
- Linkage between biotechnology and plant genetic resources work could be further strengthened by the exchange of materials between the two groups. Rice biotechnology workers should go beyond providing rice germplasm workers with solely evaluation data on samples requested from the genebank. Materials such as cloned gene sequences of importance would enable rice germplasm researchers to use them in further characterizing the existence of such valuable genes in the rest of the collection.

The time scale, extent, and method of implementing the new technologies must be studied in relation to existing facilities, staff training, and other inputs available to the different rice germplasm banks, as well as to the network system being advocated for rice genetic resources.

Genetic divergence

Y. Sano

Domesticated plants often show much greater phenotypic diversity than their wild progenitors. But precise measurement of genetic diversity depends on the evaluation techniques adopted. Isoenzyme variability is a powerful tool for detecting genetic polymorphism, but is not so efficient in detecting variants in cultivated rice species. This suggests that the genetic diversity observed in cultivated forms originates mostly from their wild progenitors. Recent molecular studies in plants dramatically revealed that genes are highly polymorphic in DNA sequences, even within a species. We do not yet know whether the numerous changes at the molecular level have any biological significance. If some of them are related to phenotypic changes, they could be conceived as allelic differences at a single locus.

The waxy (*wx*) locus in rice, which specifies the production of amylose in the endosperm, is genetically well characterized. The *Wx* allele(s) is the structural gene for a starch-bound protein responsible for amylose synthesis in the endosperm. The geographical distribution of waxy (or glutinous) rice is also well documented. The *wx* locus in rice is not essential for plant growth, and defective mutants can survive under cultivated conditions. The *wx* mutant alleles, however, seem to be slightly deleterious since the mutants are rare in wild populations, even after introgression.

Intragenic recombinations observed between waxy cultivars indicate that they often have an independent origin (Li et al 1968). African rice cultivars (*O. glaberrima*) have no waxy genotype, although the *wx* locus is found at the same chromosomal location as it is in *O. sativa* (Sano 1988). Thus, the waxy or glutinous phenotypes seem to be confined to the Asian cultivated species.

This is not the complete story for the waxy locus of rice. Our recent biochemical studies indicate that the allelic differentiation at *wx* contributes not only the lack of amylose in waxy cultivars, but could also account for the variation of amylose content among nonwaxy cultivars (Sano et al 1985, 1986). Amylose content, which is a major determinant of eating quality, varies greatly among nonwaxy rice cultivars. Most nonwaxy Asian cultivars are categorized into three amylose content groups: low, 14-20%; intermediate, 20-25%; high, 25-30%.

We used successive backcrossing to introduce the waxy locus of several lines from different amylose content groups into a waxy line (a near-isogenic line of Taichung 65 with *wx*). The results confirm that amylose content among the naturally occurring variants tested is determined primarily by allelic changes at the *wx* locus.

Table 24. Allelic differentiation at the *wx* locus of rice.

Allele ^a	Amylose content (%)	Species/ ecogeographic race ^b
<i>Wx</i> ^a	24.8-29.1	<i>O. sativa indica</i> (3) <i>O. rufipogon</i> (4) <i>O. glaberrima</i> (3) <i>O. barthii</i> (1) <i>O. longistaminata</i> (1)
<i>Wx</i> ^{int}	20.3-22.5	<i>O. sativa japonica</i> (1) <i>O. sativa javanica</i> (2) <i>O. sativa japonica</i> (2)
<i>Wx</i> ^b		<i>O. sativa japonica</i> (2)
<i>wx</i> ^{op} (<i>Wx</i> ^{op})	About 10.0	<i>O. sativa indica</i> (1)
<i>wx</i>	Nearly zero	<i>O. sativa</i> (many)

^a *Wx*^a, *Wx*^{int}, and *Wx*^b were defined by the quantitative level of the *wx* gene product bound to starch granules; *wx*^{op} (reported by Heu and Kim 1989) was modified to *Wx*^{op} by T. T. Chang in 1990 because of its 10% amylose content. ^bNumber of accessions in parentheses.

Recently, an opaque endosperm with about 10% amylose content was found in an indica cultivar from Nepal (Heu and Kim 1989). The opaque endosperm was controlled by an allele, *Wx*^{op} (gene symbol modified by T. T. Chang from *wx*^{op} to *Wx*^{op}). So far, four additional nonwaxy alleles at the *wx* locus have been identified. They have been shown to play a significant role in the variation of amylose content among cultivars (Table 24).

Although there must be other modifier genes for amylose content, it is surprising to find a range of variation in amylose content that is simply controlled by alleles at the *wx* locus. Previously, amylose content was assumed to be a quantitative trait because of its continuous variation across rice cultivars. The distribution of alleles at the *wx* locus between cultivated and wild rice species shows that the wild progenitor carries only an allele of *Wx*^a; the other mutant alleles appear to have originated from *Wx*^a. This provides evidence that during the process of domestication, it is possible to artificially select for diversification of alleles at a single locus.

The *wx* locus specifies a 60-kDa protein, which is a major protein tightly bound to the starch granules (Sano 1984). Different alleles at the *wx* locus produce different levels of the gene product. In other words, amylose content is controlled by the quantitative level of the gene product, suggesting the presence of *cis*-acting regulatory site(s) near or within the structural gene. Actually, the quantitative level of the gene product has been shown to be transcriptionally controlled. Further genetic reevaluation at the molecular level will throw more light on the phenotypic diversity of agronomically important traits.

Recommendations of working groups



Rice germplasm collecting

Field collecting plans

The working group discussed plans for collecting on a country basis. Unfortunately, some countries with rich diversity were not represented among the participants. The recommendations for field collecting during the next 4 yr were prepared by participants from Bangladesh, Brazil, and other Latin American countries, Cambodia, Malaysia, Myanmar, Philippines, Thailand, and Vietnam. Table 25 summarizes collecting plans.

Table 25. Summary of rice collecting plans, 1990-94.

Country and year	Location	Time	Type of sample ^a	
Bangladesh	1990	Jessore, Kustia	Jul/Aug	CR (aus),
		Pabna, Rajshahi, Bogra	Oct/Nov	CR (B. Aman),
		Khulna, Bagerhat, Satkhira	Nov/Dec	CR (T. Aman),
		Sylhet, Habiganj, Srimangal	Oct/Nov	WR
	1991	Kishoragonj, Netrakona,	Apr	CR (boro),
		Rangamati, Bandarban,	Jul/Aug	CR (aus),
		Chittagong		
		Dhaka, Narayanganj	Oct/Nov	CR (B. Aman),
		Munshiganj, Manikganj		
		Barisal, Patuakhali,	Nov/Dec	CR (T. Aman),
		Borguna		
	1992	Jessore, Kustia	Oct/Nov	WR
		Sylhet, Sunamganj	Apr	CR (boro),
		Pabna, Bogra, Rajshahi	Jul/Aug	CR (aus),
		Khulna, Bagerhat, Jessore	Oct/Nov	CR (B. Aman),
		Bhola, Noakhali	Nov/Dec	CR (T. Aman),
	1993	Khulna, Faridpur	Oct/Nov	WR
		Pabna, Rajshahi	Apr	CR (boro),
		Comilla, Noakhali	Jul/Aug	CR (aus),
		Faridpur, Barisal	Oct/Nov	CR (B. Aman),
		Rajshahi, Dinajpur, Rangpur	Nov/Dec	CR (T. Aman),
		Chittagong hill tracts, Noakhali	Oct/Nov	CR/WR

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Table 25 continued

Country and year	Location	Time	Type of sample ^a
1994	Dhaka, Mymensingh Khulna, Satkhira Sylhet, Habiganj, Sunamganj Kishorganj, Netrakona, Jalampur Madhupur, Jamalpur, Netrakona, Tangail	Apr Jul/Aug Oct/Nov Nov/Dec Oct/Nov	CR (boro), CR (aus), CR (B. Aman), CR (T. Aman), WR
Brazil			
1991	Amazon region	May	CR, WR
1992	Pantanal region	May	CR, WR
1993	Northeast region	May	CR, WR
1994	Northwest region	May	CR, WR
Cambodia			
1990	Kandal, Takeo, Svay Rieng, KOMPONG SPEU	Nov/Dec	CR, WR
1991	Prey Veng, Kompong Chhnang, Battambang	Nov/Dec	CR, WR
1992	Kompong Thom, Siem Reap, Koh Kong	Nov/Dec	CR, WR
1993	Mondol Kiri, Preah Vihear, Ratana Kiri	Nov/Dec	CR, WR
1994	Oddar Meanchey, Pursat	Nov/Dec	CR, WR
Indonesia			
1990	North Sumatra	Jun	CR, WR
1991	Kalimantan	Jun	CR, WR
1992	Irian Jaya	Jun	CR, WR
1993	Maluku	Jul	CR, WR
1994	South-Southeast Sulawesi	Jul	CR, WR
Latin America (except Brazil)			
1991	Uruguay	May	CR, WR
1992	Central America/Caribbean	Jul	CR, WR
1993	Paraguay	May	CR, WR
1994	Colombia	May	CR, WR
Malaysia			
1990	Sarawak	Sep/Oct	CR, WR
1991	Sarawak	Jan/Feb	CR, WR
1992	Sarawak/West Malaysia	Feb/Mar	CR, WR
1993	West Malaysia	Sep/Oct	CR
	West Malaysia	Feb/Mar	WR
1994	Collections in West Malaysia, Sarawak, and Sabah will be assessed and uncollected pockets targeted for that year.		
Myanmar			
1990	Irrawaddy Division, Yangon Division, Pegu Division, Mon State	Nov	CR, WR
1991	Magwe Division, Mandalay Division	Nov	CR, WR

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Table 25 continued

Country and year	Location	Time	Type of sample ^a
1992	Sagaing Division	Nov	CR, WR
1993	Kachin State	Nov	CR, WR
Philippines			
1990	Panay, Southern Tagalog	Dec/Jan	CR
	Palawan, Panay	Feb/May	WR
1991	Leyte, Samar, Southern Tagalog	Dec/Jan	CR
1992	Negros Oriental, Southern Tagalog, Mindoro	Dec/Jan	CR
	Mindoro	Feb/May	WR
1993	Mindanao, Southern Tagalog	Dec/Jan	CR
	Mindanao	Feb-May	WR
1994	Masbate, Southern Tagalog	Dec/Jan	CR
	Masbate	Feb/May	WR
Thailand			
1990	Northern	Oct/Nov	CR (hill rice)
		Nov	WR
1991	Northern	Oct/Nov	CR (hill rice),
	Northeast	Oct/Nov	WR
1992	Western	Nov/Dec	CR, WR
1993	Southern	Dec/Jan	CR
Vietnam			
1990	Thanh hoa	Oct	CR
	Nghe tinh	Nov	WR
1991	Mekong Delta	Dec/Jan	CR, WR
1992	Hoang lien son	Oct/Nov	CR, WR
	Lai chau		WR
1993	Dac lac	Nov/Dec	CR, WR
	Gia-lai-con-tum	Nov/Dec	CR, WR
1994	Binh Tri Thien	Nov	CR, WR

^aCR = cultivated rice, WR = wild rice.

India plans its collecting activities on an annual basis during a crop advisory committee meeting. It is expected that efforts to continue collecting rice and wild rice germplasm during the next 5 yr will be proposed by this committee.

Japan's activities on rice germplasm collecting is undertaken by scientists in the Ministry of Agriculture, Forestry and Fisheries and the Ministry of Education. On government approval and funding, scientists will participate in collecting activities in some other countries.

The United States is planning to join collecting missions in other countries and the coordinating body for rice genetic resources in the U.S. will plan participation in collecting.

The participants also discussed the considerable collecting efforts needed in the following regions:

- Parts of Africa, particularly Mozambique, should be the focus of thorough collecting for both wild and cultivated species. IITA is asked to facilitate.
- Parts of Zaire, Uganda, and Ethiopia should be explored for wild relatives of rice.

- In Laos, thorough collecting for both wild and cultivated rices should be initiated.
- In Indonesia, further collecting for wild *Oryza* species is needed, particularly in Irian Jaya and in neighboring Papua New Guinea.

Members of the working group asked that collectors unfamiliar with wild rices be provided guides to enable them to identify the rices readily. They recommend that a field book be prepared to help.

It is not clear how many distinct representative samples from a country or region are already in the base collection. Efforts should be made to get the best possible estimates, to ensure adequate representation of rice gene pools.

Where possible, large seed samples should be gathered from wild populations, to provide sufficient seeds to place samples directly into long-term storage in national genetic resources centers and to provide small samples to be sent to the base collection.

In situ conservation

For in situ conservation, three recommendations were made.

- The National Institute of Genetics in Japan should be asked to provide guidelines to help national program scientists monitor population stability and genetic change in wild populations.
- Monitoring of varietal changes in cultivated rice in selected regions, as is being undertaken in the Philippines, is recommended to other countries.
- Some habitats where wild species of *Oryza* are found, such as forests and swampy lands, should be conserved. High priority should also be given to species that produce few seeds and that are particularly difficult to maintain ex situ.

In situ conservation in wilderness areas or national parks may be appropriate for wild *Oryza* species that are components of climax ecosystems. However, in situ conservation of *Oryza* species that occupy disturbed habitats will clearly require a habitat management system that takes into account regular and irregular disturbances.

Passport data

Passport data are an essential part of germplasm documentation; they constitute the beginning of the data file. Field collectors should supply all relevant information to the germplasm documentation sector. Old records should be searched to complete the passport data files and to make this information available to germplasm users. It was recommended that

- Different data sheets be used for passport data on wild species and cultivated rices.
- A small group be assigned to reexamine and rationalize the descriptors and descriptor-states for wild species, and make them available to all genebanks conserving rice.
- A small committee list a minimum and complete set of passport data that will be adaptable to different collectors and varying circumstances.
- A committee address the following concerns:

1. Standardized country code names, following the UN/FAO system.
 2. The feasibility of developing an internationally acceptable system of standardized accession numbers. Such a system would help reduce duplicates in national collections, aid information exchange, and track down the origin of an accession. A standard registration system within the genus *Oryza* should include a) country of origin (in code/no.), b) original collection sample number, c) national genebank where the accession is available (in code/no.), and d) national accession number in the genebank. Additional information may include the crop species, originating experiment station or collector(s), and variety name in vernacular or coded number. When the accession has been deposited in IRGC and is available for wide distribution, the IRGC Acc. No. should be included as the international accession number. The data base system at IRRI has the capacity to include the national or state accession numbers and alternative variety names (vernacular or coded numbers), when such information is available.
- Standardized codes for seed sources.

Constraints on field collection

Several members of national programs indicated the need for funding and personnel to help in collecting. Individual needs are varied. Outside funding or grants are needed to stimulate conservation activities on genetic resources in national programs.

Newsletter

The IBPGR Regional Newsletter for Asia and the Pacific should insert a rice section, with a view to developing a rice genetic resources newsletter in the future. Other available outlets for information on rice genetic resources work are the *Rice genetics newsletter* and the *International rice research newsletter*.

S. D. Sharma, chairperson; D. A. Vaughan, rapporteur

Genebank management

The information NARS provided to the IRRI survey shows that many of the standards for genetic conservation by seed storage are being met by most programs. However, several national centers reported accessions with poor viability entering storage. In theory and in practice at many locations, the production or collecting of high viability seed lots of *Oryza sativa* and *O. glaberrima* is less a problem than is the case for many other crops. There are many potential causes of poor viability, especially under hot and humid tropical environments. Seed processing problems (particularly inadequate seed drying procedures) and delays in receiving accessions at national centers are two of the more likely causes.

The single most important factor in the successful maintenance of rice seed stocks in genebanks is the control of seed moisture content. Recent studies at the University of Reading support an ideal target seed storage moisture content for rice of around 4.5%. Accordingly, it is necessary to improve seed drying procedures and the capability of genebanks to approach this target. A moisture content of 6-8% is acceptable, however, for centers that can provide subzero storage conditions (typically -10°C).

While not wishing to diminish the advantages to genebanks that apply the IBPGR-preferred standards for seed drying, using a fully reactivated desiccant in the absence of more sophisticated facilities can safely dry rice seeds to the IBPGR-recommended seed storage moisture content.

It was noted that not all participants were aware of the various publications that provide advice on genebank management. IRRI and IBPGR are asked to compile a list of the relevant publications (including those referring explicitly to rice) and publish it as an appendix to these workshop proceedings. It may be helpful to also publish this list in the *Plant genetic resources newsletter*. An abridged, more easily understood manual on genebank management practices might be prepared by IBPGR.

Other difficulties raised by national center workers concern seed regeneration (a severe bottleneck for most centers), maintenance of seed moisture content (suitable containers are difficult to get), seed fumigation (concerns are the hazards of some products to genebank staff health), reliability of power supply (voltage fluctuations, supply interruptions, and lack of fuel for emergency power generators, when they are available), insulation and maintenance of cold storage rooms (how to prevent deterioration and minimize leakage), manpower development (how to motivate and keep trained staff), and monitoring the viability of stored seed.

Viability monitoring is the second most widespread concern. In collections held under poor storage conditions, it is necessary to monitor and regenerate accessions frequently, a heavy workload in addition to the risks inherent in frequent regeneration.

Means and ways to alleviate such common problems should be developed by testing and improving existing procedures and facilities, and by research to seek new methods. The use of locally available resources is imperative to sustain operations. Advice from experts and training provided by the international centers are needed.

N. Q. Ng, chairperson, T. T. Chang, rapporteur

Germplasm documentation

Data needed

1. Passport data (see recommendation of the field collecting working group).
2. Descriptors and descriptor-states for characterization and evaluation.

Standardized descriptors and descriptor-states were developed by international efforts and published as *Descriptors of rice* (IBPGR-IRRI Rice Advisory Committee 1980) and Standard evaluation system for rice (IRTP 1988). The two sets satisfy the standards of national workers, and should be followed. New descriptors of special interest to a national program may be added as needed. Abbreviated codes (acronyms) for each descriptor used by IRRI (cf. IBPGR-IRRI Rice Advisory Committee 1980) should be reexamined, standardized, and circulated. Country names may follow the UN 3-letter abbreviation system.

Location, season, cultural practices, experimental layout, and environmental data of each experiment (planting) for characterization and evaluation should be recorded. This information should accompany each set of data published or exchanged.

3. Management descriptors

Genebank curators should keep records of management information (Table 26), to better manage the genebank and to safeguard the germplasm materials.

Data base management

Software. A genebank should choose the most suitable program for its needs. Transportability is a desirable criterion in choosing a data base package. Several commercial packages are available, such as dBase, Foxbase, and ORACLE.

IRRI and IITA have developed programs (which run with some commercially available software) that facilitate the management of rice germplasm operations and data bases. Participants recommend that these programs be freely distributed to national genebanks for trial use, feedback, and further refinement. IRGC provided participants in two training courses with a preliminary version of IRRIGEN, for trial and feedback.

Hardware. For most national genebanks, using microcomputers for documentation appears to be the mainstay for the next 5 yr. Compatibility between computers is

Table 26. Management descriptors.

1.	Storage location within each store
2.	Date when seeds enter storage
3.	Initial seed germination at storage (%)
4.	Date of last germination test
5.	Germination at the last test (%)
6.	Predetermined date of next germination test
7.	Moisture content at storage (initial %)
8.	Amount of seed in storage(s)
9.	Duplication at other location(s)
10.	Month and year when the accession is multiplied
11.	Number of plants in multiplication/rejuvenation plots
12.	Multiplication site(s)
13.	Regeneration cycle

IBPGR published comprehensive descriptors in 1985 Handbook for Genebanks No. 2 (Handbook of Seed Technology for Genebanks V. 1. Principles and methodology. 210 p.)

essential for the exchange of information between genebanks. Participants recommended that national programs use an IBM-compatible personal computer, with the following minimum configuration:

512 KB RAM CPU

10 Mega Bytes hard disk

one 360 KB floppy disk drive

one 80 column printer

This configuration will allow the use of IRRIGEN.

Some assistance to NARS in procuring computing facilities and installing programs should be provided by IARCs participating in the network.

The rice germplasm information network

Participants proposed that IRRI serve as the hub of the rice germplasm information network: it has adequate computer facilities, experience in networking, and expertise in transferring data among different formats. IRRI already has a data base involving approximately 85,000 accessions.

They recommended that IITA, WARDA, and CIAT assist and coordinate regional information systems that link up with IRRI.

All national rice germplasm programs are encouraged to join the information network. They first need to document passport information on their national collections and help update this information on the existing collections held at IRRI, IITA, WARDA, and CIAT. To facilitate updating the information, IRRI, IITA, and other IARCs will provide a list of the accessions from donor countries to the appropriate national programs. The national center will validate this list and append all additional relevant information, particularly other identification numbers. This will facilitate identifying gaps in the existing collections and duplicates, to rationalize conservation efforts. This will also greatly facilitate the exchange of information among members of the network.

The data on characterization and evaluation will be added to the rice germplasm data base, thereby improving access by potential users of the information network.

N. Q. Ng, chairperson; T. T. Chang, rapporteur

Rice genetic resources network

The national programs of most rice-growing countries have on-going activities related to collecting, exchange, characterization, evaluation, computerized documentation, and conservation; these are linked to utilization. The level and pace of development of these programs, however, vary a great deal. IRRI, IBPGR, IITA, and some other international agencies are providing support to these national programs in various ways, thus encouraging suitable linkages. These linkages should be further strengthened to stimulate a collaborative approach toward key activities in conservation and management of rice genetic resources, based on mutual trust, sharing of responsibilities, active participation in the decisionmaking process, and commitment to the implementation of an agreed-upon plan of action.

The network approach will help participating countries overcome their problems and meet their needs through effective pooling of resources (including germplasm, information, and expertise). The network will also strive to keep participating countries updated on the latest developments in methodologies or techniques, through suitable publications, and will assist in organizing appropriate training programs or workshops.

National programs will benefit from the proposed network in the following areas:

- Sharing of germplasm.
 - Pooling and sharing of information, including that detailed in the data base management network.
 - Ensuring safety of collections through duplicate storage.
 - Interaction among concerned scientists.
 - Collaborative research to increase the efficiency and effectiveness of methodologies used in collecting, characterization, and safe storage of germplasm.
- The partners of the network, in turn, are expected to commit themselves to
- Free exchange of germplasm.
 - Sharing of relevant information.
 - Sharing of expertise and experience.

Work on evaluation needs to be intensified. The existing mechanism of INGER or research consortia/networks might be increasingly utilized for multilocation evaluation of germplasm collections.

Germplasm workers are urged to play a more active role in evaluation and enhancement, so they become participating members of an expanded rice improve-

ment team. On the other hand, germplasm workers deserve greater recognition of their essential inputs in crop research and improvement.

Testing and improving techniques (such as those relating to in situ conservation) are suggested as an additional activity of the network.

Gene transfer across genetic barriers has now been made attainable through rapid advances in biotechnology. Unrestricted access to germplasm has thus become even more urgent. The network will, therefore, strive to make all useful germplasm freely available to all countries for utilization in their national rice improvement programs.

To facilitate effective operation of the proposed network, the workshop recommends setting up a Rice Germplasm Committee that may meet periodically to ensure follow-up activities based on workshop recommendations or in response to urgent developments. The committee will be composed of national plant genetic resources coordinators representing regions and of representatives of international centers. Participants nominated China, India, Indonesia, and Thailand for the first term. It was agreed that IBPGR will financially support the first meeting of the committee. Representatives from continents other than Asia were suggested for inclusion. Expanded participation by regional base collection centers is also envisaged.

R. S. Rana, chairperson; P. M. Perret, rapporteur

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Appendices



Additional references on genebank practices*

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Directory of genebanks conserving rice*

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Genebank management*

T. T. Chang

While management in general refers to the coordinated implementation of various activities by many persons in an organization, it should go beyond day-to-day activities. Management policy should include long-, medium-, and short-term goals, just like seed preservation phases. Flexible and dynamic responses are needed to meet changing or unexpected shifts in direction or funding, or both. The morale of a genebank staff should be kept high and the team spirit congenial.

The managerial system of a large genebank should be based first on the scope of its mission. The scope of work will largely determine the organizational and managerial setup. However, all genebanks should have a service-oriented mission.

The primary responsibilities of a genetic resources center (genebank in a broad sense) include most or all of the following operations:

1. Collecting/acquisition/introduction
2. Multiplication/rejuvenation
3. Characterization
4. Preservation/field conservation
5. Documentation
6. Distribution/exchange
7. Research on germplasm resources
8. Training
9. Research linkage with users in conservation, evaluation, and use
10. Technical assistance to smaller genebanks or experiment stations
11. Public information

Management practices are formulated on the basis of five components: 1) planning, 2) organizational setup, 3) implementation, 4) operational control, and 5) linkage with other research institutions.

Planning

At the very beginning of setting up a genebank, its scientific and organizational mission should be well-defined in terms of goals of various storage lengths: namely, short-,

*A lecture given at different training courses. Chinese version published in 1986 by IBPGR-CAAS in *Genebank management and seed storage*, edited by K. L. Tao et al, Beijing.

medium-, and long-term. Operational setups should be linked and intermeshed. Funding sources should be assured.

Since genebanks should not operate in isolation, a body of trustees or advisors should be constituted to meet periodically, to formulate policy matters and consider improvements or amendments. Moreover, a number of advisory committees should be set up to deal with such specialized subjects as individual crops, methods of conservation, and documentation. A genebank should enlist the help of different specialists to improve its design and operations. Frequent meetings should be held to make continuous improvements or amendments and to bridge the gaps between goals and operations.

A duplicate storage site for the base collection is essential. Moreover, the help of other institutions or stations should be enlisted in the seed rejuvenation phase, especially when the crop is not adapted to the site of the genebank.

Within the genebank, annual review of program and budget, supplemented by periodic meetings among heads of laboratories (research units), are also essential in improving the plans and operations. Frequent and informal staff meetings within a lab are also helpful to coordination and productivity.

Organizational setup

A well-planned organizational system will aid the implementation of work, coordination, and monitoring of different units. Planning well in advance is required at all stages.

Division and sharing of responsibilities. Responsibilities of individual workers should be well-defined according to their training, experience, and skills. Duties should be properly delegated, so that the workers will have the authority to exercise judgment and, at the same time, be held responsible for their assignments. The supervisor will then have a valid basis to evaluate the workers' performance and personal initiative at the end of each year.

Meanwhile, every operational facet should be backed up by a knowledgeable second or even third person who can take over the essential functions when the principal worker is on leave or when an emergency arises. Such a backup setup is essential to lend continuity to a genebank, which deals with fragile biological entities having limited viability and longevity.

Research units. Research units are the laboratories necessary for scientific, administrative, and budgetary considerations. But the laboratories should not operate in such a way as to create barriers to cooperation among disciplines or fields. Workers of different units should be indoctrinated to understand that every person is an integral member of an organization that requires participation from all members to fulfill the long and complicated process of genetic conservation. In other words, the scientific mission should be placed above personal considerations.

Communication and coordination. Open and frequent communication among different disciplines or units is indispensable to the efficient working of a genebank. Every worker should know the overall process of genetic conservation and his or her individual role as an indispensable link in the entire process. The important duty of a

genebank manager is to ensure that the lackadaisical performance of one worker or of one unit will not hold up the functioning of the genebank as a whole. Workers who find free time should be encouraged to help other workers who are behind schedule because of overloading.

Implementation

Proper recruitment, decisionmaking, staff motivation, and continuous training are essential to efficient implementation of work within a genebank.

Recruitment. Work positions should be fully specified as integral links in the organizational setup. Candidates should be interviewed and selected not only for their individual capability or skill, but also for their suitability as a member of the team. A probationary and training period is required before regular employment. On-the-job training and preliminary evaluation of the person are best carried out during this period.

Decisionmaking. Decisionmaking at all levels requires the participation of all workers involved at that level. Alternatives should be considered during the decision-making process. Communication prior to making a decision will help a well-informed staff to act properly and willingly. Any decision should be subject to amendment and improvement, when needed.

Staff motivation. New ideas from staff members should be given a fair opportunity to be aired and evaluated by fellow workers. With proper incentives, staff members can come forth with improved productivity. New activities or alterations should fit into the overall process on a team basis.

Continuous upgrading of staff. Short courses or periodic seminars will help staff members broaden their understanding of the genebank's overall activities and acquire new knowledge and skills. Some training courses may be provided by other organizations. Persons who can advance themselves through educational processes should be encouraged, and successful trainees properly rewarded.

Operational control

The managerial staff at all levels should be able to exercise leading or monitoring roles in the following areas:

1. Implementation of policy and guidelines
2. Adherence to quality standards
3. Promotion of teamwork
4. Rating of individual productivity
5. Fairness in treating staff members
6. Identifying work trends and needs for improvement
7. Full use of computer facilities for records, inventories, retrieval, and analysis
8. Receptiveness to constructive criticism and needed changes
9. Willingness to perform self-reappraisal and constant improvement in operations
10. Keen interest in increasing efficiency and reducing wastage
11. Enlisting assistance and cooperation from related research agencies.

Linkage with other research institutions

A genebank is basically the custodian of plant germplasm, which was largely, or at least partly, collected and donated by numerous plant scientists outside the genebank. The variety of crop species involved may go beyond the knowledge or expertise of the genebank staff. Therefore, a national genebank must seek the cooperation and assistance of all workers concerned to ensure that the collections are comprehensive in scope and their proper conservation and use assured. Collaboration should be sought by the genebank staff from scientists in other research organizations, including colleges and universities, specialized research organizations, and commodity groups. Expertise in specific crops can be sought from advisory committees for different crops. A network of collaboration for Chinese agencies was proposed by a Rockefeller Foundation team in 1980. The plant germplasm system of the U.S. is described in two works (Anonymous 1978, Jones 1984) and, most recently, by USDA workers (Janick 1989, Knutson and Stoner 1989). A recent study of the system with recommendations for improvement was published by the Board on Agriculture of the U.S. National Research Council (1991).

Communication should be sustained by workshops and committee meetings. This role falls to the head of the national crop genetic resources center.

My personal experience and insight

I wish to share with my young colleagues the following points about genebank management:

1. Each seed sample should be treated as if it is the last accession available to you, so that it will receive proper and timely care during the long process, from collection through increase, characterization, and preservation, to use. Never plant all the seeds in a package, always save a few for emergencies or accidents.
2. Every operational step should be double-checked by another worker or by the computer to ensure accuracy. Try to foresee the loopholes.
3. Operations should be planned to be simple and least prone to error, and should be retested for reliability.
4. Be vigilant about minute details and willing to make small and continuous improvements.
5. Communicate fully and patiently with the staff so that the operational process or steps will be fully understood.
6. Exhort the staff to fully exercise the service spirit; sooner or later, it will be reciprocated by the recipients.
7. Promote teamwork among genebank staff. Maintain vigilance and high work standards, such as checking the facilities during or after heavy storms and earthquakes, observing neatness in all areas, and enforcing a non-smoking rule in fire-prone areas.
8. Persuade and convince the potential seed donors of our utmost care in looking after their collections and our willingness to return the collection to them, if needed at a later date.

9. Fulfill the needs of users by understanding their requirements, operations, and problems (the genetic evaluation and utilization approach of IRRI).
10. Be willing to learn from other disciplines and professionals, in the interest of self-improvement.
11. Adopt a business management approach to interlink the 11 components mentioned in the introduction and to redeploy available manpower at times of peak workload. Timely planning helps in all operations.
12. Make frequent contacts with the staff. It is best to visit them at their work locations rather than calling them into the manager's office.

The International Rice Germplasm Center at IRRI is privileged to have enjoyed

1. Continuity in personnel and administrative support;
2. Sustained funding;
3. Excellent cooperation from rice collectors, rice breeders, rice scientists in other disciplines, refrigeration engineers, missionaries, service volunteers, and anthropologists; and
4. Above all, a dedicated team of young workers. Personal dedication is a prime force in sustaining the myriad, often tedious, nonglamorous, and thankless but crucially important genebank services.

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Acronyms used

AICRIP = All-India Coordinated Rice Improvement Program (now Directorate for Rice Research), Hyderabad, Andhra Pradesh, India
ARI = Agricultural Research Institute, Yezin, Myanmar
ARS/USDA = Agricultural Research Service of the U.S. Department of Agriculture
BCC = Beta Coordinating Committee, Europe
BORIF = Bogor Research Institute for Food Crops, Bogor, Indonesia
BRRI = Bangladesh Rice Research Institute, Dhaka, Bangladesh
CAAS = Chinese Academy of Agricultural Sciences, Beijing, China
CARI = Central Agricultural Research Institute, Peradeniya, Sri Lanka
CENARGEN = Centro Nacional de Recursos Geneticos, Brasilia, Brazil
CGIAR = Consultative Group on International Agricultural Research
CGN = Centre for Genetic Resources, Wageningen, the Netherlands
CIAT = Centro Internacional de Agricultura Tropical, Cali, Colombia
CIMMYT = Centro Internacional de Mejoramiento de Maiz y Trigo, El Batan, Mexico
CNPAF = Centro Nacional de Pesquisa de Arroz e Feijao, Goiania, Goias, Brazil
CNRRI = China National Rice Research Institute, Hangzhou, China
CRIFC = Central Research Institute for Food Crops, Bogor, Indonesia
CRRRI = Central Rice Research Institute, Cuttack, India
DOAB = Division of Agricultural Botany, Nepal
EMBRAPA = Empresa Brasileira de Pesquisa Agropecuaria, Brasilia, Brazil
FAO = Food and Agriculture Organization of the United Nations, Rome, Italy
FOFIFA = National Center for Applied Research and Rural Development, Madagascar
GRIN = Germplasm Resources Information Network, USA
GRL = Germplasm Resources Laboratory, Beltsville, MD, USA
GRU = Genetic Resources Unit, IITA
HGBI = Hokkaido Green-Bio Institute, Naganuma-069-13, Hokkaido, Japan
IARC = International agricultural research centers in the CGIAR system
IBPGR = International Board for Plant Genetic Resources, Rome, Italy
ICAR = Indian Council of Agricultural Research, New Delhi, India
ICARDA = International Centre for Agricultural Research in Dry Areas, Aleppo, Syria

ICGR = Institute of Crop Germplasm Resources, CAAS, Beijing, China
 ICRISAT = International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Andhra Pradesh, India
 IITA = International Institute of Tropical Agriculture, Ibadan, Nigeria
 INGER = International Network for Genetic Enhancement of Rice, IRRI, Los Baños, Philippines (formerly IRTP)
 INSA = National Institute for Agricultural Sciences, Hanoi, Vietnam
 IRAT = Institut de Recherches Agronomiques Tropicales et des Cultures Vivrières, France
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 IRTP = International Rice Testing Program (now INGER)
 IRUSS = International Rice Ufra Screening Set
 ISTA = International Seed Testing Association
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 NSGC = National Small Grains Collection, USA
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 PIO = Plant Introduction Office of the USDA, Beltsville, Maryland, USA
 RDA = Rural Development Administration, Suweon, Korea
 RPIS = Regional Plant Introduction Stations, USA
 SURIF = Sukamandi Research Institute for Food Crops, Indonesia
 TAC = Technical Advisory Committee of the CGIAR, Rome
 UN = United Nations
 USAID = United States Agency for International Development
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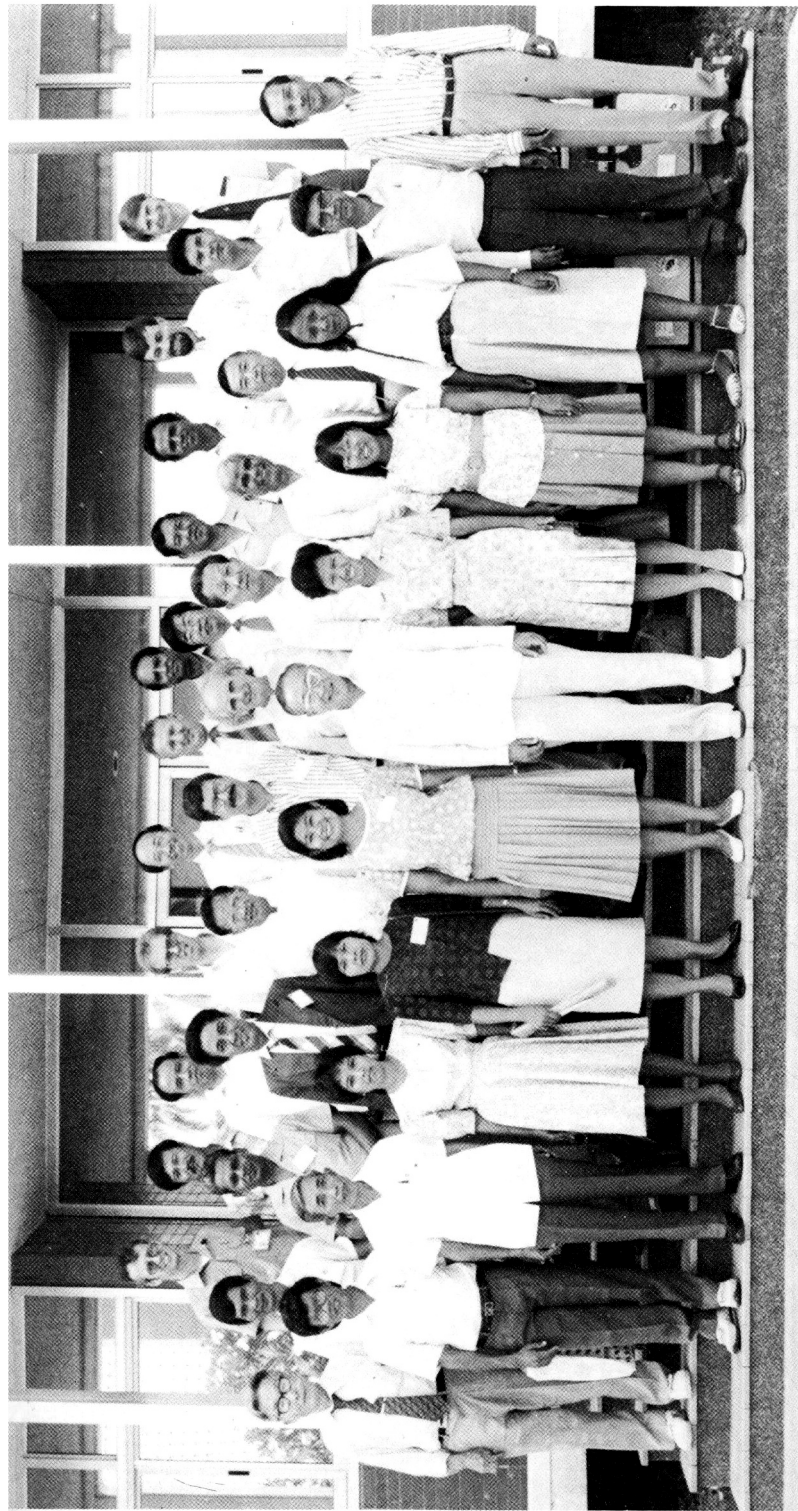
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