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Crop germplasm and wild relatives: a source of novel variation for crop improvement

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Plant genetic resources (germplasm) are the most valuable among the natural resources, as they provide building blocks for developing improved cultivars. The continuing need for improved crops cultivars to meet challenge of climate change, changes in pest scenario and changing consumer demands creates a constant need for germplasm. However, the crop germplasm pool is shrinking mainly due to negative actions of humans. Germplasm are in danger of genetic erosion, and/or local extinction because of habitat loss, alteration resulting from agriculture, loss of forest due to urbanization, pollution, invasion of exotic species, and their over exploitation. Rapid loss of plant biodiversity during the twentieth century and realization of its importance led to the collection and conservation of over 6.1 million accessions in over 1400 genebanks globally. International Agricultural Research Centers maintain over 600,000 accessions. ICRISAT genebank conserves 118,882 accessions of chickpea, pigeonpea, groundnut, sorghum, pearl-, finger, foxtail, barnyard, proso, little, and kodo millets from 144 countries (Table 1). Knowledge and management of genetic resources are critical for crop improvement programs.

Low use of germplasm

The large germplasm collections in the genebanks have not been used adequately in international and national crop improvement programs. For example, very few of the >20,000 chickpea accessions conserved in the genebank (< 1%) have been utilized in cultivar development at ICRISAT (Upadhyaya et al., 2006a). Similarly, in the national programs, the germplasm lines used in breeding programs are very limited. In China, the introduced germplasm and wild relatives have seldom been used in groundnut improvement. In USA, the cultivar ‘Dixie Giant’ was a germplasm source in all pedigrees of runner type groundnut and ‘Small White Spanish-1’ accounts for >90% pedigrees of all released cultivars. Similar situation has been reported in many crops as most plant breeders prefer to work with their own breeding lines, rather than exotic germplasm materials. Not only the limited use of germplasm is a worrisome issue, the large-scale deployment of cultivars with common genetic background complicates the whole situation even more. Sometimes, even if the number of cultivars is more, the degree of genetic diversity between them is very low and can lead to epidemics similar to the southern corn leaf blight in the USA (resulting in huge economic loss) and late blight of potato (that wiped out the potato crop resulting in famine in Europe) due to narrow genetic base of crop cultivars. One of the main reasons for low use of germplasm is the lack of information on economic traits that display high genotype x environment interactions and require multilocational replicated evaluations to identify parents for use in crop improvement.
programs. Development of core collection (10% of entire collection) representing diversity of entire collection has been suggested to overcome this.

Strategy to enhance the use of germplasm

Development of core collection

A pre-requisite before developing a core collection is to assess and characterize the diversity in the germplasm collections. At ICRISAT, we have assessed the patterns of diversity in chickpea, groundnut, pigeonpea, sorghum, pearl millet, finger millet and foxtail millet germplasm collections using data on qualitative and quantitative traits. Core collections have been developed using the information on regional patterns of diversity (Table 2).

Mini core collection

Due to its reduced size compared to entire collection, core collection is useful for scientists to identify accessions with beneficial traits for use in crop improvement programs. However, it soon became evident that developing core collections will not solve the problem of low use of germplasm, as even the size of core collection would be unwieldy for convenient exploitation by the breeders and other crop improvement scientists. This was particularly true in the crops where entire collection is too large (several thousands). To overcome this, Upadhyaya and Ortiz (2001) proposed the "mini core collection" concept using a two-stage strategy. The first stage involves developing a representative core collection (about 10%) from the entire collection using all the available information on origin, geographical distribution, and characterization and evaluation data of accessions. The second stage involves evaluation of the core collection for various morphological, agronomic, and quality traits, and then selecting a further subset of about 10% accessions from the core collection. Thus the mini core collection contains 10% of the core or ~1% of entire collection, but represents the diversity of the entire collection. At ICRISAT, mini core collections of chickpea, groundnut, pigeonpea, sorghum, and pearl millet have been established (Table 2). Mini core collections have been extensively used to identify trait specific germplasm for use in crop improvement programs.

Identifying trait specific germplasm using core/mini core approaches

The core and mini core collections of chickpea, groundnut, and pigeonpea have been evaluated extensively to identify new sources for important biotic and abiotic stresses and for agronomic traits. In chickpea, we have identified sources for early maturity (28) (Upadhyaya et al., 2007b), large-seeded kabuli type (16), high yield and other agronomic traits (39) (Upadhyaya et al., 2007a), and resistance/tolerance to drought (18) (Kashiyagi et al., 2005), salinity (12) (Vadez et al., 2007), high temperature (5), helicoverpa pod borer (5), fusarium wilt (67), botrytis gray mold (55), ascochyta blight (3), dry root rot (6), and multiple resistance (31 accessions) (Pandc et al., 2006). Similarly in groundnut scientists have identified sources for early-maturity (21)
(Upadhyaya et al. 2006b), high yield, large seed size and high shelling percentage (60) (Upadhyaya et al., 2005); resistance/tolerance to drought (18) (Upadhyaya, 2005), salinity (12); low temperature at germination (158) (Upadhyaya et al., 2008b), aflatoxin (5), rosette (3), and early leaf spot (1); in pigeonpea for early maturity (20), high yield, large seed size and high harvest index (54), resistant/tolerant to salinity (16) (Srivastava et al., 2006), sterility mosaic (11), wilt (4), Phytophthora blight (8), and two multiple resistant germplasm; in sorghum 28 germplasm with sweet stalk and 10 resistant to grain mold; 25 germplasm each in finger millet and foxtail millet for high grain yield and early maturity; several accessions for early maturity, high grain yield, and large seed size in pearl millet. The mini core collections were also evaluated by NARS partners. A total of 88 sets of core and mini core collections have been provided to scientist in 19 countries of Africa, Asia, Americas, and Europe. NARS partners identified several parents for use in breeding in India, China, Vietnam, Thailand, Mali, Niger, and UAE.

Genotyping germplasm collections:

The revolution in molecular biology, bioinformatics, and information technology has provided the scientific community with tremendous opportunities for solving some of the world’s most serious agricultural and food security issues. The Generation Challenge programme (GCP) on “Unlocking Genetic Diversity in Crops for the Resource-Poor (www.generationcp.org)” is enhancing research on this area. ICRISAT in collaboration with partners such as ICARDA, Syria; CIRAD, France; EMBRAPA, Brazil; and CAAS, China has developed the composite collections of sorghum, pearl millet, chickpea, pigeonpea, groundnut, finger millet, and foxtail millet (500 – 3500 accessions) (Table 2). The composite collections include core and mini core collections and have been genotyped using 20 to 50 SSR markers to study genetic diversity, population structure, and to establish reference sets of 200-400 genetically diverse accessions (Table 2). The composite collections were also characterized for morpho-agronomic traits at ICRISAT Center, Patancheru, India. Reference sets based on SSR markers, qualitative traits, quantitative traits, and their combinations were formed and compared for allelic richness and diversity. In chickpea, for example 48 SSR-based reference set captured 78.1% alleles of composite collection (1683 alleles) compared to 73.5% of alleles in the reference set based on 7 qualitative traits. The reference set based on both SSR and qualitative traits captured 80.5% (1354 alleles) of composite collection (Upadhyaya et al., 2008a). Similarly, in groundnut the SSR-based reference set captured 95.1% alleles (466) of composite collection (490) compared to 93.3% of alleles (457) in the reference based on 14 qualitative traits. The reference set based on both SSR and qualitative traits captured 95.9% (470) alleles of composite collection. This demonstrated that both SSR and qualitative traits were equally efficient in capturing the allelic richness in reference sets.

Use of novel alleles from wild relatives for enhancement of agronomic traits

Potential of wild relatives to enhance the resistances to biotic and abiotic stresses in cultivated species is well recognized in several crops. The wild relatives are considered agronomically poor and have seldom been considered for enhancing agronomic traits
such as early-maturity, seed size, seed yield, and harvest index. Our research at ICRISAT has indicated that the novel genes of wild relatives of chickpea, groundnut, and pigeonpea can enhance the agronomic traits of cultivated species. For instance, using two accessions of *Cicer reticulatum* (110-113 days to 50% flowering, 143-150 days to maturity, 12-16 g 100-seed weight, 2-5 g plant yield, 5.7 to 16.1% harvest index) as a parent, we have selected several progenies which took 8-21 days less to flower and 6-33 days less to mature, produced 20-103 % larger seeds, 97-217 % greater seed yield, and 6-68 % higher harvest index than the respective cultivated parents. Similarly in groundnut using an amphidiploid with very low 100-seed weight (5-8 g) and poor pod yield (2-5 g plant$^{-1}$), progenies with 60-80% higher 100-seed weight and 150-250% more pod yields were identified. This demonstrated that the novel alleles of wild relatives, that were considered to be lost in evolution to cultivated types, could be used to enhance the important agronomic traits in legumes.

**Conclusions**

Germplasm is basic to crop improvement programs for sustainable agriculture. Trait specific, genetically diverse parents are basic requirements of plant breeders for trait enhancement. Agronomically superior lines are preferable for use in breeding due to the scope for exploitation of additive genetic variance. This would reduce role of unpredictable epistatic and dominance deviation variances. Our strategic research on core, mini-core, composite collections, identifying genetically diverse trait specific germplasm and unlocking potential of wild relatives in improving agronomic traits would be helpful in achieving quantum jump and providing impetus to breeding programs in developing cultivars with a broad genetic base.

**Reference**


Allelopathy in rice can be used as a method for biological control of weeds in rice crops. We have focused on detecting QTL for allelopathic effect and identifying chemical compounds associated with allelopathic effect in rice. Firstly, we developed a reductive bioassay to assess the allelopathic effect of rice. Then, we analyzed QTL conferring allelopathic effect of rice using 12 plexes of the crosses between R317277 (allelopathic) and Bearton (non-allelopathic) and HIL marker mapped on 12 rice chromosomes. Seven QTLs for allelopathic effect were identified on chromosomes 1, 3, 5, 7, 12, and 11 and 12. Major QTLs on the chromosomes 3, 5, 6, and 7 explained 10-16% of total phenotypic variation. A single QTL on chromosome 5 showed a positive effect on allelopathic effect without QTL on chromosomes 5 and 6. QTL on chromosome 7 was responsible for inhibition of root growth and necrosis on root tips of lettuce. We also identified candidate compounds associated with allelopathic effect of rice using HPLC. Among 20 phenoic compounds identified in rice, at least 7 phenoic compounds might play primary roles in allelopathic effect of rice. QTL analysis and chemical identification will be discussed in this report.

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CS2-S1, 05 (16:20-18:40)
Developing the Wheat Phenome Atlas: Integrating 25 years of International wheat Phenotypic data with Genome Analysis
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The Wheat Phenome Atlas Project will develop an integrated diagnostic representation of the regions of the wheat genome that influence heritable phenotypic variation for agronomic, pests and disease resistance and quality traits. Developing the analytical tools to deal with data sets of 15,000 lines x 40 years x 40 traits x 100 locations x 2,000 DNA data points (10 million data points) will involve development of a new and powerful bioinformatic tools and web-based visualization software. With the consortium we are developing, we will develop a Wheat Phenome Atlas Toolbox which will be freely available to researchers worldwide. The Toolbox will enable researchers to develop other crop phenome atlases when appropriate data becomes available. It will allow for identification of elite gene blocks (eg. rust resistant), the molecular tools for rapidly introducing these elite gene blocks into new cultivars, and the prediction of cultivar performance in a range of environments, including future environments predicted by climate change models. As a pilot study we are analysing data from the Elite Spring Wheat Yield Trials (ESWY75). We are integrating the phenotypic data from 25 years of ESWY75, a total of 675 cultivars, with DARWIN data. Connecting these data sets will allow us to find specific genetic regions associated with 7 traits including resistance to 3 rusts (leaf, stem and stripe), grain yield, seed size, plant height and days to heading.

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CS2-S1, 06 (16:40-17:00)
Core Collection for Enhancement Use and Sustainable Conservation of Plant Genetic Resources: Case Studies Using Heuristic Approach for Indian Small Millets Collections
Pratap Narain Mathur, Yousuf Khan, P. Surendranath, Jayaram Gowda
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In the context of limited resources available, increasing use of genepools collections in most genebanks limits their accessibility for use in crop breeding and quality of their management. Therefore, it has been proposed that a limited set of accessions be selected containing as much genetic diversity as possible to offer a good starting point for use for new trials, and could be used for in-depth evaluation, thus increasing the knowledge about the whole collection. Frantl (1984) introduced this concept, calling it a "core collection". Brown (1994) and Brown (1995) further developed the concept. Many genebanks around the world have now been working with core collections. As a result, the concept evolved from a theoretical idea into widely applied methods with many variations and has resulted in a wide variety of methodologies for identifying core collections. Basically, the process of creating a core collection is very simple and a random selection from a collection might be considered a core collection. But the selection of a core collection to ensure representative diversity is somewhat more complicated. A most common approach being used for developing core collections

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CS2-S1, 07 (17:00-17:20)
In Situ Conservation and Characterization of Genetic Resources in the Genus Vigna Sub-Genus Ceratotropis in Thailand
Veerana Sivaswat Forrer*, Sujata Nagampogaru, Arun Masati, Chawonrath Phroutheekhov, Janalek Bloomsukhoun, Sarutee Bhuntong, Udomthbhod Jones Thamadu, Samot Cholosothron, Somphot Phonprao
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This project is part of the conservation and utilization of field crops genetic resources research project of the Thai CASA and partly funded by the FAO-CAS. The prime aim of the project was to make an inventory of known locations where Vigna species can be found. A field visit to validate the findings and make recommendations to conserve the populations found in those locations for in situ conservation of Vigna species and to raise public awareness of the importance of in situ conservation and sustainable use of Vigna species. Nine surveys were carried out between December 2005 and May 2006 and covered 12 provinces of Thailand. Found locations were recorded and GPS. Sixty-five sites from previous records were searched. It was found that 41 sites had disappeared and only 24 sites were found. Sixty-eight samples, of plant for herbarium specimens, of seed for ex situ regeneration and of seed for beneficial microorganisms, were collected. Wild Vigna in several sites had disappeared, perhaps, to threats imposed to the conservation sites, both abiotic or biotic ones. Among the threats were such as slash-and-burn, road expansion, urbanization, or herbicide application. Stress threats were such as disease, insect pests, saltwater intrusion and allelopathy effect. Many wild Vigna species distribution as well as in their sites were also displayed. Attempt, when possible, was made to relieve threats in order to sustain these in situ conservation sites. This case study should be monitored at least every 5 years.

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CS2-S1, 08 (17:20-17:40)
Allelic Richness and Diversity in Global Composite Collection and Reference Sets in Chickpea (Cicer Arietinum L.)

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In the context of limited resources available, increasing use of genepools collections in most genebanks limits their accessibility for use in crop breeding and quality of their management. Therefore, it has been proposed that a limited set of accessions be selected containing as much genetic diversity as possible to offer a good starting point for use for new trials, and could be used for in-depth evaluation, thus increasing the knowledge about the whole collection. Frantl (1984) introduced this concept, calling it a "core collection". Brown (1994) and Brown (1995) further developed the concept. Many genebanks around the world have now been working with core collections. As a result, the concept evolved from a theoretical idea into widely applied methods with many variations and has resulted in a wide variety of methodologies for identifying core collections. Basically, the process of creating a core collection is very simple and a random selection from a collection might be considered a core collection. But the selection of a core collection to ensure representative diversity is somewhat more complicated. A most common approach being used for developing core collections

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**Poster Session**

**CS2-S1, P1**

**Evaluation of Iranian Garlic (Allium Sativum L.) Genotypes Using Multivariate Analysis Method Based on Morphological Characteristics**

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Genetic evaluation of 39 Allium Sativum L. genotypes collected from different parts of Iran was carried out using morphological characteristics. Measuring of characteristics of garlic genotypes were performed based on IGPRI descriptors. Analysis of variance revealed high level of variability among all genotypes. Factor analysis was used to determine the number of main factors. The results showed, the most built characters composing the main factors. Effective characters were categorized in seven factors contributing 91.84% of total variation. For each factor, eigen value of more than 0.8 was used as significant eigen value. Cluster analysis was performed using seven factors. Garlic genotypes in distance of 10 similarity coefficient were divided into four main clusters. This study showed that multivariate analysis is a useful method for discrimination of garlic genotypes.

Keywords: Garlic, morphological characteristics, multivariate analysis, factor analysis, cluster analysis

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**CS2-S1, P2**

**Effects of Different Plant Growth Regulators and Potting Mixes on Micropropagation and Minitubertization of Potato Plants**

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For this study, Agria and Marfona cultivars of potatoes (Solanum tuberosum L.) were used. After thermotherapy and meristem isolation of cultivars, root meristems were placed on filter paper in liquid medium. In vitro micropropagation results from meristems were micropropagation of plantlets using by single node cuttings. Cultivation method. Plantlets were grown at 25°C and 16 h photoperiod with 2000 lux light intensity for one month. Then the effects of different combinations of NAA (baunin) and BAP (cytokinin) (each in four concentrations: 0.05, 1.5 and 6.0 mg/l) were investigated on rooting and growth of potato single nodes. Modified solid (MS) medium with 0.5 (2.25 mg/l) and calcium pantothenate (2 mg/l) were applied in this stage. Results showed that there are significant differences between treatments. The best medium for Agria and Marfona cultivars is the medium in which GA3 was used with NAA and BAP. Application of BAP and NAA decreases the percentage of multiple roots and the number of single nodes in medium culture. Also, after plantlets micropropagation in selective medium (control), the effects of four potting mixes on plantlets morphological traits and minituber production were studied in greenhouse. Results showed that there are significant differences between different potting mixes. The best potting mix for plantlets growth and minituber production was:

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**CS2-S1, P3**

**Local Aromatic Rice Cultivars of North Himalayas - Present Status and Future Strategies for Their Sustainable Improvement**

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Local Aromatic Rice Cultivars of North Himalayas - present status and future strategies for their sustainable improvement Ghilem Ahmed Parry, Asit Sthak, Manoj A. Agarwal, and Najib Seth

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The expansion of area under irrigated rice and the efforts made by the rice breeders during the past 5-6 decades have led to the development of improved and high yielding rice varieties that have kept a pace with the rapidly growing human population, and has guaranteed a food security for the people. However, cultivation of lower high yielding varieties, specific to a particular ecological situation, has brought about the dramatic genetic vulnerability as genetic uniformity of improved rice varieties replaced the diversity of indigenously adapted rice cultivars through cultivation over centuries. Kashmir valley has been known for large number of high quality indigenous rice cultivars for their mild rice grain characteristics and better cooking quality, with a few possessing aroma. These local cultivars are, by and large, tall, photosensitive, poor yielders and susceptible to water stress. Despite this, the production of rice grains continues to be an important agricultural activity in the Kashmir during the past 5-6 decades also led to the genetic erosion of these indigenous high quality rice cultivars. During this transition phase many of these rice cultivars/cultotypes have been lost. Among the most prominent aromatic indigenous rice cultivars of the Kashmir, Mitho Budi stands at the top followed by Mitho Budi. These cultivars are now being grown over small fragmented areas in the Srinagar and Pampore belts, and Sopra village of district Anantnag and Baramulla belt of the district Baramulla. Both these cultivars are short grown and bold seeded with excellent cooking quality. These cultivars thrive well in the field, at harvesting, in storage, during milling and polishing, cooking and while eating. The consumption of these aromatic rice varieties is now confined to special occasions and marriage festivals of the rich people of the valley. This is primarily due to the very high sale price of millet rice of these cultivars. Saltant morphological, yield and grain/tasting quality attributes of these two cultivars are given in the Table 1. 

Table 1: Morphological, yield and quality traits of aromatic rice cultivars of Kashmir. 

<table>
<thead>
<tr>
<th>Cultivar</th>
<th>Plant Height</th>
<th>Number of Leaves</th>
<th>Grain Yield (kg/ha)</th>
<th>Taste</th>
<th>Aroma</th>
<th>Cooked Grain</th>
<th>Cooking Loss</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mitho Budi</td>
<td>90 cm</td>
<td>25</td>
<td>2.5</td>
<td>Excellent</td>
<td>Strong</td>
<td>70%</td>
<td>10%</td>
</tr>
<tr>
<td>Mitho Budi</td>
<td>85 cm</td>
<td>23</td>
<td>3.0</td>
<td>Good</td>
<td>Strong</td>
<td>75%</td>
<td>5%</td>
</tr>
</tbody>
</table>

Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00. 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00 B. Yield components: A. Average grains/pot 130.2 135.2 125.0 130.0 A. Morphological (8): 1.01 1.00 1.00 1.00

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**CS2-S1, P4**

**An Assessment of Genetic Diversity in Cultivated Tea (Camellia Sinensis L.)**

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Tea (Camellia sinensis L) is the most important beverage crops in Iran and the genetic base of tea plantations originated from three parts introduced from India in 1930. For determination of genetic diversity among 30 cultivated tea clones including of national selections and introduced genotypes from Sri Lanka, Russia, India and Japan, they were evaluated using 45 RAPD markers. A total of 93 bands were produced from 16 RAPD markers that were consistent of 78 polymorphic bands and 17 monomorphic bands. Polymorphic band percentage was estimated as 82.3

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