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Identification of Soybean Cultivars Using Biochemical and Morphological Characteristics at Seed and Seedling Stage

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Seventy five cultivars of soybean were characterized for seed storage proteins, amylase isozymes, seed coat peroxidase, hypocotyl pigmentation. All the cultivars were first classified into twelve major groups based on visual characteristics *viz.* seed coat colour, hilum colour and seed coat lustre. These groups were further classified based on seed coat peroxidase reaction, hypocotyl pigmentation, amylase isozymes and seed storage protein, generating 73 groups. Thus, most of the cultivars could be uniquely identified based upon seed and seedling characteristics. Only four cultivars *viz.* JS2, Punjab1, MACS13 and MAUS71 fell into two groups each consisting of two cultivars.

Key Words: Amylase, Cultivar, Identification, Peroxidase, Soybean, SDS-PAGE

Varietal identification is essential for describing a new cultivar, testing genotypic purity and expediting DUS (distinctness, uniformity and stability) test for candidate cultivar. Various laboratory techniques employed for varietal identification range from simple methods of examining seed and seedling morphology to the more advanced procedure of analyzing DNA polymorphism (Smith and Smith, 1992; Cooke, 1995; Chen *et al.*, 1994). Seed morphology, studied by visual examination can provide useful information for differentiating genotypes (Wiesner *et al.*, 1993; Aggarwal and Powar, 1990). Examination of seedling morphology under controlled conditions of growth can be useful and cost-effective for describing and distinguishing cultivars (ISTA, 1992). SDS - PAGE and isozyme polymorphism of seed storage proteins have been found to be very useful tools in varietal identification in soybean (Abdel–Tawab *et al.*, 1993; Doong and Kiang, 1987; Cardy and Beversdorf, 1984). For rapid identification of varieties, the distinction should be made at seed and seedling stage by scoring maximum number of discriminating biochemical and morphological characteristics. Therefore, with a view to score maximum characteristics at seed and seedling stages, 75 cultivars of soybean were studied for seed coat color, hilum color, seed coat lustre, seed coat peroxidase reaction, hypocotyl coloration, SDS–PAGE of seed proteins and amylase isozymes.

Materials and Methods

Single plant progenies of 75 soybean cultivars were grown in the field at National Research Centre for Soybean, Indore. Seeds from a single plant of each of the varieties were hand harvested and studied for the following parameters.

Seed Colour

A minimum of 20 seeds from each cultivar were examined for seed coat colour, hilum color and seed coat lustre. Four seed coat colour classes *viz.* green, greenish yellow, yellow and black, four hilum categories *viz.* black, brown, imperfect black (black hilum bordered by a brown line) and gray and three seed coat lustre categories *viz.* shiny, intermediate and dull were clearly distinguishable among cultivars. Each variety was assigned to one of the classes for each of the traits.

Seed Coat Peroxidase Reaction

The method of Buttery and Buzzell (1968) was used to analyse seed coat peroxidase reaction. Cultivars were placed into one of the two groups based upon appearance (positive) or absence (negative) of reddish brown color after reacting seed coat with guiacol and hydrogen peroxide.

Anthocyanin Pigmentation on Hypocotyl

Twenty seeds of all the cultivars were sown in the germination tray under constant light. The pigmentation on hypocotyls was observed on 4th day and the cultivars were placed into one of the three groups *viz.* green, bronze or purple based upon appearance of color.

Sample Preparation for SDS-PAGE and Amylase Isozyme Analyses

Ten seeds of each cultivar were ground using pestle and mortar. The flour so obtained was defatted using petroleum ether. Hundred mg defatted flour was extracted in 1 ml of 0.05M Tris-Cl buffer (pH 6.8) and centrifuged at 10000 rpm. The supernatant was decanted and used for SDS-PAGE and Amylase analysis.

SDS-PAGE of Seed Storage Proteins

The polypeptide patterns of seed storage proteins were resolved using discontinuous SDS-PAGE system as given by Laemmli (1970). The stacking gel consisted of 5% acrylamide-bis acrylamide (29:1), pH 6.8 and separating gel consisted of 12% acrylamide-bisacrylamide (29:1), pH 8.9. The protein bands were numbered from loading well to the end of the gel. The varieties were categorized based upon presence or absence of specific bands. Rm value of each polypeptide was calculated as follows:

$$Rm = \frac{\text{Distance travelled by particular polypeptide}}{\text{Distance travelled by tracking dye}}$$

Amylase Isozymes

Amylase isozymes were resolved on native PAGE consisting of 5% stacking gel and 7% separating gel containing 0.5% starch. Isozymes were visualized by negative staining by the method given by Stoddart (1971). The varieties were categorized based on presence or absence of a particular band. Rm value of each isozyme was calculated as follows:

$$Rm = \frac{\text{Distance travelled by particular isozyme}}{\text{Distance travelled by tracking dye}}$$

Results and Discussion

Seed Colour

Based on seed coat color 75 cultivars were separated into four groups. The largest group with yellow seed coat consisted of 69 cultivars followed by black seed group consisting of four varieties and green and greenish yellow group each consisting of one variety only. For the hilum color, the largest group with brown hilum contained 42 varieties followed by black hilum group with 27 cultivars and gray hilum group consisting of 5 cultivars and imperfect black hilum group having one cultivar only. Maximum cultivars (46) displayed intermediate seed coat lustre while the group with shiny seed coat lustre comprised of 25 varieties. Only four cultivars were classified under dull seed coat luster.

Seed Coat Peroxidase Reaction

Seed coat peroxidase reaction differentiated 75 cultivars into two groups. Thirty one cultivars exhibited positive reaction and forty four cultivars exhibited negative reaction for seed coat peroxidase.

Hypocotyl Pigmentation

Among three groups, the largest group with purple pigmentation consisted of 45 cultivars followed by the group with bronze pigmentation consisting of 22 cultivars and the group with green pigmentation consisting of eight cultivars.

SDS-PAGE of Seed Storage Proteins

A total number of 35 polypeptide bands were resolved on gel with molecular weight ranging from 17 kDa to 122 kDa (Figs. 1-6). Maximum number of bands (29) were observed in Bragg and T49 while minimum number of bands (22) were observed in Hardee. Out of 35 bands, 10 bands were found to be common to all the cultivars. The common bands with their Rm values are: 3rd band (0.12), 5th band (0.14), 6th band (0.16), 7th band (0.17), 10th band (0.22), 12th band (0.24), 17th band (0.31), 19th band (0.36), 29th band (0.61), 35th band (0.82). There were some unique bands present in only one cultivar.

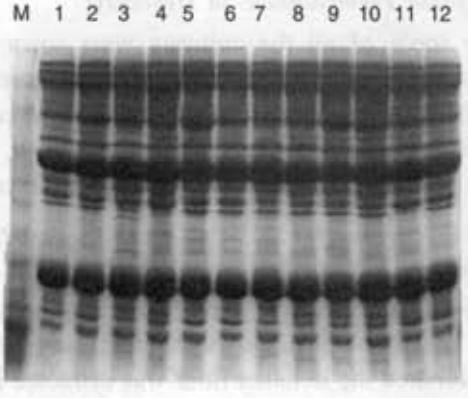

Fig.1. SDS-Page profile of soybean cultivars. Lane 1-12 represents the cultivars Lee, MACS 450, VLS 47, Pusa 24, JS 72-44, GS1, Punjabi1, PK. 327, NRC 7, VLS1, JS 72-280 and RAUS5. M represents molecular weight markers.

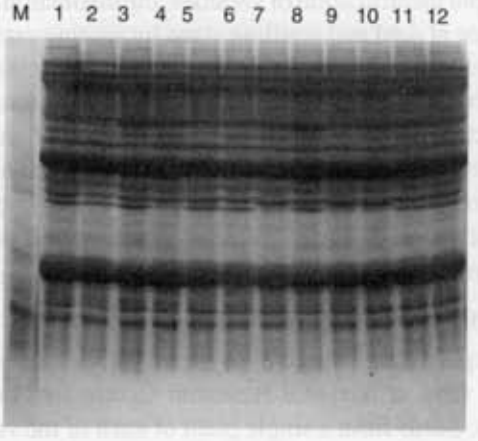

Fig.2. SDS-Page profile of soybean cultivars. Lane 1-12 represents the cultivars JS 75-MACS 124, PK 1024, JS 79-81, PK 472, ADT-1, MAUS 32, MACS13, Alankar, JS 80 MAUS 1 and NRC 37. M represents molecular weight markers.

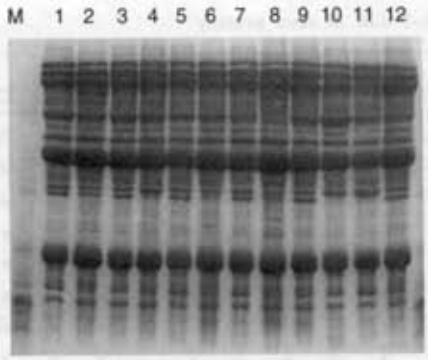

Fig.3. SDS-Page profile of soybean cultivars. Lane 1-12 represents the cultivars JS90-41, Shilajeet, Shivalik, GS2, VLS 21, Pusa37, MAUS71, MACS 58, PK 262, Improved pelican, NRC2 and JS 75-46. M represents molecular weight markers.

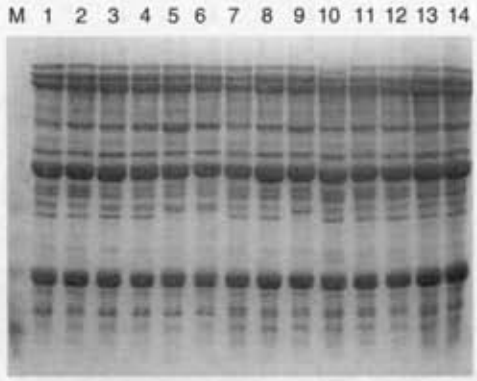

Fig.5. SDS-Page profile of soybean cultivars. Lane 1-14 represents the cultivars JS 2, PK416, MACS57, Co1, KB 79, IS 9, Harit Soya, VLS, MAUS2, JS71-05, NRC12, Pusa 16, Palam soya, PK 308. M represents molecular weight markers.

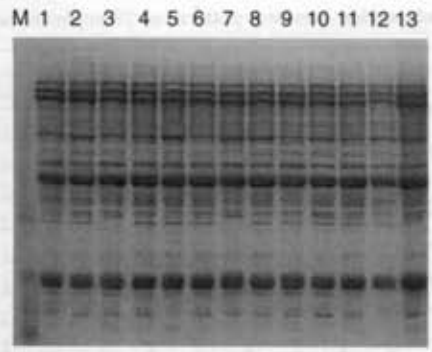

Fig.4. SDS-Page profile of soybean cultivars. Lane 1-14 represents the cultivars Pusa 40, JS 76-205, T49, PK 1042, Pusa 22, SL 295, MAUS 61-2, Pusa 20, KHSb2, An, Bragg, Kalitur, MAUS 61, PK 1092. M represents molecular weight markers.

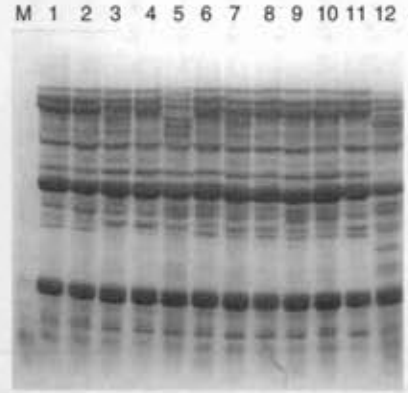

Fig.6. SDS-Page profile of soybean cultivars. Lane 1-12 represents the cultivars Birsa soya 1, PK 564, Monetta, MAUS 47, JS 335, PS1029, CO2, PK 471, SL 96, SL 459, JS 93-05, Hardee. M represents molecular weight markers.

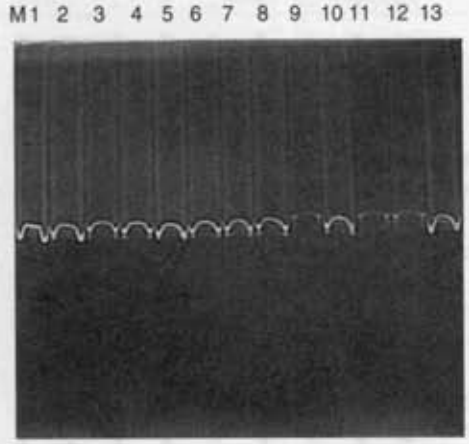

Fig.7. Electrophoretic pattern of amylase isozyme of soybean cultivars. Lanes 1-13 represent the cultivars PK 1092, MAUS71, JS79-81, Pb1, VLS2, Bragg, Lee, PK 309, Hara Soya, MAUS61, Lsb1, SL96 and JS80-21

For example, the fourth band (Rm 0.13) was present only in JS 335, 14th band (Rm 0.26) was present only in MAUS 61-2 and 21st band (Rm 0.40) was present only in MAUS 32. Rest of the cultivars were categorized based on presence or absence of any of the 25 polymorphic bands (Table 1).

Amylase Isozyme Variability

A total of four bands with Rm values 0.031, 0.45, 0.48 and 0.50 are observed. Three bands with Rm values 0.031, 0.45 and 0.50 were present in all the cultivars. The third band with Rm value 0.48 was absent in three varieties *viz.* LSb1, SL96 and Hara Soya (Fig. 7).

Varietal Identification Key

A varietal identification key was framed based on all the differentiating characters studied (Table 2). The cultivars were first classified based upon most obvious character, seed coat colour. Two cultivars, Hara Soya and JS90-41, were uniquely identified based on their seed coat colour. Remaining 73 cultivars were further sub-classified based on hilum colour. The variety Pusa

Table 1. Polypeptide banding pattern of 75 soybean cultivars derived from SDS–PAGE of seed protein

Cultivar	Band no																								
	1	2	4	8	9	11	13	14	15	16	18	20	21	22	23	24	25	26	27	28	30	31	32	33	34
Rm	.07	.08	.12	.18	.19	.23	.25	.26	.28	.29	.33	.39	.40	.42	.45	.48	.50	.53	.54	.56	.64	.67	.70	.73	.76
Lee	–	+	–	+	–	+	+	–	+	+	–	–	+	+	+	–	–	–	–	–	+	+	+	+	+
MACS450	–	+	–	+	–	+	+	–	+	+	+	–	+	+	+	–	–	–	+	–	+	+	+	+	+
VLS47	–	+	–	+	–	+	+	–	+	+	+	+	+	+	–	+	–	–	+	–	+	+	+	+	+
Pusa24	–	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	–	+	+	+	+	+
JS7244	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	–	–	+	–	+	+	+	+	+
GS1	–	+	–	–	–	+	+	–	+	+	–	+	+	+	+	–	–	–	+	–	+	+	+	+	+
Pb1	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	–	+	–	+	+	+	+	+
PK 327	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	+	+	+	–	+	+	+	+	+
NRC7	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	+	+	+	–	+	+	+	+	+
VLS1	+	+	–	+	–	+	+	–	+	+	+	–	+	+	+	–	+	+	+	–	+	+	+	+	+
JS72–280	–	+	–	+	–	+	+	–	+	+	+	–	+	+	–	–	+	+	+	–	+	+	+	+	+
RAUS5	–	+	–	–	–	+	+	–	+	+	+	–	+	+	+	–	+	+	+	–	+	+	+	+	+
JS75–46	–	+	–	+	–	–	+	+	+	+	–	+	+	+	+	–	–	+	+	–	+	–	+	+	+
MACS124	–	–	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	–	+	+	+
PK 1024	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	+	+	+
JS 79–81	–	–	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	+	+	+
PK472	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	+	+	+
ADT1	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	–	+	+	–	+	–	+	+	+
MAUS32	–	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	+	+	–	+	–	+	+	+
MACS13	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	+	+	+
Alankar	–	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	+	+	–	+	+	+	+	+
JS80–21	–	+	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	–	+	+
MAUS1	+	+	–	+	–	–	+	+	+	+	–	+	+	+	+	–	–	+	+	–	+	–	–	+	+
NRC37	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	–	–	+	+
JS 90–41	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	+	+	+
Shilajeet	–	–	–	+	–	+	+	–	+	+	–	+	+	+	+	+	+	+	+	–	+	–	+	+	+
Shivalik	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	–	+	+
GS2	–	+	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	+	+	+
VLS21	–	+	–	+	–	+	–	–	+	+	–	+	+	+	+	–	–	+	+	–	+	+	+	+	+
Pusa37	–	–	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	–	+	+	+
MAUS71	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	–	+	+	–	+	+	+	+	+
MACS58	–	–	–	+	–	+	+	–	+	+	+	+	+	+	+	+	–	+	+	–	+	–	+	+	+
PK262	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+	–	–	+	+	–	+	+	+	+	+
Imp pelican	–	+	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	–	+	+
NRC2	–	+	–	+	–	+	+	–	+	+	–	+	–	+	–	–	–	+	+	–	–	+	+	+	+
Pusa 40	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	–	–	+	–	+	+	+	+	+
JS 76–205	+	+	–	+	–	+	+	–	+	+	+	+	+	–	+	+	–	–	+	–	+	+	+	+	+
T49	–	+	–	+	–	+	+	–	+	+	+	+	+	+	–	+	+	+	+	–	+	+	+	+	+
PK1042	–	+	–	+	–	+	+	–	+	–	–	+	+	–	+	+	+	+	+	–	+	+	+	+	+
Pusa 22	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+	–	+	+	+	–	+
SI295	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+	–	+	+	+	+	+
MAUS61–2	–	+	–	+	–	+	+	+	+	–	–	+	+	+	–	+	+	+	+	–	+	+	+	+	+
Pusa20	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+	–	+	+	+	+	+
KHSb2	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	–	–	+	–	+	+	+	+	+
Ankur	–	+	–	+	–	+	–	–	+	+	+	+	+	+	+	+	–	–	+	–	+	+	+	+	+
Bragg	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	+	+	+	+	–	+	+	+	+	+
Kalitur	+	+	–	+	–	+	+	–	+	+	+	+	+	–	+	+	+	–	+	–	+	+	+	–	–
MAUS61	+	+	–	+	–	+	+	–	+	+	–	+	+	+	–	+	+	+	+	–	+	+	+	+	+
Pk1092	+	+	–	+	–	+	+	–	+	+	–	+	+	+	+	–	+	+	+	–	+	+	+	+	+

Contd.

Table 1 Contd.

Cultivar	Band no																								
	1	2	4	8	9	11	13	14	15	16	18	20	21	22	23	24	25	26	27	28	30	31	32	33	34
JS2	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+
PK416	–	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+–	–	+	+	–	+	+	+	+	+
MACS57	–	+	–	+	–	–	+	–	+	+	–	+	+	+	+	+	–	+	+	–	+	+	+	+	+
Co1	–	+	–	+	–	–	+	–	+	+	–	+	+	+	+	+	–	+	+	–	+	+	+	+	+
KB79	–	–	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	+	+	+
IS9	+	+	–	+	–	–	+	–	+	+	+	+	+	+	–	–	–	+	+	–	+	+	+	+	+
Hara soya	–	+	–	+	–	+	+	–	+	+	–	–	+	–	+	–	–	+	+	–	+	+	+	+	+
MAUS2	–	+	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	+	+	–	+	+	+	+	+
JS 71–05	–	–	–	+	+	+	+	–	+	+	–	+	+	+	+	–	–	+	+	+	+	+	+	–	+
NRC12	–	+	–	+	–	+	+	–	+	+	–	–	+	+	+	+	–	+	+	–	+	+	+	+	+
Pusa16	–	+	–	+	–	+	+	–	+	+	–	+	+	+	+	+	–	+	+	–	+	+	+	+	+
Palam soya	+	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+
Pk308	+	+	–	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+
Bsoya1	+	–	–	+	–	+	+	–	–	+	–	+	+	–	+	–	–	–	+	–	+	+	+	+	+
Pk564	–	–	–	+	–	+	+	–	–	+	–	+	+	–	+	–	–	+	+	–	+	+	+	+	+
Monetta	–	–	–	+	–	+	+	–	+	+	–	+	+	+	–	+	–	+	+	–	+	+	+	+	+
MAUS 47	–	+	–	+	+	+	+	–	+	+	–	+	+	+	–	–	–	–	+	–	+	+	+	+	+
JS335	–	–	+	+	–	+	+	–	+	+	–	+	+	+	–	+	–	+	+	+	+	+	+	+	+
Co2	–	–	–	+	+	+	+	–	+	+	–	+	+	+	+	–	–	+	+	–	+	–	+	–	+
PK471	+	+	–	+	–	+	+	–	+	–	+	+	+	+	+	+	–	+	+	–	+	+	+	+	+
SI96	+	+	–	+	–	+	+	–	–	+	–	+	+	+	+	+	–	+	+	–	+	+	+	+	+
SI459	+	–	–	+	–	+	+	–	–	+	–	+	+	–	+	+	–	+	+	–	+	+	+	+	+
JS 93–05	+	+	–	+	–	+	+	–	+	+	+	+	+	–	+	+	–	–	+	–	+	+	+	+	+
Hardee	–	–	–	+	+	–	–	–	–	–	–	+	+	+	–	–	+	+	–	–	+	+	+	+	+

Table 2. A key to differentiate Indian soybean varieties based on seed coat color, hilum color, seed coat luster, seed coat peroxidase reaction, hypocotyl pigmentation, SDS-PAGE of seed storage proteins and amylase isozyme variability

Variety	Distinguishing character					
	Morphological/chemical					Electrophoretic variability
	SCC	HC	SCL	SCP	HP	SDS - PAGE/amylase
Hara soya	G					
JS90-41	GY					
JS76-205	B	B	S			
Kalitur	B	B	I	+		
VLS1	B	B	I	_	Bz	Protein band no. 14 present
Birsasoya1	B	B	I	_	Bz	Protein band no. 14 absent
Pusa16	Y	IB				
PS1029	Y	B	S	+	Bz	
MACS450	Y	B	S	+	P	Protein band no. 1 absent
KHSb2	Y	B	S	+	P	Protein band no. 22 absent
PS1092	Y	B	S	+	P	Protein band 1&22 present
Pusa37	Y	B	S	_	Bz	Protein band no. 2 absent
Pusa24	Y	B	S	_	Bz	Protein band no. 2 present
JS71-05	Y	B	S	_	P	Protein band no. 9 present
JS93-05	Y	B	S	_	P	Protein band no. 9 absent
LSb1	Y	B	I	_	Bz	Protein band no. 3 absent
Bragg	Y	B	I	_	Bz	Protein band no. 3 present
JS335	Y	B	I	_	P	Protein band no. 4 present
JS72-44	Y	B	I	_	P	Protein band no. 23 absent
MACS13	Y	B	I	_	P	Protein band no. 1 absent
MAUS71	Y	B	I	_	P	Protein band no. 1 absent

Contd.

Table 2 Contd.

Variety	Distinguishing character					
	Morphological/chemical					Electrophoretic variability
	SCC	HC	SCL	SCP	HP	SDS - PAGE/amylase
Indirasoya9	Y	B	I	_	P	Protein band no. 1 present
NRC2	Y	B	D	+	Bz	Protein band no. 30 absent
SL295	Y	B	D	+	Bz	Protein band no. 18 absent
JS72-280	Y	B	D	+	Bz	Protein band no. 18 present
MAUS2	Y	Br	S	+	G	
MACS124	Y	Br	S	+	P	Protein band no. 30 absent
JS79-81	Y	Br	S	+	P	Protein band no. 2 absent
Pusa40	Y	Br	S	+	P	Protein band 2 & 30 present
PK308	Y	Br	S	_	G	
NRC37	Y	Br	S	_	Bz	Protein band no. 1 absent
PK564	Y	Br	S	_	Bz	Protein band no. 2 absent
MAUS1	Y	Br	S	_	Bz	Protein band 1 & 2 present
Lee	Y	Br	S	_	P	Protein band no. 27 absent
Imp.Pelican	Y	Br	S	_	P	Protein band no. 23 absent
Shilajeet	Y	Br	S	_	P	Protein band no. 2 absent
NRC7	Y	Br	S	_	P	Protein band 2, 18 & 23 present
JS2	Y	Br	S	_	P	Protein band no. 11 present
Punjab1	Y	Br	S	_	P	Protein band no. 11 present
MACS57	Y	Br	S	_	P	Protein band no. 11 absent
Hardee	Y	Br	I	+	G	Protein band no. 9 present
VLS47	Y	Br	I	+	G	Protein band 9 & 23 absent
Shivalik	Y	Br	I	+	G	Protein band no. 18 absent
PK262	Y	Br	I	+	G	Protein band no. 18 present
PK1042	Y	Br	I	+	Bz	Protein band no. 16 absent
Alankar	Y	Br	I	+	Bz	Protein band no. 23 absent
Ankur	Y	Br	I	+	Bz	Protein band no. 18 present
PK416	Y	Br	I	+	Bz	Protein band no. 22 absent
PK1024	Y	Br	I	+	Bz	Protein band no. 22 present
GS1	Y	Br	I	+	P	Protein band no. 8 absent
JS75-46	Y	Br	I	+	P	Protein band no. 11 absent
KB79	Y	Br	I	+	P	Protein band no. 2 absent
JS80-21	Y	Br	I	+	P	Protein band no. 23 absent
Pusa22	Y	Br	I	+	P	Protein band 2 & 23 present
SL96	Y	Br	I	_	G	Protein band no. 1 present
PK472	Y	Br	I	_	G	Protein band no. 1 absent
PK471	Y	Br	I	_	Bz	Protein band no. 1 present
VLS21	Y	Br	I	_	Bz	Protein band no. 1 absent
MAUS61-2	Y	Br	I	_	P	Protein band no. 14 present
CoSoy2	Y	Br	I	_	P	Protein band no. 9 present
MAUS32	Y	Br	I	_	P	Protein band no. 21 present
NRC12	Y	Br	I	_	P	Protein band no. 20 absent
MACS58	Y	Br	I	_	P	Protein band no. 2 present
MAUS61	Y	Br	I	_	P	Protein band no. 1 present
GS2	Y	Br	I	_	P	Protein band 1 & 18 absent
ADT1	Y	Br	I	_	P	Protein band no. 31 absent
PK327	Y	Br	I	_	P	Protein band no. 24 absent
T49	Y	Br	I	_	P	Protein band 18, 24 & 31 present
Co1	Y	Br	D	+	P	
MAUS47	Y	Gr	I	+	P	Protein band no. 9 present
Monetta	Y	Gr	I	+	P	Protein band no. 9 absent
RAUS5	Y	Gr	I	_	P	Protein band no. 8 absent
VLS2	Y	Gr	I	_	P	Protein band no. 8 present

SCC–Seed Coat Colour, HC–Hilum Colour, SCL–Seed Coat Lustre, SCP–Seed Coat Peroxidase, HP–Hypocotyl Pigmentation, G–Green, GY-Greenish Yellow, Y–Yellow, B-Black, IB–Imperfect black, Br–Brown, Gr–Grey, S–Shiny, I–Intermediate, D–Dull, Bz–Bronze, P–Purple

16 was differentiated from other varieties using seed coat colour and hilum colour. Differences in seed coat luster were used to differentiate the rest 72 varieties. The variety JS76-205 was uniquely identified based upon its seed coat colour, hilum colour and seed coat luster. Remaining 71 varieties were further sub-classified using seed coat peroxidase reaction. Two varieties Kalitur and Co1 were differentiated from other varieties using this additional character. Differences in hypocotyl pigmentation were used to differentiate the remaining 70 varieties. Five varieties *viz.* PS1029, MAUS2, PK308, SL96 and VLS21 were uniquely identified using this sub-classification. Rest 65 varieties were further sub-classified based upon presence or absence of amylase third band. Two varieties LSb1 and Bragg were uniquely identified using this sub-classification. Remaining 63 varieties were grouped into 12 broad groups based on this classification. SDS-PAGE pattern of the varieties falling under same group were compared and the varieties were differentiated based on presence or absence of different bands till the varieties were uniquely identified. Thus except four cultivars, all other 69 cultivars could be uniquely identified. The remaining four cultivars formed two groups of two each *viz.* JS2 and Punjab1 and MACS13 and MAUS 71.

Under Plant Variety Protection and Farmers Right Act 2001, varietal testing for Distinctness, Uniformity and Stability (DUS) is essential for protection of new plant varieties. This warrants comparison of all the candidate varieties with the varieties of common knowledge. The key developed in this study to differentiate Indian soybean varieties based upon seed coat color, hilum colour, seed coat luster, seed coat peroxidase reaction, hypocotyls pigmentation, electrophoretic variability of SDS-PAGE banding pattern and amylase isozymes can serve as a ready reckoner for varietal identification by plant breeders and seed certification officers. Moreover, it will work as fast method to group the candidate variety with similar varieties for DUS testing as distinguishing characters used in development of varietal identification key are scored at seed and seedling stages.

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Evaluation of Cucumber (*Cucumis sativus* L) Genotypes for Field Resistance to Red Pumpkin Beetle (*Aulacophora foveicollis* Lucas)

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Host preference of red pumpkin beetle (*Aulacophora foveicollis* Lucas) was studied on sixty-eight indigenous germplasm lines of cucumber during 2002. These germplasm lines were grown in randomized block design with three replications. Data were collected on infestation of red pumpkin beetle on plants at different stages like cotyledonary, true leaf, flowering and fruiting of crop. Eight germplasm lines (PCUC7, PCUC36, PCUC47, PCUC66, PCU99, PCUC102, PCUC108 and PCUC110) showed resistance against red pumpkin beetle. These genotypes may be for used in future resistance breeding in cucumber.

Key Words: Cucumber, Red pumpkin beetle, Resistance

Cucumber is an important cucurbit grown in all agro-climatic zones of India. It suffers from attack of a number of insect-pests and diseases. The red pumpkin beetle (*Aulacophora foveicollis*) is one of the most destructive pests especially during seedling stage of plants when the crop can be totally damaged (Singh *et al.*, 2003). A large number of insecticides have been tested to control this insect but their hazardous effects on health of consumer and environment necessitate research for safer methods of control.

Materials and Methods

Sixty-seven indigenous *(desi)* cucumber germplasm lines were collected from farmers field. The experiment was conducted in randomized block design with three replications each at Vegetable Research Centre (VRC) of GBPUAT, Pantnagar. These were sown in the 1st week of March 2002 with spacing of 1x1 meter. All the recommended practices for raising the crop were carried out except application of chemicals. Fertilizer dose of 60:50:60 :: N:P:K and irrigation was given at weekly intervals. The observations on infestation were recorded on five randomly selected plants in each plot at different stages *viz,* cotyledonary, true leaf, flowering and fruiting. Percent infestation data obtained through visual observation and scoring were analyzed as per Gomez and Gomez (1983) (Table 1).

Table 1. Scoring of pest infestation

Scale (% infestation)	Category
<10	Resistant
10-30	Moderately resistant
30-50	Moderately susceptible
50-70	Susceptible
>70	Highly susceptible

Results and Discussion

There were significant differences among the genotypes of cucumber with respect to red pumpkin beetle infestation at different crop stages (Table 2). At the cotyledonary leaf stage, infestation ranged between 15.0 %(PCUC32) to 70% (PCUC96) while the check Pusa Sanjog had 45% infestation. Hence, these germplasm varied between moderately resistant to susceptible. PCUC31, PCUC37, PCUC38, PCUC42, PCUC55, PCUC63, PCUC67 PCUC87, PCUC93, PCUC96, PCUC97, PCUC101, PCUC111, PCUC117, PCUC120 were found susceptible, PCUC7, PCUC25, PCUC27, PCUC29, PCUC32. PCUC35, PCUC36, PCUC40, PCUC47, PCUC48, PCUC51, PCUC53, PCUC60, PCUC61, PCUC62, PCUC65, PCUC66, PCUC69, CUC95, PCUC99, PCUC102, PCUC104, PCUC108, PCUC109, PCUC110, PCUC116, PCUC118, PCUC124 were moderately resistant and rest were moderately susceptible. At true leaf stage infestation varied between 5% (PCUC51, PCUC69) to 54% (PCUC107) while check had 20% infestation. Hence, at this stage PCUC51, PCUC69 showed resistant and PCUC107 were susceptible and PCUC14, PCUC16, PCUC19, PCUC24, PCUC25, PCUC31, PCUC37, PCUC42, PCUC46, PCUC55, PCUC57, PCUC63, PCUC67, PCUC87, PCUC93, PCUC96, PCUC97, PCUC101, PCUC111, PCUC117, PCUC120 were fond moderately susceptible and rest were moderately resistant.

At flowering stage minimum infestation was recorded on PCUC38 and PCUC61 (5%) and maximum on PCUC101 (80%) while check had 15% infestation. PCUC38, PCUC46, PCUC61, PCUC62 were found resistant and PCUC101 found highly susceptible. At fruiting stage, infestation ranged between 5% (PCUC 61, PCUC 96) to 50% (PCUC29, PCUC53, PCUC116

Table 2. **Mean percent infestation of red pumpkin beetle at different stages of cucumber crop**

Cultivar	Cotyledonary leaf stage	True leaf stage	Flowering stage	Fruiting stage
PCUC4	45.0	23.0	15.0	12.0
PCUC7	20.0	15.0	25.0	40.0
PCUC13	48.0	25.0	25.0	45.0
PCUC14	60.0	34.0	10.0	12.0
PCUC16	50.0	40.0	15.0	40.0
PCUC19	50.0	35.0	20.0	20.0
PCUC20	45.0	20.0	35.0	45.0
PCUC21	35.0	15.0	40.0	45.0
PCUC24	40.0	22.0	45.0	15.0
PCUC25	20.0	24.0	33.3	40.0
PCUC27	25.0	15.0	42.0	45.0
PCUC29	25.0	20.0	15.0	50.0
PCUC31	55.0	25.0	40.0	35.0
PCUC32	15.0	10.0	10.0	40.0
PCUC34	40.0	25.0	15.0	42.0
PCUC35	25.0	20.0	15.0	40.0
PCUC36	30.0	22.0	18.0	20.0
PCUC37	60.0	45.0	10.0	18.0
PCUC38	50.0	24.0	05.0	10.0
PCUC40	20.0	10.0	41.7	15.0
PCUC42	52.0	22.0	45.0	40.0
PCUC44	40.0	25.0	15.0	18.0
PCUC45	35.0	30.0	33.2	40.0
PCUC46	50.0	50.0	05.0	15.0
PCUC47	20.0	15.0	15.0	20.0
PCUC48	25.0	15.0	42.0	10.0
PCUC50	30.0	20.0	40.0	13.3
PCUC51	30.0	05.0	25.0	45.0
PCUC53	35.0	30.0	20.0	50.0
PCUC55	60.0	40.0	35.0	35.0
PCUC57	45.0	35.0	40.0	40.0
PCUC60	30.0	25.0	10.0	35.0
PCUC61	25.0	15.0	05.0	05.0
PCUC62	25.0	10.0	08.0	10.0
PCUC63	60.0	48.0	15.0	30.0
PCUC64	35.0	30.0	15.0	10.0
PCUC65	25.0	20.0	15.0	42.0
PCUC66	20.0	10.0	18.0	10.0
PCUC67	60.0	50.0	10.0	10.0
PCUC69	20.0	05.0	10.0	10.0
PCUC73	40.0	20.0	40.0	45.0
PCUC87	60.0	35.0	30.0	10.0
PCUC93	65.0	40.0	30.0	05.0
PCUC94	35.0	20.0	20.0	35.0
PCUC95	30.0	10.0	12.0	7.3
PCUC96	70.0	42.0	31.7	05.0
PCUC97	60.0	40.0	50.0	10.0
PCUC98	35.0	20.0	10.0	10.0
PCUC99	30.0	25.0	15.0	15.0
PCUC101	60.0	50.0	80.0	48.0
PCUC102	25.0	10.0	15.0	10.0
PCUC104	25.0	15.0	10.0	35.0
PCUC105	50.0	10.0	10.0	05.0
PCUC107	35.0	54.0	25.0	35.0
PCUC108	25.0	15.0	10.0	10.0
PCUC109	20.0	20.0	45.0	10.0
PCUC110	25.0	10.0	10.0	10.0
PCUC111	60.0	50.0	40.0	45.0
PCUC112	40.0	15.0	45.0	10.0
PCUC113	35.0	20.0	15.0	15.0
PCUC114	35.0	25.0	10.0	15.0
PCUC115	40.0	20.0	15.0	15.0
PCUC116	30.0	25.0	48.0	50.0
PCUC117	60.0	50.0	25.0	48.0
PCUC118	25.0	20.0	50.0	25.0
PCUC120	65.0	50.0	40.0	40.0
PCUC124	30.0	15.0	15.0	40.0
Pusa Sanjog (Check)	45.0	20.0	15.0	45.0
CD at 5%	16.7	12.1	12.6	12.8

and check Pusa Sanjog had 45% infestation. This study revealed that only cotyledonary stage of cucumber is highly susceptible to red pumpkin beetle. The present findings regarding host plant resistance are in accordance with earlier reports of Nayar *et al.* (1992) who mentioned that cucurbits, especially cucumber, are attacked by red pumpkin beetle in varying proportion. On the basis of the study it appeared that genotypes PCUC7, PCUC36, PCUC47, PCUC66, PCUC99 and PCUC102, PCUC108, PCUC110 had consistent field resistance against red pumpkin beetles across the crop growth stages. These genotypes may be used in future breeding programmes of cucumber to develop varieties resistant to red pumpkin beetle.

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Leafy Vegetables of North-east India

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Leafy vegetables of north-eastern region attract considerable attention due to their rich food value. Tribal people in the remote localities are basically depending upon these vegetables which they harvest from the nature. Limited attempts have been made to bring these vegetables into cultivation. There is considerable scope to collect, evaluate and improve these vegetables. Systematic cultivation can also unfold the marketing potential of these plants among the rural communities of NE region.

Key Words: Collection, Conservation, Leafy vegetables, NE region and Cultivation, Use

The north-eastern (NE) region of India is inhabited by about 26 per cent tribal population, where 119 communities are distributed in seven states. Their staple food is rice, but they largely depend on the cultivation for various kinds of vegetables. Besides, they gather some plants from the wild habitats as food plants. The topography, altitude and rainfall pattern has made the region floristically rich and diverse. Many wild plants which occur naturally, are used by local people as food. Information about the use of various plant species as leafy vegetable were available in old world tropics (Sastrapradja & Kartawinata, 1973; Ochse, 1977; Oomen & Grubgen, 1977; Martin & Rubente, 1979). The contribution of horticultural crops particularly the leafy vegetables, have so far been underestimated in this region, but they have sufficient nutritive value. The importance and use of such native food plants used in diet by the tribes have been documented by Singh and Arora (1978), Arora (1981), Arora and Nayar (1984), Haridasan *et al.* (1990). Joshi (1992) studied the leaf and grain amaranths and chenopods in detail while Joshi and Paroda (1991) have emphasized the food value on buckwheat. A preliminary attempt was made by Jana (1989) on leafy vegetable for their cultivation practice and economics of Cooch Behar district, which is adjacent to this region. There are about 700 species belonging to 125 plant families, which contribute as leafy vegetable (Peter and Devadas, 1989). 78 species are used in this region as leafy vegetables and out of this, 45 species occur in wild habitat. These are tabulated separately under cultivated (Table 1) and wild species (Table 2). Their origin and diversity is based on Zeven and Zhukovsky (1975) while for the distribution of species, Willis (1982) was consulted. Farmers of the NE region are gradually becoming interested to produce such crops which can enable them to earn limited but quick money within a very short period. Compared to other vegetables, the leafy vegetables have a low economic value but they are good sources of carotene or provitamin-A, a reasonable amount of protein, ascorbic acid, iron, folic acid and calcium (Sloten, 1984). Nutritive value of a few leafy vegetables is provided in Table 3, which can substantiate their importance as a diet.

Preference and use is another factor for consumption of a particular vegetable in a particular tribal community. This has got direct relationship with local market demand. Conventional use, culture and beliefs also count for cultivation and conservation of some species among the tribals. In some communities, using the leafy vegetables as food is a custom, which makes the food a balanced diet.

Agro-climate of the Region and Cultivation

The climatic and edaphic factors and also growing season plays a vital role for the growth of such vegetables. The region constitutes the plains and hills where the topography and climate varies, mild summer to warm summer and cold to severe cold winter. Most of the crops are rainfed and their growing period is 270 days. The rainfall remains on an average range of 1600-2600 mm per annum. The soil is shallow to deep loamy, red, lateritic and yellow, with low fertility level. Depending upon the topography and locality, heterogeneous nature of soil is found. Thus there is a variation in pH, which ranges from 4.90 to 6.65.

Tropical leafy vegetables such as *Amaranthus, Spinacea, Basella, Pisum, Raphnus, Corchorus, Cucurbita, Lagenaria, Melia, Lathyrus, Chenopodium, Enhydra, Moringa, Nymphaea, Ipomoea* and ferns like *Diplazium, Pteridium* are dominantly used in plains of the region while temperate ones like *Brassica, Colocasia, Hibiscus, Sechium, Fagopyrum, Tetragonia, Tetrastigma, Lactuca, Sauropus, Houttuynia, Corydalis, Phytolacca,*

Clerodendron, Eryngium and *Sonchus* are commonly used in the region. Most of the cultivated species are grown during winter in plains; while in hills major cultivated as well as wild species grow luxuriantly in monsoon season. Species that occur in wild are generally harvested within a month of flushing.

In plains, farmyard manure is applied, in addition to application of chemical fertilizer (N:P:K) @ 40kg : 60kg : 30kg/ha respectively. In hills, normally, humus soil and FYM are applied for the cultivation. The seeds are either broadcasted or grown on raised bund or sown by dibbling method according to the requirement of the crop. Irrigation or sprinkling of water is given depending upon the availability of soil moisture. Thinning and weeding is necessary in the herbaceous cultivated vegetable for their suitable growth. In climbers/trailing species, this requirement is very less but they need trellis for proliferation. Unfavourable climatic condition develops stresses; otherwise pest and disease problem is negligible and it can be controlled at appropriate stage, through proper care. Spraying of pesticides is not advisable for leafy vegetable, which are meant for diet. Most of these leafy vegetables are harvested when the leaves and twigs are in tender stage and suitable for consumption after cooking. When the plants start flowering, leaves are hardly used.

Preference and Use

Although, there are quite a good number of leafy vegetable occuring in this region, most of them are seasonal. Species of *Amaranthus, Raphnus, Brassica, Spinacea, Basella, Cucurbita, Pisum* are preferred over others in plain while in the hills *Brassica juncea* var. *cuneifolia* is most sought for after vegetable especially in Meghalaya, Nagaland, Arunachal Pradesh and Mizoram state. This forms an important side dish as boiled vegetable along with rice and meat, during the winter. Tribals of this region are mostly non-vegetarian, but this vegetable dish is perhaps meant for to compensate the required vitamins. The leaves of *Hibiscus subdariffa* are a delicacy to Garo tribes in Meghalaya, who often use it in dry-fish curry. Similarly, the tender twigs of *Clerodendron colebrookianum* are often used by the Mizos and consumed as vegetable stew. The leaves of *Houttuynia, Sechium, Tetragonia* and *Corydalis* are used by the Khasi tribes in fish curry preparation. The hill people of Arunachal Pradesh and Meghalaya relish the apical leaves of *Sauropus androgynus.* Dried leaves of *Colocasia esculenta* are often used in meat preparation during the off-season. Introduction of *Raphnus sativus* at high altitude of Tawang district of Arunachal Pradesh a successful, where the leaves of amaranth, buckwheat, chenopods and radish are the only leafy vegetables. The bitter leaves of *Corchorus, Azadirachta, Moringa* are used in plains of Assam and Tripura during hot summer. The twigs of *Enhydra, Ipomoea* and *Nymphaea* are succulent and consumed mostly by people residing in plains for culinary purposes. The Mikir has a preference over *Olax, Casearia, Pegia* and *Meliosma* over other wild species for various food preparations. Species belonging to Urticaceae family (Table 2) are used by the various tribes of Arunachal Pradesh after necessary processing. Both plains and hill tribes equally relish leaves of *Mentha, Coriandrum* and *Eryngium* as raw, thrashed or cooked condition as flavoring agent in curries. The fern species *Pteridium* is very delicious for its young circinate fronds, which is fried and consumed with rice.

Improvement for Better Varieties

Among these discussed species, the genetic improvement work has undertaken on *Amaranthus, Brassica, Beta, Raphnus* and *Spinacea* in India. Attempt for genetic improvement on leafy vegetable species are very little. Attention was concentrated on very limited species such as cabbage (*Brassica oleracea* var. *capitata*), lettuce (*Lactuca indica*) and radish (*Raphnus sativus*). In last decade, emphasis has been given on *Amaranthus, Fagopyrum, Chenopodium, Spinacea* for their improvement and a good number of germplasm were collected and screened under the AICRP on under-utilized plants. Leaves of many improved crop group such as millet, vegetable, tuber, bulb, pulse, fiber, condiments and medicinal plants are also used but they are particularly in leafy brassicae in this region. Cultivation of dwarf *Basella rubra* is becoming popular in cultivation in Assam plains. Similarly, the introduction of *Sauropus androgynus* can be brought under cultivation due to its popular use.

Conservation

There have been meager effort on the collection and conservation of leafy vegetable in particular in this region. However, since 1986, the NBPGR Regional Station, Umiam has collected several accessions of leafy vegetables, some of which are maintained in the field gene bank at Umiam. About 470 such accessions were assembled. These are – Cucurbits (Pumpkin and Bottlegourd) – 34; *Sechium edule* – 14; Leafy brassicae – 11; Buckwheat– 30; *Chenopodium* – 9; *Amaranthus* – 37; Spinacea – 01; *Coriandrum* – 15; *Pisum* – 5; *Allium* – 3; Radish– 02; Paederia *foetida* – 01 and *Phytolocca acinosa* – 01.

Table 1. Cultivated leafy vegetables of North-east India

Species	Family	Origin, diversity and distribution	Preferred by the community/ tribe(s) of this region	Availability in the state(s) of the region
Colocasia esculenta (L.) Schott.	Araceae	SE Asia, China, Japan	All communities of the region	Throughout the region from tropical to sub-tropical zones
Xanthosoma violaceum Schott.	Araceae	South America	All communities of the region	– do –
Xanthosoma sagittifolium (L.) Schott.	Araceae	South America	All communities of the region	– do –
Basella rubra L.	Basellaceae	South Asia	Assamese, Mizo	Assam, Manipur, Mizoram, Tripura
Beta vulgaris L.	Chenopodiaceae	Mediterranean	Khasi, Naga	Meghalaya, Nagaland
Chenopodium album L.	Chenopodiaceae	Europe	Assamese	Assam plains, Tripura
Spinacea oleracea L.	Chenopodiaceae	Afghanistan, Iran, Manchuria	Assamese	– do –
Brassica juncea Hook. f. & Th.	Brassiceae	Africa	Assamese, Mizos	Assam, Mizoram, Tripura
Brassica oleracea L. var. *capitata* L.	Brassiceae	Near eastern center	All people of plains & hills	Throughout the region from plains to 8000 ft. altitude
Brassica juncea (L.) Cz. & Coss. var. *cuneifolia* Roxb.	Brassiceae	India	All hill people	Throughout the hill region
B. campestris L. var. *sarson* Prain	Brassiceae	India	Assam and Tripura people	Plains of Assam & Tripura
B. campestris L. ssp. *Chinense* (L.) Makino	Brassiceae	China	People of high hill region	Nagaland, Arunachal Pradesh, Mizoram
Raphnus sativus L.	Brassiceae	Eastern Mediterranean	All communities of the region	Throughout the region from plains 10000 ft. altitude
Amaranthus caudatus L.	Amaranthaceae	South America, Asia	People of Assam hills & plain and Meghalaya	Tropical to sub-tropical zones of the region
Amaranthus tricolor L.	Amaranthaceae	Tropical Asia	Assam plains	Plain areas of Assam, Tripura
Corchorus olitorius L.	Tiliaceae	India, Middle east & Tropical Africa	Assam plains	Plain areas of Assam, Tripura
Pisum sativum L.	Papillionaceae	Ethiopia and Yemen	Assam, Meghalaya, Manipur	Throughout the region
Lathyrus sativus L.	Papillionaceae	West Asia and Mediterranean	Assam plains	Districts of lower Assam
Benincasa hispida (Thunb.) Cogn.	Cucurbitaceae	Java (Asia)	Almost all states	Throughout the NE region
Cucurbita moschata Duch. ex Poir.	Cucurbitaceae	–	Almost all states	Throughout the NE region
Cucurbita maxima Duch. ex Lam.	Cucurbitaceae	Secondary Center – India	Almost all states	Throughout the NE region
Lagenaria siceraria (Molina) Standl.	Cucurbitaceae	Tropical Africa	Almost all states	Throughout the NE region
Sechium edule Sw.	Cucurbitaceae	Mexico, Central America	All hill states of the region	Almost all hill states above 3000 ft. altitude
Hibiscus sabdariffa L.	Malvaceae	Africa	Meghalaya	Abundantly grown in Garo Hills
Moringa oleifera Lam.	Moringaceae	India	Assam plains	Sporadic occurrence in plains of Assam
Lactuca indica L.	Asteraceae	India, Japan, Philippines and China	All hills states	Grown in kitchen garden
Allium cepa L.	Liliaceae	Asia (Central)	Tropical to sub-tropical zones	Limited cultivation in tropical areas of the region

Contd.

Contd.

Species	Family	Origin, diversity and distribution	Preferred by the community/ tribe(s) of this region	Availability in the state(s) of the region
Allium schoenoprasum L.	Liliaceae	Europe, Asia, N. America	Hills of Meghalaya, Mizoram and Nagaland	Occurrence above 4000 ft. altitude in Christian dominated states
Coriandrum sativum L.	Apiaceae	Mediterranean and West Asia	Throughout the region, irrespective of community	Tropical to sub-tropical areas of the region
Mentha arvensis L.	Lamiaceae	Europe	Hills with high rainfall area	Meghalaya, Nagaland, Mizoram, Arunachal Pradesh
Tetragonia expansa Murr.	Aizoaceae	Chinese-Japanese Center	Sub-tropical, sub-humid areas of the region	Well adapted and naturalized in Meghalaya
Fagopyrum esculentum Moench.	Polygonaceae	Central Asia	Plains to high hills of the region	Arunachal Pradesh, Meghalaya and Assam
Azadirachta indica A. Juss.	Meliaceae	South Asia	Assam plains	Sporadic occurrence in Assam plains and not in a mass cultivation or plantations

Table 2. Wild species used as leafy vegetables in North-east India

Species	Family	Origin and diversity/ distribution	Preferred by the community /tribe(s)	Availabi lity in the state(s) of the region
***Amaranthus spinosus* L.**	Amaranthaceae	America	Village & Hill people of Assam & Meghalaya	Throughout the region
Cichorium intybus L.	Asteraceae	Europe, Mediterranean	– do –	Assam, Meghalaya, Manipur, Tripura
Enhydra fluctuans Lour.	Asteraceae	India, Malayam		Meghalaya
Sonchus oleraceous L.	Asteraceae	Eurasian	Khasi	Arunachal Pradesh
Spilanthes acmella (L.) Murr.	Asteraceae	Asia & New Guinea	Bhangni	Assam and Manipur, Tripura
Ipomoea aquatica Forsk.	Convolvulaceae	Throughout the tropics	Assamese, Manipuri	Assam
Coccinia cordifolia (L.) Cogn.	Cucurbitaceae	Tropical S. Africa	People of Lower Assam dist.	Meghalaya and Arunachal Pradesh
Sauropus androgynus (L.) Merr.	Euphorbiaceae	Southeast Asia	People of Arunachal Pradesh and Meghalaya	Assam
Paederia foetidal L.	Rubiaceae	Tropical Asia	Assamese	Arunachal Pradesh
Mussaenda roxburghii Hook. f.	Rubiaceae	Palaeotropic	Arunachalis	Assam
Dentella repens (L.) Forst.	Rubiaceae	Indomalayan	Assamese	Assam
Centella asiatica (L.) Urb.	Apiaceae	Tropical Asia	Assamese, Arunachalis and Khasis	Nagaland, Meghalaya
Eryngium foetidum L.	Apiaceae	South America	All communities of Hills	Assam hills
Oenanthe javanica (Bl.) A. Dc.	Apiaceae	Indo-China to Malaya	Assamese, Mikirs	Manipur, Assam, Tripura
Nymphaea nouchali Burm.f.	Nymphaeaceae	Tropical Asia	Manipuri, Assamese	Manipur
Tetrastigma muricatum Blanch.	Vitaceae	SE Asia	Manipuris	Arunachal Pradesh

Contd.

Species	Family	Origin and diversity/ distribution	Preferred by the community /tribe(s)	Availabi lity in the state(s) of the region
Amplectrum assamicum Clarke	Melastomataceae	Hindustani	Tribes of Arunachal Pradesh	Arunachal Pradesh
Begonia palmata L.	Begoniacea	Tropical & Sub-tropical America	Tribes of Arunachal Pradesh	Khasi Hills of Meghalaya
Houttuynia cordata Thunb.	Saururaceae	Indo-China, China, Vietnam	Khasi	Mizoram
Clerodendron colebrookianum Walp.	Verbenaceae	Indo-Burma	Mizos	Meghalaya
Lippia alba (Mill.) N.E. Br. ex Britt.	Verbenaceae	Tropical Africa	Khasi	Meghalaya
Corydalis sibiricus Pers.	Fumarieaceae	Temperate Himalaya	Khasi	Mikir Hills of Assam
Olax acuminata Wall.	Olacaceae	Indomalayan	Mikirs	Manipur
Lysimachia candida Lindl.	Primulaceae	Eastern Asia	Manipuri	Mizoram
Lepionurus oblongifolius Mast.	Opiliaceae	Indochina, Java	Mizos	Mizoram
Dysoxylum procerum Hiern.	Meliaceae	Indomalayan	Mizos	Mikir Hills of Assam
Meliosma pinnata Roxb.	Sabiaceae	Warmer part of Asia	Mikirs	Khasi Hills of Meghalaya
Campanula parviflora Benth.	Campanulaceae	Mediterranean	Khasi	Khasi Hills of Meghalaya
Zanthoxylum oxyphylla (Edgn.) Engl.	Rutaceae	Subtropical East Asia	Khasi	Meghalaya and Arunachal Pradesh
Phytolacca acinosa Roxb.	Phytolaccaceae	Tropical Asia, China, Japan	Khasi, Arunachalis	Arunachal Pradesh
Rumex nepalensis Spreng.	Polygonaceae	Nepal Himalaya	Arunachalis Hills	Arunachal Pradesh
Debregeasia longifolia (Burm. f.) Wedd.	Urticaceae	Indomalayan	High hills of Arunachal Pradesh	Arunachal Pradesh
Elatostema platyphylla Wedd.	Urticaceae	Old World	High hills of Arunachal Pradesh	Arunachal Pradesh
Laportea crenulata (Roxb.) Gaud.	Urticaceae	East Asia	High hills of Arunachal Pradesh	Arunachal Pradesh
Sarcochlamys pulcherrima Gaud.	Urticaceae	Indomalayan	High hills of Arunachal Pradesh	Throughout the region
Poikilospermum suaveolens (Bl.) Merr.	Urticaceae	E. Himalayan	Most hill tribes of the region	Meghalaya, Assam, Tripura
Alocasia macrorrhiza Schott.	Araceae	Srilanka, SE Asia	Tropical areas of Assam, Meghalaya	Arunachal Pradesh
Gnetum gnemon L.	Gnetaceae	Indomalayan	Tribes of Arunachal Pradesh	Arunachal Pradesh
FERNS				
1. *Diplazium esculentum* (Retz.) Sw.	Athyriaceae	Tropical World	Hill people of Arunachal Pradesh	Arunachal Pradesh
2. *Tectaria coadunata* (Hook. & Grev.) C. Chr.	Aspidiaceae	Pan tropical	Sikkimese	Sikkim
3. *Pteridium aquilinum* Kuhn.	Dennstaedtiaceae	Northern hemisphere and Africa	Peoples of Himalayan belt and NE region	Throughout the tropical to s ubtropical zones of the region

Table 3. Nutritive value of some wild edible leafy vegetable

Species	Moisture %	Protein %	Fat %	Carbohydrate %	Mineral Matters %	Ca %	P %	Fe+ mg/100g	Fiber %	Ash % (g)	Starch	Vitamin Rich
Amaranthus spinosus	85.0	3.0	0.3	8.1	3.6	0.8	0.05	22.9	–	–	–	–
Colocasia esculenta	93.4	0.3	0.3	4.1	1.2	0.06	0.02	0.5	0.6	–	–	–
Ipomoea aquatica	90.3	2.9	0.4	4.3	2.1	0.11	0.05	3.9	–	–	–	A, B, C
Alocasia macrorrhiza	–	–	–	–	–	–	–	–	–	–	20–45%	–
Allium cepa	86.8	1.2	0.1	11.6	–	0.18	0.05	0.7	–	–	–	–
Basella rubra	–	1.2	–	–	–	0.15	–	1.4	–	–	–	A. B_1. B_2
Hibiscus sabdariffa	86.2	1.7	1.1	10.0	–	0.18	0.04	0.0054	–	–	–	–
Moringa oleifera	75.0	6.7	1.7	13.4	2.3	4.4	7.0	7.0	0.9	–	–	A and C
Paederia foetida	–	44.6%										
(dry basis)	–	–	–	–	–	–	–	–	–	C		
Pisum sativum	–	23.6	0.6	13.0	–	0.28	0.06	–	5.4	0.9	–	–
Rumex dentatus	89.3	3.5	–	4.11	–	11.5	3.8	3.4	–	2.0	–	A, C
Sauropus androgynus	73.6	6.8	–	11.6	3.4	0.57	0.2	28.0	1.4	–	–	A, C
Sechium edule	92.6	–	2.2	–	–	6.0	4.7	0.3	–	0.8	–	A
Fagopyrum esculentum	–	4.6	0.9	–	3.6	–	–	–	8.0	–	–	–
Spinacea oleracea	92.1	2.0	0.7	2.9	1.7	7.3	21	10.9	0.6 Complex	–	–	A, K and B

Besides above accession(s) of various species of *Colocasia, Xanthosoma, Sechium, Fagopyrum, Eryngium, Clerodendron* are being maintained at the station. Rapid genetic erosion among these leafy vegetables was also found as the indigenous vegetables are replaced by the introduced species. Due to change of local environment and surrounding habitat destructions, many wild species are also facing problem to survive. Tribal are the inventors of many wild species, which are edible. Attention is to be given seriously on such new plants having nutritive value, which can broaden the avenue for possible introduction and utilization extensively. According to their propagative plant parts, endeavor can be made for their conservation either in their habitat or in *ex-situ* and *in-vitro* conditions.

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Evaluation of Wild Relatives of Chickpea (*Cicer* spp.) for Resistance to Pod Borer, *Helicoverpa armigera* (Hubner)

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The legume pod borer, *Helicoverpa armigera*, is a major constraint to chickpea production worldwide. The levels of resistance in the cultivated chickpea germplasm are moderate, and therefore, we evaluated 93 accessions of annual wild relatives of chickpea in the field, and 141 accessions under greenhouse conditions for resistance to *H. armigera*. Under field conditions, 24 accessions showed a leaf feeding score of <2.0 compared to 6.0 to 6.5 of the *Cicer reticulatum* accession IG 69975. These accessions also had less than 2 eggs and/or larvae of *H. armigera* and <2 larvae of *Spodoptera exigua* per plant at the flowering/podding stages. Based on leaf feeding, larval survival, and larval weights in the detached leaf assay, 41 accessions showed low leaf feeding, reduced larval weights, and / or low larval survival. Accessions IG 69947, IG 70002, IG 70003, IG 70009, IG 70019, IG 70022, ICC 17125, IG 69979 ICC 17122, ICC 17156, IG 70006, and ICC 17187 (*C. bijugum*), IG 69995 and IG 70030 (*C. judaicum*), and IG 69988, IG 69999 IG 70021, IG 70025, and IG 70028 (*C. pinnatifidum*) showed low leaf feeding, low larval weights, and low host suitability index. These accessions can be exploited for introgressing resistance genes from the wild relatives into the cultivated chickpeas to increase the levels and diversify the basis of resistance to *H. armigera*.

Key Words: *Cicer* spp., *Helicoverpa armiger*, Host plant resistance, pod borer

Chickpea (*Cicer arietinum* L.) is one of the most important grain legumes in Asia, parts of East and North Africa, and the Mediterranean Europe. In recent years, it has gained importance in Australia, Canada, and USA. Pod borer, *Helicoverpa armigera* (Hubner), *Fusarium* wilt, *Aschochyta* blight, *Botrytis* gray mold, and drought are the major constraints limiting the production and productivity of this crop worldwide. Of these, *H. armigera* has been estimated to cause a loss of $325 million annually in the semi-arid tropics (ICRISAT 1992). Because of excessive use of insecticides to control this pest on cotton, grain legumes, vegetables and other high value crops, this pest has developed high levels of resistance to the commonly used insecticides (Kranti *et al.*, 2002). Therefore, there is a need to focus on alternative methods, including host plant resistance for integrated pest management in chickpea (Sharma, 2001). However, only low to moderate levels of resistance are available in the cultivated germplasm of chickpea (Lateef, 1985; Lateef and Sachan, 1990). Therefore, there is a need to identify wild relatives of chickpea with high levels of resistance to this pest. Some of the accessions of wild relatives of chickpea have shown high levels of resistance to cyst nematode, wilt, gray mold, leaf miner and the bruchids (Malhotra *et al.*, 2002). However, there is no information on the relative susceptibility of wild relatives of chickpea to the pod borer, *H. armigera*. Therefore, all the accessions of annual wild relatives of chickpea available at the ICRISAT genebank, were evaluated for resistance to *H. armigera* under field and greenhouse conditions.

Materials and Methods

Evaluation of wild relatives of chickpea for resistance to Helicoverpa armigera under field conditions

To evaluate the relative resistance or susceptibility of annual wild relatives of chickpea to *H. armigera*, 93 accessions were planted in the field during the 2001/02 post-rainy season at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India. However, only 51 accessions germinated or survived in the field. Of these, 20 accessions belonged to *Cicer bijugum*, 1 to *C. cuneatum*, 2 to *C. judaicum*, 11 to *C. pinnatifidum*, 16 to *C. reticulatum*, and 1 to *C. yamashitae*. Three chickpea cultivars (ICC 506 EB – moderately resistant; ICCV 2 – susceptible Kabuli type, and Annigeri - local check) were included as controls. During the 2002/03 post-rainy season, 93 accessions were planted in the field. Out of the 92 accessions that germinated, 23 accessions belonged to *C. bijugum*, 2 to *C. cuneatum*, 23 to *C. judaicum*, 14 to *C. pinnatifidum*, 25 to *C. reticulatum*, 3 to *C. yamashitae*, 1 to *C. chorassanicum* and 1 to

C. echinospermum. Each entry was sown in a one-row plot, 2-m long, and there were five plants in each row. There were two replications in a randomized complete block design. The seeds of the wild relatives were scarified at one end with a sharp knife, soaked in water for 24 h, and treated with thiram (3 g per kg of seed) before sowing to enhance water absorption and faster germination. The seeds of cultivated chickpeas were sown without scarification. The trial was planted on ridges 60-cm apart on deep black soils (Vertisols). The seeds were sown in hills at a spacing of 50-cm between the hills at a depth of 5-cm below the soil surface. Normal agronomic practices were followed for raising the crop (basal fertilizer N: P: K :: 50: 60: 40 kg ha^{-1}). Interculture and weeding operations were carried out as needed. The field was irrigated immediately after sowing, and at intervals of one month thereafter. At the flowering stage, data were recorded on eggs and larvae per 5 plants and leaf damage on a 1 to 9 scale (1 = <10% leaf area damaged, and 9 = >80% leaf area damaged).

Evaluation of Wild Relatives of Chickpea for Resistance to H. armigera under Greenhouse Conditions

During the 2002 postrainy season, 141 accessions of annual chickpea wild relatives, along with three cultivated chickpea genotypes (ICC 506 – moderately resistant, ICCV 10 commercial check, and Annigeri – susceptible local landrace) were evaluated for resistance to *H. armigera* under no-choice conditions using the detached leaf assay (Sharma *et al.*, 2002b). The plants were grown in plastic pots (30-cm diameter, 30-cm deep) in the greenhouse. The pots were filled with a potting mixture of black soil (Vertisols), sand, and farmyard manure (2: 1: 1). The seeds were scarified at one end, treated with thiram (3 g per kg of seed) and placed in a Petri dish containing agar-agar (0.5%) for germination. After germination, the plants were transplanted into the soil and watered immediately. One seedling was transplanted in each pot, and the plants were watered as needed. There were five plants for each accession. The pots were arranged in a completely randomized design. The greenhouse was cooled by desert coolers to maintain the temperature at 27 ± 5°C, and relative humidity >65%. Additional lighting was provided (14 h photoperiod) to induce flowering and pod formation.

Detached Leaf Assay

The accessions grown under field and/or greenhouse conditions were tested for resistance to *H. armigera* at the vegetative stage (50 days after germination) using the detached leaf assay. Terminal branches (2 to 3 fully expanded leaves and a bud) of chickpea seedlings were used to measure genotypic resistance to *H. armigera* (Sharma *et al.*, 2002b). The chickpea branches were cut with scissors, and immediately planted in a slanting manner into 3% agar-agar medium in a 250 ml plastic cup. There were five replications for each accession in a completely randomized design. Ten neonate larvae of *H. armigera* raised in the laboratory (Sharma *et al.*, 2001) were released on the chickpea leaves with a camel hairbrush. The cups were kept in the laboratory at 27±2° C, and 45 to 75% relative humidity. Observations were recorded 5 days after releasing the larvae on the leaves, when the differences between the resistant and susceptible checks were maximum. First, the plants were scored for leaf feeding on a 1 to 9 scale (1 = <10% leaf area damaged, and 9 = >80% leaf area damaged). The number of larvae surviving after the feeding period were recorded, and placed in 25 ml plastic cups. The weights of larvae were recorded 4 h after separating them from the food. The data were expressed as percentage larval survival and mean weight of the larvae. Data on leaf damage rating, larval survival and larval weights were used to compute host suitability index (resistance index) for each accession.

Resistance (host suitability) index = Larval weight/ damage rating x larval survival) (low values indicating high levels of resistance, and high values denoting low resistance/high susceptibility).

Statistical Analysis

Data were subjected to analysis of variance using GENSTAT release 5.0. The significance of differences between the treatments was measured by *F*-test at *P* 0.05. The treatment means were compared using least significant difference (LSD) at $P \leq 0.05$.

Results

Reaction of different accessions of wild relatives of chickpea to Helicoverpa armigera under field conditions

Under field conditions, 24 accessions showed a leaf damage rating of <2.0 compared to 6.0 to 6.5 of the *Cicer reticulatum* accession IG 69975 (Table 1). These accessions also had less than 2 eggs and larvae of *H. armigera* and *S. exigua* per plant at the flowering stage. High egg and larval numbers were recorded on IG 69975, IG 70020, IG 72937, IG 72942, IG 72938, IG 72944,

Table 1. Screening of wild chickpea accessions for *Helicoverpa armigera* in the field (ICRISAT, Patancheru, 2002/03 post-rainy season)

Accession	Alternate accession identifier	Species	Damage rating*		*Helicoverpa armigera* Eggs + larvae per plant	*Spodoptera exigua* Larvae per plant
			2001/02	2002/03		
IG 69942	ILWC 3	*C. yamashitae*	*	2.3	1.0	1.7
IG 69946	ILWC 7	*C. bijugum*	3.0	4.0	4.0	5.0
IG 69947	ILWC 8	*C. bijugum*	5.4	3.0	3.0	1.7
IG 69959	ILWC 20	*C. judaicum*	*	1.0	0.0	1.0
IG 69960	ILWC 21	*C. reticulatum*	6.0	2.3	3.0	1.0
IG 69968	ILWC 29	*C. pinnatifidum*	1.1	2.0	1.0	0.0
IG 69969	ILWC 30	*C. judaicum*	*	1.3	2.0	0.0
IG 69970	ILWC 31	*C. judaicum*	*	2.0	1.0	0.0
IG 69972	ILWC 33	*C. pinnatifidum*	1.5	–	*	*
IG 69974	ILWC 35	*C. echinospermum*	*	2.0	2.3	1.0
IG 69975	ILWC 36	*C. reticulatum*	6.5	6.0	8.0	0.0
IG 69976	ILWC 37	*C. cuneatum*	*	1.5	3.0	1.0
IG 69977	ILWC 38	*C. judaicum*	*	1.0	0.0	0.0
IG 69979	ILWC 40	*C. cuneatum*	1.0	1.0	0.0	1.0
IG 69980	ILWC 41	*C. judaicum*	*	1.0	2.0	0.0
IG 69981	ILWC 42	*C. bijugum*	*	3.3	3.7	2.5
IG 69982	ILWC 43	*C. judaicum*	*	1.3	3.0	1.0
IG 69986	ILWC 47	*C. judaicum*	*	3.0	2.0	0.0
IG 69987	ILWC 48	*C. judaicum*	*	1.0	5.3	1.0
IG 69988	ILWC 49	*C. pinnatifidum*	2.0	3.3	0.0	1.5
IG 69989	ILWC 50	*C. judaicum*	*	2.0	0.0	0.0
IG 69990	ILWC 51	*C. pinnatifidum*	1.0	3.3	0.0	1.0
IG 69992	ILWC 53	*C. yamashitae*	*	3.3	2.7	1.5
IG 69993	ILWC 54	*C. judaicum*	*	4.0	3.0	1.0
IG 69994	ILWC 55	*C. yamashitae*	0.4	2.0	4.0	2.0
IG 69995	ILWC 56	*C. judaicum*	*	1.0	2.0	1.0
IG 69996	ILWC 57	*C. judaicum*	*	1.5	1.0	0.0
IG 69997	ILWC 58	*C. judaicum*	*	2.0	0.0	3.0
IG 69998	ILWC 59	*C. judaicum*	*	3.5	1.0	0.0
IG 69999	ILWC 60	*C. pinnatifidum*	*	2.3	3.0	1.5
IG 70000	ILWC 61	*C. judaicum*	*	1.0	1.0	1.0
IG 70001	ILWC 62	*C. bijugum*	*	2.7	5.0	2.0
IG 70002	ILWC 63	*C. bijugum*	2.5	2.7	5.7	2.7
IG 70003	ILWC 64	*C. bijugum*	2.5	2.7	2.0	3.3
IG 70004	ILWC 65	*C. bijugum*	2.5	3.0	12.0	2.0
IG 70005	ILWC 66	*C. bijugum*	4.1	2.5	3.0	0.0
IG 70006	ILWC 67	*C. bijugum*	3.5	3.3	4.0	2.7
IG 70007	ILWC 68	*C. bijugum*	3.0	3.0	5.0	2.0
IG 70008	ILWC 69	*C. bijugum*	2.5	3.5	3.0	1.0
IG 70009	ILWC 70	*C. bijugum*	3.5	3.3	4.0	1.0
IG 70010	ILWC 71	*C. bijugum*	3.0	2.3	5.0	1.5
IG 70011	ILWC 72	*C. bijugum*	4.5	3.0	0.0	2.5
IG 70012	ILWC 73	*C. bijugum*	4.1	2.7	5.0	4.5
IG 70013	ILWC 74	*C. bijugum*	3.5	2.7	7.5	2.0
IG 70014	ILWC 75	*C. bijugum*	3.1	2.7	3.0	3.7
IG 70015	ILWC 76	*C. bijugum*	2.5	3.0	5.0	2.0
IG 70016	ILWC 77	*C. bijugum*	2.4	2.7	6.0	3.5

Accession	Alternate accession identifier	Species	Damage rating*		*Helicoverpa armigera* Eggs + larvae per plant	*Spodoptera exigua* Larvae per plant
			2001/02	2002/03		
IG 70017	ILWC 78	*C. pinnatifidum*	0.9	2.0	0.0	2.0
IG 70018	ILWC 79	*C. bijugum*	5.0	2.7	2.5	2.3
IG 70019	ILWC 80	*C. bijugum*	3.5	3.0	1.5	2.0
IG 70020	ILWC 81	*C. reticulatum*	4.0	2.3	12.0	17.0
IG 70021	ILWC 82	*C. pinnatifidum*	*	2.0	0.0	2.0
IG 70022	ILWC 83	*C. bijugum*	*	3.0	1.5	1.0
IG 70023	ILWC 84	*C. bijugum*	3.5	3.3	10.0	3.0
IG 70024	ILWC 85	*C. pinnatifidum*	1.9	2.0	1.0	3.0
IG 70025	ILWC 86	*C. pinnatifidum*	1.5	1.5	2.0	1.0
IG 70026	ILWC 87	*C. pinnatifidum*	1.0	1.3	2.0	1.0
IG 70027	ILWC 88	*C. pinnatifidum*	*	2.7	0.0	0.0
IG 70028	ILWC 89	*C. pinnatifidum*	1.1	2.3	1.5	1.5
IG 70029	ILWC 90	*C. chorassanicum*	*	2.0	0.0	1.0
IG 70032	ILWC 93	*C. judaicum*	0.4	1.3	3.0	0.0
IG 70033	ILWC 94	*C. judaicum*	*	1.0	5.0	0.0
IG 70034	ILWC 95	*C. judaicum*	*	2.0	1.5	2.0
IG 70035	ILWC 96	*C. pinnatifidum*	*	2.0	1.5	0.0
IG 70036	ILWC 97	*C. pinnatifidum*	1.1	2.0	1.0	1.5
IG 70037	ILWC 98	*C. judaicum*	*	1.3	1.0	0.0
IG 70038	ILWC 99	*C. judaicum*	*	1.0	2.0	2.0
IG 70039	ILWC 100	*C. pinnatifidum*	*	3.0	3.5	0.0
IG 72930	ILWC 101	*C. judaicum*	*	1.0	5.0	1.0
IG 72931	ILWC 102	*C. judaicum*	1.4	1.5	6.5	1.0
IG 72932	ILWC 103	*C. judaicum*	*	1.3	1.0	2.0
IG 72933	ILWC 104	*C. reticulatum*	*	2.3	1.7	2.0
IG 72934	ILWC 105	*C. reticulatum*	*	2.0	2.0	1.0
IG 72935	ILWC 106	*C. reticulatum*	*	2.0	4.0	1.0
IG 72936	ILWC 107	*C. reticulatum*	*	3.0	2.5	1.0
IG 72937	ILWC 108	*C. reticulatum*	3.0	2.0	11.0	33.0
IG 72938	ILWC 109	*C. reticulatum*	*	2.7	5.3	0.0
IG 72939	ILWC 110	*C. reticulatum*	*	3.0	3.5	2.0
IG 72940	ILWC 111	*C. reticulatum*	3.5	2.0	3.7	2.0
IG 72941	ILWC 112	*C. reticulatum*	4.5	2.3	1.3	1.5
IG 72942	ILWC 113	*C. reticulatum*	5.5	2.0	5.7	1.0
IG 72943	ILWC 114	*C. reticulatum*	*	2.7	2.5	2.0
IG 72944	ILWC 115	*C. reticulatum*	4.0	2.7	9.5	2.0
IG 72945	ILWC 116	*C. reticulatum*	4.0	2.5	1.5	0.0
IG 72946	ILWC 117	*C. reticulatum*	5.5	1.0	7.0	1.0
IG 72948	ILWC 119	*C. reticulatum*	*	2.3	3.7	6.0
IG 72949	ILWC 120	*C. reticulatum*	7.0	3.3	3.0	2.0
IG 72951	ILWC 122	*C. reticulatum*	3.5	3.3	2.0	4.0
IG 72952	ILWC 123	*C. reticulatum*	6.0	2.7	3.3	5.7
IG 72953	ILWC 124	*C. reticulatum*	5.5	2.0	3.0	1.5
IG 72955	ILWC 126	*C. reticulatum*	5.1	3.0	1.0	2.0
IG 72958	ILWC 129	*C. reticulatum*	*	3.0	7.0	1.0
IG 72959	ILWC 130	*C. reticulatum*	4.5	2.0	2.0	2.0
Mean				2.3	3.1	2.0
SE				±0.73	±2.84	±2.29

* Damage rating (1 = <10% leaf area damaged, and 9 >80% leaf area damaged).

IG 72946 and IG 72958 (*C. reticulatum*), IG 69987, IG 70033 and IG 72930, (*C. judaicum*), and IG 7004, IG 70007, IG 70010, IG 70012, IG 70013, IG 70015, IG 70016 and IG 70023 (*C. bijugum*). Since cultivated chickpeas matured much earlier than the wild relatives, no data were recorded on them for comparison with the wild relatives.

Reaction of wild relatives of chickpea grown under field conditions for resistance to neonate larvae of H. armigera–detached leaf assay

In the plants grown under field conditions, leaf damage rating varied from 2.4 in ICC 506 to 9.0 in IG 69968, and five accessions showed a leaf damage rating of <5.0, compared to 2.4 and 3.0 in ICC 506, and 5.5 and 6.2 in Annigeri in the first and second experiments, respectively (Table 2). The larval weights varied from 1.20 to 6.59 mg in the first experiment, and 1.47 to 6.07 mg in the second experiment. The larval weights of *H. armigera* were less than half on IG 69947, IG 70002, IG 70006, IG 70009, IG 70010, IG 70013, and IG 70016 (*C. bijugum*), IG 69979 (*C. cuneatum*), and IG 70017 (*C. pinnatifidum*) as compared to larval weights on the cultivated chickpea, ICCC 37 (first experiment) or ICCV 2 (second experiment). The larval survival varied from 52 to 95% in the first experiment, and 70 to 98% in the second experiment. Based on resistance index, accessions IG 69947, IG 70006, IG 70016, IG 70003, and IG 70008 (*C. bijugum*), IG 69979 (*C. cuneatum*), and IG 70025, IG 70028, IG 70036, and IG 70017 (*C. pinnatifidum*) showed evidence for high levels of resistance to *H. armigera*. The leaf damage ratings in general were greater in the detached leaf assay than those observed under natural field conditions. It may be because of low levels of infestation in the field, and/or existence of oviposition non-preference as one of the components of resistance to *H. armigera*.

Reaction of wild relatives of chickpea grown under greenhouse conditions for resistance to H. armigera

The accessions were tested in five sets of 30-35 accessions, along with the resistant and susceptible checks of the cultivated chickpeas to maintain precision and timely observations (Table 3). In the first experiment, the leaf feeding scores ranged from 3.8 in IG 69947 to 9.0 in IG 70031, IG 70021 and IG 70035 in the wild relatives, compared to 6.6 in ICCC 37 and 5.0 in Annigeri (Table 3). The larval weights were <1.50 mg on 16 accessions of the wild relatives compared to 2.45 mg on ICCV 10 (moderately resistant check) and 4.23 mg on ICCC 37 (susceptible check). The resistance index of these genotypes was <1.5 compared to 2.93 of ICCV 10 and 6.28 of ICCC 37. Larval survival ranged from 54% on IG 69990 to 98% on ICCC 37. Accessions IG 69947 and IG 70002 (*C. bijugum*), and IG 69988 (*C. pinnatifidum*) showed low leaf feeding, low larval weights, and low host suitability index.

In the second experiment, 10 accessions showed leaf damage rating of <5.2 compared to 7.6 in ICC 506, and 8.8 in ICCV 10. The larval weights on these accessions were <1.34 mg compared to 2.63 mg on ICC 506, and 3.39 mg on ICCV 10. Larval survival was 56 to 68% on 7 accessions of the wild relatives compared to 72% on ICC 506 and ICCV 10, and 82% on Annigeri. Accessions IG 70003 (*C. bijugum*), IG 69995 and IG 70030 (*C. judaicum*), IG 69999 IG 70021, IG 70025, and IG 70028 (*C. pinnatifidum*) showed high resistance (resistance index <1.5 compared to 2.43 of Annigeri, and 2.49 of ICC 506).

In the third experiment, five accessions showed leaf-feeding scores of <5.0 compared to 9.0 in ICC 506 and 8.5 on Annigeri. Larval weights were <1.5 mg on 13 accessions compared to 3.93 mg on ICC 506 and ICCC 37, and 5.61 mg on Annigeri. Larval survival was <60% on eight accessions compared to 90% on IG 69994, 76% on ICC 506, and 88% on Annigeri. Accessions IG 70009, IG 70019, and IG 70022, (*C. bijugum*) showed evidence for low leaf feeding and reduced larval weights. Host suitability index was poor (<1.47 compared to 3.32 on ICC 506 and 5.78 on Annigeri) on 12 accessions, of which IG 70009, IG 70019, and IG 70022 (*C. bijugum*) suffered low leaf damage, and the larval weights and larval survival were also very low.

In the fourth experiment, ICC 17125, IG 69979, ICC 17198, and ICC 17211 showed leaf damage rating of <5.4 compared to 8.5 on Annigeri. Larval weights were <1.5 mg on 19 accessions, as compared to 5.61 on Annigeri. Thirteen accessions showed poor host suitability index (<1.55 compared to 3.32 of ICC 506 and 5.78 of Annigeri), of which ICC 17125 and IG 69979 (*C. bijugum*) also showed evidence for low leaf feeding and low larval weights.

In the fifth experiment, leaf-feeding scores ranged from 4.6 on ICC 17122 to 9.0 on ICC 17212, ICC 17126, ICC 17152, ICC 17153, ICC 17155, and ICC 17209 as compared to 5.4 on ICC 506 and 8.8 on ICCC 37.

Table 2. Relative susceptibility of wild relatives of chickpea grown under field conditions to *Helicoverpa armigera* – detached leaf assay (ICRISAT, Patancheru, India 2002 post-rainy season)

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
I^st^ experiment					
IG 69946	*C. bijugum*	5.8	2.13	86	3.16
IG 69947	*C. bijugum*	7.8	1.51	68	1.32
IG 70002	*C. bijugum*	6.2	1.78	86	2.47
IG 70006	*C. bijugum*	4.4	1.20	56	1.53
IG 70007	*C. bijugum*	6.6	2.36	88	3.15
IG 70009	*C. bijugum*	4.8	1.72	88	3.15
IG 70010	*C. bijugum*	6.8	1.74	92	2.35
IG 70011	*C. bijugum*	7.0	1.94	90	2.49
IG 70013	*C. bijugum*	5.2	1.86	88	3.15
IG 70016	*C. bijugum*	5.8	1.66	82	2.35
IG 70018	*C. bijugum*	4.2	2.03	92	4.45
IG 70023	*C. bijugum*	6.6	1.94	98	2.88
IG 69979	*C. cuneatum*	5.8	1.62	72	2.01
IG 72931	*C. judaicum*	7.4	2.31	88	2.75
IG 70032	*C. judaicum*	7.8	2.61	70	2.34
IG 70025	*C. pinnatifidum*	8.8	2.93	52	1.73
IG 69975	*C. reticulatum*	4.4	3.65	76	6.30
IG 72937	*C. reticulatum*	5.9	4.85	82	6.74
IG 72941	*C. reticulatum*	6.4	2.88	68	3.06
IG 72944	*C. reticulatum*	5.6	6.59	90	10.59
IG 72946	*C. reticulatum*	5.0	5.00	92	9.20
IG 72949	*C. reticulatum*	6.4	3.74	92	5.38
IG 72951	*C. reticulatum*	5.4	4.83	86	7.69
IG 72953	*C. reticulatum*	7.2	3.89	78	4.21
IG 72959	*C. reticulatum*	7.2	4.76	86	5.69
IG 69994	*C. yamashitae*	8.5	3.85	95	4.30
Cultivated chickpea					
ICC 506 EB	*C. arietinum*	2.4	3.27	72	9.81
ICCC 37	*C. arietinum*	2.8	3.82	62	8.46
Annigeri	*C. arietinum*	5.5	3.74	69	4.69
SE		±0.56	±0.33	±7.14	
LSD		2.13	1.21	19.7	

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
II^nd^ Experiment					
IG 70003	*C. bijugum*	4.2	2.92	92	6.40
IG 70004	*C. bijugum*	8.0	2.80	96	3.36
IG 70005	*C. bijugum*	8.8	3.54	84	3.38
IG 70008	*C. bijugum*	6.2	3.06	86	4.24
IG 70012	*C. bijugum*	5.8	2.73	94	4.42
IG 70014	*C. bijugum*	7.0	3.26	98	4.56
IG 70015	*C. bijugum*	7.8	3.33	98	4.18
IG 70019	*C. bijugum*	8.0	2.45	78	2.39
IG 69961	*C. pinnatifidum*	8.6	2.22	88	2.27
IG 69968	*C. pinnatifidum*	9.0	3.57	88	3.49
IG 69972	*C. pinnatifidum*	8.8	3.14	74	2.64
IG 69988	*C. pinnatifidum*	8.8	4.06	92	4.24
IG 69990	*C. pinnatifidum*	8.8	3.14	86	3.07
IG 70017	*C. pinnatifidum*	9.0	1.47	76	1.24
IG 70024	*C. pinnatifidum*	8.8	3.70	92	3.87
IG 70026	*C. pinnatifidum*	8.4	4.08	94	4.57
IG 70028	*C. pinnatifidum*	7.2	3.94	80	4.38
IG 70036	*C. pinnatifidum*	7.6	3.01	84	3.33
IG 69960	*C. reticulatum*	7.6	5.21	90	6.17
IG 70020	*C. reticulatum*	5.5	4.90	96	8.55
IG 72940	*C. reticulatum*	6.8	4.55	88	5.89
IG 72942	*C. reticulatum*	7.6	4.50	94	5.57
IG 72945	*C. reticulatum*	8.4	5.66	94	6.33
IG 72952	*C. reticulatum*	8.2	6.07	84	6.22
IG 72955	*C. reticulatum*	7.6	5.42	90	6.42
Cultivated chickpea					
ICC 506	*C. arietinum*	3.0	2.40	70	5.60
ICCV 2	*C. arietinum*	4.3	4.06	74	6.99
Annigeri	*C. arietinum*	6.2	2.37	80	3.06
SE		±1.20	±0.93	±15.64	
LSD		16.4	25.6	17.9	

*Damage rating (1 = <10% leaf area consumed, and 9 = >80% leaf area consumed).

Table 3. Relative susceptibility of wild relatives of chickpea grown under greenhouse conditions to *Helicoverpa armigera* – detached leaf assay (ICRISAT, Patancheru, India 2002)

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
I^st^ experiment					
IG 69947	*C. bijugum*	3.8	0.72	78	1.48
IG 69981	*C. bijugum*	6.0	1.02	86	1.46
IG 70002	*C. bijugum*	5.2	1.07	86	1.77
IG 70009	*C. bijugum*	8.4	1.13	90	1.21
IG 69976	*C. cuneatum*	6.8	1.54	70	1.59

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
IG 69943	*C. judaicum*	7.6	1.75	84	1.93
IG 69980	*C. judaicum*	7.0	1.80	82	2.11
IG 69982	*C. judaicum*	7.8	1.83	80	1.88
IG 69948	*C. pinnatifidum*	8.2	1.32	76	1.22
IG 69968	*C. pinnatifidum*	8.6	1.20	68	0.95
IG 69972	*C. pinnatifidum*	8.6	0.98	70	0.80

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
IG 69988	*C. pinnatifidum*	5.4	1.64	90	2.73
IG 69990	*C. pinnatifidum*	8.8	1.98	54	1.22
IG 69999	*C. pinnatifidum*	8.8	0.75	66	0.56
IG 70021	*C. pinnatifidum*	9.0	1.04	74	0.86
IG 70026	*C. pinnatifidum*	8.0	1.45	62	1.12
IG 70027	*C. pinnatifidum*	8.4	1.08	76	0.98
IG 70031	*C. pinnatifidum*	9.0	1.12	58	0.72
IG 70035	*C. pinnatifidum*	9.0	0.94	70	0.73
IG 69960	*C. reticulatum*	6.2	1.26	80	1.63
IG 69975	*C. reticulatum*	6.2	1.60	68	1.75
IG 72933	*C. reticulatum*	6.4	1.33	72	1.50
IG 72934	*C. reticulatum*	7.4	1.76	72	1.71
IG 72941	*C. reticulatum*	7.7	1.75	62	1.41
IG 72942	*C. reticulatum*	7.2	1.92	72	1.92
IG 72943	*C. reticulatum*	8.0	1.40	74	1.30
IG 72949	*C. reticulatum*	8.2	2.19	80	2.14
IG 69942	*C. yamashitae*	8.4	2.32	78	2.15
IG 69992	*C. yamashitae*	8.2	1.51	74	1.36
Cultivated chickpea					
Annigeri	*C. arietinum*	5.0	3.83	86	6.59
ICCV 10	*C. arietinum*	7.2	2.45	86	2.93
ICCC 37	*C. arietinum*	6.6	4.23	98	6.28
SE		±1.30	±0.45	±6.61	
LSD at 5%		2.14	0.75	18.5	
II[nd] experiment					
IG 70003	*C. bijugum*	2.8	0.57	72	1.47
IG 70004	*C. bijugum*	3.8	1.15	78	2.36
IG 70007	*C. bijugum*	4.0	1.13	64	1.81
IG 70008	*C. bijugum*	5.0	1.2	80	1.92
IG 70010	*C. bijugum*	4.4	1.30	76	2.25
IG 69995	*C. judaicum*	7.8	1.39	78	1.39
IG 69998	*C. judaicum*	5.4	2.18	62	2.50
IG 70000	*C. judaicum*	3.8	1.33	78	2.73
IG 70030	*C. judaicum*	6.4	0.99	86	1.33
IG 70034	*C. judaicum*	7.0	1.62	82	1.90
IG 69999	*C. pinnatifidum*	7.8	0.92	56	0.66
IG 70021	*C. pinnatifidum*	8.2	1.32	66	1.06
IG 70025	*C. pinnatifidum*	8.2	1.51	64	1.18
IG 70028	*C. pinnatifidum*	7.2	0.89	70	0.87
IG 72936	*C. reticulatum*	4.2	1.34	74	2.36
IG 72937	*C. reticulatum*	3.0	0.90	82	2.46
IG 72939	*C. reticulatum*	6.4	1.95	70	2.13
IG 72944	*C. reticulatum*	5.6	2.16	66	2.55
IG 72945	*C. reticulatum*	6.2	2.32	72	2.69
IG 72952	*C. reticulatum*	5.4	1.97	80	2.92
IG 72953	*C. reticulatum*	5.0	1.31	68	1.78
IG 72955	*C. reticulatum*	6.0	1.68	84	2.35
IG 72958	*C. reticulatum*	5.0	1.22	80	1.95
IG 72959	*C. reticulatum*	5.2	1.24	80	1.91

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
Cultivated chickpea					
ICC 506	*C. arietinum*	7.6	2.63	72	2.49
ICCV 10	*C. arietinum*	8.8	3.39	72	2.77
Annigeri	*C. arietinum*	7.8	2.31	82	2.43
SE		±1.2	±0.81	±14.28	
LSD at 5%		1.9	1.34	23.65	
III[rd] experiment					
IG 69946	*C. bijugum*	5.4	0.99	74	1.36
IG 70009	*C. bijugum*	3.8	0.69	70	1.27
IG 70011	*C. bijugum*	6.2	1.20	74	1.43
IG 70012	*C. bijugum*	4.6	1.07	74	1.72
IG 70013	*C. bijugum*	6.2	1.25	72	1.45
IG 70014	*C. bijugum*	5.2	1.22	84	1.97
IG 70015	*C. bijugum*	5.0	1.49	66	1.97
IG 70018	*C. bijugum*	5.6	1.37	78	1.91
IG 70019	*C. bijugum*	4.2	0.89	50	1.06
IG 70022	*C. bijugum*	4.4	0.63	52	0.74
IG 70023	*C. bijugum*	5.6	2.61	52	2.42
IG 70029	*C. chorassanicum*	8.6	1.45	52	0.88
IG 69974	*C. echinospermum*	8.2	2.41	78	2.29
IG 69970	*C. judaicum*	7.0	1.69	70	1.69
IG 69977	*C. judaicum*	7.4	3.13	54	2.28
IG 69987	*C. judaicum*	7.8	1.63	78	1.63
IG 70032	*C. judaicum*	6.4	1.74	70	1.90
IG 70033	*C. judaicum*	7.6	1.54	76	1.54
IG 70038	*C. judaicum*	8.2	1.63	74	1.47
IG 69961	*C. pinnatifidum*	7.8	1.33	60	1.02
IG 70024	*C. pinnatifidum*	8.4	1.63	62	1.20
IG 70036	*C. pinnatifidum*	8.8	1.85	50	1.05
IG 70039	*C. pinnatifidum*	8.2	1.13	54	0.74
IG 70020	*C. reticulatum*	7.6	2.00	80	2.11
IG 72940	*C. reticulatum*	7.2	1.76	74	1.81
IG 69994	*C. yamashitae*	7.8	1.81	90	2.09
Cultivated chickpea					
ICC 506	*C. arietinum*	9.0	3.93	76	3.32
ICCC 37	*C. arietinum*	7.6	3.93	68	3.52
Annigeri	*C. arietinum*	8.5	5.61	87.5	5.78
SE		±1.10	±0.55	±14.89	
LSD at 5%		1.83	0.92	24.72	
IV[th] experiment					
ICC 17125	*C. bijugum*	5.0	0.97	80	1.55
IG 69979	*C. cuneatum*	5.2	1.25	76	1.83
ICC 17148	*C. judaicum*	7.1	1.08	78	1.19
ICC 17149	*C. judaicum*	6.0	1.35	80	1.80
ICC 17150	*C. judaicum*	6.2	1.40	68	1.54
ICC 17191	*C. judaicum*	8.4	1.39	82	1.36
ICC 17192	*C. judaicum*	7.6	1.58	96	2.00
ICC 17193	*C. judaicum*	6.2	1.25	60	1.21

Accession	Species	Damage rating*	Larval weight (mg)	Larval survival (%)	Resistance index
ICC 17195	*C. judaicum*	7.4	1.18	92	1.47
ICC 17197	*C. judaicum*	5.6	1.05	80	1.50
ICC 17198	*C. judaicum*	5.4	1.57	78	2.27
ICC 17199	*C. judaicum*	7.8	1.90	72	1.75
ICC 17204	*C. judaicum*	8.0	1.15	76	1.09
ICC 17205	*C. judaicum*	6.6	1.17	82	1.45
ICC 17208	*C. judaicum*	8.0	1.49	86	1.60
ICC 17211	*C. judaicum*	4.4	1.18	86	2.31
IG 70032	*C. judaicum*	7.2	1.20	70	1.17
IG 70033	*C. judaicum*	6.4	1.50	62	1.45
IG 70034	*C. judaicum*	7.4	1.38	66	1.23
IG 70038	*C. judaicum*	7.0	1.01	64	0.92
IG 72931	*C. judaicum*	7.4	0.88	76	0.90
ICC 17200	*C. pinnatifidum*	8.4	2.05	68	1.66
ICC 17201	*C. pinnatifidum*	6.4	2.23	82	2.86
ICC 17203	*C. pinnatifidum*	8.4	2.07	68	1.68
ICC 17121	*C. reticulatum*	7.0	2.07	82	2.42
ICC 17123	*C. reticulatum*	7.8	3.26	56	2.34
ICC 17124	*C. reticulatum*	7.0	2.09	66	1.97
ICC 17163	*C. reticulatum*	5.8	1.94	84	2.81
ICC 17117	*C. yamashitae*	8.2	1.49	86	1.56
Cultivated chickpea					
ICC 506	*C. arietinum*	9.0	3.93	76	3.32
ICCC 37	*C. arietinum*	7.6	3.93	68	3.52
Annigeri	*C. arietinum*	8.5	5.61	88	5.78
SE		±1.28	±0.06	±15.23	
LSD at 5%		2.11	1.05	25.2	
Vth experiment					
ICC 17122	*C. bijugum*	4.6	0.77	90	1.51
ICC 17156	*C. bijugum*	4.8	1.32	82	2.26
ICC 17157	*C. bijugum*	8.4	2.58	82	2.52
ICC 17187	*C. bijugum*	5.4	1.01	86	1.61
IG 70001	*C. bijugum*	8.6	1.17	86	1.17
IG 70005	*C. bijugum*	6.6	1.16	90	1.58
IG 70006	*C. bijugum*	5.4	1.00	92	1.70
IG 70016	*C. bijugum*	7.0	0.82	84	0.98
ICC 17162	*C. cuneatum*	8.0	1.28	88	1.41
ICC 17151	*C. judaicum*	8.8	2.25	70	1.79
ICC 17188	*C. judaicum*	8.0	1.48	66	1.22
ICC 17189	*C. judaicum*	8.6	2.08	80	1.93
ICC 17190	*C. judaicum*	8.8	1.92	76	1.66
ICC 17194	*C. judaicum*	8.8	1.66	70	1.32
ICC 17196	*C. judaicum*	8.4	1.92	72	1.65
ICC 17207	*C. judaicum*	8.6	1.67	88	1.71
ICC 17212	*C. judaicum*	9.0	1.93	80	1.72
IG 69959	*C. judaicum*	8.8	2.12	90	2.17
IG 69969	*C. judaicum*	8.8	2.82	86	2.76
IG 72932	*C. judaicum*	8.8	1.85	78	1.64
ICC 17126	*C. pinnatifidum*	9.0	2.10	76	1.77
ICC 17152	*C. pinnatifidum*	9.0	1.48	90	1.48
ICC 17153	*C. pinnatifidum*	9.0	1.46	82	1.33
ICC 17155	*C. pinnatifidum*	9.0	1.94	86	1.85
ICC 17209	*C. pinnatifidum*	9.0	2.72	78	2.36
ICC 17210	*C. pinnatifidum*	8.6	1.55	80	1.44
IG 70039	*C. pinnatifidum*	8.6	1.60	84	1.56
ICC 17160	*C. reticulatum*	7.2	1.50	94	1.96
IG 70037	*C. reticulatum*	8.6	1.99	90	2.08
IG 72943	*C. reticulatum*	8.2	1.67	94	1.91
IG 72951	*C. reticulatum*	8	2.81	82	2.88
IG 72964	*C. reticulatum*	8.4	2.88	82	2.81
ICC 17116	*C. yamashitae*	8.6	2.75	82	2.62
Cultivated chickpea					
Annigeri	*C. arietinum*	8.4	5.83	82	5.69
ICC 506E	*C. arietinum*	5.4	4.12	90	6.87
ICCC 37	*C. arietinum*	8.8	6.25	92	6.53
SE		±0.95	±0.75	±13.29	
LSD at 5%		1.06	1.25	21.94	

*Damage rating (1 = <10% leaf area consumed, and 9 = >80% leaf area consumed).

Larval weights were <1.5 mg on 13 accessions of the wild relatives compared to 4.1 mg on ICC 506 and 5.83 mg on Annigeri. Larval survival ranged from 66% on ICC 17188 to 92% on ICCC 37 as compared to 90% on ICC 506 and 82% on Annigeri. Ten accessions showed poor host suitability index, of which ICC 17122, ICC 17156, IG 70006, and ICC 17187 showed low leaf feeding, low larval weights, and/or poor host suitability index.

Discussion

Several genotypes have been found to be less susceptible to *H. armigera* in the cultivated germplasm of chickpea (Lateef, 1985). However, the expression of resistance varies over seasons and locations. Therefore, wild relatives of chickpea can be exploited as useful sources of genes to increase the stability of resistance to this pest. Accessions belonging to *C. bijugum*, *C. pinnatifidum*, and *C. echinospermum* have shown resistance to leaf miner (*Liriomyza cicerina* Rondani) and bruchids (*Callosobruchus chinensis* L.) (Singh *et al.*, 1990, 1997, 1998). Numbers of pod borer larvae have been found to be lower on the annual species *C. echinospermum*, *C. judaicum*, *C. pinnatifidum* and *C. reticulatum* as compared to *C. arietinum* (Kaur *et al.*, 1999; Sharma *et al.*, 2002b).

Accessions IG 69947, IG 70002, IG 70003, IG 70009, IG 70019, IG 70022, ICC 17125, IG 69979, ICC 17122, ICC 17156, IG 70006, and ICC 17187 (*C. bijugum*), IG 69995 and IG 70030 (*C. judaicum*), and IG 69988, IG 69999 IG 70021, IG 70025, and IG 70028 (*C. pinnatifidum*) showed high levels of resistance to *H. armigera*. The major component of resistance to *H. armigera* in the wild relatives of chickpea is antibiosis, which could be because of the poor nutritional quality of the food or the presence of secondary metabolites. Leaf feeding and larval survival, in general, were greater on the wild relatives than on the cultivated chickpeas, while the larval weights on many wild relatives were much lower than those on the cultivated chickpeas, indicating existence of antibiosis effect on *H. armigera* in wild relatives of chickpea. Several isoflavones have been identified from wild relatives of chickpea (Stevenson and Veitch, 1996, 1998), which have shown antifeedant and antibiotic activity towards the larvae of *H. armigera* (Simmonds and Stevenson, 2001). Developing seeds of wild relatives of chickpea have also shown a significant variation in trypsin inhibitors for the *H. armigera* gut proteinases (Patankar *et al.*, 1999). Therefore, there is a possibility of introgressing diverse resistance genes from the wild relatives of chickpea into the cultivated genotypes for increasing the levels and diversifying the basis of resistance to *H. armigera.*

There has been little success in introgressing resistance genes from the tertiary gene pool into the cultigen. The possibility of gene transfer from *C. reticulatum* and *C. echinospermum* to the cultigen is quite high (Singh and Ocampo 1993, 1997; Badami *et al.*, 1997; Sheila *et al.*, 1992), and the accessions of these species showing resistance to *H. armigera* can be exploited to increase the levels and diversify the basis of resistance to this pest. Since use of wild relatives for introgression of useful genes into the cultivated types will result in the transfer of a number of undesirable traits, marker assisted selection may be useful to improve the efficiency for selection of the desirable traits (Sharma *et al.*, 2002a). Since there is limited polymorphism in the cultigen, lines derived through wide hybridization may be more useful for construction of genetic linkage maps. Development of techniques to overcome compatibility barriers and chromosome engineering may lead to increased utilization of wild relatives of chickpea for resistance to *H. armigera.*

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Extent of Genetic Variation in Indigenous Scented Rice Varieties of Assam

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Forty indigenous scented rice varieties of Assam (locally known as *Joha*) including an introduction from Thailand were screened for the extent of genetic variation for yield and yield attributing traits, and for a few biochemical parameters. The results indicated that there was considerable variation among the varieties for all the traits. The estimates of genotypic and phenotypic coefficients of variation were found to be high for grains per panicle, 100-grain weight, flag leaf area, grain yield per plant, effective tillers and biochemical parameters studied.

Key Words: Genetic advance, Genetic variation, Heritability, Scented rice

There is a great diversity of rice germplasm in North Eastern India, particularly in Assam. Among the various classes of rice cultivated in Assam, scented rice locally known as "joha" occupies a premium position in the local market due to its unique aroma. But these varieties are low yielding, photoperiod sensitive and prone to lodging. Considering the socio-economic importance of the crop, there is a need to genetically improve these varieties. The principal chemical of rice is starch followed by protein content. Apart from starch and protein, rice provides other nutrients like sugars, minerals, fats and some B-complex vitamin. Improvement in nutritional quality of the indigenous scented rice varieties should also get due consideration in order to make them more acceptable in national and international markets. The present studies were, therefore, initiated with an objective to know the extent of genetic variation in indigenous scented (joha) rice varieties for yield and yield attributing characters and for a few biochemical parameters.

Materials and Methods

Forty indigenous scented rice varieties were evaluated in a randomized block design with 3 replications during the *Sali* season, 2003. The experiment was conducted in the experimental field of Regional Agricultural Research Station (RARS), Titabor (26°55'N and 90°10'E). Row length was 2 m with a spacing of 20 cm x 15 cm. Fertilizers were applied on the basis of recommendation for indigenous rice (20 kg N, 10 kg P_2O_5 and 10 kg K_2O/ha). In the field experiment, data on individual plant basis were recorded on five randomly sampled plants in each replication leaving the border rows and border plants. Observations were recorded for days to maturity, plant height (cm), number of effective tillers per plant, panicle length (cm), grains per panicle, grain length (cm), grain breadth (cm), L/B ratio, sterility percentage and 100-grain weight (g). For the laboratory experiment, total soluble sugar was estimated by using Anthrone method given by Yem and Willis (1954). Reducing sugar was estimated by the method described by Miller (1959) and non-reducing sugar by subtracting the percentage of reducing sugar from the percentage of total soluble sugar. Starch content was estimated by the method described by Chopra and Konwar (1976). The data were subjected to analyses of variance and the variance components, phenotypic and genotypic coefficients of variation were estimated according to Burton (1952). Heritability and genetic advance were also estimated by the formula given by Johnson *et al.* (1955).

Results and Discussion

In the analysis of variance, existence of significant variation for grain yield per plant and other yield attributing and grain characters was recorded. High estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for grains per panicle, 100-grain weight, grain length, grain breadth and days to maturity (Table 1). Direct selection would be effective for these characters in improving grain yield. High estimates (>20%) of GCV and PCV were observed for 100-grain weight, grains per panicle, flag leaf area, grain yield per plant and effective tillers per plant. Out of these characters, relative magnitudes of GCV and PCV estimates indicated relatively higher influence of environment for grain yield per plant and effective tillers per plant. This was also reflected in the estimation of heritability. Plant height, days to maturity and panicle length with less than 10% GCV exhibited lower genetic variation. Rest of the characters exhibited moderate genetic variation (10-20%). High estimates of h^2 and GA for grains per panicle indicated that the character is ideal for selection without progeny testing as it is apparently governed by additive gene. For other characters with high heritability (>80%) corresponding GA estimates

were low indicating influence of non additive genes. For these characters, progeny testing will be required with selection.

The range for different characters are also presented in the Table 1. The plant height was found to be minimum in the varieties Badsabhog (121.7 cm). Effective tillers per plant were found to be maximum in the variety Bogi joha (12.9). Considering the panicle characteristics, panicle length were found to be maximum in the variety Nepali joha (32.93 cm). Grains per panicle were found be highest in Krishna joha (303.33) while sterility percentage was found to be minimum in the variety Tulsi joha (15.63%). The highest performance of grain yield per plant was exhibited by the variety Kon joha-1 (42.71 g) and this higher yield may be due to its better performance for plant height, 100-grain weight, flag leaf breadth, flag leaf area and grain breadth. The variety Nepali joha was found to be a better performer for the traits 100-grain weight, flag leaf length, flag leaf breadth, flag leaf area, grain breadth and L/B ratio. Grains per panicle were found to be maximum in the variety Krishna joha with the longest duration while the shortest duration variety was the Bogi joha with maximum number of effective tillers per plant. Badshabhog was recorded as the tallest among the varieties under study. Highest flag leaf length was exhibited by the variety Govindbhog and L/B ratio was by the variety Koli joha. Cheniguti and Boga Tulsi were two long grained varieties with comparatively higher yield. In the present investigation, analysis of variance was found to have significant variation among the varieties for the various biochemical parameter. Though, estimates of GCV, PCV and h^2_{bs} were found to be high for all the traits but GA (%) was found to be very low except for starch percentage. High heritability, with low genetic advance indicated the involvement of non-additive genes and thus, there will be need for progeny testing for selection to be effective (Table 2). In the present investigation, analysis of variance was found to have significant variation among the varieties for the various biochemical parameters. The range of total soluble sugar was found to be 0.412% to 0.764% while reducing sugar was from 0.121% to 0.264% and non reducing sugar was from 0.256% to 0.628%. Starch percentage was found to be ranging from 65.81% to 81.89%.

Table 1. Estimates of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (h^2_{bs}), genetic advance (GA) and range for different characters.

Character	GCV	PCV	h^2_{bs}	GA in % of mean	Range
Plant height (cm)	6.85	7.72	78.7	18.61	121.7-166.67
Effective tillers/plant (No)	20.47	27.65	54.8	2.68	4.30-12.90
Days to maturity (days)	3.50	3.74	87.5	10.03	135-157
Flag leaf length (cm)	12.26	15.96	59.0	6.20	24.60-41.33
Flag leaf breadth (cm)	15.16	17.14	78.3	0.32	0.88-1.84
Flag leaf area (cm^2)	24.26	27.78	76.3	16.15	25.55-69.32
Panicle length (cm)	8.63	10.12	72.6	4.11	21.70-32.93
Grains per panicle (No.)	29.53	32.79	81.1	110.22	96.67-303.3
Sterility percentage (%)	11.61	20.14	33.2	3.12	15.63-30.83
100-grain weight (g)	31.36	31.99	96.1	1.05	0.65-2.86
Grain length (cm)	18.07	18.55	94.8	0.27	0.52-1.13
Grain breadth (cm)	15.24	16.25	87.9	0.07	0.19-0.30
L/B ratio	14.44	16.31	78.4	0.83	2.33-4.50
Grain yield per plant (g)	24.26	32.69	55.0	9.64	5.57-42.71

Table 2. Estimates of genotypic and phenotypic efficient of variance (GCV and PCV), heritability, genetic advance (GA)and range for different biochemical parameters

Character	GCV	PCV	h^2_{bs}	GA in % of mean	Range
Total soluble sugar (%)	16.61	16.66	99.4	0.19	0.412 - 0.764
Reducing sugar (%)	14.27	15.66	83.1	0.04	0.121 - 0.264
Non-reducing sugar (%)	22.63	22.81	98.4	0.19	0.256 - 0.628
Starch percentage (%)	4.68	4.69	99.5	7.17	65.81 - 81.89

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Collection and Characterization of Paddy Germplasm in High Altitude and Tribal Area Zone of Visakhapatnam

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A study was conducted on characterization of paddy germplasm of high altitude and tribal area zone of Visakhapatnam district during the year 2000-2001. 81 germplasm entries collected from the tribal areas of the district were characterized for 18 growth and yield attributing characters. Among the eleven characters, green leaf sheath, glabrous leaf moderately exerted panicle, with short and partly awned grain, straw-coloured hull having easy threshability were noticed to have higher absolute frequency. Aroma was present in 32per cent of the entries. Correlation studies have revealed a significant and positive correlation of grain yield per plant with days to flowering, days to maturity, leaf length and aroma.

Key Words : Characterization, Correlation, Exploration, Frequency, High Altitude and Tribal Area Zone (HAT), Paddy germplasm

Paddy is the major food crop of the tribals in the Visakhapatnam district of Andhra Pradesh. It is the staple food of all the sects of tribal people in this area. The crop is grown in upland, direct seeded and transplanted conditions. The crop is cultivated to the largest extent amongst all the field crops. Tribals usually grow local/ primitive cultivars of paddy that are long statured, long duration, low yielding, having aroma and other desirable traits carefully conserved through generations of domestication, *in situ* conservation, natural selection and evolution methods. The genetic erosion of this valuable germplasm material initiated and accelerated through the introduction of short-statured, early duration, high yielding paddy cultivars is on constant rise in this area. This area being in proximity with the secondary centre of paddy origin, a huge wealth of paddy biodiversity exists which needs to be collected, conserved, documented, characterized and evaluated for all the desirable traits and as useful base material for different breeding programme. Germplasm resources not only helps in avoiding genetic vulnerability to pests and diseases, but will also help to use the advances in transferring genes across sexual barriers (Swaminathan, 1988). Presence of a wide pool of plant genetic diversity is the pre-requisite for crop improvement. Occurrence of scented rice germplasm to a higher frequency has been observed in this area on par with the new aromatic paddy landraces.

Materials and Methods

Exploration trips were undertaken in the Tribal Area of Madhya Pradesh, Orissa and in the high altitude and tribal area of Visakhapatnam district of Andhra Pradesh. Eighty-one germplasm accessions of paddy collected from the different areas of the district (Fig. 1) were sown during the *kharif* 2000 and 2001 for characterization of 18 morpho-agronomic growth and yield attributing characters. The mean value of five observations for each character was taken for further statistical analysis. As any particular landrace is rarely homogenous in genetic composition, random samples of panicles were collected from fields grown for a particular variety. Attempts were made to avoid duplicates during collection. The passport characters were also recorded at the collecting site. Each collection has been assigned a collector number and later a unique IC number were assigned by National Bureau of Plant Genetic Resources (NBPGR), New Delhi.

Each entry was sown in 2m x 1m plots in the red sandy loam soils of the main block of Regional Agricultural Research Station, Chintapalle. It is located at an altitude of 780 m, soils are slightly acidic, low in organic carbon content, low in nitrogen and phosphorus and medium in potash availability. The rainfall during the years 2000 and 2001 was 976.2 mm and 911.9 mm respectively and was less than normal. The crop was grown under rainfed conditions in 20 cm solid rows. The entries were fertilized with 60-20-40 kg NPK/ha. Split application of nitrogen in the form of urea was given at active tillering and panicle initiation stages. The crop was weeded twice at 30 and 45 days after sowing. Observations on the characters *viz.*, leaf sheath colour, leaf blade colour, leaf

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pubescence, leaf length, leaf width, days to flowering, panicle exertion, stigma colour, apicule colour, plant height, panicle length, panicle type, awning, days to maturity, hull colour, threshability, aroma and grain yield per plants were recorded for characterization of these germplasm. Characterization was done using the minimal descriptors (Mahajan *et al.*, 2000).

The range, mean, standard error of mean, coefficient of variation of some important morph-agronomic traits were recorded.

Results and Dicussion

Characterization of the germplasm indicated (Table 1) that out of the eleven qualitative characters, the absolute frequency was very high for green leaf sheath colour (74.1), glabrous type of leaf pubescence (82.7) and intermediate type of panicle (71.6). Among the various entries short and partly awned grains, easy threshability of straw and non-aromatic grains showed moderately high frequency. Entries with the characters of light purple margins on leaf sheath, purple margin on leaf, purple coloured apiculus compact type of panicle and purple type of hull colour were found to show very less distribution. Most of the entries were had brown apiculus, white stigma in flowers and straw-coloured hull. Aroma was present in 32% of the entries. The results are in conformity with the findings of Patra (2000).

Correlation studies (Table 2) of grain yield per plant with different plant characters revealed that days to flowering, days to maturity and aroma in grains are positively and significantly correlated with grain yield at 5% level of significance. Among the individual characters, leaf length (cm) and leaf colour are significantly and negatively correlated with each other. Similar is the case with plant height (cm).

Leaf colour and days to flowering, leaf length (cm) and apiculus colour, leaf length and plant height, awn and leaf colour, days to flowering and days to maturity, leaf sheath colour and threshability, days to maturity and threshability, days to maturity and aroma were found to be significantly and positively correlated with each other. The results are in corroboration with Sharma and Hore (1989). The study shows that in the germplasm studied, wide variation exists with respect to days to flowering, days to maturity and aroma. This enables the rice breeders to tailor high yielding varieties suitable to the zone.

Table 1. Frequency distribution of accessions for different descriptors

Sl. No.	Descriptor state	Colour Code	Absolute frequency	Relative percentage (%)
	Basal			
1	**Leaf sheath colour**			
	Green	1	60	74.1
	Purple lines	2	8	9.9
	Light purple	3	1	1.2
	Purple	4	12	14.8
2	**Leaf blade colour**			
	Light green	1	40	49.4
	Green	2	40	49.4
	Purple margin	5	1	1.2
3	**Leaf pubescence**			
	Glabrous	1	67	82.7
	Intermediate	2	9	11.1
	Pubescent	3	5	6.2
4	**Panicle exertion**			
	Well exerted	1	23	28.4
	Moderate exerted	3	38	46.9
	Just exerted	5	14	17.3
	Partly exerted	7	6	7.4
	Enclosed	9	–	
	Others	99	–	
5	**Stigma colour**			
	White	1	31	38.3
	Light Green	2	19	23.4
	Yellow	3	5	6.2
	Purple	5	20	24.7
	Others	99	6	7.4
6	**Apiculus colour**			
	White	1	7	8.7
	Brown	3	35	43.2
	Red apex	5	15	18.5
	Purple	6	6	7.4
	Purple apex	7	17	21.0
	Others	99	1	1.2
7	**Panicle type**			
	Compact	1	5	6.2
	Intermediate	5	58	71.6
	Open	9	17	21.0
	Others	99	1	1.2
8	**Awning**			
	Short and partly awned	1	51	63.0
	Short and fully awned	5	1	1.2
	Long and fully awned	7	16	19.7
	Others	9	2	2.5
		99	11	13.6
9	**Hull colour**			
	Straw	1	28	34.6
	Golden	2	–	0.0
	Golden Brown	3	21	25.9
	Brown ferrous on straw	4	10	12.4
	Purple	5	2	2.5
	Purple furrows on straw	6	4	4.9
	Brown (fanny)	7	8	9.8
	Black	8	7	8.6
	Others	99	1	1.2
10	**Threshability**			
	Easy	1	54	66.7
	Intermediate	2	27	33.3
	Difficult	3	–	–
	Others	99	—	—
11	**Aroma**			
	Absent	0	55	67.9
	Present	1	26	32.1

Table 2. Correlation Matrix

	LFS Clr	LF Clr	LF Pub	LF Lt (Cm)	LF Wd (Cm)	Day Flw	Pan Exe	Stig Clor	Apic Clr	PT HT (Cm)	Pa Nlt (Cm)	Pan Tp	Awn	Day Mat	Hull Clr	Thresh	Aroma	Grainyld
Lfs Clr	1.00000	0.09131	–0.16229	0.02102	0.12529	0.17989	0.04360	0.13149	-0.07853	0.15190	–0.15097	–0.23059	0.01937	0.09693	–0.13569	0.23516	0.00576	–0.17090
Lf Clr		1.00000	–0.04706	–0.30604	–0.04352	0.24742	0.16672	–0.11500	0.00226	-0.37637	–0.24965	–0.03031	0.46175	0.20838	0.07812	–0.02774	–0.04719	0.04370
Lf Pub			1.00000	0.18731	–0.04421	–0.01758	0.13701	–0.06034	0.10196	0.10204	–0.02289	0.10054	–0.18162	–0.04319	0.09397	–0.01586	–0.14887	0.00687
Lf Lt (Cm)				1.00000	0.02836	–0.04111	0.01279	0.08215	0.23717	0.39943	0.08431	–0.13767	–0.43636	–0.07598	–0.10338	–0.09536	–0.08166	–0.04738
Lf Wd (Cm)					1.00000	–0.23267	0.04365	0.00935	–0.12977	0.06216	–0.13537	–0.06219	–0.02645	–0.26802	0.06639	–0.18811	–0.05292	–0.14919
Day Flw						1.00000	0.16328	0.08873	–0.05219	–0.13494	–0.09131	–0.01760	0.19778	0.94374	–0.12659	0.18732	0.11644	0.27938
Pan Exe							1.00000	0.10081	–0.04179	–0.06325	–0.19453	–0.02522	0.22702	0.15812	0.04607	0.06041	0.15363	0.06214
Stig Clor								1.00000	0.08308	0.12803	–0.07402	–0.21270	–0.04880	0.05698	–0.16250	0.06189	0.06725	0.18903
Apic Clor									1.00000	0.08466	0.13065	–0.18932	–0.07520	–0.05530	0.10035	0.01356	0.04413	–0.04881
Pt Ht (Cm)										1.00000	0.23699	0.00867	–0.34646	–0.16537	–0.07340	0.06110	–0.08031	–0.06984
Pan Lt (Cm)											1.00000	0.01947	–0.18404	–0.06528	0.06273	0.10707	0.03252	0.06551
Pan Tp												1.00000	–0.15678	0.10617	0.09399	0.20558	0.11305	0.14561
Awn													1.00000	0.05697	0.20151	–0.20569	–0.19592	0.01263
Day Mat														1.00000	–0.144898	0.33483	0.26187	0.33878
Hull Clr															1.00000	–0.20067	–0.18693	–0.19397
Thresh																1.00000	0.24309	–0.01874
Aroma																	1.00000	0.29276
Grain Yld/Pl																		1.00000

Significance Levels	0.05	0.01	0.005	0.001
LI Correlation =>	0.21852	0.28467	0.30902	0.35892
Y1 = 1.3703 + 0.05878 x 6	Day Flw	2.5862	0.0115	
Y1 = –1.9879 + 0.06464 x 14	Day Mat	3.2004	0.0020	
Y1 = 6.1636 + 2.33636 x 17	Aroma	2.7213	0.0080	

Table 3 shows the range for different plant characters. The mean values indicate that most of the varieties are of medium duration (137 days) with a grain yield of 6.9 grams per plant. Higher coefficient of variation was observed for leaf sheath colour, panicle exertion, hull colour, aroma and grain yield per plant.

In all, germplasm mainly constituted entries with green leaf sheath colour, glabrous type of leaf pubescence and intermediate type of panicle having significant correlation of grain yield per plant with days to flowering, days to maturity and aroma in grains.

Table 3. Range, Standard Deviation and Coefficient of Variation of Different Descriptors

Pooled n=81		Lowest	Highest	Mean	Std Dev.	Std. Error	CV%
LFS CLR	X1	1.00	4.00	1.56	1.08	-0.12	69.08
LF CLR	X2	1.00	5.00	1.54	0.63	0.07	41.04
LF PUB	X3	1.00	3.00	1.23	0.55	0.06	21.85
LFLT (CM)	X4	20.00	58.00	43.19	9.44	1.04	23.94
LFWD (CM)	X5	0.50	1.30	0.85	0.20	0.02	18.89
DAY FLW	X6	65.00	140.00	94.30	17.81	1.98	56.75
STIG CLOR	X8	0.00	99.00	4.71	15.18	1.68	46.01
APIC CLR	X9	0.00	7.00	4.22	1.94	0.21	16.54
PTHT CM)	X10	55.00	144.00	95.60	15.81	1.75	24.54
PAN LT(CM)	X11	0.00	46.00	18.98	4.65	0.51	24.50
PAN TP	X12	0.50	9.00	5.56	2.09	0.23	37.64
DAY MAT	X14	104.00	187.00	137.71	19.64	2.18	14.26
HULL CLR	X15	0.00	8.00	3.41	2.40	0.26	70.40
THRESH	X16	1.00	2.00	1.33	0.47	0.05	35.57
GRAIN YLD/PL	Y1	2.00	20.00	6.91	3.74	0.41	54.22

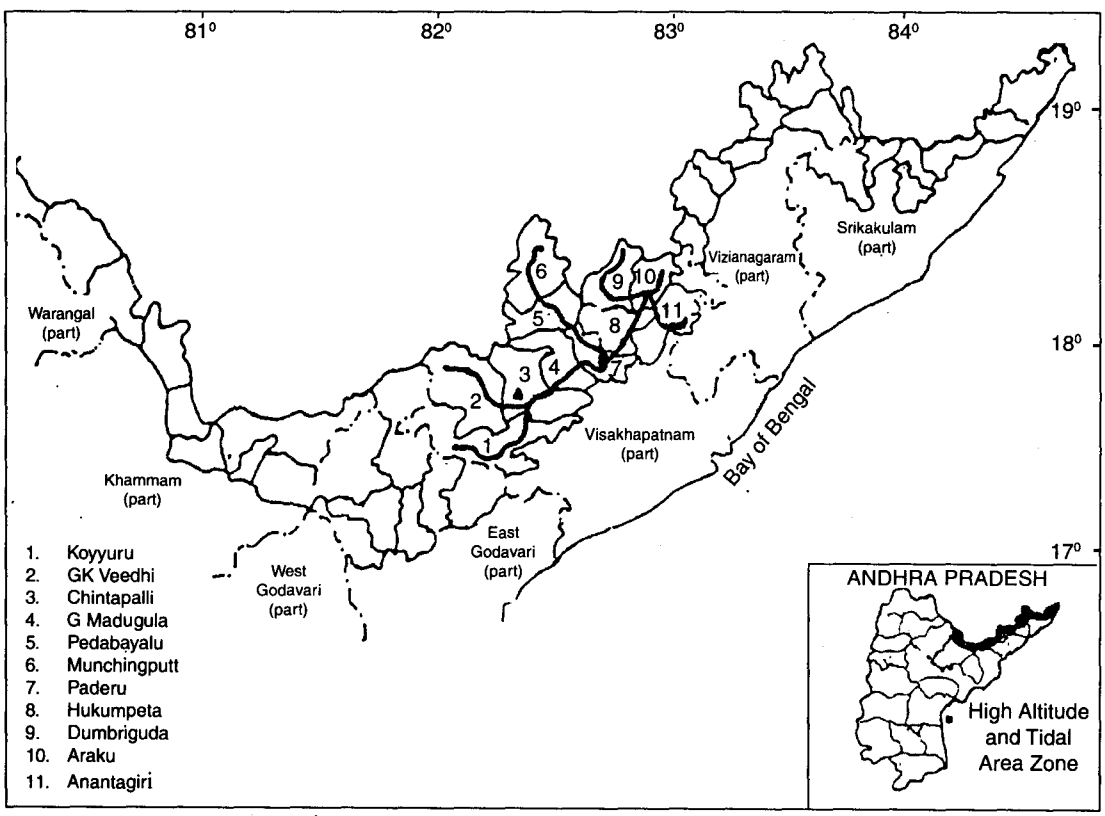

Fig. 1: Route map of paddy germplasm collection

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Resistance Sources Against Predominant Pathotypes of Yellow Rust in Winter Wheat

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Thirty-four lines of winter wheat were screened for yellow rust resistance against predominant pathotypes of northern India. Four of these were found to be resistant against all the four pathotypes. Breeding wheats involving these sources of resistance may diversify the Indian wheats and reduce the impact of new pathotypes.

Key Words: Sources of resistance, Winter wheat, Yellow rust

Yellow rust caused by *Puccinia striiformis* sp *tritici* is one of the most devastating diseases of wheat. The disease is more destructive in cooler regions. The spread of this rust is fast due to prevalence of low temperature in the north-western region of India during the months of January and February which affects tillering and grain development of the plant. Wheat cultivars derived from "Veery" germplasm had Lr26 linked with Yr9 and Pm8 genes located on 1B/1R translocation, were resistant and provided safety against losses due to leaf and stripe rusts till 1995. However, the evolution of new pathotype designated as 46S119 which is virulent on Yr9 and Yr2 has changed the situation (Nayar, 1996). So far in India, about 27 stripe rust races or their biotypes have been identified out of which 14 races were picked up from Nilgiries (Nayar *et al.* 2000). About 27 potentially useful genes are known to condition resistance against stripe rust pathogens (McIntosh *et al.* 1998). Winter wheats are supposed to be a good source of yellow rust resistance besides providing winter hardiness and yield advantage. In northern India, pathogens viz., 46S102, 46S103, 46S119 and 47S103 have been found to be predominant and hence, an attempt was made to identify new sources of resistance which could be utilized for the development of varieties resistant to yellow rust.

Materials and Methods

Seeds of thirty four winter wheat lines along with two spring wheat check varieties and one susceptible check (Agra local) were space planted in aluminium trays (29 X 12 X 7 cm) containing a mixture of loam soil and farm yard manure in the ratio of 3:1. The trays were kept in a spore proof glass house having sufficient light. The trays were watered regularly to keep the soil moist for proper germination of seeds. Seven days old seedlings were inoculated with uredospores of four predominant isolates of yellow rust separately as per the method described by Luthra (1966). The inoculated seedlings were atomized with water and kept for 48 hrs in the humid chamber for germination of spores. The seedlings were then shifted to glass house benches. The 15-20 days old seedlings were evaluated against predominant pathotypes of yellow rust during 2000-01 and 2001-02 and seedling reaction against each of the pathotypes was recorded according to Nayar *et al.*, (1997). The seedlings showing $ (naught fleck), # (fleck), 1-2 reaction were classified as resistant while seedlings with reaction 3 and 3+ were regarded as susceptible.

Results and Discussions

Response of winter wheat lines against predominant pathotypes of yellow rust is presented in Table 1. Four winter wheat lines *viz.*, Moro, Cappelle-Desprez, Mega and Maris-Hunstman showed resistant reaction against all the four predominant pathotypes of yellow rust. The genotype Kavkaz has shown resistance against 46S102, 46S103 and 47S103 races of yellow rust in both the years of testing. *T. spelta album*, Riebsel and Joss Combier have also been found to be resistant against these three pathotypes with escape for some pathotype in one year. Besides, Vilmorin, Bezostaya and Compair have also been found resistant against most prevalent race 46S119 which is virulent on Yr2 and Yr9 (Table 2). Discrepancies in the disease appearance for different years were due to disease escape which is very common for yellow rust (Nayar, 1996) and hence some more confirmation about the resistant lines is required.

Nayar *et al.*, (2001) postulated the presence of Yr9 and Yr18 either singly or in various combinations in 95 among 136 released varieties of wheat in India and emphasized the need of diversification of resistance against yellow rust. Similarly, Kumar and Bhatnagar (2000) reported the presence of Yr9 in 44% of the advanced elite lines of wheat generated during 1996-

Table 1. **Seedling reaction of winter wheats against yellow rust pathotypes during 2000-2002**

Genotype / Variety	Pathotypes							
	2000-01				2001-02			
	46S102	46S103	46S119	47S103	46S102	46S103	46S119	47S103
T. spelta album	$	$	$	$	–	$	3	#
Riebesel	1-2	#	3+	#	–	#	3+	$
Moro	$	$	#	#	1	$	–	$
Aurora	3+	3+	3+	3+	3+	–	3+	–
Vilmorin	2+3	3+	$	1-2	3+	2	#	3
CappelleDesprez	1-2	$	#	1-2	1	2	#	$
Mega	#	#	#	#	$	$	#	$
Maris-Huntsman	#	$	$	$	$	–	#	–
Hobbit	#	$	$	1-2	1	3	3	#
Bon-Fermier	3+	2+3	2+3	3+	3+	3+	3+	3
Chinese-166	3+	$	$	3+	–	$	3	3
Joss Combier	1-2	$	12	#	–	2	3+	2
HeinesVII	1-2	2+3	2+3	2+3	1	3+	3	3+
Peko	3+	1-2	3+	3+	3+	3+	3	3+
Heines Kolbin	3+	3+	2+3	3+	3+	3+	–	3+
Elgin	–	3+	–	–	3	3+	3+	3+
Kavkaz	#	#	3+	$	$	$	3+	#
Altas-66	3+	3+	3+	3+	3+	3+	3+	3+
Bezostaya	3+	3+	$	3+	3+	3+	–	3+
Blue boy	3+	–	3+	3+	3	3	3+	3+
Centurk	2+3	3+	3+	3+	3	3	3+	3
Dacia	1-2	3+	3+	3+	#	#	3+	#
Demar 4	#	3+	3+	3+	$	3+	3+	2
Sava	3+	3+	3+	3+	–	3+	3+	$
Bolal	3+	3+	3+	3+	3+	3+	–	–
Burgas-2	1-2	3+	3+	3+	$	3+	3+	#
Favorit	#	3+	3+	3+	$	3+	–	#
Moldova	$	3+	3+	3+	$	3+	3+	3
PD Extreme	#	$	3+	#	–	3+	3+	#
Rousalka	#	3+	3+	3+	2	3+	3+	3
Opal	#	3+	1-2	1-2	#	$	3+	$
Lee	3+	3+	3+	3+	3+	3+	3+	3+
Compair	3+	3+	#	#	3+	$	#	$
Chancellor	1-2	3+	3+	3+	3	3+	3+	1
HS 240	#	$	3+	#	#	$	3+	#
VL 738	#	$	3+	#	–	$	3+	$
Agra Local	3+	3+	3+	3+	3+	3+	3+	3+

Infection type: $ (naught fleck = immune) # (fleck= very resistant) 1-2 (resistant) 3 (moderately susceptible) 3+ (highly susceptible)

Table 2. Response of winter wheats against yellow rust

Pathotype	Resistant lines
46S102, 46S103, 46S119 and 47S103	Moro, Cappelle – Desprez, Mega and Maris – Hunstman
46S102, 46S103 and 47S103	Kavkaz, T. Spelta album, Riebsel and Joss – Combier
46S119	Vimorin, Bezostaya and Compair

99 at IARI, Regional Station, Shimla. Widespread occurrence of Yr9 in Indian wheat, has necessitated diversification of germplasm with new sources of resistance against yellow rust. In present study the winter lines detected as resistant against predominant pathotypes of yellow rust may serve as good sources of resistance for breeding yellow rust resistant cultivars in India. The spring wheats derived involving such winter stocks may also

broaden the genetic architecture of the cultivars and reduce the frequent evolution of new pathotypes.

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Preliminary Evaluation of *Corchorus* spp. for Resistance to Yellow Mite [*Polyphagotarsonemus latus* (Banks)], Semilooper (*Anomis sabulifera* Guen.) and Stem Weevil (*Apion corchori* Marshall)

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Yellow mite [*Polyphagotarsonemus latus* (Banks)], semilooper (*Anomis sabulifera* Guen.) and stem weevil (*Apion corchori* Marshall) are major economic pests of cultivated jute (*Corchorus* spp.). Eighty accessions of *Corchorus* species were evaluated under field infestation, in an augmented randomized block design, against Yellow mite, semilooper and stem weevil. Based on the damage caused by these pests, accessions WCIN-009, WCIN-006, NYM-2860 (*C. aestuans*); WCIJ-116 (*C. fascicularis*); WCIJ-009, KBA-230 (*C. tridens*); WCIJ-031 (*C. pseudo-capsularis*); WCIJ-121 and WCIJ-132 (*C. trilocularis*) were identified as moderately resistant against one or more of these three pests. It was also found that none of the accessions evaluated showed high level of resistance against all the three pests together. Further studies under greenhouse / artificial infestation conditions are required to substantiate the results.

Key Words: *Corchorus* species, Jute, Screening, Semilooper, Stem weevil, Yellow mite

Jute (*Corchorus capsularis* L. and *C. olitorius* L.), an important fibre crop is cultivated mainly in the north-eastern region comprising states of West Bengal, Assam, Bihar, Orissa, Uttar Pradesh and some parts of Meghalaya and Tripura. The yellow mite [*Polyphagotarsonemus latus* (Banks)], semilooper (*Anomis sabulifera* Guen.) and stem weevil (*Apion corchori* Marshall) are the major economic pests of jute in India. The damage caused varies with the pests (Singh, 1981). Jute stem weevil exists throughout the jute crop season (i.e. March-July) and causes damage to the crop from early stage till harvest. Female weevil punctures the stem near base of petiole for egg deposition and developing grub tunnels into pith damaging the fibre tissue. A 'knot' is formed at the point of injury that causes defect in fibre quality. The green semilooper appears in the field in the first week of June and continues to damage the jute plants till harvest. The larvae damage tender apical leaves of jute plants causing reduction in growth and consequently fibre yield. In severe cases, semilooper larvae destroy the growing points, which induce branching thus affecting both fibre yield and quality. The yellow mite feeds on the apical leaves, which roll and bend, consequently arresting the growth. It appears in field in the first week of May and continues to damage the crop for about two months.

A number of management strategies have been investigated to prevent crop losses from these pests. These methods include selection of resistant varieties, suitable date of sowing, inter-cultural operations, use of insecticides/ bio-pesticides and crop rotation (Das and Singh, 1999). The objective of this study was to evaluate germplasm of wild and cultivated *Corchorus* species for resistance to the major insect-pests under field conditions, which would provide useful information for breeding resistant varieties against these pests.

Materials and Methods

The experimental material (Table 1) for the present investigation consisted of 80 accessions of *Corchorus* species collected under International Jute Organization (IJO) Germplasm Project (1988-89) and National Agricultural Technology Project – Conservation of Agrobiodiversity (Sustainable Management of Plant Biodiversity: Jute and Allied Fibres). Of these, 67 accessions belonged to seven wild species and 13 accessions to cultivated species (*C. capsularis* and *C. olitorius*). The accessions were screened for resistance to yellow mite, semilooper and stem weevil under conditions of natural infestation in the field at Central Research Institute for Jute and Allied Fibres, Barrackpore (22° 45' N, 88° 16' E and 30 m altitude) in March. The experimental material was grown in an augmented randomized complete block design with four checks in four blocks. Each entry was grown in a single row, 3 m long. The rows were 30 cm apart, and plants were thinned to a spacing of 7-10 cm within the row. Recommended agronomic practices were used for raising the crop. No insecticide/fungicide was applied during the growth of the crop.

Jute yellow mite, semilooper and stem weevil damage was assessed visually. Based on the extent of incidence,

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Table 1. Yellow mite, semilooper and stem weevil incidence (mean values) in different *Corchorus* species evaluated during 2002

Species	Accession	Source country	Incidence percentage (mean)		
			YM	SL	SW
C. aestuans	WCIJ-037	Tanzania	28.32 (34.19)*	31.44 (30.86)	29.09 (27.31)
	WCIJ-044	Tanzania	9.92 (15.79)	23.22 (22.64)	1.01 (0.00)
	WCIJ-100	Tanzania	22.28 (18.67)	-1.70 (0.00)	16.21 (18.67)
	WCIJ-135	Tanzania	29.59 (31.48)	17.61 (17.55)	24.33 (25.24)
	WCIJ-153	Thailand	26.44 (32.31)	22.78 (22.20)	20.88 (19.10)
	WCIJ-144	China	22.84 (28.71)	0.58 (0.00)	21.63 (19.85)
	WCIN-009	India	15.06 (20.93)	0.58 (0.00)	13.68 (11.90)
	WCIN-005	India	20.70 (26.57)	17.01 (16.43)	28.35 (26.57)
	WCIN-003	India	15.93 (21.80)	0.58 (0.00)	26.31 (24.53)
	WCIN-006	India	8.16 (14.03)	0.58 (0.00)	1.78 (0.00)
	WCIN-007	India	28.58 (30.47)	0.06 (0.00)	16.11 (17.02)
	WCIN-008	India	26.72 (30.61)	22.69 (22.63)	24.57 (25.48)
	YBM-78	India	28.46 (34.33)	0.58 (0.00)	1.78 (0.00)
	NYM-2855	India	20.70 (26.57)	0.58 (0.00)	1.78 (0.00)
	NYM-2860	India	19.61 (25.48)	0.58 (0.00)	17.57 (15.79)
	NYM-2846	India	37.83 (33.68)	12.36 (11.30)	12.90 (11.30)
	NYM-2835	India	28.98 (25.37)	-1.70 (0.00)	16.17 (18.63)
	KBA-186	India	25.95 (21.80)	1.06 (0.00)	1.60 (0.00)
C. fascicularis	WCIJ-005	Kenya	35.02 (40.89)	32.89 (32.31)	42.67 (40.89)
	WCIJ-014	Kenya	37.34 (39.23)	26.63 (26.57)	35.36 (36.27)
	WCIJ-025	Kenya	11.03 (12.92)	20.76 (20.70)	30.72 (31.63)
	WCIJ-028	Kenya	20.65 (22.54)	29.07 (29.01)	19.15 (20.06)
	WCIJ-052	Kenya	15.30 (21.17)	0.58 (0.00)	22.95 (21.17)
	WCIJ-085	Kenya	15.38 (11.77)	23.96 (25.66)	14.32 (16.78)
	WCIJ-116	Kenya	5.45 (7.34)	18.33 (18.27)	-0.92 (0.00)
	WCIJ-055	Tanzania	20.60 (22.49)	20.49 (20.43)	27.03 (27.94)
	WCIJ-140	Tanzania	12.29 (14.18)	18.49 (18.43)	21.06 (21.97)
	WCIJ-086	Thailand	13.07 (14.96)	23.28 (23.22)	11.94 (12.85)
C. pseudo-capsularis	WCIJ-007	Kenya	28.80 (24.65)	18.21 (17.15)	18.74 (17.14)
	WCIJ-031	Kenya	16.54 (18.43)	15.95 (15.89)	-0.92 (0.00)
	WCIJ-041	Tanzania	26.52 (22.91)	-1.70 (0.00)	15.09 (17.55)
C. pseudo-olitorius	WCIJ-034	Kenya	10.23 (16.10)	14.48 (13.90)	13.08 (11.30)
	WCIJ-092	Kenya	14.72 (16.61)	16.42 (16.36)	9.35 (10.26)
	WCIJ-125	Kenya	16.69 (13.08)	14.40 (16.10)	6.75 (9.21)
C. tridens	WCIJ-009	Kenya	19.87 (16.26)	16.54 (18.24)	17.60 (20.06)
	WCIJ-017	Kenya	44.35 (40.20)	1.06 (0.00)	25.69 (24.09)
	WCIJ-042	Tanzania	3.61 (0.00)	22.39 (24.09)	17.01 (19.47)
	WCIJ-068	Kenya	42.84 (39.23)	37.53 (39.23)	24.11 (26.57)
	WCIJ-149	Tanzania	30.31 (26.16)	17.83 (16.78)	23.47 (21.87)
	WCIJ-137	Tanzania	17.24 (13.63)	33.56 (35.26)	21.63 (24.09)
	WCIJ-147	Tanzania	25.80 (22.20)	30.61 (32.31)	19.74 (22.20)
	KBA-230	India	19.94 (15.79)	1.06 (0.00)	1.60 (0.00)
	NYM-2863	India	51.67 (47.60)	1.06 (0.00)	1.60 (0.00)

Contd...

Table 1 Contd...

Species	Accession	Source country	Incidence percentage (mean)		
			YM	SL	SW
C. trilocularis	WCIJ-008	Kenya	26.83 (23.22)	21.52 (23.22)	17.01 (19.47)
	WCIJ-016	Kenya	40.69 (37.08)	–1.70 (0.00)	34.62 (37.08)
	WCIJ-022	Kenya	17.05 (13.44)	17.50 (19.20)	14.08 (16.54)
	WCIJ-026	Kenya	18.32 (14.71)	19.35 (21.05)	15.66 (18.12)
	WCIJ-033	Kenya	13.95 (10.34)	16.42 (18.12)	23.64 (26.10)
	WCIJ-061	Kenya	20.46 (16.31)	22.32 (21.26)	17.91 (16.31)
	WCIJ-065	Kenya	22.34 (18.19)	21.49 (20.43)	19.79 (18.19)
	WCIJ-071	Kenya	21.70 (17.55)	18.61 (17.55)	16.73 (15.13)
	WCIJ-079	Kenya	31.08 (26.93)	1.06 (0.00)	17.70 (16.10)
	WCIJ-091	Kenya	23.08 (19.47)	19.71 (21.41)	9.70 (12.16)
	WCIJ-103	Tanzania	23.62 (19.47)	18.40 (17.34)	21.07 (19.47)
	WCIJ-111	Kenya	17.41 (13.26)	28.37 (27.31)	22.86 (21.26)
	WCIJ-121	Kenya	11.61 (13.50)	0.06 (0.00)	12.59 (13.50)
	WCIJ-039	Tanzania	24.85 (20.70)	25.79 (24.73)	20.03 (18.43)
	WCIJ-131	Tanzania	17.59 (13.44)	35.77 (34.71)	27.38 (25.78)
	WCIJ-132	Tanzania	16.08 (17.97)	0.06 (0.00)	17.06 (17.97)
	WCIJ-133	Tanzania	4.15 (0.00)	30.33 (29.27)	20.84 (19.24)
	WCIJ-134	Tanzania	22.71 (19.10)	25.87 (25.57)	19.74 (22.20)
	KBA-62	India	4.15 (0.00)	46.06 (45.00)	25.69 (24.09)
	KBA-80	India	30.31 (26.16)	17.84 (16.78)	23.47 (21.87)
	KBA-222	India	20.25 (16.10)	24.15 (23.09)	14.68 (13.08)
	KBA-227	India	21.97 (17.82)	31.06 (30.00)	16.08 (14.48)
C. urticifolius	WCIJ-070	Kenya	31.89 (37.76)	21.28 (20.70)	16.26 (14.48)
	WCIJ-112	Kenya	38.87 (35.26)	35.56 (35.26)	32.80 (35.26)
C. capsularis	CIM-022	India	29.43 (31.32)	25.54 (25.48)	18.28 (19.19)
	CIN-012	India	33.36 (39.23)	15.54 (14.96)	28.35 (26.57)
	CIN-088	India	33.36 (39.23)	19.01 (18.43)	16.74 (14.96)
	CIN-358	India	38.87 (35.26)	20.93 (22.63)	13.33 (15.79)
	CEX-012	Taiwan	32.20 (34.09)	0.06 (0.00)	18.84 (19.75)
	CEX-054	Brazil	35.29 (31.68)	13.52 (15.22)	22.07 (24.53)
C. olitorius	OIJ-018	Kenya	22.20 (24.09)	27.63 (27.57)	19.27 (20.18)
	OIJ-026	Kenya	20.31 (22.20)	22.26 (22.20)	14.59 (15.50)
	OIJ-097	Tanzania	25.93 (31.80)	0.58 (0.00)	18.56 (16.78)
	OIJ-229	Nepal	26.67 (28.56)	9.78 (9.72)	25.66 (26.57)
	OIN-046	India	16.30 (18.19)	18.97 (18.91)	20.14 (21.05)
	OIN-507	India	31.21 (37.08)	0.58 (0.00)	1.78 (0.00)
	OMU-017	India	26.15 (32.02)	0.58 (0.00)	27.44 (25.66)
Varietal mean	N = 80		22.99	15.91	18.26
Checks	JRO 524		8.80 (17.15)	5.73 (11.84)	11.42 (19.13)
	JRO 632		18.60 (25.29)	15.01 (22.60)	12.64 (20.73)
	JRO 878		26.60 (31.01)	9.64 (15.73)	8.38 (16.37)
	JRC 212		24.43 (28.72)	14.79 (21.74)	10.91 (18.92)
	JRC 321		31.41 (33.79)	19.21 (25.88)	11.02 (19.36)
Check mean	N =5		27.19	19.56	18.50
LSD (0.05)	N = 80		12.15	21.76	11.13

YM = Yellow mite, SL = Semilooper, SW = Stem weevil, * = Angular values in parenthesis

the plants were rated for pest damage using the scale: highly resistant (infestation 0.00 %), resistant (infestation from 1-10 %), moderately resistant (infestation from 11-20 %), moderately susceptible (infestation from 21-50 %), susceptible (infestation from 51-75 %) and highly susceptible (infestation from 76-100 %). The incidence percentage values calculated on the basis of number of plants infested in a row were transformed using inverse sin angular transformation. Although no artificial infestation was done, field level infestation was high during the crop growth period. The statistical analysis was done using Indostat statistical software package, developed by Indostat Pvt. Ltd., Hyderabad, India.

Results and Discussion

Yellow Mite

Significant differences were detected in accessions of wild species evaluated for yellow mite damage. Out of 80 accessions (Table 1), 2 accessions each of *C. aestuans* WCIJ-044 (9.92 %), WCIN-006 (8.16 %) and *C. trilocularis* KBA-62 (4.15 %), WCIJ-133 (4.15 %); one each of *C. fascicularis* WCIJ-116 (5.45 %) and *C. tridens* WCIJ-042 (3.61 %) were resistant to yellow mite. All the accessions of *C. pseudo-olitorius* (WCIJ-034, WCIJ-092, WCIJ-125) were moderately resistant to yellow mite. Amongst wild species, accessions WCIJ-017 (44.35 %) and NYM-2863 (51.67 %) of *C. tridens* were moderately susceptible and susceptible, respectively. None of the accessions were highly susceptible to yellow mite.

Semilooper

Among the 80 accessions (Table 1) tested, 2 of *C. aestuans* (WCIJ-100, NYM-2835); one of *C. pseudo-capsularis* (WCIJ-041) and one of *C. trilocularis* (WCIJ-016) were highly resistant to semilooper infestation. Accessions of *C. pseudo-olitorius* WCIJ-034 (14.48 %), WCIJ-092 (16.42 %) and WCIJ-125 (14.40 %) were moderately resistant to semilooper infestation. Maximum mean damage percentage was observed in accessions of *C. trilocularis* KBA-62 (46.06 %) followed by WCIJ-068 (37.53 %) of *C. tridens*. None of the accessions were highly susceptible to semilooper infestation.

Stem Weevil

Five aceessions of *C. aestuans* (WCIJ-044, WCIN-006, YBM-78, NYM-2855, KBA-186); one each of *C. fascicularis* (WCIJ-116), *C. pseudo-capsularis* (WCIJ-031), *C. trilocularis* (WCIJ-091) and two of *C. tridens* (KBA-230, NYM-2863) exhibited resistance against stem weevil infestation. Accessions WCIJ-034, WCIJ-092 and WCIJ-125 of *C. pseudo-olitorius* were moderately resistant to stem weevil infestation. Maximum mean damage percentage was observed in accession of *C. fascicularis* WCIJ-005 (42.67 %) and *C. trilocularis* WCIJ-016 (34.62 %).

Among cultivated species, accessions CEX-012, OIJ-097, OIN-507 and OMU-017 were identified as resistant genotypes to semilooper infestation. Amongst check varieties, JRO 524 was found resistant to yellow mite (8.80 %) and semilooper (5.73 %) infestation and moderately resistant against stem weevil (11.42 %). However, JRO-878, JRC 212 and JRC 321 were moderately susceptible to yellow mite infestation. Chaudhury *et al.* (1999) reported that in tossa jute accessions KEN/DS/041 and KEN/DS/061 were identified as donor parents for resistance on the basis of low incidence of jute semilooper. Similarly, Palve *et al.* (2002) also found accessions of wild species *C. aestuans*, *C. trilocularis* and *C. tridens* highly resistant against semilooper infestation.

Accessions of wild species of *Corchorus* identified for resistance to these major pests can be used in interspecific hybridization for improving cultivated varieties of jute. Further studies under artificial infestations are needed for confirming the results obtained under natural infestation.

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Ethnobotany of Minor Millets and Related Grasses from the Tribal Area of Rajasthan

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An ethnobotanical survey of tribal area of Southern Rajasthan was carried out for minor millets and other related wild species of grasses. Ethnobotanical information on this group of plants is based on the exhaustic interviews with local farmers, village headmen, priest and other community leaders. Ethnobotany of 8 minor millets and 18 related wild species of grasses have been given from the study area. Enumeration of these plants with their botanical name, local name, locality of collection, their herbarium number and ethnobotanical uses are given.

Key Words: Ethnobotany, Grasses, Minor millets, Southern Rajasthan, Tribals

The term millets commonly refers to any of the broad range of small seeded cereals and forages. Millets are also referred to as miscellaneous cereals or coarse grains, are members of the family Poaceae. Compared to other cereal grains minor millets can grow in less fertile soils, and survive intense heat and low rainfall conditions. In addition, they require shorter growing season. Under such conditions, minor millets and other related grasses are of immense importance in a state like Rajasthan where famine due to recurrent drought occur rather frequently. There is an old saying in relation of famine about the state *viz* "Teejo Kurio Athwon Akal" which means that the state is bound to be hit by 'Kurio' or state of quasi-famine every third year and by a state of acute or grave famine every eighth year. During famine conditions, the tribals of southern Rajasthan totally depend on minor millets and other related grasses for the food when other cultivated crops have failed.

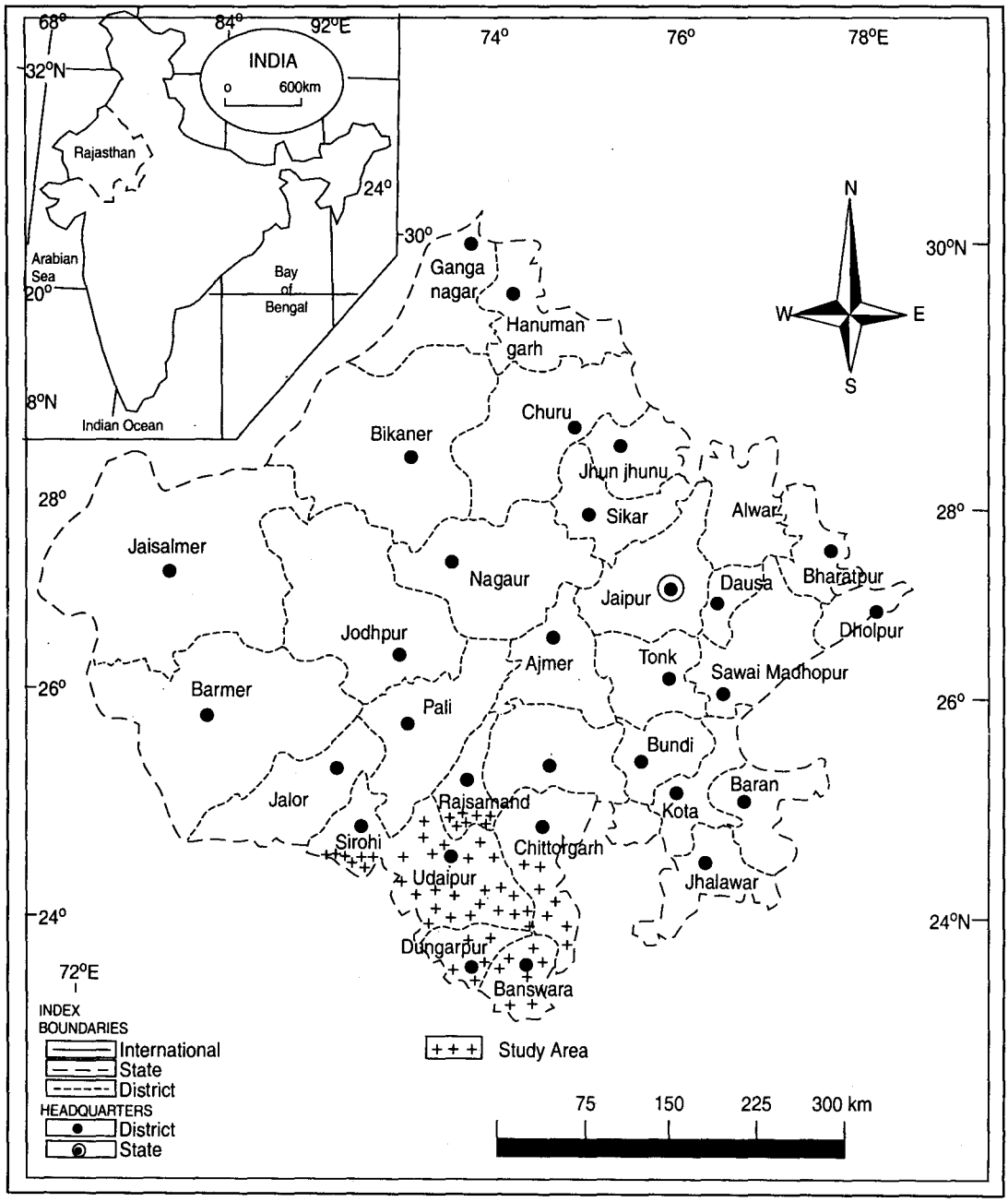
Aravalli hills of Southern Rajasthan are extremely rich in grasses. Being the food of the poorest segment of the society, little attention has been paid on minor millets and to other related wild species of grasses which are very important food of the tribals during difficult period. Considerable work on grasses have been carried out by Caius (1937), Bor (1960), Seetharam (1982, 1983), Katewa and Tiagi (1984), Doshi (1995), Mathur (1996), Sharma (1996), Singatwadia (2000), Katewa *et al.* (2001). A perusal of literature reveals that no ethnobotanical work has been carried out on these group of plants.

Therefore, in the present paper an attempt has been made to study the ethnobotany of minor-millets and related wild species of grasses from the tribal dominated area of southern Rajasthan (Map 1)

Materials and Methods

An ethnobotanical survey of tribal dominated and other rural populated area of the southern Rajasthan was carried out repeatedly in different seasons. The information was recorded about minor millets and related grasses from the study area. The information is based on the interviews with the tribals. Before actually launching into the field work, rapport was established with one or two persons preferably the chief, guidance sought and contact was then established with other tribals of the locality. The linguistic fluency, personality and social standing are crucial for establishing rapport between the participant involved. The local informants were the farmers working in the field, village headmen, priests and other community leaders. Generally two types of interviews were taken of individuals and of groups. For individuals persons were selected at random on the way or entering a hut finding out knowledgeable individuals from the village or village priest, our purpose explained and interviews taken.

To determine the authenticity of information collected during fieldwork, repeated verification of data from different time was done. Thus only the specific and reliable information cross checked with many informants has been incorporated in the present study. All the collected specimens are deposited in the herbarium of the Laboratory of Ethnobotany and Agrostology, Department of Botany, College of Science, ML Sukhadia University, Udaipur (India) for authentication of information and further reference. Number of voucher specimens are also provided. The ethnobotanical information about the minor millets and related grasses are given alphabetically by mentioning their botanical name, local name (if available), ecology, ethnobotany, flowering and fruiting.



Map 1: Distribution of local land races in the study area

Enumeration

(A) Minor Millets

Brachiaria ramosa (Linn.) Stapf. EA* 28

Local name – Kuri **Locality:** Dungarpur

Ecology – An annual grass, common in rainy season on hills, plains etc.

Ethnobotany – *Chapattis* made from the grains flour are eaten by the tribals during famine. Sugar is mixed in grain flour and cooked with milk. This delicious preparation locally called 'Kheech' is eaten by the tribals. The grass is good fodder for cattle. According to tribals, there is no effect of termites/ pests on seed up to 30 years. The ash of the plant is used as an ointment on burns.

Fls. and Frts. – August–September

Echinochloa crusgalli (Linn.) P. Beauv. EA 88

Local name – Batt **Locality** – Banswara

Ecology – It grows on light soils. It is also cultivated with rice.

Ethnobotany – The grains are eaten by tribals either making *chapatti, khitchdi* or *raab* (local preparation). The plant is used in disease of spleen and for checking haemorrhage by the tribals. Extract of whole plant is taken orally in nostril haemorrhage by the tribals.

Fls. and Frts. – August–October

*EA = Ethnobotany and Agrostology Herbarium.

Echinochloa frumentacea Link. EA 417

Local name – Batti **Locality** – Salumber

Ecology – It is grown in moist area.

Ethnobotany – According to tribals it is the quickest growing of all millets. It is grown as a subordinate crop of sorghum and maize by the tribals. Grains are either cooked in water like rice or parched or boiled with milk and sugar by the tribals. The grains are useful in biliousness and constipation.

Fls. and Frts. – August–September

Eleusine coracana (Linn.) Gaertn. EA 418

Local name – Maal **Locality** – Chotta nala

Ecology – An annual and cultivated grass of southern Rajasthan

Ethnobotany – Tribals of southern Rajasthan cultivate this grass and grains are eaten during summer months. According to tribals the nutritive value of grains of this grass is higher than that of rice and equal to that of wheat. Grains can be safely stored for a period of 30-40 years. Grains may also be malted and flour of malted grains is used as nourishing food for infant by the tribals. The grains are used in diabetes by the tribals. The leaf extract is given to woman in childbirth and the plant is reported to be diaphoretic, diuretic. The plant is used in leprosy, liver disease, measles, pneumonia and small pox by the tribals.

Fls. and Frts. – September–November.

Panicum miliaceum Linn. EA 374

Local name – Cheena **Locality** – Chotta nala, Jhadol

Ecology – An annual grass. It is only minor millet which is cultivated during summer months in the southern Rajasthan. The grains are very slippery and shinning.

Ethnobotany – The flour of grains is used for making *chapattis, raab* (local preparation) etc. The grains can be stored safely for many years.

Fls. and Frts. – April-June

Paspalum scrobiculatum Linn. EA 360

Local name – Kodra Locality – Banswara

Ecology – A perennial grass, commonly found near ponds, tank etc. or near marshy places.

Ethnobotany – The grains are used as food by the tribals of Rajasthan. According to tribals it requires more water and is more nutritious as compared to other millets. It contain poisonous narcotic constituent in younger stage, which cause vomiting and vertigo. Paste of whole plant is used for skin diseases and is effective on boils and sores. Mature grains are used to cure diarrhoea.

Fls. and Frts. – August-September

Setaria glauca (Linn.) P. Beauv. EA 422

Local name – Hamli **Locality** – Bili kheda, Banswara

Ecology – An annual grass, very common in protected grassland area.

Ethnobotany – The grains are mixed with the grains of maize to make the chapatis during scarcity of food grains. Powder of grains is mixed in the urine of goat and about two teaspoonful of it is taken orally with water for about a week to cure syphilis.

Fls. and Frts. – September–October

Setaria italica (Linn.) P. Beauv. EA 423

Local name – Kangni **Locality** – Banswara

Ecology– An annual grass, cultivated or growing in gardens at shady places.

Ethnobotany– According to tribals the grains are said to posses heating properties and when taken alone sometimes cause diarrhoea, so the grains are powdered and mixed with flour of cultivated cereals to make the *chapatis*. The straw is thin and considered a good fodder. It is generally fed to cattle without chaffing. The straw makes a good hay when cut in flowering stage. The straw is used for thatching and bedding. The grains are

astringent, diuretic and laxative and are useful externally in rheumatism.

Fls. and Frts. – June–November

(B) Other Related Grasses

Acrachne racemosa (Heyne) Ohwi. EA 14

Local name–Phundale ghass **Locality**–Banswara, Salumber

Ecology – An annual grass, mostly found along the margin of cultivated land.

Ethnobotany – The tribals use the grains during famine condition and also as fodder for the cattle.

Fls. and Frts. – July–September

Alloteropsis cimicina (Linn.) Stapf. EA 13

Local name – Basanti ghass **Locality** – Banswara

Ecology – An annual grass, common in the rainy season to moist and shady places.

Ethnobotany – The grains are used as famine food by the tribals. It is also used as fodder. Root paste is used in toothache.

Fls. and Frts. – August–September.

Apluda mutica Linn. **EA 12**

Local name – Bhangtu, Gunderi **Locality**–Jhadol

Ecology – An annual grass commonly found in hedges by the tribals and amongst bushes.

Ethnobotany – It is considered as a good fodder. The grains are also used as famine food by the tribals. Poultice of whole plant is used to cure mouth sores of cattle. It is also given to cattle with small fishes to cure flatulence. The grass is tied in compact bundles, which are used for thatching of tribal huts.

Fls. and Frt. – August-September

Brachiaria reptans (Linn.) Gard. et. C.E. Hubb. EA 27

Local name – Soraya **Locality** – Jhadol

Ecology – An annual grass, often found in cultivated growing fields with slender creeping stem rooting at lower nodes. An excellent soil binding grass.

Ethnobotany – Grains are used as famine food by the tribals. It is also used as fodder.

Fls. and Frts. – July–September

Cenchrus ciliaris Linn. EA 54

Local name – Dhaman **Locality** – Salumber

Ecology – A perennial grass.

Ethnobotany – This grass is considered to be the most nutritious fodder grass by the tribals. It increases the quantity of milk in milch cattle. Grains are used as famine food by the tribals during severe famine conditions.

Fls. and Frts. – August–October.

Coix lacryma jobi Linn. EA 41

Local name–Garelo **Locality**–Gorana Dam, Sayara

Ecology – An annual grass, common in wet places along streams and ditches.

Ethnobotany – The false fruits known as jobs tears are used as beads for making necklaces by the tribals. Boiled grains are eaten by the tribals. Boiled grains are also eaten to cure dysentery. Grains of this grass are mixed with the grains of *Zea mays* and used for making porridge by the tribals. The leaf extract is given orally in urinary complaints.

Fls. and Frts. – August–September.

Dactyloctenium aegyptium (Linn.) P. Beauv. EA 65

Local name – Malicha **Locality** – Jhadol

Ecology – An annual grass of cultivated field and along roadsides, preferring sandy substratum.

Ethnobotany – The grains are ground to flour by the tribals for making chapatis during scarcity of food. Powder of grains is taken orally with water by the tribals in stomachache.

Fls. and Frts – August–October

Echinochloa colonum (Linn.) Link. EA 90

Local name – Sama **Locality** – Chittorgarh

Ecology – An annual grass, common in waterlogged areas frequently occuring in ditches etc. with muddy soil, often partially under water.

Ethnobotany – It is valued as a quick growing fodder grass by the tribals. It is relished by cattle at all stages and its nutritive value is enhanced when in grain stage. The grains are eaten as rice by the poor tribals. Boiled grains are also eaten by women during the fast of 'Sama pancham'

Fls. and Frts. – August–September

Eleusine indica (Linn.) Gaertn. EA 83

Local name – Chitki **Locality** – Jhadol

Ecology – Annual, common in wet places on the margin of cultivated field.

Ethnobotany – Grains are used as famine food by the tribals and also used as fodder

Fls. and Frts. – July–October.

Haecklochloa granularis (Linn.) O. Ktze. EA 96

Local name – Majri Hankli **Locality** – Bansi

Ecology – An annual grass of rare occurrence, restricted to moist places in open grassland.

Ethnobotany – It is a good fodder grass and used as scarcity food by the tribals.

Fls. and Frts. – September-December

Ischaemum rugosum Salisb. EA 419

Local name – NA **Locality** – Dungarpur

Ecology – An annual grass, growing in wet marshy places especially in rice field.

Ethnobotany – It is used as forage. It is a serious weed in many crops, particularly in rice field. It also provide suitable material for compost. In times of food scarcity the grains are eaten by the tribals.

Fls. and Frts. – September–October.

Panicum paludosum Roxb. EA 420

Local name – NA **Locality** – Sitamata wild life sanctuary

Ecology – A perennial grass with spongy culm often seen growing in submerged water, common on margin of slow flowing streams and puddles.

Ethnobotany – It is used as fodder or famine food by the tribals.

Fls. and Frts. – August–September

Paspalidium flavidium (Retz.) A. Camus. EA 421

Local name – NA **Locality** – Banswara

Ecology – An annual grass of marshy places.

Ethnobotany – The grains are used as food by most of the tribals of the area. It is also used as fodder by the tribals.

Fls. and Frts. – August–October

Setaria paniculifera (Steud.) Fourn. **EA 424**

Local name – NA **Locality** – Banswara

Ecology – A perennial shade loving grass of hilly tracks, usually indicate damp, humus–impregnated soil.

Ethnobotany – The grains are used as famine food during period of food scarcity.

Fls. and Frts. – September–October

Setaria tomentosa (Roxb.) Kunth. EA 426

Local name – NA **Locality** – Dungarpur

Ecology – An annual grass, very common in moist habitats and shady places.

Ethnobotany – The grains are used as famine food in the period of food shortage.

Fls.and Frts. – August–October

Setaria verticillata (Linn.) P. Beauv. **EA 94**

Local name – Jhetudi ghass **Locality** – Jhadol

Ecology – An annual grass, commonly found in sandy clay soil, particularly along irrigation channels, dam-sides and waste places. It is a weed of the garden in shady and neglected places. This species can very easily recognized by its readily sticking spikes to once clothing.

Ethnobotany – It is good fodder grass for the cattle. The grains are eaten by tribals as famine food.

Fls. and Frts. – August–October

Sorghum halepense (Linn.) Pers. EA 425

Local name–Baruri ghass **Locality**–Kodiyat, Udaipur

Ecology – A perennial grass, grow as a wild around and inside the cultivated field.

Ethnobotany – According to tribals this grass is very poisonous in the early stage of growth, which is fatal to cattle. Extract of whole plant is taken orally along with pinch of common salts in fever by the tribals.

Fls. and Frts. – October–January

Urochloa panicoides P. Beauv. EA 427

Local name – NA **Locality** – Kodiyat

Ecology – A tufted annual grass, common in cultivated fields.

Ethnobotany – A very good fodder grass for the cattle. The grains are collected during shortage of food.

Fls.and Frts. – August–September

Results and Discussion

From the ethnobotanical survey it was noted that the tribals of southern Rajasthan, in addition to cultivation of *Zea mays* (as staple crop), also cultivate the traditional minor millets for consumption during the summer months especially when there is shortage of food due to famine. Tribals cultivate minor millets either singly or with *Zea mays*. The crop of minor millets mature within 2-3 months after sowing. All the minor millets except *Panicum miliaceum* are cultivated on the onset of monsoon while *Panicum miliaceum* is cultivated in the end of February or beginning of March. The crop of *Panicum miliaceum* is harvested in the month of June. Though the minor millets are cultivated in a very small area but nutritionally they are considered far superior by the tribals in comparison to other cereals like wheat, rice, maize etc. as one chapati of these minor millet is sufficient to quench the hunger of tribals for whole day. According to tribals out of 8 cultivated minor millets, *Paspalum scrobiculatum* is considered as the most nutritious minor millet. The area of cultivation of these minor millets is shrinking because of division of land in to nuclear families from joint families.

From the ethnobotanical survey it was noted that the tribals consume the minor millets either mixing with other cereals or by boiling the grains. The health, vitality and longevity enjoyed by the tribals have been attributed by them, especially by the elders, to these minor millets and other related wild species of grasses. This belief was substantiated, as some of the grasses used as food have medicinal value.

Due to modernization and urbanization, food habits of tribals have changed. The area of cultivation of minor millets is decreasing year by year. The number of other related wild species of grasses is also decreasing due to overgrazing and recurrent droughts. So the documentation and conservation of these plants is assuming great significance in the light of the food problem likely to be faced in the near future.

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Evaluation of Genetic Diversity in *Pinus gerardiana* Wall. Using Isozymes

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Pinus gerardiana or chilogoza pine is a very important conifer species which is distributed very sparsely and is threatened due to reckless cone harvest leading to almost complete lack of natural regeneration. The present study was carried out to assess genetic variation among ten different populations of the species in Himachal Pradesh using isozymes. A total of nine isozyme loci were recorded for four enzyme systems and fifteen alleles were assigned for different isozymes. The isozyme loci such as PER-I, EST-II and AAT-II were the most variable in terms of allele frequency. For each locus one allele was most common, not only with respect to its frequency, in the population but also with respect to the number of populations which contained it. The isozyme loci PER-II and NADH-I appeared heterozygous. Most of the genetic variation parameters showed a range of variation in different population and also revealed low variation in some of the isolated populations of *P. gerardiana* and perhaps is result of inbreeding in small populations. On the basis of similarity coefficient and genetic distances it is concluded that various populations of *P. gerardiana* differ substantially i.e. upto 7 per cent of total variation can be attributed to the population differences which is generally high for any conifer. It is also concluded that species is highly heterozygous in nature as indicated by negative F-statistics.

Key Words: Genetic diversity, Isozymes, *Pinus gerardiana*.

Pinus gerardiana Wall. (chilgoza pine) is distributed very sparsely in the world. It is confined to the mountains of eastern Afghanistan, parts of Pakistan and scattered patches in dry inner Himalayas. In India, the chilgoza pine is restricted to the dry inner valleys of North-west Himalayas where it grows at altitude of 1600 to 3300 m above mean sea level. As a timber tree, *P. gerardiana* is of little importance and used only where other timber species are not available. However, there is no other conifer species, which can match *P. gerardiana* in terms of its nutritional nuts that have carbohydrates, proteins and fats. Tribals of Kinnaur are largely dependent on the domestic and foreign sale of its nuts and it constitutes the backbone of their economy. Besides, this species is a good soil binder, and thus checks soil erosion. Though chilgoza pine has not been tapped commercially for oleoresin owing to its limited distribution and to avoid destruction of the trees, in order to get more valuable nuts, yet there is great scope for resin extraction. The species is facing a threat due to reckless cone collection by tribals which adversely effects its natural regeneration. Thus, *P. gerardiana* deserves immediate attention for genetic conservation and improvement. The basic pre-requisite for genetic improvement and conservation of genetic resources is the study of genetic variability in existing populations. In order to identify the level of diversity, marker systems have almost become indispensable. During the last two decades, isozymes have been widely used to study genotypic variation in populations (Hamrick and Godt 1989). Unlike quantitative traits, isozymes are not generally influenced by environmental variation, ontogenetically stable and conditionally expressed. The technique fulfils the aim of tree geneticist to detect genetic differences as close as possible to the DNA level because these are direct gene products.

Material and Methods

Seeds of *P. gerardiana* were collected from ten different sites delimited by natural features, such as streams and mountains. These sites lie on both sides of river Sutlej, which divides the chilgoza forests into two mountainous ranges. These sites were Akpa, Rispa, Skiba, Shongthong, Boktu, Kalpa, Dubling, Kanam, Spilow and Morang. The sites Akpa, Skiba, Boktu, Rispa were at the centre of distribution range while Dubling and Morang at the extremes and most isolated. Ten trees were sampled from each site. Megagametophytic tissue from 10-15 seeds was used for enzyme extraction from each tree sampled. Seeds were soaked in 1% hydrogen peroxide for three days and then germinated on moist filter paper at 25°C. When radical emerged out of seed coat by 2 to 5 mm, the megagametophytic tissue was separated and

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homogenised in pre-chilled pestle and mortar using extraction buffer (1:5 w/v). The extraction buffer contained 0.05 M tris base, 0.008 M citric acid (pH 8.3), 0.1% ascorbic acid, 0.1 % cystein hydrochloride and 1 % polyethyelene glycol (PEG). The homogenates thus obtained were centrifuged at 15,000 rpm for 20 minutes at 4°C and stored in a refrigerator in tightly capped tubes till use. Horizontal polyacrylamide gel electrophoresis was carried out to separate the various enzyme systems. The isozymes were fractioned at 4°C at a constant current of 50mA in polyacrylamide gel in electrophoresis tank containing lithium borate buffer (pH 8.3) (Scandalios, 1969). The staining procedure followed for various enzyme systems were according to Conckle *et al.* (1984) with slight modifications. Locations of isozymes were specified by relative mobility (Rm) values, which were calculated according to Kuhn and Fretz (1978). The isozymes of each enzyme system obtained on the gel were named according to Rajora and Zesuffa (1988). The fastest anodal zone was designated as locus 1 for enzyme encoded by multiple loci. Further, the isozymes at a locus were denoted by alphabets A, B, C etc. where A represents the fastest, and B, C, progressively, slower forms. Various genetic parameters such as allele frequency, proportion of polymorphic loci (Nei, 1978), polymorphic index (Allard *et al.*, 1978), observed and expected heterozygosity (Nei, 1978), average allele per locus, effective number of allele per locus (Crow and Kimura, 1970), Wright's F statistic, similarity index (Pontikis *et al.*, 1980) and genetic distance (Nei, 1978) were calculated for each population.

Resuits and Discussion

Only four enzyme systems out of twelve tested were resolved with sufficient activity and clarity, hence were selected for final analysis. These were peroxidase (PER), esterase (EST), nicotinamide adenine dinucleotide dehydrogenase (NADH) and aspartate amino transferase (AAT).

Peroxidase-The investigation revealed that peroxidase isozymes showed two loci and two bands for each locus. Neale *et al.* (1984) also found two zones of activity for peroxidase in Douglas fir. Similarly, Mowrey *et al.* (1990) and Gibson and Hamrick (1991) found two peroxidase loci in *Prunus* spp. and *Pinus pungens*, respectively. Thus, peroxidase seems to be a diamer in *Pinus gerardiana*. The locus PER-I shows a lot of polymorphism while locus PER-II showed a more consistent banding pattern as evidenced from their allele frequencies in various populations.

Esterase-Three different loci were observed for this enzyme system in the sampled genotypes of *P. gerardiana*. The loci EST-I and EST-II had only one band whereas, EST-II had two bands and showed polymorphism. Huang *et al.* (1994) observed three single band zones for esterase in Masson pine.

Nicotinamide adenine dinuleotide dehydrogenase-For this enzyme system two loci were observed and both were polymorphic with two alleles. The allele frequencies at NADH-I did not vary much among the populations. The allele frequencies at locus NADH-II showed variation, NADH-IIA being the most common allele.

Aspartate amino transferase-Two loci were detected for the enzyme aspartate amino transferase activity. The locus AAT-I had only one allele and was monomorphic over all the populations while AAT-II had two alleles, AAT-IIA being the most common allele in all the populations. The result are in agreement with those of Myburg and Harris (1997) who also recorded two loci for AAT activity with one allele at each locus in *P. kesia* and with Yeh and O'Malley (1980) who recorded two loci with two alleles at each locus in Douglas fir. However, some other workers such as Goncharenko *et al.* (1993), Timerjanov (1997), Scaltsoyiznnes *et al.* (1994) and Beaulien and Simon (1994) have recorded three loci for AAT activity in various conifer species.

Genetic interpretations-A total of nine isozyme loci were recorded for four enzyme systems and fifteen alleles were assigned for different isozymes. The allele frequencies for fifteen alleles at nine loci for different populations are listed in Table 1. The loci such as PER-I, EST-II, and AAT-II were most the variable and most of populations did not differ much at loci PER-II, EST-I, EST-III, NADH-I, NADH-II and AAT-I in terms of allele frequencies. It can also be seen that for every locus, there is a most common allele not only with respect to its frequency in a population, but also with respect to number of populations contained it. In the present investigation the per cent polymorphism varied from 33.33 to 66.67 per cent. It is interesting to note that populations which lie in the centre of the distributional range such as Akpa, Rispa, Shongthong, Spilow except Skiba depicted a high per cent polymorphism as compared to the isolated populations such as Dubling, Moorang and Boktu. In pines a wide variation in percentage of polymorphic loci have been reported in literature ranging from 5 per cent in *P. palustris*

Table 1. Probable genotype, allele(s), allele frequency, of *Pinus gerardiana* at different sites based on isozymes

Loci	Sites/ Parameters		Dubling	Moorang	Skiba	Akpa	Rispa	Kanam	Spilow	Shongthong	Boktu	Kalpa
PER–I	Genotype		BB	BB&AB	BB	BB&AB	BB&AB	BB&AB	BB&AB	BB&AB	BB	BB&AB
	Allele frequency	A	0	0.33	0	0.43	0.20	0.20	0.33	0.20	0	0.33
		B	1	0.67	1	0.57	0.80	0.80	0.67	0.80	1	0.67
PER–II	Genotype		AB	AB	AB	AB	AB	AB	AB	AB&AA	AB	AB
	Allele frequency	A	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.67	0.50	0.50
		B	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.33	0.50	0.50
EST–I	Genotype		BB	BB	BB	BB	BB	BB	BB	BB	BB	BB
	Allele frequency	A	0	0	0	0	0	0	0	0	0	0
		B	1	1	1	1	1	1	1	1	1	1
EST–II	Genotype		AA	AA	AA	AA&AB	AA&AB	AA&AB	AB	AA&AB	AA&AB	AA&AB
	Allele frequency	A	1	1	1	0.67	0.67	0.67	0.50	0.80	0.57	0.80
		B	0	0	0	0.33	0.33	0.33	0.50	0.20	0.43	0.20
EST–III	Genotype		AA	AA	AA	AA	AA	AA	AA	AA	AA	AA
	Allele frequency	A	1	1	1	1	1	1	1	1	1	1
		B	0	0	0	0	0	0	0	0	0	0
NADH–I	Genotype		BB&AB	AB	AB	AB	AB	AB	AB	AB	AB	AB
	Allele frequency	A	0.33	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50
		B	0.67	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50
NADH–II	Genotype		AA&Nil	AA&AB	AB	AA&AB	AA&AB	AB	AB	AB	AB&Nil	Nil
	Allele frequency	A	1	0.80	0.50	0.80	0.57	0.50	0.50	0.50	0.50	
		B	0	0.20	0.50	0.20	0.43	0.50	0.50	0.50	0.50	
AAT–I	Genotype		AA	AA	AA	AA	AA	AA	AA	AA	AA	AA
	Allele frequency	A	1	1	1	1	1	1	1	1	1	1
		B	0	0	0	0	0	0	0	0	0	0
AAT–II	Genotype		AA	AA&AB	AA&AB	AA&AB	AA&AB	AA&AB	AA&AB	AB	AA&AB	AB
	Allele frequency	A	1	0.57	0.57	0.57	0.67	0.57	0.67	0.50	0.67	0.50
		B	0	0.43	0.43	0.43	0.33	0.43	0.33	0.50	0.33	0.50

(Synder and Hamaker, 1978) to 100 per cent in *P. heplensis* (Agundez *et al.*, 1999), *P. henryi* (Guo *et al.*, 1998) and *P. taeda* (Schmidtting *et al.*, 1999). The average number of alleles per locus varied from 1.22 to 1.67, which also followed the same trend i.e. lower number of alleles per locus was observed in isolated populations. In 20 species of *Pinus*, the mean of average number of alleles per locus was observed to be 2.29 (Ledig, 1986). Thus in present studies less number of alleles per locus was observed than the average reported in the literature.

The expected mean heterozygosity for various populations in the present study ranged from 0.10 to 0.32, again some of the isolated populations being on the lower side in this parameter also (Table 2). The expected heterozygosity for the species as a whole was recorded to be 0.30, which is on the higher when compared with expected heterozygosities reported in 37 *Pinus* species, which ranged between 0-0.362 with a mean of 0.174 (Ledig, 1986). Direct comparison with other studies may not however be reliable as type of the enzymes, the number of enzymes and the total loci studied vary from study to study. In many cases workers take into account all the loci including the monomorphic ones for calculation of the genetic parameters, whereas, others exclude them. This may lead to differences in the calculated values. The estimate of the fixation index was negative for all the populations studied except for the population at Dubling. The negative values of fixation index reflect the predominance of heterozygotes in these populations. In conifers excess of heterozygotes is an important factor, which can be ascribed to large differences in male and female allelic frequencies. Significant predominance of heterozygotes is common in mature stands of conifers (Muller-Strack *et al.*, 1983; Morgante *et al.*, 1993).

Similarity index-The similarity index values (Pontikis *et al.*, 1980) between and within various populations are directly based on isozyme phenotypes. The maximum similarity coefficient value was found between the populations of Rispa and Kanam followed by that between Kanam and Spilow, which lie at central part of distributional range of *Pinus gerardiana* (Table 3). Minimum similarity index value was recorded between Dubling and Spilow, Dubling being an isolated population. For the populations such as Dubling, Moorang, the within population similarity coefficient was high which indicates higher relatedness.

Table 2. Genetic variation parameters of different populations of *Pinus gerardiana*

Site Parameters	Dubling	Moorang	Skiba	Akpa	Rispa	Kanam	Spilow	Shongthong	Boktu	Kalpa	In total in the species
Total number of loci	9	9	9	9	9	9	9	9	9	8	9
Total number of allele in all loci	11	14	13	15	15	15	15	15	14	13	15
Per cent polymorphic loci	33.33	55.56	44.44	66.67	66.67	66.67	66.67	66.67	55.56	62.50	66.67
Polymorphic index	0.11	0.25	0.22	0.30	0.26	0.30	0.32	0.29	0.27	0.28	0.30
Average number of allele/locus	1.22	1.56	1.44	1.67	1.67	1.67	1.67	1.67	1.56	1.63	1.67
Effective average number of allele/locus	0.12	0.15	0.14	0.20	0.16	0.16	0.16	0.19	0.15	0.17	0.30
Mean observed heterozygosity	0.17	0.39	0.42	0.47	0.44	0.50	0.56	0.44	0.47	0.47	0.42
Mean expected heterozygosity	0.10	0.25	0.22	0.30	0.30	0.30	0.32	0.29	0.27	0.28	0.30
F-statistics	0.32	-0.15	-0.17	-0.32	-0.28	-0.38	-0.48	-0.28	-0.30	-0.36	-0.40

Table3. Intra- and inter-population similarity matrix between ten different populations of *Pinus gerardiana* based on isozymes

	Dubling	Moorang	Skiba	Akpa	Rispa	Kanam	Spilow	Shongthong	Boktu	Kalpa
Dubling	0.96									
Moorang	0.81	0.94								
Skiba	0.89	0.84	0.86							
Akpa	0.78	0.89	0.84	0.85						
Rispa	0.88	0.85	0.72	0.83	0.84					
Kanam	0.76	0.86	0.80	0.85	0.90	0.85				
Spilow	0.61	0.81	0.86	0.85	0.88	0.89	0.90			
Shongthong	0.72	0.86	0.84	0.72	0.84	0.86	0.85	0.90		
Boktu	0.78	0.80	0.84	0.71	0.84	0.88	0.84	0.79	0.82	
Kalpa	0.78	0.83	0.75	0.81	0.77	0.79	0.74	0.74	0.81	0.91

Table 4. Genetic distance matrix between ten different populations of *Pinus gerardiana* based on isozymes

	Dubling	Moorang	Skiba	Akpa	Rispa	Kanam	Spilow	Shongthong	Boktu	Kalpa
Dubling										
Moorang	0.046									
Skiba	0.060	0.029								
Akpa	0.072	0.018	0.058							
Rispa	0.079	0.021	0.182	0.011						
Kanam	0.156	0.031	0.189	0.023	0.001					
Spilow	0.102	0.054	0.056	0.023	0.004	0.009				
Shongthong	0.086	0.060	0.028	0.209	0.064	0.019	0.026			
Boktu	0.076	0.061	0.029	0.224	0.018	0.009	0.017	0.024		
Kalpa	0.130	0.060	0.060	0.060	0.053	0.048	0.068	0.024	0.072	

The mean values of within population similarity coefficient and between population similarity coefficients were 0.883 and 0.813, respectively. This indicates that about 7 per cent variation is due to their interpopulation differences. This means that genetic variation in *P. gerardiana* is high in local populations and the same allele tends to be distributed throughout the whole range of the species. The results are in agreement with those of Hamrick and Godt (1989) who concluded that conifer species have approximately 6.8 per cent of their variation among populations.

Genetic distance-The Nei's genetic distances are also estimation of the inter-population genetic variability. The genetic distance almost followed the same trend as that of similarity coefficient (Table 4). The mean genetic distance for all possible pairs of populations was 0.06 showing that differentiation among populations was substantially high.

Although average inter-population genetic distances within populations for most of the conifers is rather low viz., 0.003 in Russian population of *P. koraiensis* (Potenko and Velikov, 1998), 0.013 in *Larix sukaczewii* (Timerjanov, 1997), 0.008 in *P. thunbergii* (Kim *et al.*, 1997), 0.017 in *P. sylvestris* (Goncharennko *et al.*, 1994) and 0.0037

in Doublas fir (Yeh and O'Malley, 1980). However, Scaltsoyiannes (1999) observed very high genetic distance between population of *Cedrus libani* (upto 0.487).

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International Treaty on Plant Genetic Resources for Food and Agriculture: An Assessment

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The sustainable use of plant genetic resources (PGR), has been a common concern of humankind. The conservation and sustainable use of PGR is of critical importance for meeting the food, health and other needs of the growing world population. Earlier PGR were considered a common heritage of mankind and were freely available for acquisition and utilization, but with the Convention on Biological Diversity (CBD) coming into force with effect from December 29, 1993, the sovereign rights of the nations over their biological resources have been recognised and the nations are responsible for conservation of biological diversity and using it in a sustainable manner. The access to and sharing of both, genetic resources and technologies, are essential, as most of the countries depend largely on PGR for food and agriculture that originated elsewhere. Nations may, therefore, mutually benefit from creation of an effective system for facilitated access to these resources, while exercising their sovereign rights over their plant genetic resources for food and agriculture (PGRFA). It was, thus considered appropriate to formulate an international agreement within the frame work of the Food and Agriculture Organization (FAO) of the United Nations to achieve the objectives in harmonization with the provisions made under CBD. After years of negotiations, a treaty named "International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) was adopted in November, 2001 at the 31st Conference of the UN Food and Agricultural Organisation (FAO, 2001).

Genesis of the Treaty

In 1983, the FAO Conference established the inter-governmental Commission on Plant Genetic Resources (now the Commission on Genetic Resources for Food and Agriculture) and adopted a non-binding International Undertaking (IU) on Plant Genetic Resources. The objectives of IU were to ensure that "PGR of economic and or social interest, particularly for agriculture will be explored, preserved, evaluated and made available for plant breeding and scientific purposes" This undertaking was based on the universally accepted principle that PGR are a heritage of mankind and consequently should be available without restriction.

After 1993, when CBD was adopted during Rio Earth Summit of the United Nations, the authority to determine access to genetic resources became the responsibility of national governments, which was to be determined on the principles of prior informed consent (PIC) and mutually agreed terms (MAT).

In 1993, the FAO adopted a resolution (7/93) for the revision of IU to bring it in harmony with CBD, and to address other outstanding issues of access to PGR held in *ex situ* collections by Consultative Group of International Agricultural Research Centres (CGIAR), and the realization of farmers rights. These issues were not addressed by IU earlier.

The revised text of IU was submitted to the FAO Conference on 3rd Nov, 2001 and adopted as "The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA).

Salient Provisions

Objectives of the Treaty: The objectives of the Treaty are "the conservation and sustainable use of PGRFA and the fair and equitable sharing of benefits arising out of their use, in harmony with the CBD, for sustainable agriculture and food security". The objectives are proposed to be attained by closely linking this Treaty to the FAO of the United Nations and to the CBD.

Entry and termination of the Treaty: The Treaty was open for signature at the FAO from 3 November 2001 to 4 November 2002 by all members of FAO and other states that are not members of FAO but are members of either the United Nations, or any of its specialized agencies. However, this Treaty is subject to ratification, acceptance or approval by the members and non-members of FAO as referred above. The Treaty shall come into force on 29th June 2004, after 90 days of the deposit of the 40th instrument of ratification and acceptance[1].

A contracting party at any time, after two years of the Treaty coming into force, may notify in writing for its withdrawal from the Treaty. The withdrawal shall be effective after one year of receipt of the notification. The Treaty shall be automatically terminated if and when,

as a result of withdrawals, the number of contracting parties drops below forty, unless the remaining contracting parties unanimously decide otherwise. In the event of termination the disposition of assets shall be governed by the financial rules to be adopted by the Governing Body.

Relevant terms in the Treaty: For the purpose of this Treaty, some important terms have been defined as follows:

- "*In situ* conservation" means the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated plant species, in the surroundings where they have developed their distinctive properties.
- "*Ex situ* conservation" means the conservation of plant genetic resources for food and agriculture outside their natural habitat.
- "Plant genetic resources for food and agriculture" means any genetic material of plant origin of actual or potential value for food and agriculture.
- "Genetic material" means any material of plant origin, including reproductive and vegetative propagating material, containing functional units of heredity.
- "Centre of origin" means a geographical area where a plant species, either domesticated or wild, first developed its distinctive properties.
- "Centre of crop diversity" means a geographical area containing a high level of genetic diversity for crop species in *in situ* conditions.

Obligations on part of Contracting Parties

Each contracting party of the Treaty shall ensure the conformity of its laws, regulations and programmes with the provisions of the Treaty. Each contracting party shall, subject to national legislation, and in cooperation with other contracted parties where appropriate, promote an integrated approach to the exploration, conservation and sustainable use of PGRFA and shall in particular, as appropriate, undertake some of the activities like:

(i) Survey and inventory of PGRFA;

(ii) Promote the collection of PGRFA and relevant associated information on those PGR that are under threat or are of potential use;

(iii) Promote or support, as appropriate, farmers and local communities' efforts to manage and conserve on-farm their PGRFA;

(iv) Promote *in situ* conservation of wild crop relatives and wild plants for food production;

(v) Cooperate to promote the development of an efficient and sustainable system of *ex situ* conservation, giving due attention to the need for adequate documentation, characterization, regeneration and evaluation;

(vi) Take steps to minimize or, if possible, eliminate threats to PGRFA.

The contracting parties are also obligated to develop and maintain appropriate policies and legal measures to promote sustainable use of PGR for sustainable agriculture and food security, and international cooperation, in the following manner.

(a) At national level by

(i) development and maintenance of diverse farming systems;

(ii) strengthening research which enhances and conserves biological diversity by maximising intra and inter specific variation;

(iii) promoting breeding efforts for development of varieties adapted to social, economic and ecological conditions;

(iv) broadening genetic base of crops;

(v) promoting locally adapted crops and varieties;

(vi) supporting the wider use of diversity of varieties and species in on-farm management;

(vii) reviewing policies for varieties release and seed production as appropriate

(b) At the international level by

(i) cooperating with other contracting parties, directly or through FAO and the relevant international organizations in the conservation and sustainable of PGRFA.

(ii) cooperating in establishment or strengthening the capabilities of developing countries and countries with economies in transition with respect to conservation and sustainable use of PGRFA.

The Multilateral System of access and benefit sharing

In exercise of sovereign rights of nations over their plant genetic resources for food and agriculture, the Treaty envisages the establishment of a multilateral system (MS) covering a list of 35 food and 29 forage crops (Annexure 1 of the Treaty) selected on the criteria of food security and interdependence. It shall include all PGRFA of the listed crops that are under the management and control of the contracting parties and in public domain. The

contracting parties shall also take appropriate measures to encourage national and legal persons within their jurisdiction, holding PGRFA of the listed crops, to include such PGRFA in the MS. The MS shall also include the PGRFA as listed, and held in the ex situ collections of the International Agricultural Research Centres of the CGIAR.

The access to PGRFA shall be provided solely for the purpose of utilization and conservation for research, breeding and training for food and agriculture, provided that such purpose does not include chemical, pharmaceutical and/or other non-food/feed industrial uses (Article 12.3 a). The access is to be accorded expeditiously without the need to track individual accessions and either no fee or fee, not exceeding the minimal cost involved, is to be charged. It is also envisaged in the Treaty that all the available passport data, subject to applicable law, and any other associated available non-confidential descriptive information should be made available with PGRFA being provided. However, as per Article 12.3 (d), the recipient shall not claim any intellectual property or other rights that limit the facilitated access to PGRFA, or their genetic parts or components, in the form received from MS. The MS also makes it mandatory (Article 12.3 g) on the part of recipient to continue to make the accessed and conserved material available to MS.

Article 13 of the Treaty describes about the benefit sharing mechanisms in the MS. It has been indicated that the benefits arising from the use, including the commercialization of PGRFA under MS shall be shared fairly and equitably through different mechanisms like the exchange of information, access to and transfer of technology, capacity building, and the sharing of the benefits arising from commercialization, taking into account the priority activity areas in the rolling Global Plan of Action, under the guidance of the Governing Body.

Article 13.2 d (ii) of the Treaty states that "a recipient who commercializes a product that is a PGRFA and that incorporates material accessed from MS, shall pay to the mechanism, such as Trust Account, as referred in the Article 19.3 f of the Treaty, an equitable share of the benefits arising from commercialization of that product, except whenever such a product is available without restriction to others for further research and breeding, in which case the recipient who commercializes shall be encouraged to make such payment".

The facilitated access to PGRFA shall be provided in pursuance of standard material transfer agreement (MTA), which shall be adopted by the Governing Body and contain the provisions of the Articles 12.3 (a, d, g) and 13.2 d (ii) and other relevant provisions of the Treaty as referred above. The conditions of MTA shall also apply to the transfer of PGRFA to another person or entity, as well as to any subsequent transfers of these PGRFA.

It has been emphasized under the Article 13.3 of benefit sharing that the benefits arising from the use of PGRFA that are shared under MS should flow primarily, directly or indirectly, to the farmers in all countries, especially in developing countries, and countries with economies in transition, who conserve and sustainably utilize PGRFA. This component of Treaty will largely depend upon the effectiveness of implementation of the Global Plan of Action and the funding strategy, particularly for the developing countries and countries with economies in transition, especially in centres of diversity and the least developed countries.

Farmers' Rights

It has been very well recognized in the Treaty (Article 9) that the local and indigenous communities and farmers of all regions of the world, particularly those in the centres of origin and crop diversity have made enormous contributions and will continue to make for the development and conservation of plant genetic resources which constitute the basis of food and agriculture. The responsibility for realizing the farmers' rights related to PGRFA rests with the national governments and accordingly, as appropriate and subject to its national legislation, take measures to protect and promote farmers' rights with respect to (i) protection of traditional knowledge related to PGRFA, (ii) right to equitable share of the benefits arising out of use of PGRFA and (iii) the right to participate in decision making, at national level on matters related to conservation and sustainable use of PGRFA.

Also, the Treaty shall not limit any rights that farmers have to save, use, exchange and sell farm saved seed/ propagating material, subject to national law and as appropriate.

Supporting Components

Four major components supportive to the effective working of the Treaty have been recognized. These are:

(1) Effective implementation of Global Plan of Action (FAO, 1996), where 20 activities have been identified to be pursued through national actions.

(2) Recognising the importance of *ex situ* collection of PGRFA held in trust by International Agricultural Research Centres (IARCs) of the CGIAR with the Treaty, the Contracting Parties have called upon IARCs to sign agreements with the Governing Body with regard to *ex situ* collections listed as well as non-listed crops with certain terms and conditions such as:

(i) PGRFA listed in Annex 1 of the Treaty and held by the IARCs shall be made available as per standard MTA to be adopted by the Governing Body.

(ii) PGRFA not listed in Annex 1 of the Treaty and collected before CBD that are held by IARCs shall be made available as per MTA currently in use pursuant to the agreements between IARCs and FAO. The MTA shall be modified by the Governing Body not later than its second regular session.

(iii) The Contracting Parties in whose territory the PGRFA were collected from *in situ* conditions shall be provided with samples of such PGRFA on demand, without MTA.

(3) The existing cooperation in the international networks on PGRFA should be encouraged to be developed on the basis of existing arrangements and consistent with the terms of the Treaty.

(4) The contracting parties should cooperate in development and strengthening of a global information system to facilitate exchange of information, based on existing information systems, on scientific, technical and environmental matters related to PGRFA.

The Institutional and Financial Provisions

The Governing Body (GB) of this Treaty shall be composed of all contracting parties. All the decisions will be taken by consensus. The functions of the GB shall be to promote the full implementation of the Treaty keeping in view its objectives particularly, for the operation of MS and establishment of an appropriate mechanism, like as a Trust Account, for receiving and utilizing financial resources that will accrue to it for purpose of implementing this Treaty.

The Secretary of GB shall be appointed by the Director General of FAO, with the approval of the GB. The Director General of FAO shall be the Depositary of this Treaty.

For financial resources, the contracting parties have to make a funding strategy for the effective implementation of the Treaty. The funding strategy shall be to enhance the availability, transparency, efficiency and effectiveness of the provisions of the financial resources. To mobilize funds for priority activities, plans and programmes, in particular to the developing countries and countries with economies in transition, the GB shall periodically set targets for such funding. The effectiveness and efficiency in implementation of programmes and policies of the Treaty in building capacity in PGRFA in developing countries and countries with economies in transition will mainly depend on the effective allocation of funds by the Contracting Parties, particularly by the developed countries.

The other component of the funding strategy is to get revenue through the benefits arising out of the commercial utilization of PGRFA (Article 13.2 d). Voluntary contributions may also be provided by the Contracting Parties, the private sector, non-governmental organizations and other sources. The GB shall consider modalities of a strategy to promote such contributions.

Assessment and Perception of the Treaty

The International Undertaking (IU) adopted by FAO in 1983 came to a close when an international binding agreement "The International Treaty on Plant Genetic Resources for Food and Agriculture" was adopted. This treaty was necessitated to harmonize the provisions made under Convention on Biological Diversity (CBD) particularly with respect to the sovereign rights of the nations over their biological resources, fair and equitable sharing of the benefits arising out of the use of biological resources, facilitating access and conservation and sustainable use of biological resources. This has paved a way to understand the value of biological resources, and the significance of farmers and communities in the development and conservation of biological resources.

The Contracting Parties should see that the emphasis laid under article 7.2 (a) for the international cooperation to be mainly directed towards establishing or strengthening the capabilities of developing countries and countries with economies in transition, associated with centres of crop diversity should be carried out in letter and spirit so that the important objective of the Treaty to promote conservation of the PGRFA is not vitiated.

Concerns Regarding Conditions of Access: The issue related to access to PGRFA should be made clear on

the point (i) whether the material has to be accessed through a single window system (Nagamine, 2004) or (ii) it has to be at accessed directly from the concerned party.

It will be desirable if the access is made through single window system. IARC should sign the agreement with FAO, who will hold the material in trust and supply the materials to the indenting party through MTA. By this way, a uniform system will be developed for utilization of biological resource under the MS.

Crops and forages covered: In the agreement arrived at, after consideration of various thoughts, where some countries wanted every crop to be brought under MS, the biodiversity-rich developing world managed to keep back some valuable crops from the common system. India favoured retaining all crops dealt under CGIAR system. Ultimately, it was agreed to included the selected crops based on food security and interdependence amongst countries. The 35 food crops and 29 forages (listed in Annex 1) were selected. This list represents about 85 percent of the crops important for food security. However, there seems to be some major gaps in the list, if the criteria of food security is considered. Crops like soybean, groundnut, sugarcane tomato and most tropical forages are excluded, while asparagus and strawberry are included (Fowler, 2004).

Regarding the number of crops and forages, there are apprehensions. Some countries feel it to be exhaustive, while others have rated them to be a low number (Chawdhary, 2002). To add crops and forages to the list will be a matter of 'amendment' now, which can be proposed once the Governing Body is established. But that too will not be a easy job since the amendment need to be approved by all, due to the 'consensus' clause of the Treaty.

The fear of biopiracy expressed by the author (Chawdhary, 2002), about the uncovered crops seems to be unfounded. The author had expressed that the Treaty may increase the threat to the diversity of genetic resources, escalate biopiracy and inactivate identification, collection, documentation and conservation of PGR excluded from MS. But, It has been reaffirmed under CBD as well as in the Treaty that the states have sovereign rights and are responsible for conservation and sustainable use of their biological biodiversity with a fair and equitable sharing of benefit arising from use of the genetic resources. This leaves no scope for such suspicions. Accordingly, the Biological Diversity Act 2002 has been passed in India and access to PGR by foreigners would be as per provisions of the Act. The access and regulations of PGR for each and every crop will be controlled by National Biodiversity Authority. Apart from this, the ex situ collections of all the crops held in trust by IARCs are to be supplied as per the standard MTA which forbids applying for any IPR over the acquired germplasm.

Provision of Farmers Rights and Intellectual Property Rights: The holders of biological resources have taken a right step in bringing only those crops and forages under the Treaty which are important for food security and interdependence of many countries. The other crops and forages would either be, handled through bilateral agreements or amendments made in the Treaty at later stages. The main aspect where conflicts or the differences of opinions have surfaced are the Farmers Rights, benefits sharing and the IPRs related to biological resources. The Treaty clearly envisages the farmers rights under Article 9 with respect to protection of their traditional knowledge, right to equitable sharing of use of PGRFA and their participation in decision making related to PGRFA conservation and sustainable uses. Article 13.3 states that the benefits sharing from the use of PGRFA should primarily, directly or indirectly, flow to farmers. But the responsibility of all these aspects rests with the national governments, who have to make laws, plans and policies in cognizance of these issues. This may be possible at the national level but there should be a commitment from the international agency like FAO to take care of these issues of the international level also, since the Treaty allows claiming IPRs, if not in their original forms, but on their modified forms, as could be interpreted from the Article 12.3 (d) that mentions as not to claim any IPR "in the form received". Since patents are being allowed on the processes of varietal development and even for a 'gene' extracted from a plant in some developed countries, the commercialization aspect definitely creeps in and therefore, the authority at the international level should see how to extract claims of benefit sharing arising out of use of the biological resources.

Involvement of Private Sector towards benefit sharing: Value addition being an important component of PGRFA, it would be desirable to involve private sector and food industries to exploit the commercialization aspect of PGRFA to the fullest extent to take advantage of benefit sharing and enhance the allocation to the funding strategy, as provided in Article 13.6, where the contracting parties are advised to consider modalities for voluntary benefit

sharing contributions by food processing industries that benefit from PGRFA.

Conclusion

The PGRFA are the most essential component of food security, the world over. As most of the countries largely depend on the PGRFA that originated elsewhere, it is necessary to make provisions for the access and sharing of PGRFA at the global level. The recognition of sovereign rights of the nations over their genetic resources, after adoption of CBD in 1993, brought out a major shift in national germplasm exchange policies, and therefore, it became essential, at the international level, to formulate the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) for conservation and sustainable utilization of PGRFA in harmony with CBD provisions.

Presently 64 crops have been covered in the multilateral system (MS). PGRFA will be exchanged through MS where material transfer agreements (MTA) are likely to take care of IPR issues. It should be considered as an opportunity by member countries to regain mutual exchange of PGRFA and related technologies for ushering in food and nutritional security for the human population. The list of crops may be expanded at the later stage by the Governing Body. The treaty envisages the protection of farmers rights as well, in terms of their traditional knowledge and involvement in management of PGRFA. The ITPGRFA will ultimately benefit the humankind at the global level while signifying the sovereign rights of the nations over their biological resources and taking care of benefit sharing and sustainable use of the resources.

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International Treaty on Plant Genetic Resources for Food and Agriculture: An Assessment

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The sustainable use of plant genetic resources (PGR), has been a common concern of humankind. The conservation and sustainable use of PGR is of critical importance for meeting the food, health and other needs of the growing world population. Earlier PGR were considered a common heritage of mankind and were freely available for acquisition and utilization, but with the Convention on Biological Diversity (CBD) coming into force with effect from December 29, 1993, the sovereign rights of the nations over their biological resources have been recognised and the nations are responsible for conservation of biological diversity and using it in a sustainable manner. The access to and sharing of both, genetic resources and technologies, are essential, as most of the countries depend largely on PGR for food and agriculture that originated elsewhere. Nations may, therefore, mutually benefit from creation of an effective system for facilitated access to these resources, while exercising their sovereign rights over their plant genetic resources for food and agriculture (PGRFA). It was, thus considered appropriate to formulate an international agreement within the frame work of the Food and Agriculture Organization (FAO) of the United Nations to achieve the objectives in harmonization with the provisions made under CBD. After years of negotiations, a treaty named "International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) was adopted in November, 2001 at the 31st Conference of the UN Food and Agricultural Organisation (FAO, 2001).

Genesis of the Treaty

In 1983, the FAO Conference established the inter-governmental Commission on Plant Genetic Resources (now the Commission on Genetic Resources for Food and Agriculture) and adopted a non-binding International Undertaking (IU) on Plant Genetic Resources. The objectives of IU were to ensure that "PGR of economic and or social interest, particularly for agriculture will be explored, preserved, evaluated and made available for plant breeding and scientific purposes" This undertaking was based on the universally accepted principle that PGR are a heritage of mankind and consequently should be available without restriction.

After 1993, when CBD was adopted during Rio Earth Summit of the United Nations, the authority to determine access to genetic resources became the responsibility of national governments, which was to be determined on the principles of prior informed consent (PIC) and mutually agreed terms (MAT).

In 1993, the FAO adopted a resolution (7/93) for the revision of IU to bring it in harmony with CBD, and to address other outstanding issues of access to PGR held in *ex situ* collections by Consultative Group of International Agricultural Research Centres (CGIAR), and the realization of farmers rights. These issues were not addressed by IU earlier.

The revised text of IU was submitted to the FAO Conference on 3rd Nov, 2001 and adopted as "The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA).

Salient Provisions

Objectives of the Treaty: The objectives of the Treaty are "the conservation and sustainable use of PGRFA and the fair and equitable sharing of benefits arising out of their use, in harmony with the CBD, for sustainable agriculture and food security". The objectives are proposed to be attained by closely linking this Treaty to the FAO of the United Nations and to the CBD.

Entry and termination of the Treaty: The Treaty was open for signature at the FAO from 3 November 2001 to 4 November 2002 by all members of FAO and other states that are not members of FAO but are members of either the United Nations, or any of its specialized agencies. However, this Treaty is subject to ratification, acceptance or approval by the members and non-members of FAO as referred above. The Treaty shall come into force on 29th June 2004, after 90 days of the deposit of the 40th instrument of ratification and acceptance[1].

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Relevant terms in the Treaty: For the purpose of this Treaty, some important terms have been defined as follows:

- "*In situ* conservation" means the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated plant species, in the surroundings where they have developed their distinctive properties.
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(b) At the international level by

(i) cooperating with other contracting parties, directly or through FAO and the relevant international organizations in the conservation and sustainable of PGRFA.

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The Multilateral System of access and benefit sharing

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Concerns Regarding Conditions of Access: The issue related to access to PGRFA should be made clear on

the point (i) whether the material has to be accessed through a single window system (Nagamine, 2004) or (ii) it has to be at accessed directly from the concerned party.

It will be desirable if the access is made through single window system. IARC should sign the agreement with FAO, who will hold the material in trust and supply the materials to the indenting party through MTA. By this way, a uniform system will be developed for utilization of biological resource under the MS.

Crops and forages covered: In the agreement arrived at, after consideration of various thoughts, where some countries wanted every crop to be brought under MS, the biodiversity-rich developing world managed to keep back some valuable crops from the common system. India favoured retaining all crops dealt under CGIAR system. Ultimately, it was agreed to included the selected crops based on food security and interdependence amongst countries. The 35 food crops and 29 forages (listed in Annex 1) were selected. This list represents about 85 percent of the crops important for food security. However, there seems to be some major gaps in the list, if the criteria of food security is considered. Crops like soybean, groundnut, sugarcane tomato and most tropical forages are excluded, while asparagus and strawberry are included (Fowler, 2004).

Regarding the number of crops and forages, there are apprehensions. Some countries feel it to be exhaustive, while others have rated them to be a low number (Chawdhary, 2002). To add crops and forages to the list will be a matter of 'amendment' now, which can be proposed once the Governing Body is established. But that too will not be a easy job since the amendment need to be approved by all, due to the 'consensus' clause of the Treaty.

The fear of biopiracy expressed by the author (Chawdhary, 2002), about the uncovered crops seems to be unfounded. The author had expressed that the Treaty may increase the threat to the diversity of genetic resources, escalate biopiracy and inactivate identification, collection, documentation and conservation of PGR excluded from MS. But, It has been reaffirmed under CBD as well as in the Treaty that the states have sovereign rights and are responsible for conservation and sustainable use of their biological biodiversity with a fair and equitable sharing of benefit arising from use of the genetic resources. This leaves no scope for such suspicions. Accordingly, the Biological Diversity Act 2002 has been passed in India and access to PGR by foreigners would be as per provisions of the Act. The access and regulations of PGR for each and every crop will be controlled by National Biodiversity Authority. Apart from this, the ex situ collections of all the crops held in trust by IARCs are to be supplied as per the standard MTA which forbids applying for any IPR over the acquired germplasm.

Provision of Farmers Rights and Intellectual Property Rights: The holders of biological resources have taken a right step in bringing only those crops and forages under the Treaty which are important for food security and interdependence of many countries. The other crops and forages would either be, handled through bilateral agreements or amendments made in the Treaty at later stages. The main aspect where conflicts or the differences of opinions have surfaced are the Farmers Rights, benefits sharing and the IPRs related to biological resources. The Treaty clearly envisages the farmers rights under Article 9 with respect to protection of their traditional knowledge, right to equitable sharing of use of PGRFA and their participation in decision making related to PGRFA conservation and sustainable uses. Article 13.3 states that the benefits sharing from the use of PGRFA should primarily, directly or indirectly, flow to farmers. But the responsibility of all these aspects rests with the national governments, who have to make laws, plans and policies in cognizance of these issues. This may be possible at the national level but there should be a commitment from the international agency like FAO to take care of these issues of the international level also, since the Treaty allows claiming IPRs, if not in their original forms, but on their modified forms, as could be interpreted from the Article 12.3 (d) that mentions as not to claim any IPR "in the form received". Since patents are being allowed on the processes of varietal development and even for a 'gene' extracted from a plant in some developed countries, the commercialization aspect definitely creeps in and therefore, the authority at the international level should see how to extract claims of benefit sharing arising out of use of the biological resources.

Involvement of Private Sector towards benefit sharing: Value addition being an important component of PGRFA, it would be desirable to involve private sector and food industries to exploit the commercialization aspect of PGRFA to the fullest extent to take advantage of benefit sharing and enhance the allocation to the funding strategy, as provided in Article 13.6, where the contracting parties are advised to consider modalities for voluntary benefit

sharing contributions by food processing industries that benefit from PGRFA.

Conclusion

The PGRFA are the most essential component of food security, the world over. As most of the countries largely depend on the PGRFA that originated elsewhere, it is necessary to make provisions for the access and sharing of PGRFA at the global level. The recognition of sovereign rights of the nations over their genetic resources, after adoption of CBD in 1993, brought out a major shift in national germplasm exchange policies, and therefore, it became essential, at the international level, to formulate the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) for conservation and sustainable utilization of PGRFA in harmony with CBD provisions.

Presently 64 crops have been covered in the multilateral system (MS). PGRFA will be exchanged through MS where material transfer agreements (MTA) are likely to take care of IPR issues. It should be considered as an opportunity by member countries to regain mutual exchange of PGRFA and related technologies for ushering in food and nutritional security for the human population. The list of crops may be expanded at the later stage by the Governing Body. The treaty envisages the protection of farmers rights as well, in terms of their traditional knowledge and involvement in management of PGRFA. The ITPGRFA will ultimately benefit the humankind at the global level while signifying the sovereign rights of the nations over their biological resources and taking care of benefit sharing and sustainable use of the resources.

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ANNEX I

List of Crops Covered under the Multilateral System

FOOD CROPS

Crop	Genus	Observations
Breadfruit	Artocarpus	Breadfruit only.
Asparagus	*Asparagus*	
Oat	*Avena*	
Beet	*Beta*	
Brassica complex	*Brassica et al.*	Genera included are: *Brassica, Armoracia, Barbarea, Camelina, Crambe, Diplotaxis, Eruca, Isatis, Lepidium, Raphanobrassica, Raphanus, Rorippa*, and *Sinapis*. This comprises oilseed and vegetable crops such as cabbage, rapeseed, mustard, cress, rocket, radish, and turnip. The species *Lepidium meyenii* (maca) is excluded.
Pigeon Pea	*Cajanus*	
Chickpea	*Cicer*	
Citrus	*Citrus*	Genera *Poncirus* and *Fortunella* are included as root stock.
Coconut	*Cocos*	
Major aroids	*Colocasia, Xanthosoma*	Major aroids include taro, cocoyam, dasheen and tannia.
Carrot	*Daucus*	
Yams	*Dioscorea*	
Finger Millet	*Eleusine*	
Strawberry	*Fragaria*	
Sunflower	*Helianthus*	
Barley	*Hordeum*	
Sweet Potato	*Ipomoea*	
Grass pea	*Lathyrus*	
Lentil	*Lens*	
Apple	*Malus*	
Cassava	*Manihot*	*Manihot esculenta* only.
Banana / Plantain	*Musa*	Except *Musa textilis*.
Rice	*Oryza*	
Pearl Millet	*Pennisetum*	
Beans	*Phaseolus*	Except *Phaseolus polyanthus*.
Pea	*Pisum*	
Rye	*Secale*	
Potato	*Solanum*	Section tuberosa included, except *Solanum phureja*.
Eggplant	*Solanum*	Section melongena included.
Sorghum	*Sorghum*	
Triticale	*Triticosecale*	
Wheat	*Triticum et al.*	Including *Agropyron, Elymus*, and *Secale*.
Faba Bean / Vetch	*Vicia*	
Cowpea *et al.*	*Vigna*	
Maize	*Zea*	Excluding *Zea perennis, Zea diploperennis*, and *Zea luxurians*.

FORAGES

Genera	Species
Legume Forages	
Astragalus	*chinensis, cicer, arenarius*
Canavalia	*ensiformis*
Coronilla	*varia*
Hedysarum	*coronarium*
Lathyrus	*cicera, ciliolatus, hirsutus, ochrus, odoratus, sativus*
Lespedeza	*cuneata, striata, stipulacea*
Lotus	*corniculatus, subbiflorus, uliginosus*
Lupinus	*albus, angustifolius, luteus*
Medicago	*arborea, falcata, sativa, scutellata, rigidula, truncatula*
Melilotus	*albus, officinalis*
Onobrychis	*viciifolia*
Ornithopus	*sativus*
Prosopis	*affinis, alba, chilensis, nigra, pallida*
Pueraria	*phaseoloides*
Trifolium	*alexandrinum, alpestre, ambiguum, angustifolium, arvense, agrocicerum, hybridum, incarnatum, pratense, repens, resupinatum, rueppellianum, semipilosum, subterraneum, vesiculosum*
Grass Forages	
Andropogon	*gayanus*
Agropyron	*cristatum, desertorum*
Agrostis	*stolonifera, tenuis*
Alopecurus	*pratensis*
Arrhenatherum	*elatius*
Dactylis	*glomerata*
Festuca	*arundinacea, gigantea, heterophylla, ovina, pratensis, rubra*
Lolium	*hybridum, multiflorum, perenne, rigidum, temulentum*
Phalaris	*aquatica, arundinacea*
Phleum	*pratense*
Poa	*alpina, annua, pratensis*
Tripsacum	*laxum*
Other Forages	
Atriplex	*halimus, nummularia*
Salsola	*vermiculata*

Evaluation and Classification of Sugarcane Germplasm using Hierarchical Cluster Analysis

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Hierarchical cluster analysis (UPGMA-method) was carried out for the classification of 50 sugarcane clones based on 14 yield and quality characters, which resulted in the formation of 5 clusters having 2 to 22 clones. Cluster II had the maximum (22) and cluster I had minimum (2) clones. It has classified germplasm accession according to their degree of similarity or dissimilarity. Dendrogram was prepared using rescaled distances.

Key Words: Hierarchical cluster analysis, Germplasm, Sugarcane.

Sugarcane is one of the important crops which produces more than 60 per cent of world sugar. India contributes around 13 per cent of the world and 41 per cent of Asian sugar production. It contributes 2 per cent to national GDP. The other byproducts of sugarcane are jaggery, *khandsari*, ethanol, paper, cattle feed, fuel, etc. For improving complex characters like yield and sugar recovery, choice of the parents is very important and it becomes easier if the germplasm is evaluated and classified properly and systematically on the basis of given set of characters. Cluster analysis is a technique which determines the degree of similarity or dissimilarity in the germplasm and is the best basis to define commonness, thereby eliminating redundancy and characterize the germplasm on the basis of degree of diversity (Peeters and Martinelli. 1989; Brown, 1991; Ordas *et al.*, 1994; Smith *et al.*, 1995). Therefore, the present study was conducted to evaluate, categorize and classify the sugarcane clones on the basis of 14 yield and quality characters.

Materials and Methods

The present study, comprising 50 clones, was conducted at CCS HAU, Regional Research Station, Uchani (Karnal) during 2001-02. Observations were recorded on 14 variables viz., number of millable canes/clump, cane height, cane thickness, number of internodes per cane, internode length, leaf length, leaf breadth, leaf area, single cane weight, cane yield/clump, Brix%, Pol%, Purity% and CCS%.

Data were recorded on five canes each from five randomly selected clumps of each genotype and average was computed. Cluster analysis was carried out on 50 clones and 14 variables using computer programme SPSS.

UPGMA (Unweighted pair-group method using arithmetic averages) with city block distances was used as it is suggested to be the best and most commonly used method (Romesburg, 1984). Dendrogram (Fig 1) was prepared using the rescaled distances. Based on the method suggested by Romesburg (1984) the dendrogram was cut to form the clusters.

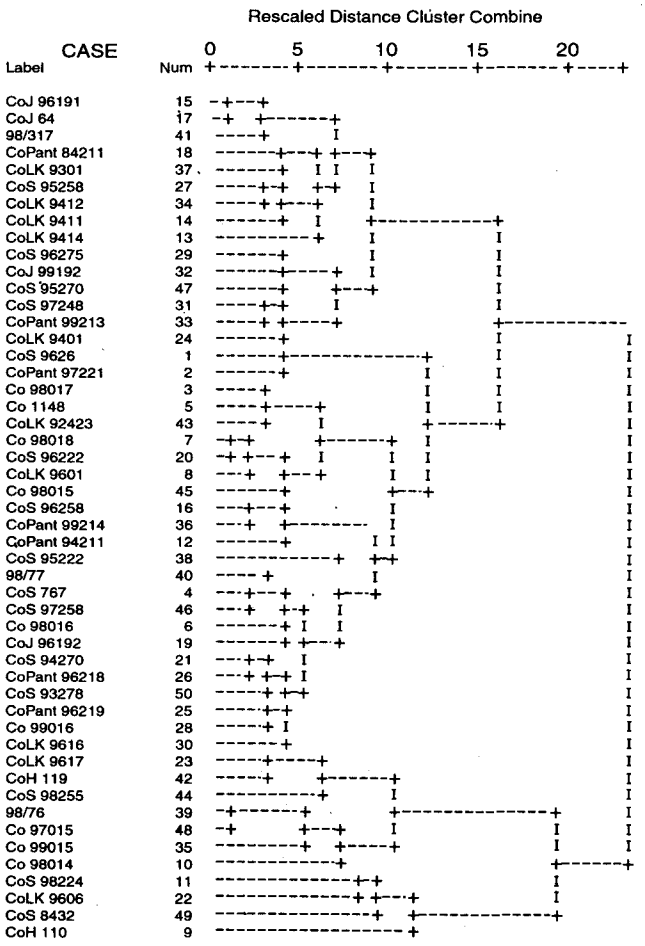

Fig. 1. Dendrogram portraying clustering pattern of different genotypes

Results and Discussion

Hierarchical cluster analysis identified five clusters (Table 1) containing two to twenty-two clones. Cluster II had twenty-two clones, cluster I had only two, cluster III had four, cluster IV had seven and cluster V had fifteen clones. Much information is not available on application of cluster analysis in sugarcane yet some of the workers viz., Nair and Sreenivasan (1992) studied 94 genotypes of sugarcane and grouped them into nine clusters with considerable diversity being observed among the clusters. White (1993) used cluster analysis to assess early line trials of *Saccharum* interspecific hybrids for resistance to sugarcane borer. Chatwachirawong and Srinives (1999) used cluster analysis to determine relationship among 26 clonal cultivars of sugarcane and pedigree of all cultivars was traced back to 11 original ancestors. Pathak *et al.* (2000) studied 22 clones of sugarcane and grouped them into five clusters, Tai and Miller (2002) used cluster analysis to classify the core collection of 75 clones of sugarcane, Cluster II and V had five clones while others had four each.

Mean performance of different clusters calculated for different characters revealed wide variation for the characters under study (Table 2). Cluster I with only two clones was found to be better in number of millable canes, number of internodes, Brix%, Pol%, CCS% and Purity% and poor in cane height, cane thickness, leaf length, leaf breadth and leaf area. Cluster II with 22

Table 1. Cluster membership profile of different genotypes (UPGMA-City block distances)

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
	CoS 96268	Co 98017	CoH 110	Co 98014	CoLK 9414
	CoPant 97221	CoS 767	CoS 98224	CoLK 9617	CoLK 9411
		Co 1148	CoLK 9606	Co 99015	CoJ 96191
		Co 98016	CoS 8432	98/76	CoJ 64
G		Co98018		CoH 119	CoPant 84211
E		CoLK 9601		CoS 98255	CoLK 9401
N		CoPant 94211		Co 97015	CoS 95258
O		CoS 96258			CoS 96275
T		CoJ 96192			CoS 97248
Y		CoS 96222			CoJ 99192
P		CoS 94270			CoPant 99213
E		CoPant 96219			CoLK 9412
S		CoPant 96218			CoLK 9301
		Co 99016			98/317
		CoLK 9616			CoS 95270
		CoPant 99214			
		CoS 95222			
		98/77			
		CoLK 92423			
		Co 98015			
		CoS 97258			
		CoS 93278			
No. of Genotypes	2	22	4	7	15

Table 2. Cluster mean for different characters in sugarcane (UPGMA-city Block)

Clusters	C1	C2	C3	C4	C5	General Mean
Characters						
No. of millable canes	3.83	3.45	3.27	3.06	3.28	3.34
Cane height (cm)	97.57	177.75	217.00	191.77	153.12	176.13
Cane thickness (cm)	1.90	2.18	2.48	2.36	2.03	2.17
No. of internodes	21.80	19.50	22.43	19.76	18.39	19.53
Inetrnode length (cm)	10.20	10.66	10.65	11.37	9.85	10.5
Leaf length (cm)	91.85	118.98	129.63	119.24	111.64	116.58
Leaf breadth (cm)	2.70	3.40	3.73	3.21	3.07	3.27
Leaf area (cm^2)	167.67	287.23	342.49	272.18	244.25	271.87
Single cane weight (g)	764.15	763.64	1326.18	1027.83	506.55	768.52
Yield/clump (kg)	2.45	2,60	3.40	3.04	1.97	2.53
Brix%	18.80	18.65	18.72	17.94	19.29	18.75
Pol%	36.33	35.55	35.75	34.48	36.91	35.85
CCS%	11.85	11.50	11.68	11.50	11.96	11.67
Purity%	91.97	90.77	91.59	91.98	91.17	91.17

Table 3. Inter and Intra (in bold)-cluster distances (UPGMA-City Block distances)

Clusters	C1	C2	C3	C4	C5
C1	**110.00**	301.90	884.50	474.73	439.36
C2		**204.33**	737.97	404.12	397.11
C3			**247.03**	493.02	1067.48
C4				**202.95**	681.35
C5					194.65

clones was found to be good for number of millable canes and leaf characters and medium in yield and quality characters. Cluster III with 4 clones was better in yielding attributes and moderate in quality characters. Cluster IV having 7 clones was better in Purity% and yield characters but poor in number of millable canes, Brix% and Pol%. Cluster V having 15 clones was better in quality characters but poor in cane yield.

The maximum inter-cluster distances was observed between cluster V and Cluster III followed by cluster III and cluster I. Minimum inter-cluster distances was observed between cluster II and cluster I followed by cluster V and cluster II (Table 3). Maximum intra-cluster distances was observed in cluster III followed by cluster II and minimum intra-cluster distances in cluster I. Cluster V had better quality attributes and cluster III had better yield attributes. The hybridization aiming diverse clones viz., clones from cluster V and III and cluster III and I are likely to produce heterotic hybrids and desirable transgressive segregants for better quality as well as yield traits in further generations. Clones with better mean values can be selected among all the clusters depending upon the objective of breeding programme. Romesburg (1984) observed that findings of similar alternatives reduce the decision problem to two stages i.e., first, to select the cluster that can best achieve the planning objectives and second to select the best alternative within the best cluster.

The association among the different clones is presented in the form of dendrogram (Fig. 1) prepared using rescaled distances. The clones lying nearer to each other in the dendrogram are similar to one another than those lying apart. The resemblance coefficient between two clones is the value at which their branches join. The dendrogram also showed the relative magnitude of resemblance among the different clusters.

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Variability Estimates and Search for Earliness in a Large Heterogeneous Population of Groundnut (*Arachis hypogaea* L.) Germplasm

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Seven hundred sixty eight Spanish bunch groundnut germplasm were screened for earliness using eight short duration elite cultivars as check in the field condition during rainy season 2001. The population showed wide range of variation for pod weight per plant, kernel weight per plant, shelling percent, hundred kernels weight and pod maturity percent recorded at eighty days after germination (DAG). Forty-two genotypes recorded more than seventy percent pod maturity at eighty days after germination. Sixteen genotypes out of forty-two selected genotypes confirmed their earliness in next post rainy season also having other desirable agronomic characters. These short duration germplasm would be useful as such or in the breeding program as donor parents.

Key Words: *Arachis hypogaea*, Earliness, Germplasm, Groundnut, Screening

Groundnut is one of the most important cash crops and has wide potential adaptability as *kharif*, pre-*rabi*, *rabi* and summer crop. However, groundnut cultivation as pre-*rabi* and *rabi* crop in river belt and paddy fallow land, respectively, provide maximum return with a productivity range of 1500-2500 q. Growing groundnut as the second crop after harvest of rice in residual moisture or with minimal irrigation will not only boost the country's groundnut production but also more remunerative than the rice–rice sequence besides cutting the water requirement, breaking the built up of pest load and increasing the fertility of soil. Indeed, short-duration high yielding groundnut variety would be a criteria to take the advantage of residual moisture of paddy fallow land and decrease the risk of yield loss by pre-monsoon shower during maturity stage. Hence, to search for elite early maturing genotypes in this germplasm, a screening programme was undertaken.

Materials and Methods

The present study was a part of maintenance, evaluation and characterization program of 3000 groundnut gene pools maintained at Out-reach Center of National Research Centre for Groundnut, Bhubaneswar, Orissa. All 768 Spanish bunch germplasm under the variety *vulgaris* of species *Arachis hypogaea* available at the centre were used in the experiment.

Experiment 1

Seven hundred sixty eight accessions were sown in augmented design having eight blocks during first week of July 2001 at Central Experimental Horticultural Station, Bhubaneswar, Orissa. Seven hundred sixty eight accessions distributed equally in eight blocks having 96 accessions in each blocks. Eight elite popular cultivars (AK-12-24, TAG-24, Jl-24, GG-2, TG-3, ICGS-11, ICGS-44 and OG52-1) were also sown as checks in all eight blocks. Each block contained 96 germplasm accessions and eight check varieties. Eight check varieties were sown in randomization at an interval of 12 germplasm accessions within the block. Each germplasm accession as well as check variety were sown for three lines in five meter bed with line to line and plant to plant spacing of 45 x 10 cm. Recommended NPK fertilizers for the crop were applied as basal dose in the ratio of 20:40:40. Standard crop management and plant protection measures recommended for groundnut crop were used for the experiment. Five plant samples were collected from the each check variety as well as germplasm accessions at 80 days after germination (DAG). Observations were recorded for total number of pods per plant, number of mature pods per plant, pod weight per plant, kernel weight per plant and 100 kernel weight from five plant samples. Shelling percentage was calculated by dividing kernel weight per plant with pod weight per plant and expressed in percentage. Pod maturity percent per plant was considered as one of the criteria for earliness, worked out by dividing number of matured pod per plant with total number of pods per plant, and expressed in percentage. Data was analyzed according to Agarwal and Sapra (1995).

Experiment 2

Forty-two short listed accessions on the basis of higher

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maturity percent than better performing check variety at 80 days after germination in experiment 1 were re-evaluated for confirmation during post-rainy season. Forty-two accessions along with 8 check varieties (AK-12-24, TAG-24, Jl-24, GG-2, TG-3, ICGS-11, ICGS-44 and OG52-1) were sown in randomized block design with three replications during first week of January, 2002 at Central Rice Research Institute, Cuttack, Orissa. Both test entries and check varieties were sown for three lines of 5 meters bed with row to row and plant to plant spacing of 45 x 10 cm. Similar crop management practices and plant protection measures described for experiment-1 have been followed in experiment 2. Five competitive plants sample was collected from each test entries and check at 80 DAG. Observation were recorded on number of total pods per plant, number of mature pods per plant, pod weight per plant, kernel weight per plant, 100 kernel weight from five plants sample. Pod maturity percent and shelling percentage were calculated as described earlier. Pod maturity percent at 100 DAG was also recorded in these forty-two accessions.

Results and Discussion

Experiment 1

Variance and histogram for frequency distribution of pod weight per plant, kernel weight per plant, shelling percent, 100 kernel weight and pod maturity percent have been presented in Table 1 and Figures 1-5.

Pod weight per plant: The population of 768 germplasm accessions was distributed into three different classes (Fig. 1) for pod weight per plant. The class, 0-5 represented the modal class containing 577 accessions followed by class 6-10 and class 10-15 with 150 accessions and 10 accessions, respectively. The mean pod weight per plant of the population was 3.75 though it ranged from 0.42 (ICG No. 1193) to 13.40 (ICG No. 6769). The high coefficient of variation (53.77) indicated wide range of variability within the population for the trait.

Kernel weight per plant: Frequency distribution of the population for kernel weight per plant spread over two

Table 1. Genetic parameters for yield and its related traits in a population of 768 groundnut germplasm accessions

Characters	Mean	Range	CV%
Pod weight per plant (g)	3.75	0.42-13.40	53.77
Kernel weight per plant	2.64	0.24-9.66	53.89
Shelling percent	70.21	33.33-86.26	9.10
100 kernel weight (g)	33.22	16.32-52.60	18.79
Pod maturity percent at 80 DAG	58.70	31.31-97.29	14.83

DAG denotes days after germination

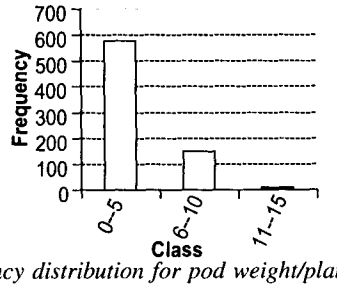

Fig. 1. Frequency distribution for pod weight/plant (g)

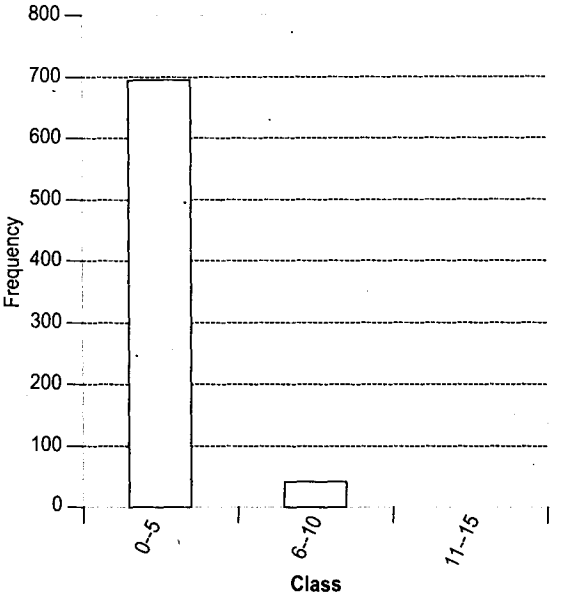

Fig. 2. Frequency distribution for kernel weight/plant (g)

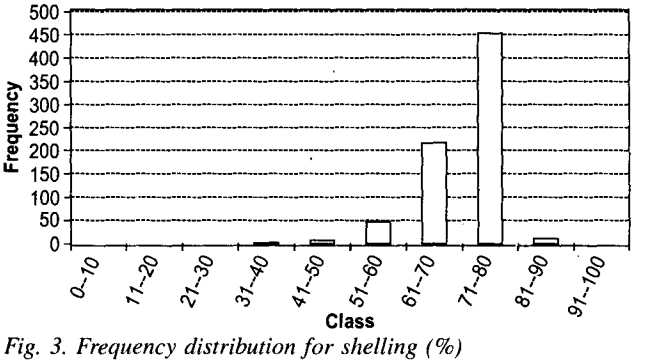

Fig. 3. Frequency distribution for shelling (%)

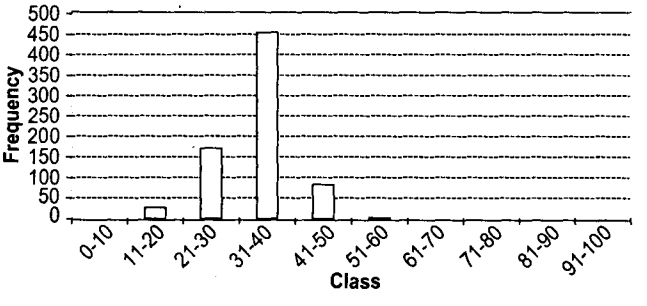

Fig. 4. Frequency distribution for 100 kernel weight (g)

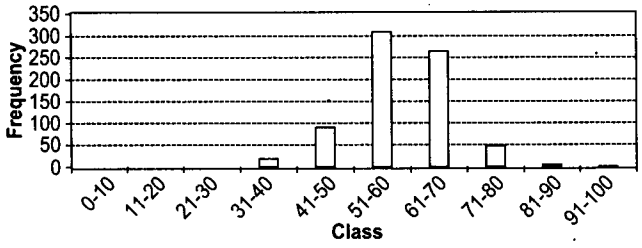

Fig. 5. Frequency distribution for pod maturity % at 80 DAG

classes (Fig. 2). Class 0-5 represented the modal class with 695 accessions followed by next higher class 5-10 with 92 accessions. Population mean of the trait was 2.64 and it ranged from 0.24 (ICG No. 1193) to 9.66 (ICG No. 6769) Higher coefficient of variation (53.89) revealed the existence of large diversity within the population for the trait.

Shelling percent: Population under study grouped into six different classes (Fig. 3) for shelling percent. The class 71-80 represented the modal class sharing 454 accessions followed by previous class, 61-70 with accessions. Only 11 accessions registered more than eighty percent of shelling percent. The mean shelling percent (70.21) of the population indicated that majority of the accessions characterized with high shelling percent. Though it ranged from 33.33 (ICG No. 3698) to 86.26 (ICG No. 1873) however, lower coefficient of variation (9.10) predicted symmetric nature of the population with comparatively less diversity for this trait.

100 kernel weight: Histogram for 100 kernel weight of the population showed five different classes (Fig. 4). The class 31-40 formed the modal class having 455 accessions followed by previous class, 21-30 with 171 accessions. Only two accessions registered 100 kernel weight more than fifty gram. Average 100-kernel weight of the population was 33.22 and value ranged from 16.32 (ICG No.10772) to 52.60 (ICG No. 3621). Moderate range (16.32-52.60) and coefficient of variation (18.79) predicted less degree of variation in the population for this trait.

Pod maturity percent at 80 DAG: Population has been distributed into seven different classes (Fig. 5) for pod maturity. The class 51-60 registered as modal class containing 309 accessions followed by next higher class 61-70 with 265 accessions. The mean pod maturity percent of the population was 58.70. The value ranged from 31.31 (ICG No.7614) to 97.29 (ICG No.10321) indicating wide range of variation in the population. However, lower coefficient of variation (14.83) indicated the symmetric nature of the population grouping majority of the genotypes under modal class and very few in the extreme classes. ANOVA and mean pod maturity percent of eight check varieties were presented in Tables 2 and 3. There was no significant block effect on checks as well as test entries and no significant difference between mean pod maturity percent among checks. However, all check varieties failed to have an appreciable level of pod maturity. The pod maturity percent of eight check varieties ranged from 53.80 to 61.51. Variety, ICGS-44 showed highest level (61.51) of pod maturity percent among eight checks. Hence, 70 percent pod maturity was considered as confidence limit and accessions having equal to or more than 71 percent pod maturity were taken into account for further study. Accessions having equal to or more than 70 percent pod

Table 2. ANOVA for eight check varieties over eight blocks

Source of variation	D.F	S.S.	M.S.S.	F. Value
Block	7	661.12	94.45	1.98 NS
Check	7	438.02	62.57	1.31 NS
Error	49	2340.51	47.77	

NS denotes not significant

Table 3. Mean pod maturity percent of eight check varieties over eight blocks

Sl. No.	Checks	No. of total pods/pl.	Pod maturity %
1	AK-12-24	14.72	60.32
2	GG-2	12.45	56.18
3	ICGS-11	13.25	58.70
4	ICGS-44	14.67	61.51
5	JL-24	15.26	58.21
6	OG 52-1	12.00	53.80
7	TAG-24	13.50	54.90
8	TG-3	12.00	54.80

maturity were listed in Table 4. The ICG No. 10321 showed highest pod maturity (97.29) percent followed by ICG Nos. 4551, 2077, 12421, 12409 and 3508. The pod maturity of these selected forty two accessions recorded at 100 DAG (Table 4) surprisingly was less than the pod maturity at 80 DAG. While, in some other accessions pod maturity at 100 DAG has increased considerably over the pod maturity at 80 DAG (Table 5). The pod maturity at 100 DAG decreased in the accessions, which attained more than 70-80 percent pod maturity at 80 DAG. However, it increased in accessions, which showed less than 50 percent pod maturity at 80 DAG. Decrease in pod maturity percent at 100 DAG over 80 DAG in some accessions would be the result of I) the pod loss during harvest due to over maturity or II) damage of mature pods by soil born pathogen/insect like termite/pod rot due to delay in harvest of comparatively early accessions. Hence, delay in harvest till maturity of every pod in a plant could be detrimental in groundnut especially in non synchronous flowering type. Hence, harvesting at critical maturity level is very important to avoid such yield loss. Critical maturity time of a

Table 4. Accessions with higher pod maturity % over better performing check at 80 days after germination

Sl. No.	ICG No.	No. of total pods/pl.	Maturity% at 80 DAG	Sl. No.	ICG No.	No. of total pods/pl.	Maturity% at 80 DAG
1	1201	12.31	74.66 (66.58)	22	4551	14.76	90.00 (72.44)
2	1208	14.02	71.56 (60.00)	23	6069	12.04	71.56 (65.88)
3	1330	14.78	77.08 (73.89)	24	6449	12.31	75.85 (61.00)
4	1354	15.00	75.82 (70.54)	25	6595	13.02	71.56 (63.94)
5	1489	14.08	73.57 (70.91)	26	6654	14.02	72.54 (67.21)
6	1496	13.31	71.56 (72.05)	27	7055	12.39	78.46 (74.66)
7	1572	12.04	75.82 (57.86)	28	7064	11.04	74.66 (73.68)
8	1631	13.35	90.00 (40.34)	29	7098	14.33	71.56 (64.38)
9	2077	14.00	77.08 (60.40)	30	7106	13.70	71.56 (65.88)
10	2092	15.04	71.56 (59.41)	31	7111	13.31	74.66 (65.88)
11	2210	12.20	72.54 (60.87)	32	7507	10.39	75.82 (62.65)
12	2220	13.15	74.66 (67.94)	33	7529	14.72	74.66 (72.15)
13	3497	13.04	75.82 (66.74)	34	7539	15.78	72.54 (74.66)
14	3508	16.74	80.02 (74.11)	35	10321	15.31	97.29 (64.90)
15	3540	15.70	77.08 (64.52)	36	10327	16.33	71.56 (76.82)
16	3572	14.08	71.56 (65.88)	37	10368	13.04	72.51 (73.78)
17	4038	11.67	71.56 (69.73)	38	10382	12.78	75.82 (73.46)
18	4102	13.74	71.56 (70.54)	39	12173	13.08	73.57 (53.13)
19	4112	14.00	77.08 (68.19)	40	12341	15.33	75.82 (62.87)
20	4117	16.35	72.54 (78.76)	41	12409	10.76	80.02 (71.09)
21	4549	11.35	75.82 (70.54)	42	12421	13.31	81.87 (65.88)

Value in parentheses denotes maturity % at 100 da43ys after germination

Table 5. Some of the genotypes with less than 50 % pod maturity at 80 days after germination

Sl. No.	ICG No.	No. of total pods/pl.	Maturity% at 80 DAG	Sl. No.	ICG No.	No. of total pods/pl.	Maturity% at 80 DAG
1	1180	9.36	47.29 (72.84)	11	4598	11.33	48.45 (74.66)
2	1391	11.51	48.45 (75.58)	12	6240	9.85	45.57 (76.06)
3	3202	14.24	49.60 (68.87)	13	6757	10.56	47.57 (68.19)
4	3260	10.23	47.29 (68.61)	14	7548	12.54	45.67 (68.36)
5	3264	11.10	47.87 (70.54)	15	10419	11.00	46.72 (70.54)
6	3268	8.36	47.87 (69.30)	16	10559	9.88	45.57 (77.75)
7	3463	9.56	48.45 (75.70)	17	10665	10.75	49.02 (74.21)
8	3630	10.58	42.13 (69.91)	18	11514	12.00	43.55 (75.35)
9	3653	9.45	39.23 (68.87)	19	11617	9.50	48.45 (72.44)
10	4568	10.03	45.00 (75.00)	20	11618	10.01	32.58 (71.56)

Value in parenthesis denotes maturity % at 100 days after germination

particular genotype vary with the genotypes and environments and could be determined only after evaluation of a variety in a particular environmental condition. Similarly, harvesting of this forty-two genotypes at 80 DAG may be produce more *number of mature pod per plant than harvesting at 100 DAG.*

Experiment 2

Number of total pods per plant, pod maturity percent, pod weight per plant, kernel weight per plant, 100-kernel weight and shelling percent recorded at 80 DAG are presented in Table 6. Sixteen accessions out of forty two selected accessions repeated their earliness over better performing check (ICGS-11). ICG No.2220 showed highest pod maturity percent (90) followed by ICG No. 3497, 6654, 2077, 1496, 7111 and 10368 which were also better than mean (68.48) pod maturity.

Table 6. Early maturing accessions over better check

ICG No.	No. of total pods/pl.	Maturity %	Pod wt./pl. (g)	Kernel wt./pl. (g)	100 kernel wt.(g)	Shelling percent
1354	18.00	65.98	9.84	6.99	30.24	70.54
1496	15.13	68.78	8.39	5.49	33.17	65.95
2077	16.00	68.85	9.43	6.14	39.08	65.85
2092	17.40	66.52	9.43	5.97	29.44	61.68
2210	15.20	65.25	8.11	5.15	31.69	63.11
2220	14.51	90.07	8.97	5.63	30.42	62.76
3497	15.40	70.42	8.36	5.32	30.79	62.84
4038	1367	65.20	8.58	5.27	35.86	62.06
4549	11.53	65.85	7.21	4.49	31.28	62.79
4551	16.67	64.53	8.98	6.47	32.16	72.23
6654	16.20	69.60	11.04	5.63	40.43	50.34
7111	15.13	68.56	8.02	4.79	29.61	59.79
7507	12.93	66.44	6.89	4.26	25.7	60.41
10327	19.33	66.85	10.72	7.70	31.52	71.98
10368	15.40	68.49	8.83	5.40	35.57	60.99
12409	11.67	67.65	6.86	3.81	31.87	55.95
(ICGS-44 (Better check)	15.00	65.20	10.31	5.83	35.36	56.80
Mean	15.25	68.48	8.82	5.55	32.60	62.71
SE±	2.05	5.83	1.23	.096	3.67	5.65

These genotypes also recorded sixty percent or more shelling percent except ICG No. 6654. Hence, these accessions may be evaluated further in multi-locations and introduced for the area featured with end season moisture stress or limited source of irrigation.

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VRIS: An Information System for Varieties of Pulse Crops

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Variety Research Information System (VRIS) specifically addresses the management need by producing a user-friendly, menu driven system that generates data collection forms, queries and reports and maintains a cumulative database for statistical analysis and interpretations. The present VRIS for pulse crops *viz.*, chickpea, pigeonpea, mungbean, urdbean, lentil, lathyrus, fieldpea and rajmash was developed during 2001–2002 at the Indian Institute of Pulses Research, Kanpur, India. It accommodates data on various characteristics of varieties using six tables for structure data entry. The software was developed using a numbers of forms/sub-forms that were designed in MS- ACCESS 2000 and operates on Windows 98/Windows NT Workstation 4.0. VRIS helps in interactive retrieval and updating of the data. Details of record, query and report can be accessed through variety name as primary key. VRIS has information on more than 435 varieties of pluses released from 1949-50 to 2001-2002. The database provides safe data storage that can be secured and shared over local Area Network (LAN) at Institute level and liking with the Institute's website (http://www.iipr.ernet.in/vris.htm) for access by pulse growers and other industry members.

VRIS is simple to use and does not require programming knowledge. This Information System directly and specifically addresses the needs for comprehensive information on varieties of pulse crops available for cultivation in different agro-climatic zone of the country.

Key Words: Information System, LAN, MS-ACCESS 2000, QBE, SQL, Visual Basic 6.0, VRIS, Windows NT.

From nutrition point of view for human beings and improving soil fertility and texture, pulses play very important role as they are protein rich and fix nitrogen in soil through biological process, respectively. These two are major factors responsible for cultivation of pulses by farmers throughout the country. Spectacular progress in development of high yielding varieties of pulse crops during the last 25-30 years has been made in India (Chaturvedi and Ali, 2002). To raise the production of these crops, it is essential to transfer the knowledge about these varieties to farmers, research managers, scientists, planners and administrators in selection of appropriate varieties to maximize their profit. Indian council of Agricultural Research (ICAR) is shouldering the responsibility of coordinating the agricultural research in India. The Indian Institute of Pulses Research (IIPR) and All India Coordinated Pulse Improvement Project has been given the responsibility to undertake the research on pulse crops and to develop improved varieties and management practices. Proper selection of varieties and transfer of technology from research station to farmer's field is of utmost importance for raising national food production in general and pulses in particular as more than 435 varieties of different pulse crops have been released for cultivation in different agro–ecological zones/states of the country.

Information on different varieties of crops is available in various publications of the Department of Agriculture and Cooperation, Government of India and the Indian Council of Agricultural Research (Ali *et al.*, 1994, Astana *et al.*, 1986, Agrawal, 1984 & Govt. of India, 1988). At present, the information on various characteristics of varieties is managed manually and the records are maintained in the register at the Institute and the Coordinating units. Under this system of record-keeping, there are certain problems *viz.*, lack of complete information on varieties at one place, delay in retrieving the required information, timely upgradation, lack of proper documentation, lack of clarity in selection of appropriate variety for a particular agro-ecological zones etc. The data available on various characteristics of released varieties are effectively utilized by scientists, government and extension officials for promoting good cultivars by improving awareness of favourable features among farmers. VRIS may provide opportunity to industrialists and various other agencies involved in seed production and also carrying out plant breeding research to develop new varieties as per need.

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In light of above discussion, it is clear that a large number of organizations require information on pulse varieties, but the great amount of repetitive work requires a manpower and time. With the advent of computer technology, it has become essential to develop a Database and information retrieval system for varieties of pulse crops. No commercial software was available that fulfills these requirements especially in the fields of pulses. Hence, the project on "Variety Research Information System (VRIS) for pulses" was initiated at IIPR, Kanpur during 1997-98 with aim to design an appropriate information system for accurate and efficient data collection and entry, generate forms and reports and combine with modern statistical tools in the most effective manner for storing, retrieving, summarizing and presenting acquired data. For potato genetic resources, an information system has been developed by Sarkar *et al.* (1966) which utilizes dBASE III plus.

System Specifications

Variety Research Information System for pulses is developed in MS-ACCESS 2000 and operates on Windows 98 or Windows NT 4.0 workstation. For development of a relational database for sugarcane the same software was used by Stafne *et al.* (2001). The system requires as IBM compatible personal computer with Pentium or higher processor, at least 16 MB RAM, hard and floppy disk drives, mouse and a VGA or higher display monitor with printer. A colour monitor, if available, will greatly enhance the use of menu driven features (consider Fig. 3-4).

System Description and Operation

The flows of information generated at different stages of varietal release process are presented in Fig. 1. It indicates that the Indian Institute of Pulses Research has strong linkage with a large number of organizations and individuals. The All Indian Coordinated Research Project related to pulses was trifurcated into All Indian Coordinated Research Project (AICRP) on Chickpea, AICRP on Pigeonpea and AICRP on MULLARP (Mungbean, Urdbean, Lentil, Lathyrus, Rajmash and Pea). All the relevant information on varieties starting from the evaluation of a genotype in the coordinated trial(s) at field level till the variety is notified is maintained at the Institute level. The system takes care of all varieties which are developed and entered into coordinated trials, identified for release, notified and denotified.

Initially, a suitable Performa covering all information collected on a particular variety was prepared for system analysis and design following Morris and Raykowski (1993). Based on the information the final data input sheets were designed to collect the information. Individual codes were standardized and designed using the principal of relational database management system (RDBMS).

Tables, Forms, Queries and Reports

Creation of tables and designing forms, reports, queries and switchboards are the main activities in VRIS. The relationship between different tables is defined in the relationship window using primary key and foreign key in another table (Fig. 2). Primary key is used to identify each record uniquely in a table.

- **Table** is an object that maintains data in records (rows) and fields (columns) similar to spreadsheets. Every table in our database focuses on one subject. The proposed system comprises six tables. Their detailed descriptions are presented in Table 1.
- **Form** is often the most convenient layout for entering, changing and viewing records in the database. Forms display and print data form table(s) based on query by the user. Forms are deigned and created by using form wizard. These forms can be customized by using design view to move controls, add a label and edit label text, change the appearance of text and adjust how the form looks and works. Sub-forms can also be created within a form. A sub-form can display a set of records associated with the record on the main form. Sub-forms are especially effective for viewing data from tables or queries with a one- to-many relationship. A total of 6 forms which contain 5 sub- forms are designed in the system. Data are entered from the forms to be saved in a designed table. Fig. 3 illustrates the format of a form (i.e., general information for variety developed) where data is entered in the varietal database.
- **Query** is a SQL (Structured Query Language) statement that allows the user to view, change, and analyze data in different ways. User can also use it as a source of records for forms and reports. Queries can be created using query wizard. The bottom half of the widows contains the Query-by-example (QBE) grid, in which the user can define the criteria of a query. For example, to find the name of chickpea varieties released during

Table 1. Examples of table structure and associated fields used in VRIS database for pulse crops

Table Name	Field Name	Type	Size	Indexed Field Description
1. General information for released variety				
Crop Name	Text	50	Yes	Name of pulse crop
Variety Name*	Text	50	Yes	Name of variety/hybrid
Pedigree	Text	75	No	Pedigree of variety
Source of Introduction	Text	01	No	Source of introduction
Name of Instt./Agency	Text	50	No	Name of originating source/Institution
Year in which Released	Number	04	Yes	Year of release
Breeding Method	Text	01	No	Breeding method
Original Name of Variety	Text	50	No	Original name of variety/hybrid
2. Information on morphological character				
Leaf Colour	Text	25	No	Leaf colour
Leaf Shape	Text	25	No	Leaf shape
Seed Colour	Text	25	No	Seed colour
Seed Shape	Text	15	No	Seed shape
Seed Size	Text	15	Yes	Seed size
Growth habit/plant Type	Text	30	No	growth habit/plant type
Protein (%)	Number	06	Yes	Protein Content (%)
Any Other Information	Text	50	No	Any other Information
3. Reaction of Diseases/Insect/Pest				
Zone Code	Number	01	Yes	Code of zone/state
Disease Type	Text	01	Yes	Disease type
Disease Name	Text	50	No	Disease name
Tolerance to Abiotic/biotic	Text	50	No	Reaction to biotic/abiotic stresses
4. Yield Performance				
Average Yield	Number	10	Yes	Average yield
Potential Yield	Number	10	No	Potential yield
5. Zone wise Information				
Zone Code	Number	01	Yes	Code of zone/state
Recomm Zone/State	Text	25	Yes	Name of recommended Zone/State
Maturity days	Number	03	Yes	Days to maturity
Any Other Remark	Text	50	No	Any other remarks
6. Variety Release Information				
Notification Number	Text	15	No	Notification Number
So Date Time	Date/	08	Yes	Notification date
Any Other Relevant Information	Text	50	No	Reason(s) for de-notification

*Variety Name is common for all tables included in the database

1980-90, which are suitable for the North West plain zone having more than 20 q/ha yield. Queries can also be constructed through SQL statement using clauses such as SELECT–FROM–WHERE, ORDER BY, etc.

- **Report** is an effective way to present data in a printable format. Data in report comes from tables or/and queries. User can use a report to show the summarized data by grouping data and showing grand totals as well as sub-totals. Reports can be created by using reports wizard and can be customized using design view
- Switchboard provides entry point to database. It also has buttons that user can click to open forms and reports (or open other switchboards to access open additional forms and reports), quit MS-ACCESS or customize the switchboard. A switchboard form can be created using switchboard manager. Each activity is selected form VRIS are presented through the main switchboard (Fig. 4).

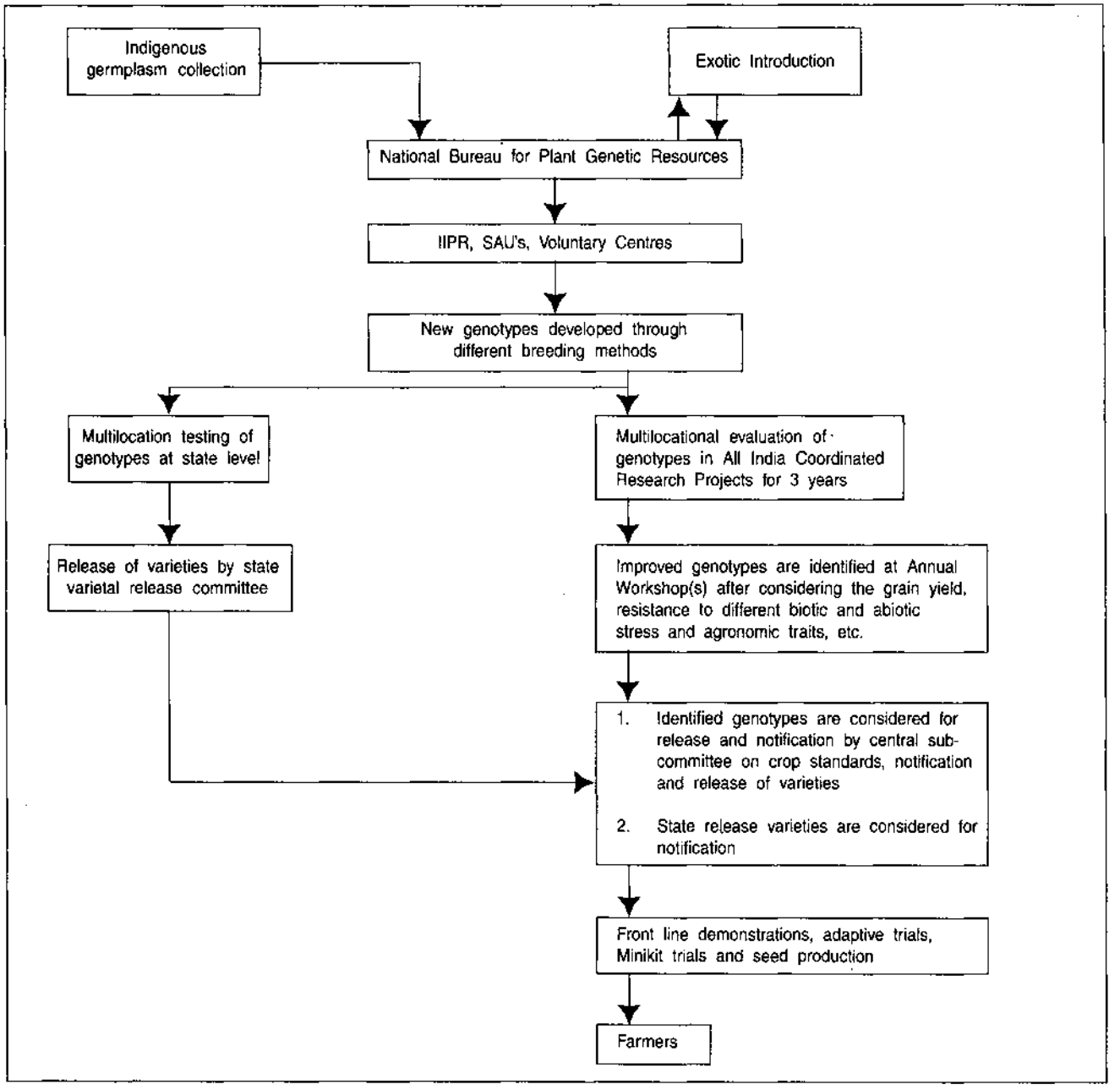

Fig. 1: Flow of information for variety release process in pulse crops

Result and Discussion

Selection of pulse varieties requires the efficient integration of large number of various characteristics related to area, growing condition, disease and insect pest resistance, environmental stress condition etc. To fulfill the information requirements in optimum ways, various output reports and queries are designed by grouping similar information. The effort has been made to present the information in best possible way from the user's point of view. In designing the output for the system, it was taken into consideration whether the information is to be presented in the form of query or report or to create documents. During 2000, the database on chickpea varieties was prepared and demonstrated to the users (Devraj *et al.*, 2000 and Dua *et al.*, 2001). The present VIRS database contains different released varieties of chickpea (122), pigeonpea (95), mungbean (74), urdbean (64), lentil (21), fieldpea (25), lathyrus (3) and rajmash (14). A total of 7 reports and 4 queries were included in the database in addition

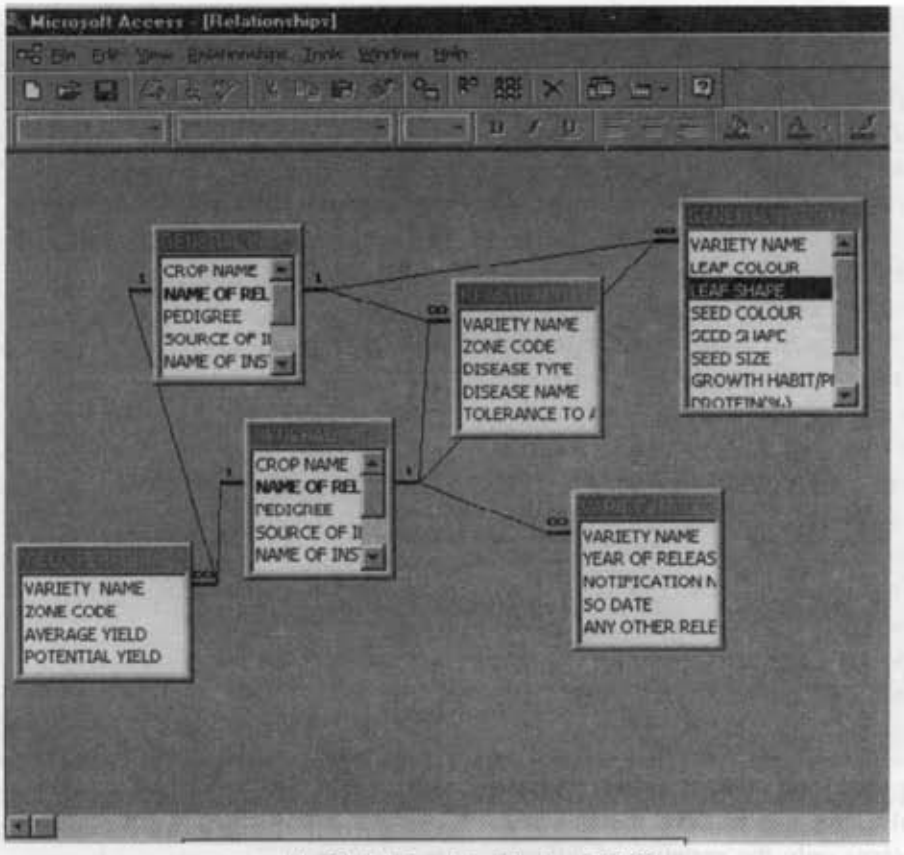

Fig. 2. Relationships Window in VRIS

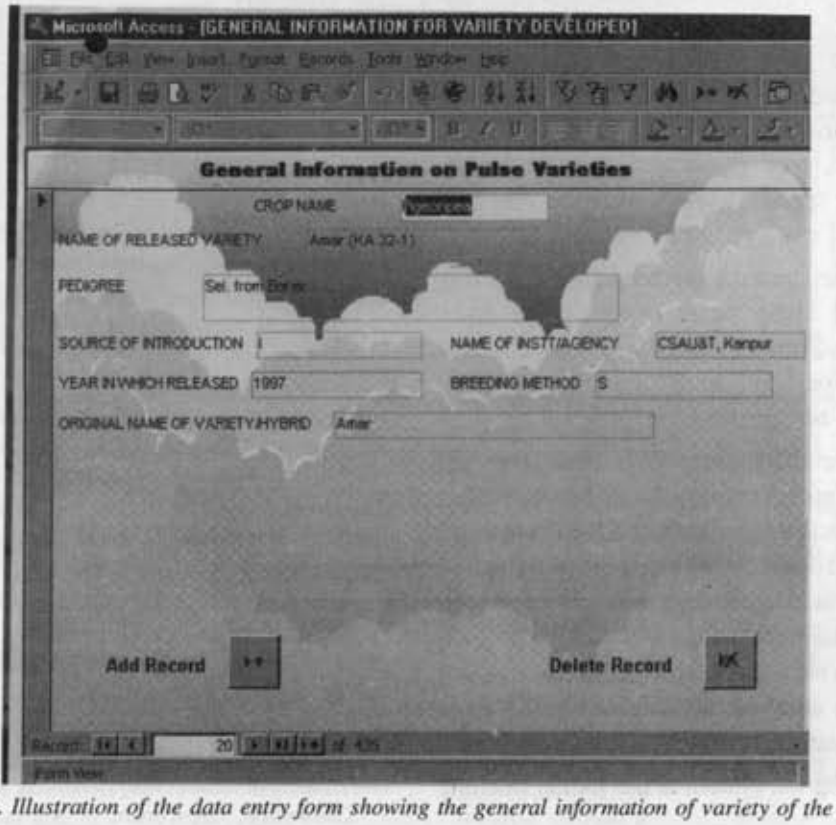

Fig. 3. Illustration of the data entry form showing the general information of variety of the VRIS

to complete report on a particular variety, list of varieties released for cultivation during the year, information on plant protection, morphological characters, release information yield performance, zone wise information, number of varieties released during a period, ranking of varieties on yield and disease characters in a specific zone and other related characters independently. Summary reports (i.e., general information on varieties) created in landscape format (Fig. 5), provides information regarding all varieties of different pulse crops. Like most commercial database software's, VIRS is user friendly and completely menu-driven with options for data entry, updating of existing variety list for a particular crop and printing reports. This system generates quick and accurate reports as per the user's choice and requirement to efficient sorting and searching techniques. The system is being successfully for the past year and has considerably reduced. The manpower and processing time required for compilation and preparation of reports.

Future Direction

The system is being tested and implemented in a phased manner with several addition under development where the first phase concerns only the varieties of different pulses which have been released upto 2001-2002 have been included. The system will be implemented for varieties which are entered into coordinated trials, identified for released and denotified. During the next phase the information on molecular characterisation, plant breeder rights, seed production, area under the crops or area under specific variety over the year will be included.

From farmers view point a pictorial guide covering major diseases and insect pests of the pulse crops will be included so that farmers can identify the diseases (s)/insect pest (s) and appropriate control methods will also be available in VIRS.

From the above discussion, it is clear that the variety database is going to be a large database (i.e., each variety contains approximately 8 KB information) and software will support various queries. Thus to meet the requirement of the day, it is proposed that system will be modified using MS-ACCESS 2000 as back end and Visual Basic 6.0 as front end for designing the forms and Visual Basic's crystal Repots 8.0 for better outputs.

For implementing the system at the Indian Institute of Pulses Research, Kanpur, the concerned crop coordinators and breeders will be involved in monitoring and updating of system at ARIS-IIPR computer centre. Data available on IIPR local server can be accessed through the Institute website (http://www.iirp.ernet.in) *via* ERNET service.

It is proposed to connect the hardware placed at IIPR through Leased line/VSAT to an existing National Agricultural Network (ARISNET) which will take care of the communication problems associated with the operation of existing system. This will result into efficient dissemination of the information to various users through the district computer centers of National Informatics Centre. Request for information concerning this system, including source code can be sent to devraj@iipr.ernet.in or drmichra_1969@yahoo.co.in

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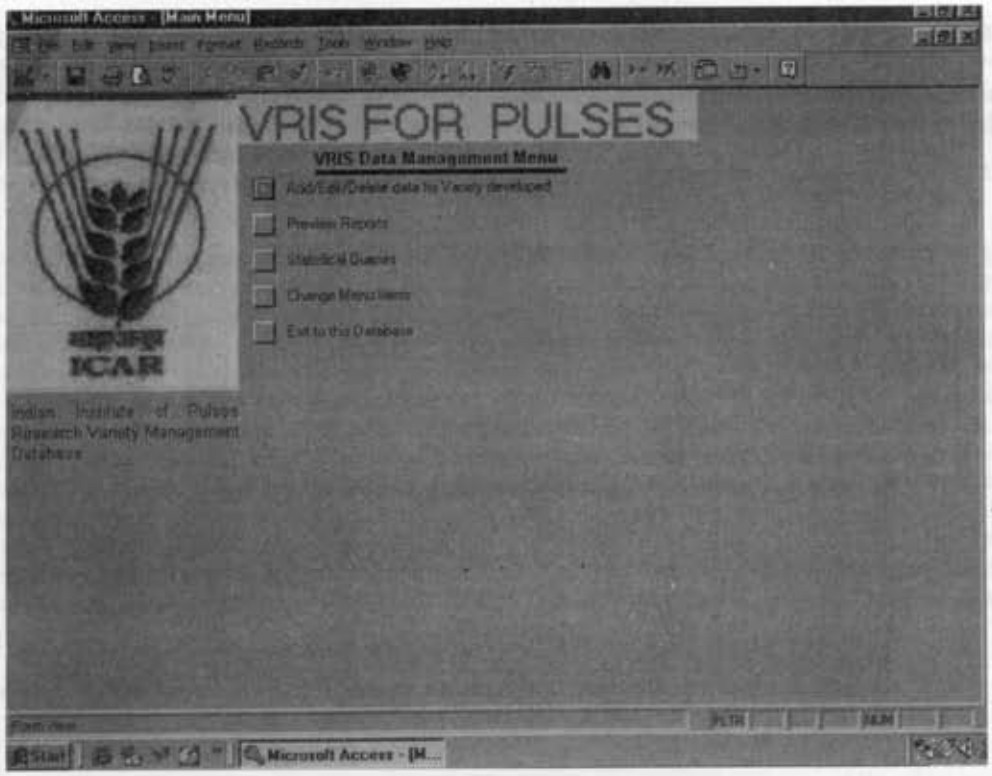
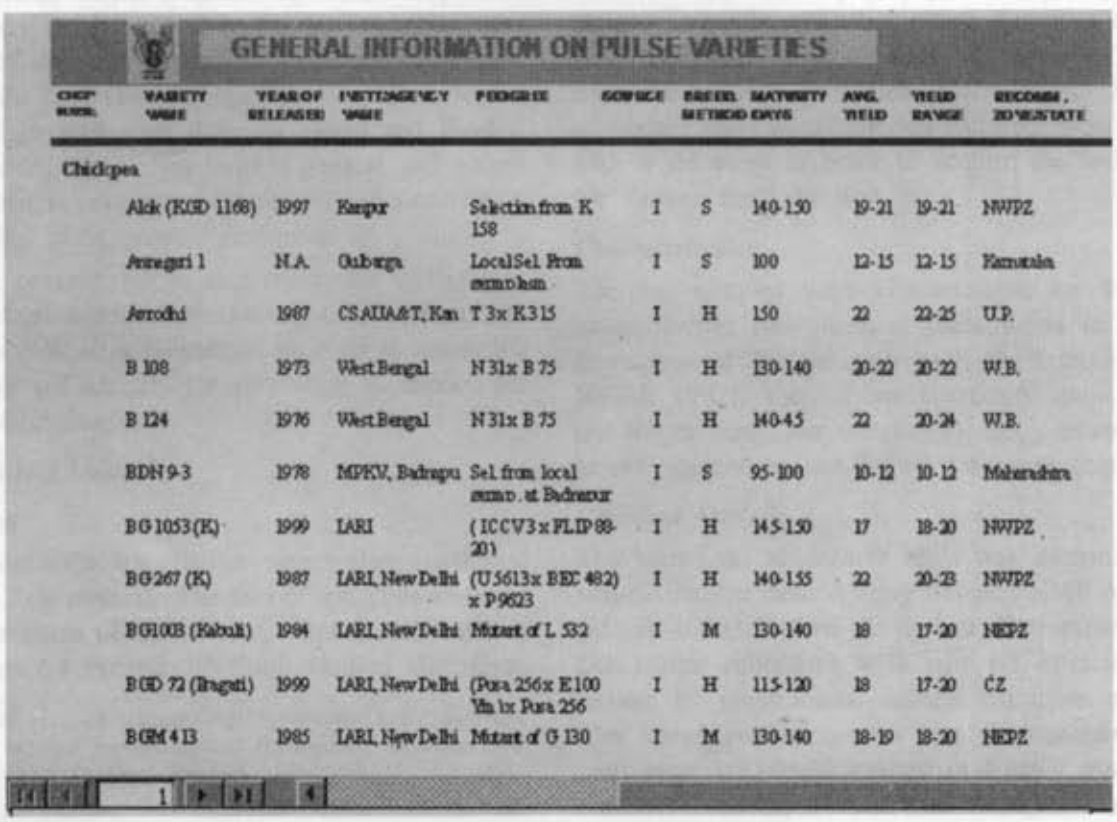


Fig. 4. The main switchboard for the pulse varieties database of IIPR, which facilitates navigation



GENERAL INFORMATION ON PULSE VARIETIES

CROP NAME	VARIETY NAME	YEAR OF RELEASE	INSTITUTE/AGENCY NAME	PEDIGREE	SOURCE	BREED. METHOD	MATURITY DAYS	AVG. YIELD	YIELD RANGE	RECOMM. ZONE/STATE
Chickpea										
	Alok (KGD 1168)	1997	Kanpur	Selection from K 158	I	S	140-150	19-21	19-21	NWPZ
	Annegiri 1	N.A.	Gulbarga	LocalSel. From germplasm	I	S	100	12-15	12-15	Karnataka
	Avrodhi	1987	CSAUA&T, Kan	T 3x K 315	I	H	150	22	22-25	U.P.
	B 108	1973	West Bengal	N 31x B 75	I	H	130-140	20-22	20-22	W.B.
	B 124	1976	West Bengal	N 31x B 75	I	H	140-45	22	20-24	W.B.
	BDN 9-3	1978	MPKV, Badnapu	Sel. from local germp. at Badnapur	I	S	95-100	10-12	10-12	Maharashtra
	BG 1053 (K)	1999	IARI	(ICCV3 x FLIP 88-20)	I	H	145-150	17	18-20	NWPZ
	BG 267 (K)	1987	IARI, New Delhi	(US613x BEC 482) x P 9623	I	H	140-155	22	20-23	NWPZ
	BG 1003 (Kabuli)	1994	IARI, New Delhi	Mutant of L 552	I	M	130-140	18	17-20	NEPZ
	BGD 72 (Bragati)	1999	IARI, New Delhi	(Pusa 256x E 100 Yellow x Pusa 256	I	H	115-120	18	17-20	CZ
	BGM 413	1985	IARI, New Delhi	Mutant of G 130	I	M	130-140	18-19	18-20	NEPZ

Fig. 5. A summary report on general information of chickpea varieties generated through the VRIS

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Collection, Characterization and Evaluation of Walnut (*Juglans regia* L) Germplasm from North-Western Himalayas

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From the different agro-ecological habitats of North-Western Himalayan region of India, 422 accessions of *Juglans* landrace diversity from naturalized populations were collected. The area studied was in Uttaranchal (170), Jammu and Kashmir (150) and Himachal Pradesh (102), lying between 30°35'E latitude and 75°79' N longitude. Exploration trips were made from January 2000 onwards in forest, villages and farmer backyards which are mostly inaccessible. These *Juglans* landrace diversity were characterized for quantitative and qualitative traits in order to be utilized as variety, in respective of agro-ecological regions as well as for conservation in the field gene bank for future utilization and breeding programme. The large variation in nut weight, nut length, nut shape, nut diameter, shell texture, shell colour, shell seal, kernel percentage, kernel percentage, kernel colour, kernel filling, kernel protein and kernel oil were recorded within and between agroecological zones. The range of in shell nut weight, kernel percentage and kernel oil varied from 7.68-18.45g, 28.51-55.55%, 53.00-79.54% in Uttaranchal; 6.29-27.16g, 33.05-66.26%, 58.38-7244% in Jammu and Kashmir and 9.18-19.98g, 34.10-57.88%, 13-81-74.92% in Himachal Pradesh, respectively. The nut shape varied from ovate, round, elliptic, broad elliptical, short trapezoid and long trapezoid. Kernel colour ranged form light amber to extra light with moderate to very easy removal of kernel halves.

Key Words: Collection, Characterization, Evaluation, Germplasm, *Juglans*, Walnut.

Nut fruits have great potential for their further utilization in North-Western Himalayan region of India. Among the nut fruits, walnut (*Juglans regia* L.) occupies an important place because they are are nutritious, with long shelf-life and require less care in cultivation. It has rich land race diversity in Himalayan region due to high ecological diversity (Joshi and Pandey, 1996, Pandey, 1998). Nut fruits in general, and walnut in particular, is an excellent example of under-utilization of existing plant genetic resources.

The present paper describes the collection, characterization and evaluation of walnut germplasm from North-Western Himalayas in order to assess the variability and identify the promising accessions for future utilization.

Material and Methods

Collection

Germplasm collection missions were undertaken during the year 2000 onwards. The area of collection involved from the states of Uttaranchal, Jammu and Kashmir and Himachal Pradesh of North-Western Himalayan region of India between 30°35'E latitude and 75°79'N longitude. Climatic conditions are warm tropical to arctic/arid terperate. Topography is mostly hilly terrain along with gently undulating plains. Sampling strategy was determined through selective methods, mostly from the farmer's backyards. Sufficient nut samples of *Juglans regia* were collected and trees were market with white paint in order to acquire the bud sticks for further multiplication.

Characterization

The nut samples were characterized for different morphometric and chemical traits based on IPGRI descriptors of *Juglans regia* with slight modification IPGRI, 1997). The various characters studied were nut length (cm), nut weight (g), nut diameter (cm) kernel percentage and kernel thickness (mm).

Chemical Analysis

The kernel oil of *Juglans regia* was determined by non-destructive method using Newport NMR Analyzer (Model-4000, Oxford Analytical Instruments, Ltd. U.K.) after calibrating with pure oil extracted with hexane by conventional solvent extraction method. The kernel protein content was determined by the conventional Kjeldahl method in Kjeltec Auto 1030 Analyser (Tecator, Sweden) and multiplication factor

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6.25 was used to convert nitrogen in protein (Jayaraman, 1981).

Results and Discussion

The study was based on ecological diversity along with collection and characterization of juglans landrace diversity from the region.

Ecological Diversity

The North-Western Himalayas comprises the states of Jammu and Kashmir, Himachal Pradesh, Uttaranchal hills and Shiwalik hills having four distinct ecological zones. The vegetation is in general, drought resistant and cold tolerant. The area usually receives low rainfall, but get heavy snowfall or rain in winters.

The region has a number of land races of *Juglans*. Other characteristic vegetation consist of extensive stands of pines (*Pinus roxburghii*), deodar (*Pinus deodar*), oak (*Quercus dilatata* and *Q. incana*), *Rhododendron* sp. and *Hippophae rhmamnoides*. The soils are extermely varied. The foot and plain valley have deposits of gravel and coarse sand alluvial and red loams. On mountains the forests soils are clayey and gravely porous sandy loam rich in humus. Marshy low lying comprises peaty soils.

All the landrace diversity of *Juglans regia* show considerable variation with respect no tel to different soil, rainfall and temperature. *Juglans* can be successfully grown on wide range of soil types including rocky soils. Some of *Juglans* landrace have been found to grow even on rocky soil along with water streams in Uttaranchal hills. Generally, no serious diseases and insect were observed on the naturally occurring trees except leaf spot in *Juglans*.

Collection

The Indian Council of Agricultural Research carried out an extensive programme under the National Agricultural Technology Project (Plant Biodiversity) for the collection of indigenous *Juglans* landraces from the North-Western Himalayan region of India. This programme has been carried out in collaboration with research institutes/state agricultural universities. non-governmental organization along with farmer participations. The project has been implemented from Januany 2000 and several exploration trips were carried out in the respective states. The areas surveyed were Anmantnag, Budgam, Srinagar, Pulwama and Baramulla districts of Jammu and Kashmir (J&K), Uttarkashi, Dehradun, Tehri, Almora, Champawat and Nainital districts of Uttaranchal; Kallu, Chamba, Linnaur, Solan, Shimla and Sirmaur districts of Himachal Pradesh. A total of 422 diverse landraces of *Juglans regia* have been collected (Table 1) The diversity collected are from Uttaranchal (170), Himachal Pradesh (102) and Jammu and Kashmir (150). These materials were collected from different altitudes and include villages, forests and farmers backyards of the repective agro-ecological zones.

Table 1. Areas explored and *Juglans* diversity collected from North-Western Himalayan region of India

Areas surveyed and explored	Diversity Collected
Anantnag, Budgam. Srinagar, Kupwara, Pulwama, and Baramulla districts of Jammu & Kashmir	150
Dehradun, Uttarkashi, Tehri, Almora, Champawat, and Nainital districts of Uttaranchal	170
Kallu, Chamba, Kinnaur, Solan, Shimla and Srimaur	102
Total diversity collected	**422**

Characterization

Uniform descriptors were followed by all the institutions involved in the collection, evaluation, documentation and conservation of *Juglans*. Considerable variability exists for nut fruits size sape, kernel percentage, kernel colour, kernel protein and kernel oil content. The *Juglans* fruits posses thin shell, papery shell, semi-hard and hard shell along with creamy white kernel colur. The kernel oil and protein in some of landraces are quite high, from >70% and 20% respectively. Apart from use as dry fruits, the walnut oil is commercially used for making soap, oil and other cosmetic pruducts.

Net Characteristics

A large variation in nut weight, nut length, nut shape and nut diameter were recorded within and between the different agro-ecological zones. The range of nut weight was varied from 7.68-18-45 g in Uttaranchal, 6.29-27.16g in J&K and 9.18-19-98g in Himachal Pradesh (Table 2). Aslam (1993) reported that average in shell, nut weight varied between 9.37 to 12.96 g in case of indigenous selection and 8.45 to 10.46g in case of exotic cultivars. In the present study the high nut weight was recorded in some of the accessions, and similar nut weight was observed by Paunovic (1990), and higher than found in Himachal Pradesh and Uttaranchal by Gautam (2000) and Lal and Singh

Table 2. Characterization of *Juglans* diversity based on nut and kernel characters

Characters	Range of variation for important traits.		
	Uttaranchal	Jammu & Kashmir	Himachal Pradesh
Nut Characters			
Nut length (cm)	3.22-5.06	2.22-5.10	3.01-4.90
Nut diameter (cm)	2.60-3.75	2.68-4.55	2.98-3.77
Nut weight (g)	7.68-18.45	6.29-27.16	9.18-19.98
Nut shape	*R, O, LT, BE	*R,O, ST, BE. LT, T	*BO, ST, BE, O,LT
Shell thickness (mm)	1.30-3.23	1.0-3.0	1.40-2.36
Shell texture	Smooth to Rough	V. Smooth to Rough	Smooth to Rough
Shell colour	Light to Dark	Light to dark	Light to V. dark
Shell seal	V. weak to Strong	V. weak to strong	Weak to very strong
Kernel characteristics			
Kernel (%)	28.51-55.55	33.05-66.26	34.10-57.88
Kernel oil (%)	53.00-79.54	58.38-66.66	13.81-74.92
Kernel protein (%)	11.15-28.80	14.38-21.16	11.81-26.89
Kernel colour	*ET to LA	*ET to LA	*ET to LA
Kernel filling	Poor to V. Good	Poor to Excellent	Poor to Good

*R=Round, O=Ovate, LT=Long Trapezoid, BE=Broad Elliptic, ST=Short Trapezoid,
T=Triangular, BV=Broad Ovate, C=Circular, ET=Extra Light, LA=Light Amber

(1978), respectively. Similarly the nut length and nut diameter ranged from 3.22-5.06 and 2.60-3.75cm in Uttaranchal; 2.22-5.10 and 2.68-4.55cm in and 3.01-4.94 and 2.98-3.77 cm in Himachal Pradesh respectively and a sizeable number of accessions have either at par or more than that suggested by Serr and Ford (1954) in all .the three states. The nut shape varied from round, ovate, long trapezoid, short trapezoid, broad elliptic, elliptic, broad ovate and triangular amongst the different region. Shell texture and shell colour were smooth to rough and light to dark in Uttaaranchal (1.30-3.23mm) and Himachal Pradesh (1.11-2.36mm). Similar observations have been reported by other workers (Rue and Yang, 1990; Lal and Singh 1978; Paunovic, 1990 and Gautam, 2000).

Kernel Characterstics

Considerable variability exists in kernel characteristics amongst the hill regions of India. There is large variation in kernel percentage, which varied 28.51-55.55% in Uttaranchal, 33.05-66.26% in and 34.10-57.88% in Himachal Pradesh. Thus there is great scope for selection of walnut variety on the basis of kernel recovery as suggested by Serr and Ford (1954). Similar results were also reported by Bhat *et al.* (1992) that high kernel percentage from 54.20 to 63.20 in whereas contrary to this Qureshi & Dalal (1985) reported 30-35 percent kernel in seedlings from Kinnaur district of Himachal Pradesh but nut size of this selection was very small. Pieklo and Czynczyk (1990) reported 37.60 to 53.10 per cent in Italy (Radicarti *et al.* 1990). Wang *et al.* (1990) and China and Armenia repectively,

Amongst the *Juglans* land race diversityfew important accessions collected from North-Western Himalayas could be used as a potential lines in breeding for imcorporation of various traits viz; bearing habit, nut quality, kernel percentage, high percentage of kernel protein, kernel oil and precocity as well as resistance to various diseases and insects.

Acknowledgements

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SHORT COMMUNICATION

Sources of Resistance Against Root-knot Nematode, *Meloidogyne incognita* (Kofoid & White) Chitwood in Mungbean and Urdbean

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Key Words: ***Meloidogyne incognita*, Root-knot nematode, Resistant sources, *Vigna mungo*, *Vigna radiata***

Mungbean, *Vigna radiata* (L.) Wilczek and urdbean, *Vigna mungo* (L.) Hepper are the major pulse crops grown in India. Despite progress in genetic improvement of these crops, the production has remained static during the past several years due to a number of biotic factors. Nematodes play an important role in crop production (Sasser, 1989). Several phytoparasitic nematodes are known to be associated with mungbean and urdbean. Among them, root-knot nematode, *Meloidogyne incognita* (Kofoid & White) Chitwood is a major pest causing 18-65% and 23-49% losses in mungbean and urdbean, respectively (Ali, 1997). Due to prohibitive cost and environmental hazards, the use of chemicals is discouraged and growing resistant cultivars is advocated which would be cost-effective as well as ecofriendly. In view of above, greenhouse experiments were conducted to identify sources of resistance in these crops, which could be exploited in breeding programme to develop a commercial variety possessing resistance against this nematode.

Advanced breeder's seed material entries for multilocational testing under All India Co-ordinated Research Project on MULLaRP (Mungbean, Urdbean, Lentil, Lathyrus, Rajmash and Fieldpea) were included in this study, as these entries are high yielding. Promising seeds of mungbean and urdbean were surface sterilized in 0.2% mercuric chloride solution and were sown separately under completely randomized design with three replications in 15 cm diameter earthen pots containing 1 kg of steam sterilized soil. Fifteen hundred freshly hatched second stage juveniles of *M incognita* were inoculated around each plant at 2-3 leaf stage. After 45 days of inoculation the plants were uprooted and washed gently in running tap water. Galls that developed on the roots were counted. Resistance/susceptibility was determined as follows: no galls = highly resistant (HR), 1-10 galls = resistant (R), 11-30 galls = moderately resistant (MR), 31-100 galls = susceptible (S), > 100 galls = highly susceptible (HS).

The results are shown in Table 1. None of the accessions of mungbean and urdbean were found highly resistant. However, AKU 9802, AKU 15, UG 1017, TPU 4, Phule U 9417-5, OBG 17 and USTD 102 of urdbean and ML 131, IPM 99-125-and Pusa

Table 1. Response of mungbean and urdbean genotypes against *M. incognita*

Varieties		No. of galls	Host reaction
Mungbean	**Urdbean**		
ML 131, IPM 99-125, Pusa172	AKU 9802, AKU 15, UG1017, TPU 4, Phule U 9417-5, OBG 17, USJD 102	1-10	R
Pusa 2072,VGG72,UPM 99-3, Pusa 105, ML 1108, BM 4, PBMR 145, NDM 97-1, CoGG912	NDU 99-2, TV 94-2, OBG 19, USJD 111, VGG 2009, KU 96-3, UK 17, TV 2000-27, CoBG630, KU 99, CoBG 631	11-13	MR
MSJ 118, MH 96-1, ML 5, TM 98-37, AKM 9801, TM 94-2	KU 99-4, VSJD 113, TV 95-5-1, UG 950, AKU 99-01	31-100	S
ML 818, TM 99-47, MH 98-1	TU 2000-28, OBG 15	Above 100	HS

172 of mungbean were found resistant. Varieties TU 2000-28 and OBG 15 of urdbean and ML 818, TM 99-47 and MH 98-1 of mungbean were highly susceptible. Rest of the varieties were found moderately resistant to susceptible. In absence of highly resistant donors in mungbean and urdbean against this nematode screening should further be extended on a large scale to encompass almost all the existing lines/germplasm collection of other national and international research centres. In due course of time however, cultivation of these crops in *M. incognita* infested fields could be carried out employing chemicals and other agronomic practices which suppress root-knot population.

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SHORT COMMUNICATION

Adaptability of Some Groundnut Breeding Lines under Residual Moisture of Paddy Fallow

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Key Words: Groundnut Germplasm, Stability, Rice Fallow

In India, the average productivity of groundnut in post-rainy season is fairly high (1500 kg/ha) and quite stable but its contribution to National groundnut basket is only 32 percent. Pre-*rabi*/*rabi* groundnut, grown either on residual moisture situation or with minimal irrigation after harvest of *kharif* rice is one of the most remunerative cash crop in the state of Orissa. Groundnut cultivation under residual moisture condition of paddy fallows in the state has touched the area of 0.2 million hectare with an average productivity of 2 tonnes/hectare (Ghosh, 1995). However, biggest problem towards productivity of groundnut under paddy fallows is non-availability of improved location specific variety suitable for existing cropping pattern and quality seed materials. Hence, merit to assess the performance and adaptability of groundnut genotypes towards further pushing up and sustaining the groundnut productivity.

Thirty-nine water use efficient and short duration groundnut varieties received from ICRISAT, Patancheru, Andhra Pradesh and local variety, AK-12-24 as check have been used in the present study. Experiments were conducted at the farm of Central Rice Research Institute, Cuttack, Orissa during post-rainy season after harvest of *kharif* rice in the year 1999, 2000 and 2001. Forty genotypes were sown in Randomized Block Design, replicated thrice during first week of January every year. Each genotype was sown in five lines of five meters length with 45 x 10 cm spacing between and within lines, respectively. Recommended cultural practices for groundnut were followed for conducting experiments in every year. Observation on plant height, number of primary branches, biological yield, pod yield per plant, total pods per plant, matured pods per plant, shell thickness kernel yield per plant, hundred kernels weight, pods length and breadth, kernel length and breadth were recorded on ten randomly selected plants from each plots at harvest. Harvest index based on kernel yield, pod length and breadth ratio and kernel length and breadth were calculated. Pod yield per plant was utilized to work out stability parameters following Eberhart and Russell (1966).

The joint regression analysis (Table 1) revealed that genotypes and environment mean sum of square for pod yield per plant were significant indicating wide variability among the genotypes for expression of the character and warrant further studies. Yadav and Kumar (1979) and Kumar *et al.* (1984) observed similar results for hundred pods mass and shelling percent, the two yield contributing characters in different set of genotypes. Significant genotype x environment (linear) interaction might be responsible for high (linear) adaptation in relation to yield contributing characters. The variance due to pooled deviation (nonlinear) was also significant reflected considerable genetic diversity in the material (Perkins and Jinks, 1968). Such nonlinear deviation may be of practical value to construct and test the utility of multiple regression models to know critically the complex mechanism of adaptation. A variety is likely to be stable over different environments if it shows high mean value (above average performance), unit or less than linear regression coefficient (bi) with lowest deviation (non-significant) from the linear regression (bi). Twenty-five genotypes (Table 2) either registered at per or higher pod yield per plant in comparison to check, while only five genotypes viz, ICGV-91112, ICGV-92215, ICGV-86607, ICGV-88409 and ICGV-91124 produced significantly higher pod yield per plant than check. Out of these, ICGV-92215 could be promising and stable in any environment for its lower S^2d_i nearer to unit b_i values. On the other hand

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Table 1. ANOVA for pod yield/plant (g) in groundnut

Source of variation	d.f	M.S.S
Genotype (G)	39	8.67**
Environment (E)	2	202.22**
G x E	78	4.79**
E (Linear)	1	404.45**
G x E (linear)	39	4.93**
Pooled Deviation	40	4.53**
Pooled error	234	2.55**

Table 2. Estimates of stability parameters based on three environments for pod yield/plant (g)

Genotypes	Mean	B_i	S^2d_i
ICGV-91129	9.16	0.74	10.79**
ICGV-92195	7.22	0.95	8.48**
ICGV-93382	9.36	0.19	-0.85
ICGV-91146	9.62	0.86	-0.33
ICGV-91131	9.47	1.21	-0.71
ICGV-92234	6.80	1.33	-0.20
ICGV-92199	9.26	0.68	1.78
ICGV-92229	6.40	0.06	19.23**
ICGV-87160	9.42	1.02	6.40
ICGV-91112	10.93	2.77* *	-0.10
ICGV-92222	9.89	1.89	0.26
ICGV-91114	7.56	0.65	0.28
ICGV-87354	8.71	1.78	16.55**
ICGV-92198	8.64	1.35	-0.47
ICGV-91117	9.98	1.55	17.02**
ICGV-92215	11.56	1.25	0.42.
ICGV-86031	9.07	1.37	0.87
ICGV-93379	8.58	0.47	2.09*
ICGV-87358	9.36	1.41	5.58**
ICGV-92196	9.26	1.20	2.80**
ICGV-91151	9.49	1.69	4.39**
ICGV-86607	11.16	-0.19	0.34
ICGV-93407	7.20	0.83	21.24**
ICGV-93373	8.47	1.34	-0.85
ICGV-88398	7.60	0.00	-0.85
ICGV-92224	4.09	0.00	1.57
ICGV-93396	7.82	0.56	9.27**
ICGV-88409	11.10	-0.01	7.97**
ICGV-86590	7.90	0.01	1.57
ICGV-92206	7.76	0.55	-0.78
ICGV-92196	9.02	1.10	4.91**
ICGV-93438	9.53	1.65	3.57**
ICGV-91123	7.16	0.21	-0.47
ICGV-86707	7.82	1.16	-0.85
ICGV-92226	8.64	1.68	0.47
ICGV-92269	9.64	2.05	-0.85
ICGV-86742	6.27	0.72	-0.24
ICGV-91124	10.76	2.04	-0.77
ICGV-86754	7.84	1.72	6.25**
AK-12-24	9.42	0.09	1.67
Mean	**8.73**	**1.00**	
SE of mean (±)	**1.50**	**0.66**	

ICGV-91112 and ICGV-91124 may be promising for only in favourable environments due to their lower S^2d_i and higher bi values while; ICGV-86607 may be more adaptive poor environment for its lower S^2d_i and negative b_i value (Jatasara and Paroda 1980). In spite of higher pod yield per plant the adaptability of ICGV-88409 was conspicuous due to its significantly higher S^2d_i value. The genotypes, ICGV-92215, ICGV-91112, ICGV-86607 and ICGV-91124 registered appreciable kernel wt per plant and harvest index (Table 3) may be suitable alternative to push further rice based groundnut productivity under residual moisture situation.

Table 3. Pooled mean for seven yield related traits of seven selected genotypes

Genotypes	Pods yield/pl.	Kernel yield/pl (g)	Biological yield/pl (g) (g)	Harvest Index (%)
ICGV -91112	10.93	9.82	26.44	37.15
ICGV -91124	10.76	8.23	24.56	33.51
ICGV -92215	11.56	8.28	26.49	31.24
ICGV-86607	11.16	6.56	26.13	25.10
ICGV-88409	11.10	6.70	35.27	19.00
AK 12-24	9.42	7.97	22.00	36.06
Mean	**10.82**	**7.93**	**26.82**	**30.34**
S. E. of mean (±)	**1.07**	**1.31**	**3.14**	**0.77**

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SHORT COMMUNICATION

Preliminary Field Screening for Reaction to Rust and Powdery Mildew Diseases of Wheat Germplasm

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Wheat diseases particularly yellow rust, brown rust and powdery mildew cause significant losses in yield. Although a large number of chemicals are available in the market for controlling the diseases but they are costly and local farmers are not able to purchase them. Hence, the cultivation of resistant/tolerant varieties is the only alternative to prevent the losses. The present study reports the reaction of some elite lines to yellow rust, brown rust, black rust and powdery mildew.

Four hundred twenty five accessions of indigenous as well as exotic material in wheat germplasm were screened under epiphytotic conditions at the NBPGR Regional Station, Bhowali during Rabi 2002-2003, which is known as hot spot for rust and several other wheat diseases. The accessions were sown in three rows, 2 meter long with 23 cm spacing. Normal dosages of manures, fertilizers and other cultural practices were used. The outbreak and scoring of diseases were recorded under natural infestation. This centre provides good feasibility for screening the germplasm of wheat especially for yellow rust (*Puccinia striiformis*), brown rust (*Puccinia recondita*) and powdery mildew (*Erysiphe graminis* var. *tritici*) because of the appearance of the disease in sufficient spectrum for effective screening of germplasm. Percentage of leaf covered by yellow rust, brown rust, black rust and powdery mildew were calculated, taking 10 hills from each micro plots randomly at fortnightly intervals beginning 45 days after transplanting (DAT). The disease intensity was also recorded simultaneously on a 0-9 scale.

Wheat is popularly grown in *Rabi* season in rain fed/irrigated areas of Uttaranchal due to its increased demand for food as well as low cost of cultivation. Powdery mildew of wheat is essentially a disease of the hills where it appears in severe form. Of late, it has been reported in plains also but so far its incidence is not high. At times it is reported from isolated places in Tarai areas.

Out of the four hundred twenty five accessions based on disease intensity, 07 entries for yellow rust, brown rust and black rust 07 entries for powdery mildew and 02 for yellow rust, brown rust, black rust and powdery mildew, respectively were found highly resistant (<1 score) are listed below:

Yellow Rust, Brown Rust and Black Rust

EC-339599, EC-374931, EC-374939, EC-331630, IC-82401 IC-104630 & IC-104577.

Powdery Mildew

EC-339591, EC-339600, EC-339604, EC-339608, IC-35155, IC-82133, & IC-325775

Yellow Rust, Brown Rust, Black Rust and Powdery Mildew

EC-339597 & EC-339630.

These accessions showed a good promise for multiple resistance to various wheat diseases and can be utilized for evolving disease resistant varieties. Breeding for disease resistant cultivars has been taken up by different centers under the All India Co-ordinated Wheat Improvement Project. Therefore, the present results will be quite useful to the wheat breeders of the country.

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SHORT COMMUNICATION

Studies on Genetic Divergence in Aromatic Rice

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Nature of genetic divergence among the thirty aromatic rice genotypes was measured using Mahalanobis D^2 analysis for eleven agronomic characters. Significant variation was observed for all the characters studied. On the basis of D^2 values the genotypes were grouped into five clusters. The cluster I was the largest with 10 genotypes and cluster V had the least 3 genotypes. No relationship was observed between clustering pattern and the geographic distribution of the genotypes. The characters like grain yield/plant and plant height showed maximum contribution towards divergence. The cluster III and V showed maximum and II and III minimum inter cluster distance. So the genotypes from these clusters are suggested as parental donors to obtain high heterotic combination.

Key Words: Aromatic rice, Cluster analysis, Genetic divergence

Aromatic rice germplasm collected from different parts of India provides a good genetic diversity due to presence of high degree of phenotypic variability. Crosses between the parents with maximum divergence has been found to be most effective for genetic improvement. The importance of nature and magnitude of genetic divergence in aromatic rice and its utilization for selection of desirable parents or donors. Either exploitation of hybrid vigour or to get desirable recombinations the multivariate analysis developed by Mahalanobis D^2 analysis is a valuable tool to quantify the degree of divergence among the population. The present study was undertaken to know the nature and magnitude of genetic divergence among the aromatic rice collected from different parts of India.

The experimental material comprised thirty aromatic genotypes collected from different parts of India. The experiment was conducted in a Randomised Block Design in *kharif* season-2002 at Central Rice Research Institute, Cuttack with three replications. Thirty days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and between plants respectively. Onservations were recorded on ten randomly selected plants of eleven quantitative characters *viz.* days to 50% flowering, plant height, panicle number, plant panicle length, spikelets/ panicle, grains/panicle, 1000-grain weight, grain length, grain breadth, length/breadth ratio and grain yield/plant. The mean values over three replications were used for statistical analysis. The analysis of genetic divergence using Mahalanobis D^2 analysis was carried out and grouping of the genotypes into different clusters by Tocher's method (Rao 1952).

The analysis of variance showed significant variability among the genotypes for all the characters studied indicating adequate scope for selection of superior and diverse genotypes. On the basis of D^2 values the thirty genotypes were grouped into five clusters. The cluster I consisted of maximum number of ten genotypes. Cluster II have seven genotypes, Cluster III consisted of four genotypes, Cluster IV consisted of six genotypes and Cluster V consisted of three genotypes. Though PPS-50, PPS-55, PPS-58, PPS-85 and Punjab basmati-1

Table 1. Clustering pattern of aromatic rice genotypes

Cluster	No. of Genotypes	Origin	Genotypes
I	10	Haryana,	Pusa basmati, HKR-228
		M.P.	Kalimochi
		U.P.	Basmati-370, Kalajira-286
		Punjab	PPS-55, PPS-85
		Tamil Nadu	Pusa-33, ADT-9
		Bihar	Kamini
II	7	Punjab	PPS-50
		M.P.	Vishnubhog
		Haryana	Karnal basmati, HKR-241
		Bihar	Kamod
		Orissa	CRM-8-30
		Assam	Tulsibhog
III	4	Orissa	Sugandha
		Karnataka	Kusum
		M.P.	Madhuri
		Rajasthan	BK-79
IV	6	Tamil Nadu	ADT-32, ADT-41
		U.P.	Narendra-118
		Maharashtra	PBN-1
		Punjab	Punjab basmati-1
		M.P.	Basmatibahar
V	3	Orissa	IET-12016
		M.P.	Dubaraj
		Punjab	PPS-58

Table 2. Cluster mean values for eleven characters in aromatic rice

	Days to 50% flowering	Plant height (cm).	Panicle number/ plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	1000-grain weight (gm)	Grain length (mm)	Grain breadth (mm)	Length/ breadth ratio	Grain Yield/ plant (g)
I	106.0	**140**	6.2	24.2	**60.2**	**40.4**	20.2	10.2	1.96	5.2	**4.5**
II	**117.0**	125	7.5	**22.1**	90.5	65.2	18.5	9.7	**2.11**	4.6	6.2
III	**98.0**	**112**	**8.2**	23.5	93.4	60.1	19.8	10.8	1.96	5.5	8.7
IV	115.0	130	6.0	22.3	**160.3**	**120.4**	**16.3**	**7.6**	**1.85**	**4.1**	**15.3**
V	108.0	128	**5.6**	**24.6**	98.2	55.3	**21.8**	**11.0**	1.96	**5.6**	7.2

Bold figures indicate highest and lowest values for each character

originated in Punjab but they are placed in different clusters. Vivekanandan and Subramanian (1993) viewed that this clustering pattern may due to varied agroclimatic region prevailing in different states of India. The genotypes in cluster I originated from six different states showed maximum diversity and grouped in one cluster. There is no parallalism existing between the genetic diversity and geographical distribution. Similar reports have been reported by Ushakumari and Rangaswamy (1997) and Gupta *et al.* (1998). Selvakumar *et al.* (1989) also reported that the genetic drift and selection in different environments can produce greater diversity than geographic diversity.

The contribution of different characters towards divergence have greater emphasis on clustering pattern of genotypes and best choice of parents in hybridization programme. It was observed that grain yield/plant contributed maximum (28.2%) followed by plant height (15.2%) whereas lowest contribution was observed by length/breadth ratio (2.5%) towards total divergence. Vivekanandan and Subramanian (1993), Ushakumari and Rangaswamy (1997) also emphasized the greater contribution of grain yield/plant and plant height towards total divergence.

The intracluster distance varied from 6.1(II) to 21.7(V). The maximum intercluster distance 24.4 was observed between cluster III and V. Since the genotypes found in cluster III and V are more divergent, so the selection of parents from these two cluster for hybridization programme to obatin high heterotic combination and desirable transgressive segregants which was supported by Soni *et al.* (1999).

The genetic divergence among the clusters are reflected in the cluster mean values. The cluster mean values (Table 2) showed wide difference for various characters studied. Cluster I showed highest values for plant height (140.0 cm) and lowest values for spikelets per panicle (60.2), grains/panicle (40.4) and grain yield per plant (4.5 g). The cluster II have highest mean values for days to 50% flowering (117 days), grain breadth (2.11 cm) and lowest for panicle length (22.1 cm). The cluster III have highest panicle number (8.2) and lowest for days to 50% flowering (98 days), plant height (112 cm). The cluster IV have highest value for spikelets/panicle (160.3), grains/panicle (120.4), grain yield/plant (15.3 g) and lowest values for 1000 grain weight (16.3 g), grain length (7.6 mm), grain breadth (1.85 cm) and length/breadth ratio (4.1). Cluster V have highest values for panicle length (24.6 cm), 1000-grain weight (21.8 g), grain length (11.0 mm), length/ breadth ratio (5.6) and lowest for panicle number (5.6). The genotypes with high mean values can be directly used for adaptation or can be used as parents in hybridization programme through recombination breeding. Among the clusters, cluster V is the best cluster for genotypes.

Table 3. Average intra (bold) and inter cluster distance (D) values

	I	II	III	IV	V
I	**12.7**	13.8	12.8	11.2	19.6
II		**6.1**	7.0	15.4	22.8
III			**7.3**	14.5	24.4
IV				**7.1**	16.6
V					21.7

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