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SEEDLING AND ADULT PLANT RESISTANCE TO LEAF RUST IN WHEAT

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Forty exotic genetic stocks of bread wheat were tested in glasshouse and isolated single race nurseries against three pathotypes of race 77 and with mixture of pathotypes to observe their seedling and adult plant resistance to leaf rust. Twenty five genotypes showed adult plant resistance and significant genetic differences were detected to enable their grouping in 8 distinct classes. Fifteen genetic stocks depicted seedling resistance at the seedling and adult plant stages when tested against race 77-5 and were placed in three distinct groups. The study indicated that adequate variability for seedling and adult plant resistance to leaf rust exists in these germplasm accessions when tested against native pathotypes of leaf rust.

Key words : Plant resistance, durable resistance, leaf rust, wheat, *Puccinia recondita* f. sp. *tritici*

The food security of India depends on the increased production of wheat and rice. The stability and sustainability of wheat production is greatly influenced by biotic and abiotic stress factors. Leaf rust of wheat caused by *Puccinia recondita* Rob. ex Desm. f. sp. *tritici* Erikss and E. Henn. is important in all the wheat growing regions of the country and causes serious yield losses (Swaminathan, 1978). A number of pathotypes of race 77 have evolved with increasing virulence to a number of *Lr* genes (Kadam *et al.*, 1977; Nayar *et al.*, 1980), thereby making resistance of many bread wheat cultivars ineffective to which these genes have been deployed. In recent decade, there has been an increasing interest on adult plant leaf rust resistance (APR) genes because most of the sources of APR have been found to confer durable resistance. Knowledge of genetic diversity for APR may help in deploying novel APR sources towards breeding for durable resistance against this rust. The present investigation was, therefore, undertaken in 40 exotic genetic stocks of wheat leaf rust germplasm pool to detect variation for adult plant leaf rust resistance against the most virulent forms of race 77 (77-5), (Nayar *et al.*, 1992).

MATERIALS AND METHODS

The materials of the present study comprised of 40 genetic stocks obtained from the National Bureau of Plant Genetic Resources. The pedigree details are mentioned in Table 1. The leaf rust pathotypes 77-1, 77-2 and 77-5 whose

Table 1. Pedigree of genetic stocks in wheat leaf rust germplasm pool (WLRGP) 1993

Entry No.	Name or Cross/Pedigree
1	4777(2)/ /Fkn/Gb/3/Vee'S'/4/Buc'S'/Pvn'S'/5/Ald'S'/3/CC//Inia/Bb
2	67109/Frd//P101/Fw71002/3/2*Vee#6
3	Au//Kal/Bb/3/Bon/4/Bow'S'
4	Au//Kal/Bb/3/Bon/4/Bow'S'
5	Au//Kal/Bb/3/Bon/4/Kvz//Cno/Pj62
6	Bage/Hork'S'//Aldan'S'/4/Au/Kal/Bb/3/Bon
7	Bow'S'/Vee'S'//71St2959/Crow'S'
8	Buc'S'/Dga//Hpo'S'
9	CHAM2/Vee'S'
10	Carpentrio/Carp/4/G11/Yr-Resel(B)/3/Au//Kal/Bb
11	Genaro.81/Snb'S'
12	Genaro.81/Vee'S'
13	Ghurab
14	Glennson.81/Kea'S'
15	G11/YrResl(B)/3/Au//Kal/Bb/4/Yr/Pam'S'
16	Gv/Adl'S'//Bow'S'
17	Gv/Adl'S'/Mji//Bow'S'
18	Hahn'S'/Mji//Lira'S'
19	Jcan/Emu'S'//Chrc'S'/4/las20//
20	KAUZ'S'
21	Kvz//Cno/Pj62/4/T.Ast//Kal/Bb/3/Sq48/A1/Cno'S'(2)//Cno(4)
22	Maya74'S'/On//1160-147/3/Bb/G11/4/Chat'S'5/Maya74-'S'/On//1160
23	Myna'S's/3/F35.70/Mo//Nac
24	Ns732/Her
25	Seri82/5/Ald'S'/4/Bb/G11//Cno67/7C/3/Kvz/Ti
26	Seri82/5/Ald'S'/4/Bb/G11//Cno67/7C/3/Kvz/Ti
27	Sn64/Hn4'/Rex/3/Edch/Mex/4/Sls'S'/5/Bow'S'

28	TALLO 3
29	Tsi/Vee#5#S'
30	Ures.81/Genaro.81
31	Ures/Bow'S'
32	Ures/Bow'S'
33	VCee#5'SBow'S'
34	Vee'S'//GV/Ald'S'
35	Vee'S'//Sannine/Ald'S'
36	Vee'S'//Sannine/Adl'S'
37	Vee'S'/3/Tast/Mo//Nac
38	Vee'S'/5/Gv/4/D6301/Nai/Wrm/3/Cno*3/Chr
39	Vee'S'/5/Skh8/4/Rrv/Ww15/3/Bj'S'//On*/Bon
40	Vee'S'/5/kh8/4/Rrv/Ww15/3/Bj'S'//On*3/Bon

avirulence and virulence formulae are given below, were obtained from the Directorate of Wheat Research Station, Shimla

77-1	=	Lr21, Lr23/Lr1, Lr2, Lr3, Lr10, Lr11, Lr12, Lr13, Lr15, Lr16, Lr17, Lr20, Lt26, Lr27+31, Lr30
77-2	=	Lr26/Lr1, Lr2, Lr3, Lr10, Lr11, Lr12, Lr13, Lr15, Lr16, Lr17, Lr20, Lr21, Lr23, Lr27+31, Lr30
77-5	=	Lr21/Lr1, Lr2, Lr3, Lr10, Lr11, Lr12, Lr13, Lr15, Lr16, Lr17, Lr20, Lr23, Lr26, Lr27+31, Lr30
Common avirulence	=	Lr9, Lr18, Lr19, Lr24, Lr25, Lr28 and Lr29
Common virulence	=	Lr14, Lr22, Lr33, Lr34

Seedling studies

Six to eight wheat seedlings of genetic stocks were planted as hill and raised in trays in triplicate. Ten days old seedlings were inoculated with uredospores suspended in Tween 20. The inoculated plants were placed in humidity chambers overnight at 10° to 15°C and transferred to glasshouse chamber. The infection types (ITs) were recorded after 12-14 days on 0-4 scale (Stakman 1962). Infection type data from only one replicate are reported because there was no significant variations in ITs of the other two replicates.

Adult plant resistance studies

The adult plant resistance was monitored for 3 years (1995., 1996 and 1997) against 77-1, 77-2 and 77-5 chosen for virulence on seedling resistance genes and also with the mixture of prevalent races of leaf rust. Forty genetic stocks alongwith susceptible check (Agra-Local) were planted in isolated

nurseries at IARI farms in 1.25 m long rows 23 cm apart and inoculated with individual pathotypes. Spreader rows were planted periodically between the rows. The nursery was bordered on all sides with two rows of mixture of Agra Local and Lal Bahadur, followed by two rows of oats spaced 23 cm apart to trap foreign spores if any.

Artificial leaf rust epiphytotic was initiated by injecting urediospore-water-Tween 20 suspension in leaf sheaths of spreader plants 60 days old with hypodermic syringe. Rust severity and response were measured at the terminal stage of plant growth for individual pathotype (Loegering, 1959), while disease ratings were made thrice at fortnight intervals when tested with mixture of pathotypes in 1995 and 1996.

RESULTS AND DISCUSSION

Adult plant resistance

Out of 40 genotypes under study 25 genotypes were susceptible at the seedling stage with the seedling infection type (IT) 33+ to 4 while 15 genotypes were resistant 0 to 2 when tested with leaf rust race 77-5, which is the most aggressive race and covers most of the virulences available in the country. The genetic stocks were tested at the adult plant stage with the same race (77-5) besides other pathotypes of race 77 (77-1 and 77-2). Based on the identical response pattern for each pathotype, 25 genotypes can be classified in 9 distinct groups (Table 2).

Group I	:	It comprises of 12 stocks with very low (VL) response to 77-5, 77-1, 77-2 and mixture of pathotypes of leaf rust.
Group II	:	The second group comprises of 4 stocks, wherein very low (VL) disease ratings were obtained for 77-1 and 77-2 and comparatively high (L) for 77-5.
Group III	:	It comprised of one stock Entry 12 which gave very low responses to 77-1 and 77-2 but high (H) to 77-5.
Group IV	:	Entry 2 and 16 constituting this group in which APR factors are effective against 77-1 and 77-2 but ineffective against 77-5.
Group V	:	The APR source is effective against 77-1 and 77-5 (Ent 35) but ineffective against 77-2.
Group VI	:	It embodies unique APR of race specific type which is effective to race 77-1 only (Ent. 33).
Group VII	:	This APR source (Entry 25 and 26) showed race specific adult plant resistance to 77-1 like group 6, however, the entries in this group gave high response to mixture of races during 1995 and 1996.
Group VIII	:	Low reaction to 77-2 is the characteristic of this APR source (Entry 10).
Group IX	:	It involves Entry 1 with susceptible check Agra local which lack any APR component.

Table 2. Categorising adult plant resistance to leaf rust : Seedling infection type with leaf rust race 77-5 in glasshouse and adult plant response patterns of 25 genotypes of WLRGP-93, with specific leaf rust pathotypes and mixture of leaf rust pathotypes in isolated field nurseries.

Group I	Entry	SIT	77-1			77-2			77-5			Mixture 1995			Mixture 1996		
			1995	1995	1995	1995	1996	1996	1997 ^a	1997 ^b	(L)	I	II	III	I	II	III
			(VL)			(VL)											
	6	3+	10MR	5MR	5MR	TR	TR	TR	-	-	-	5MR	10MR	20MS	TR	TR	TR
	7	4	-	5MR	5MR	TR	TR	TR	5MR	5MR	5MR	5MR	10MR	5MRMS	5MR	10MR	10MR
	9	4	5RMR	5MR	5MR	TMS	-	-	5MR	5MR	5MR	10RMR	20MR	40MRMS	-	-	-
	13	3+	TR	TR	TR	TR	TR	10S	10MR	5MR	5MR	10R	10RMR	20MR	5R	10RMR	10MR
	14	3+	5R	10MSS	TS	TS	10S	10S	10MS	10MS	10MS	5MR	5MR	10MRMS	5MR	10MR	10MR
	15	4	10MR	5MR	10MSS	TS	TS	10S	10MS	10MS	10MS	10MS	5MR	5MR	10MRMS	5MR	10MR
	20	3+	10MRMS	TR	TR	TR	TR	TR	TMR	20MR	20MR	10MR	20MR	30MRMS	-	-	-
	23	4	TR	TMR	TMR	TR	TR	TR	TR	5MR	5MR	TMR	5MR	5R	-	-	-
	28	3c	5R	5MR	5MR	TR	5MS	TR	TR	10MR	10MR	5MR	5MR	20MRMS	5MR	10MR	10MRMS
	36	3+	TMR	TR	TR	TR	TR	TR	TR	TMR	TMR	TR	TR	TR	5R	5R	5R
	39	33+	5R	10MR	TMR	TMR	20MR	TR	TR	TR	TR	5MR	10MR	10MRMS	-	-	-
	40	33+	30MS	TR	-	-	20MS	-	-	-	-	10MR	20MRMS	30MRMS	10MS	30MS	40MSS
Group II	3	3+4	(VL)	5RMR	10MR	TR	10S	20MSS	30S	30S	(L)	10MR	20MSS	50MS	20MS	30MS	40MSS
	4	33+	20MR	20MR	TR	TR	30S	10MSS	30S	30S	10MRMS	10MRMS	10MS	40MS	20MS	30MSS	40MSS

(Table Contd. on next page)

Table 2 contd.

		77-1		77-2		77-5		Mixture 1995			Mixture 1996		
		77-1	77-2	77-2	77-2	77-5	77-5	77-5	77-5	77-5	77-5	77-5	77-5
5	4	10MR	20MRMS	TR	TR	10MR	10MR	10MR	10MR	10MR	10MR	10MR	10MR
29	3	10MR	20MRMS	TR	10MR	10MR	10MR	10MR	10MR	10MR	10MR	10MR	10MR
Group III	(VL)	(VL)			(H)								
	3+	10MR	10S	TR	-	40S	40S	40S	40S	40S	40S	40S	40S
Group IV	(L)	(L)	(L)			(H)							
	3	40MS	30MS	TMR	40S	-	-	20MR	40S	60S	30MS	40S	50S
Group V	3+	20MR	30MR	-	-	60S	60S	10MR	-	20MSS	20MS	20MSS	30MSS
	(L)	(L)	(H)			(L)							
35	3+	40MSS	50S	-	-	20S	30S	10MS	20MSS	50S	20MSS	50S	60s
Group VI	(L)	(L)	(H)			(H)							
	3+	40MSS	50S	-	40-S	10MSS	-	10MR	10MRMS	30MSS	-	-	-
Group VII	(L)	(L)	(H)			(H)							
	4	60MS	80S	-	20S	-	-	30MS	50S	70S	40S	50S	70S
26	4	-	80S	-	20S	20MSS	60S	30MS	60S	80S	50S	60S	80S
Group VIII	(L)	(L)	(L)			(H)							
	4	60S	30S	-	-	10MS	60S	20MS	40S	60S	40S	50S	60S
Group IX	(H)	(H)	(H)			(H)							
	33+	50S	60S	40S	-	-	60S	60MRMS	40S	60S	40S	60S	60S
AL	4	70S	80S	70S	60S	70S	100S	70S	70	80S	70S	80S	30S

VL = 0-20mR; L = 20MS-30MSS; H = 40S-100S; SIT = Seeding Infection type; A = Agra local

Table 3. Seedling resistance : Seedling infection type with leaf rust race 77-5 in glasshouse and adult plant response patterns of 15 genotypes of WLRGP-93, with specific leaf rust pathotypes and mixture of leaf rust pathotypes in isolated field nurseries.

Entry	SIT	77-1			77-2		77-5		Mixture 1995			Mixture 1996		
		1995	1995	(VL)	1996	1996	1997 ^a	1997 ^b	I	II	III	I	II	III
Group I														
8	2+	(VL)	TR	(VL)	TR	5MS	TR	TR	5R	5R	5R	TMR	5MR	5MR
18	2+	TR	TR	TR	TR	-	TR	TR	TMR	TR	TR	-	-	-
19	1-2-	TR	10MR	10MR	TR	-	TMR	10MR	TMR	10MR	20MR	5MR	10MR	10MR
21	22+	5R	TR	TR	TR	-	TR	TMR	5R	5R	10MRMS	-	-	-
22	22+	5MR	20MR	20MR	TMR	TR	TMR	5MR	5MR	20MS	30MS	10MR	20MRMS	20MS
24	2-	TR	TR	TR	TR	TR	TR	TR	TR	0	TR	TR	-	-
27	2+	10MR	20MR	20MR	TMR	5MS	10MS	20MS	10MR	30MRMS	-	10MR	30MR	30MR
30	2	20MRMS	20MR	20MR	TMR	5MRMS	10MS	10S	10MR	10MSS	-	5MS	10MS	20MS
31	1+2-	TR	10MR	10MR	TR	5MR	10MR	10MS	5MR	10MR	10MR	5MR	10MS	20MRMS
32	22+	10R	5MR	5MR	TR	TMR	5MS	10MS	5MR	10MR	10MRMS	10MR	10MR	20MRMS
34	2+	10MR	-	-	TMR	TR	TMR	5MR	10MR	10MR	20MS	10MR	10MS	20MSS
38	1+2	TR	TR	TR	TR	TR	TMR	TR	TR	5R	5MR	10MR	5MR	5MR
11	2+	(VL)	5MR	(VL)	TR	20S	30S	30S	10MRM _S	20MSS	50S	30S	40S	60S
Group II														
Group III														
17	2+	(H)	50S	(H)	-	-	10MSS	50S	20MS	40S	60S	30S	40S	60S
37	2+	90S	80S	80S	-	60S	60S	70S	20MSS	60S	70S	30MSS	40S	60S

Seedling resistance

Group I embodies 12 genotypes possessing high seedling resistance to all the pathotypes which remains effective throughout the life of plant (Table 3). Entry 11 (Group 2) was distinct in the sense that it gave low resistance response to race 77-5. Genotypes 17 and 37 showed seedling resistance in glasshouse but were susceptible to 77-1, 77-2 and 77-5 races of leaf rust at adult plant stage. Similar cases were also reported by Bahadur *et al.*, 1993.

Studies have indicated that the genetic stocks are available with seedling resistance as well as adult plant resistance to the most virulent forms of leaf rust (77 group). Both types of resistances are valuable, since the interaction of major seedling resistance genes with adult plant resistance genes has been suggested as one of the means to achieve durable resistance (Sawhney *et al.*, 1992, Sawhney and Joshi, 1996). Pyramiding of seedling resistance genes with adult plant resistance genes can be an effective strategy to breed for durable resistance to leaf rust in wheat.

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GENETIC DIVERGENCE IN HIMALAYAN RICE

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Fifty genotypes of rice (*Oryza sativa* L.) from the Himalayan belt were studied for their genetic divergence for a set of ten characters using Mahalanobis D^2 statistics. The genotypes were grouped into 11 clusters. The genetic diversity was not related to geographic diversity. Based on divergence and superior cluster means, crosses between genotypes from cluster IX and I, II, VI, XI may result in superior types.

Key words : Rice, genotype, genetic divergence, heterosis

Genetic diversity in a population provides the basis of any crop improvement programme. The use of diverse parents gives better opportunities to a breeder for selection and development of a superior variety. Estimation of genetic divergence through the use of Mahalanobis D^2 statistics has been emphasized by many workers (Murty and Arunachalam, 1966; Singh and Bains, 1968; Singh and Gupta, 1968), because of its usefulness in forming parental combinations before effecting actual crosses.

MATERIALS AND METHODS

The experimental material consisted of 50 germplasm lines from Himachal Pradesh (11), Jammu & Kashmir (3), Uttar Pradesh (1), Bihar (7), Assam (7), Arunachal Pradesh (3), Meghalaya (14), Nagaland (3), Manipur (1). All the 50 lines were grown in complete randomised block design with two replications under low land conditions at Barapani (900m), Meghalaya during *Kharif* 1992 and 1993. One month old seedlings from the nursery were transplanted under the recommended levels of fertilizers with a spacing of 30cm $\times$ 15 cm. Each plot consisted of two meter long, three rows. Observations were recorded on well guarded randomly chosen ten plants per replication for each entry for ten characters. The mean values were subjected to Mahalanobis D^2 statistics to measure genetic divergence as suggested by Rao (1952) and the clusters were formed by Tocher's method (Rao, 1952).

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RESULTS AND DISCUSSION

The analysis of variance exhibited highly significant differences among the genotypes for all the ten characters. On the basis of D^2 values, all the 50 genotypes were grouped into 11 clusters (Table 1). The maximum number of genotypes were in cluster I (19 genotypes) whereas cluster VIII to XI contained only single genotype each. Since the cluster I included genotypes from different areas along the long stretch of Himalaya from west to east, this indicated that there is no association between clustering pattern and eco-geographical distribution of the genotypes. Many rice workers (De and Rao 1987; Mishra and Dash, 1997) have revealed that geographical diversity is not necessarily related to genetic diversity.

The clustering of genotypes from different eco-geographical locations into one cluster could be attributed to possible free exchange of breeding materials or even varieties from one place to another (Verma and Mehta, 1976). This may also be due to the fact that the unidirectional selection practiced for a particular trait in several places produced similar phenotypes which were aggregated in one cluster irrespective of their distant geographic origin (Singh and Bains, 1968). On the other hand many genotypes originating from one place were scattered over different clusters (Table 1). Such genetic diversity among the

Table 1. Distribution of 50 genotypes of rice in different clusters

Cluster No.	No. of genotype	Genotypes/Germplasm lines	Origin/source
I	19	BD18, BD133, BDS 7/378, BDS 7/383, BDJ 1253, C 1003, C 1630, C 1926, C 1946, C 1999, DKH 74, Gnob, IC 81400, IC 81396, NG 6/42, NKG 1160, NKG 1154, NKG 1211, P 532.	Assam (3) Arunachal Pradesh (2) Bihar (3) Himachal (4) J & K (2) Meghalaya (2) Nagaland (2) U.P. (1)
II	9	BD 10, BD 19, BD 38, BD 71, BD 77, BD 93, BD 99, BD 101, Manipuri	Meghalaya (8) Manipur (1)
III	5	C 1981, DKH 60, NKG 1046, NKG 1047, NKG 1161	Assam (1) Bihar (1) Himachal (3)
IV	4	C 1800, C 1875, NKG 1120, NKG 1209	Bihar (1) Himachal (3)
V	3	BD, BD 2, DKH 89	Assam (1) Meghalaya (2)
VI	3	BD 118, C 1947, C 1964	Bihar (2) Meghalaya (1)
VII	3	C 1645, MMH 6/6, MMH 6/26	Assam (2) J & K (1)
VIII	1	BD 57	Meghalaya (1)
IX	1	BDS 7/376	Arunachal (1)
X	1	NH 6/27	Nagaland (1)
XI	1	NKG 1192	Himachal (1)

genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murty and Arunachalam, 1966). The intra-and inter-cluster divergence among the genotypes was of varying magnitude (Table 2). The intra-cluster D^2 values have been found to be zero for clusters VIII to XI as they included only single genotype whereas it was maximum in cluster VII (8.90). The maximum inter-cluster distance was obtained between clusters VI and VIII (35.97) while the minimum inter-cluster distance has been observed between clusters III and VII (12.18) indicating close relationship between these clusters. The greater the distance between clusters, wider the genetic diversity between the genotypes.

Table 2. Intra (bold) and inter-cluster distance among 11 clusters in rice

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	8.47	16.70	16.34	12.31	17.38	19.14	13.83	22.26	16.60	15.50	23.40
II		7.92	22.15	14.31	25.39	31.99	22.44	14.55	28.88	14.21	31.59
III			6.18	14.61	15.22	15.25	12.18	24.56	19.09	16.73	25.26
IV				8.09	15.77	23.01	13.36	17.76	22.44	12.53	26.15
V					7.11	18.02	12.19	26.40	21.73	20.08	21.98
VI						7.54	16.10	35.97	12.88	27.68	19.68
VII							8.90	26.24	19.97	17.96	24.94
VIII								0.00	34.49	16.36	34.76
IX									0.00	27.34	17.19
X										0.00	29.92
XI											0.00

The cluster means for each character are presented in Table 3. The single genotype, BDS 7/736, in the cluster IX showed the highest grain yield performance accompanied by the highest means for panicle weight, grains per panicle, and maximum days to maturity as well as the lowest number of tillers and panicles. NKG 1192 in cluster XI possessed the highest number of tillers and panicles and the heaviest 100-grain weight. The genotypes (BDS 118, C 1947, C 1964) of cluster VI were characterised by the longest duration for days to flower and days to maturity. The maximum plant height was found in genotypes of cluster III but these had the lowest 100-seed weight. Cluster II means showed maximum panicle length for the genotypes it contained. BD 57 in cluster VIII possessed the lowest mean values for days to flower, days to maturity, panicle weight and grain yield per plant. The genotypes in

Table 3. Cluster means for ten characters in 50 genotypes of rice

Cluster number	Plant height (cm)	Tiller number	Days to flower	Panicles per plant	Panicle length (cm)	Days to maturity	Panicle weight (g)	Grains per panicle	100-seed weight (g)	Yield per plant (g)
I	105.17	8.01	138.73	7.81	23.20	161.49	2.53	110.97	2.40	17.11
II	100.42	7.55	118.00	7.31	24.00**	150.00	2.46	95.38	2.59	16.35
III	121.37**	8.01	141.80	7.76	23.37	173.00	1.80	107.68	1.74*	11.29
IV	82.41	9.63	130.25	9.08	21.19	161.50	2.29	93.90	2.41	12.99
V	94.15	7.90	142.00	7.73	20.40	175.70	1.69	92.77	2.62	6.87
VI	117.35	9.10	154.70**	8.73	21.87	194.00**	1.99	105.83	1.98	15.62
VII	83.92	10.10	141.67	8.80	21.58	173.00	1.70	79.60	2.17	11.87
VIII	110.00	7.90	113.00*	7.80	23.50	145.00*	1.59*	109.10	2.15	4.25*
IX	85.95	7.50*	154.00	6.50*	22.35	194.00**	3.28**	128.60**	2.50	21.35**
X	81.65*	9.10	116.00	6.50*	19.00*	151.00	2.12	104.30	2.00	8.55
XI	111.30	10.30**	138.00	10.00**	22.70	159.00	2.56	104.90	2.95**	11.20
Grand mean	102.47	8.27	135.29	7.92	22.75	168.36	2.30	103.25	2.34	14.54
CV(%)	16.34	15.11	1.49	14.52	4.44	1.06	6.68	5.45	3.98	7.63

*, ** lowest and highest means respectively.

clusters I, IV, V possessed medium mean values for all the characters. The coefficient of variation for different characters indicated that major forces of discrimination were plant height, tiller and panicle number and grain yield, which is in agreement with the findings of Mishra and Dash (1997). It is noteworthy that cluster IX consisting of a single genotype (BDS 7/736) from Arunachal Pradesh had superior mean values for grain yield, grain number/panicle, panicle weight combined with the longest maturity duration.

On the basis of divergence and grain yield and components of grain yield, it is suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of clusters IX and cluster I, II, VI as well as cluster XI. This information may be useful to the breeders engage in varietal improvement programmes in the Himalayan belt.

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SCREENING LENTIL GERMPLASM ACROSS TWO FERTILITY REGIMES

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A set of fifty lentil genotypes was used to study its response to extra nitrogen application through foliar spray of urea. The response was measured in terms of plant height, number of pods per plant, number of secondary branches per plant, days to maturity and grain yield per plant. Different genotypes responded differentially. A positive response was observed for yield and its determinants in 12 genotypes.

Key words : Lentil, germplasm, yield, fertilizer, evaluation

Pulses have been cultivated on marginal lands for ages. This has resulted in the erosion of genetic variability responsive to better management conditions (Jain, 1981). Lentil is second most important *rabi* pulse crop of India. It is considered to be one of the oldest food crops of mankind. Traditionally, lentil has been considered to have a lower fertilizer requirement (Lal, 1989). This concept, however, has been one of the important reasons for its low productivity at 6.7 q/ha (Sharma, 1995). One of the potential strategies to increase its productivity is to breed for response to better management including higher fertilizer doses. The present investigation was, therefore, undertaken to screen lentil germplasm across two fertility regimes to identify responsive characters and genotypes.

MATERIALS AND METHODS

A set of fifty diverse genotypes of lentil were sown in a RBD in six replications at the research farm of the Institute during *rabi* 1993-94. Along with all other standard agronomic practices, a basal dose of 20 kg N/ha was given. Additionally, 20 kg urea/ha was applied in form of foliar spray only to three replications at the end of flowering, thus creating two sets of experiment each with three replications, one with only 20 kg N/ha (F₁) and the other

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with an additional 20 kg urea/ha (F_2). The data were recorded on plant height (cm), number of pods per plant, number of secondary branches per plant, days to maturity and grain yield per plant (g). Individual and pooled RBD analyses were performed subsequently.

RESULTS AND DISCUSSION

Application of extra nitrogen through foliar spray of urea caused changes in three characters, number of secondary branches per plant, number of pods per plant and grain yield per plant among various genotypes studied (Table 1). The maturity duration was increased only for VL 110 by 3.3 per cent. There was no significant change in any genotype for plant height. Mean number of pods per plant increased by 16.7 per cent in F_2 as compared to F_1 . A total of 21 genotypes showed significant increase for this character. The maximum increase of 53.3 per cent was observed in PL 81-340.

Table 1. Mean, coefficient of variation (CV) and genotypes* showing positive response

Sl.No.			No. of pods per plant	No. of secondary branches per plant	Grain yield per plant
1.	Mean F_1		49.6	6.2	2.81
	F_2		57.9	8.0	3.62
2.	CV F_1		23.6	10.7	20.20
	F_2		23.8	12.7	23.90
3.	Genotypes showing increase	No.	21	23	25
		Names	PL81-340 (53)	VL 109 (55)	VHC 396 (52.8)
			NP 59A (42)	VL 119 (55)	L 4076 (50.8)
			VL 109 (48)	DPL 510 (51)	K 301 (45.7)
			VL 118 (47)	VL 110 (46)	DPL 504 (46.6)
4.	Genotypes showing no change	No.	29	27	25
		Names	NP 6565	NP 43	NP 6565
			VH 8801	VHL 8801	NP 44
			DPL 507	DPL 507	DPL 507

*Values in parentheses indicate the amount of change in %.

Table 2. Pooled ANOVA for yield and other characters in lentil under two fertility regimes

Parameter	Plant height (cm)	No. of pods per plant	No. of secondary branches per plant	Days to maturity	Grain yield per plant (g)
Mean squares					
Fertility regime	1.61	6.75	1.98	0.05	0.08
Genotype	65.60**	1128.30*	5.40*	10.60**	0.36**
Fertility regime × Genotype	0.80	28.80	0.59	0.14	0.02
Other Parameters					
Pooled mean	28.60	47.80	6.20	194.00	1.43
SE (Mean)	2.20	3.09	0.64	1.17	0.19
Critical difference at p = 0.05	6.11	8.58	1.81	3.24	0.55
Coefficient of variation	11.40	28.40	15.10	6.70	19.10

**Significant at p = 0.01.

A total of 23 genotypes showed an increase in number of secondary branches per plant increasing the average value of F_2 for this character by 29% as compared to that of F_1 . The maximum increase (56.8%) was observed on VL 109. Half of the genotypes studied showed an increase in grain yield per plant, the maximum being 52.8% for VHC 396. The mean grain yield per plant increased by 28.9%. There were a total of 12 genotypes viz., VL 105, VL 4, VL 109, PML 8803, VL 111, VL 107, VL 110, HUL 12, VL 119, VL 106, VL 117 and VL 120 which showed an increase for all the three characters. The results indicate at the hidden potential in lentil germplasm for utilization in breeding programmes.

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EVALUATION OF RAMIE GERMPLASM

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The present investigation was carried out with forty diverse ramie genotypes to evaluate their performance for fibre yield per plant and other yield attributes. The mean performance estimates revealed that amongst the forty genotypes, four genotypes namely SC-12, R- 1420, SC-7 and R-67-34 exhibited high mean performance for fibre yield per plant over all the environments. The genotypes SC-12 and SC-7 also exhibited high mean performance for all other remaining traits. Of these, four genotypes, R-1420 recorded high mean performance for all the traits except number of leaves, fresh weight of plant and cane while the genotype R-67-34 exhibited high mean performance for all the traits except plant height, number of leaves and leaf area. These genotypes deserve consideration for further improvement and as parents in hybridization programme.

Key words : Ramie, *Boehmeria nivea*, fibre yield, mean performance, yield attributes

Ramie (*Boehmeria nivea* (L) Gaud) is a fast growing underexploited but promising fibre crop which is considered as the strongest among all the natural fibres (Roy, 1984). The ramie fibre has great commercial importance and possesses excellent fibre qualities and mainly used in textile industry for manufacturing different types of clothings by blending with synthetic and natural fibres (Ganguli and Sarma, 1982). Now-a-days ramie fibre has got importance as a commercial source of textile industry and industrial demand of ramie fibre is increasing day-by-day. Therefore, the present investigation was aimed at to assess the mean performance of the genotypes for fibre yield per plant and other related traits so that we can identify and exploit the superior germplasm of ramie for further improvement.

MATERIALS AND METHODS

The materials utilized in the present investigation comprised of forty indigenous and exotic ramie genotypes collected from Ramie Research Station (ICAR), Sorbhog, Assam and some other districts of Assam (Table 1). The trial was conducted in a randomized block design with three replications

Table 1. Ramie germplasm used in the experiment

S.No.	Designation	Name of genotype
1	G ₁	R-1410 (<i>B. utilis</i>)
2	G ₂	R-1411 (Florida common)
3	G ₃	R-1412 (E 53-42)
4	G ₄	R-1413 (E 51-71)
5	G ₅	R-1414 (E 50-76A)
6	G ₆	R-1415 (Pl. London)
7	G ₇	R-1416 (E 50-59)
8	G ₈	R-1417 (Tatsut Tall)
9	G ₉	R-1418 (Kagasai)
10	G ₁₀	T-1420 (E 50-21)
11	G ₁₁	R-1421 (Miyasai 112)
12	G ₁₂	R-1422 (Tatsut Short)
13	G ₁₃	R-1424 (Kamargaon, Assam)
14	G ₁₄	R-1425 (Jorhat, Assam)
15	G ₁₅	R-1426 (Nowgoam, Assam)
16	G ₁₆	R-1427 (J.A.R.I., W.B.)
17	G ₁₇	R-1428 (Puna, Small leaf)
18	G ₁₈	R-1429 (Puna, Large leaf)
19	G ₁₉	R-1438 (J.A.R.I., Hyb. 9)
20	G ₂₀	R-1445 (J.A.R.I., Hyb. 2757)
21	G ₂₁	R-1451 (Tat Lal Sel)
22	G ₂₂	R-1452 (E 51-71 Sel)
23	G ₂₃	R-67-45 (Sel)
24	G ₂₄	R-68-34 (Sel E 50-76)
25	G ₂₅	R-67-51 (Sel)
26	G ₂₆	R-67-52 (Sel)
27	G ₂₇	SC-3 (Collected from Banekuchi, 3 km west from Nalbari)
28	G ₂₈	SC-4 (Collected from South Bongaigaon)
29	G ₂₉	SC-5 (Collected from South Bongaigaon near North Salmara)
30	G ₃₀	SC-7 (Nalbari, Barkhata, Dist-Goalpara (Dhiren Ravai])
31	G ₃₁	SC-8 (Namati, Tihu, Dist.-Nalbari)
32	G ₃₂	SC-9 (Mukaria, Dharamtala, Mayong Black, Dist. -Now gaon)
33	G ₃₃	SC-10 (Salmara, Abhoyapuri, Dist.-Goalpara)
34	G ₃₄	SC-11 (Sonapur, Dumuria Black, Dist.-Kamrup)
35	G ₃₅	SC-12 (Teragagaon, Dist. -Kokrajhar)
36	G ₃₆	SC-14 (Bahalpur, Dist.-Goalpara)
37	G ₃₇	SC-15 (Soulmari, Dist.-Barpeta)
38	G ₃₈	SC-16 (Dool Hati, North Lakhimpur)
39	G ₃₉	RH-I (Philippines, Dr. D.P.Singh)
40	G ₄₀	Philippines Var.

considering three dates of cuttings as three environments in the Experimental Farm of the Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat. For raising the crop, land was thoroughly and deeply ploughed and farm yard manure was applied @ 7-10 tonnes/ha. The rhizome cuttings were planted in the field maintaining a spacing of 45 cm × 60 cm in horizontal position in 5-6 cm deep furrow. After two months of planting a fertilizer mixture of N : P₂O₅ : K₂O was applied @ 20:10:10 kg/ha. Moreover, after each harvest/cutting fertilizer mixture of N : P₂O₅ : K₂O was applied @ 30 : 15 : 15 kg/ha (Sarma *et al.*, 1979). Observations were recorded for nine traits *viz.* plant height, number of effective canes, number of leaves, leaf area, basal stem diameter, fresh weight of plant, fresh weight of cane, fresh weight of fibre and dry weight of fibre. The mean data of each genotype for different traits over three environments were analyzed to study the mean performance of different genotypes.

RESULTS AND DISCUSSION

The mean performance of different genotypes over different environments is presented in Table 2. The studies revealed that for plant height the mean performance of the genotypes ranged from 68.88-138.19 cm. The maximum plant height of 138.19 cm was recorded for the genotype G₁₀ (R-1420) followed by G₂₃ (R-67-46), G₃₅ (SC-12), G₃₀(SC-7), G₁₃ (R-1424), G₃₄ (SC-11), G₁₄ (R-1425), G₁₅ (R-1426) and G₃₃ (SC-10). The number of effective canes ranged from 5.58-13.83. The maximum number of 13.83 was noted for G₃₅ (SC-12) followed by G₁₀ (R-1420), G₃₀ (SC-7), G₁₅ (R-1426), G₁₈ (R-1429), G₁₄ (R-1425), G₂₆ (R-67-52), G₂₄ (R-67-34) and G₃₄ (SC-11). For number of leaves, the range was 62.92-108.17. The highest number of 108.17 was recorded for the genotype G₃₅ (SC-12) followed by G₃₀ (SC-7). The leaf area ranged from 1551.48-7388.65 cm². The highest leaf area of 7388.65 cm² was exhibited by the genotype G₃₅ (SC-12) followed by G₃₀ (SC-7), G₁₀ (R-1420) and G₂₃(R-67-46). The mean performance for basal stem diameter ranged from 0.99-1.28 cm. The maximum diameter of 1.28 cm was revealed by the genotype G₃₀ (SC-7) followed by G₂₄ (R-67-34), G₃₅ (SC-12), G₁₀ (R-1420), G₂₃ (R-67-46) and G₃₇(SC-15). The fresh weight of plant of the genotypes ranged from 236.92-1043.54 g. The highest fresh weight of 1043.54 g was exhibited by the genotype G₃₅ (SC-12) followed by G₂₄ (R-67-34), G₃₀ (SC-7) and G₃₃ (SC-10). The range for mean fresh weight of cane was 149.42-565.33 g. The genotype G₃₅ (SC-12) showed maximum fresh weight of cane of 565.33 g followed by G₃₀ (SC-7) and G₃₃ (SC-10). The range for mean fresh weight of cane was 149.42-565.33 g. The genotype G₃₅ (SC-12) showed maximum fresh weight of cane of 656.33 g followed by G₃₀ (SC-7), G₁₃ (R-1424), G₃₄ (SC-11), G₁₅ (R-1426), G₂₄ (R-67-34), G₂₉ (SC-15), G₁₈ (R-1429) and G₁₄ (R-1425). The fresh weight of fibre of the genotypes ranged from 11.21-36.21 g. The maximum of 36.21 g was recorded for the genotype G₃₅

Table 2. Mean performance of forty ramie genotypes for fibre yield per plant and other yield attributes over three environments

Geno- type	Plant height (cm)	Num- ber of effec- tive canes	Num- ber of leaves	Leaf area (cm ²)	Basal stem dia- meter (cm)	Fresh weight of plant (g)	Fresh weight of cane (g)	Fresh weight of fibre (g)	Dry weight of fibre (g)
G ₁	76.94	5.92	74.00	1960.34	1.13	260.17	159.42	15.21	6.29
G ₂	77.19	6.92	68.71	2132.93	1.13	253.96	253.96	149.42	16.58
G ₃	104.47	8.67	69.04	2800.44	1.17	547.96	246.09	19.34	9.00
G ₄	91.33	8.75	68.08	2498.52	1.05	315.63	196.17	20.46	11.46
G ₅	68.88	5.58	65.38	1551.48	0.99	236.92	162.59	11.21	5.21
G ₆	108.08	9.33	70.96	3241.11	1.15	548.65	266.54	19.76	8.59
G ₇	82.09	10.25	67.04	3013.28	1.18	383.63	207.29	26.09	11.88
G ₈	106.7	9.58	72.95	3147.82	1.19	576.69	270.08	26.08	14.17
G ₉	105.32	10.17	66.75	2944.81	1.11	430.67	221.75	19.25	10.21
G ₁₀	138.19	13.50	84.71	6494.42	1.26	644.94	304.38	30.17	17.92
G ₁₁	115.06	10.67	80.38	4087.65	1.20	627.00	278.00	20.30	11.75
G ₁₂	101.04	7.00	62.96	2543.06	1.13	204.88	188.34	17.50	8.88
G ₁₃	124.07	10.67	75.96	4070.34	1.21	622.17	478.43	20.88	11.09
G ₁₄	121.78	12.08	82.04	4522.38	1.22	692.46	431.13	24.83	12.58
G ₁₅	120.55	12.83	79.55	4375.01	1.22	794.05	456.25	26.25	14.30
G ₁₆	92.15	9.42	72.21	3298.75	1.04	327.13	193.42	12.84	7.34
G ₁₇	101.54	7.50	64.50	2972.76	1.00	289.29	177.13	13.88	6.71
G ₁₈	111.42	12.58	86.73	4225.99	1.20	772.88	437.67	26.17	15.79
G ₁₉	99.29	7.42	69.58	3108.63	1.03	321.29	199.75	12.21	7.75
G ₂₀	96.85	5.67	65.38	3036.06	1.00	297.29	181.42	21.50	8.05
G ₂₁	88.64	9.83	70.96	3409.63	1.15	339.92	195.98	21.92	12.00
G ₂₂	102.99	11.33	68.33	3098.20	1.17	393.92	256.55	26.54	14.25
G ₂₃	135.82	11.83	83.19	6014.95	1.26	628.38	349.96	27.38	16.96
G ₂₄	119.82	12.00	81.54	4392.47	1.27	957.00	442.34	28.92	17.00
G ₂₅	90.88	8.83	63.38	2213.67	1.17	330.59	184.29	22.67	11.54
G ₂₆	111.77	12.08	74.54	3082.38	1.19	538.21	266.30	27.46	14.21
G ₂₇	111.19	10.92	74.96	3003.19	1.20	785.58	320.17	27.42	14.59
G ₂₈	112.11	10.42	84.63	4808.55	1.17	607.50	363.63	22.54	12.67

(Table contd. on next page)

Geno- type	Plant height (cm)	Num- ber of effec- tive canes	Num- ber of leaves	Leaf area (cm ²)	Basal stem dia- meter (cm)	Fresh weight of plant (g)	Fresh weight of cane (g)	Fresh weight of fibre (g)	Dry weight of fibre (g)
G ₂₉	114.48	10.17	78.54	4107.65	1.17	719.88	438.21	19.88	12.67
G ₃₀	126.92	13.08	103.63	6746.81	1.28	940.99	560.81	29.09	17.38
G ₃₁	97.04	8.08	68.84	3886.65	1.13	389.71	272.75	15.59	6.97
G ₃₂	113.32	11.58	68.50	4193.76	1.21	610.50	346.80	21.71	12.30
G ₃₃	120.36	11.42	78.33	4564.80	1.24	851.30	394.42	24.96	14.30
G ₃₄	124.03	12.00	81.46	4982.52	1.24	706.59	462.21	24.42	14.50
G ₃₅	127.03	13.83	108.17	7388.65	1.27	1043.54	565.33	36.21	22.58
G ₃₆	105.31	9.08	73.00	3245.34	1.19	663.67	385.63	16.80	8.46
G ₃₇	113.59	10.33	78.63	4078.91	1.25	779.88	338.25	23.29	13.00
G ₃₈	115.40	10.75	79.75	4324.21	1.15	611.88	338.21	22.79	13.80
G ₃₉	106.25	10.75	71.79	2945.02	1.20	406.85	273.38	23.25	13.42
G ₄₀	109.95	11.50	76.63	3635.37	1.19	574.71	340.59	24.79	12.46
Range	68.88- 138.19	5.58- 13.83	62.96- 108.17	1551.48- 7388.65	0.99- 1.28	236.92- 1043.54	149.42- 565.33	11.21- 36.21	5.21- 22.58
SED	3.41	0.76	3.48	183.61	0.03	47.35	22.97	1.48	1.24

(SC-12) followed by G₁₀ (R-1420), G₃₀ (SC-7), G₂₄ (R-67-34), G₂₆ (R-67-52), G₂₇ (SC-3) and G₂₃ (R-67-46). A range of 5.21-22.58 g was recorded for dry weight of fibre. The maximum dry weight of fibre of 22.58 g was observed for the genotype G₃₅ (SC-12) followed by G₁₀ (R-1420), G₃₀ (SC-7) and G₂₄ (R-67-34).

The estimates of mean performance analysis revealed that amongst the forty ramie genotypes high fibre yield per plant of 22.58 g, 17.92 g and 17.00 g respectively was recorded for the genotype G₃₅ (SC-12), G₁₀ (R-1420), G₃₀ (SC-7) and G₂₄ (R-67-34). The two genotypes G₃₅ (SC-12) and G₃₀ (SC-7) also exhibited high mean performance for the remaining traits. Of the four genotypes, G₁₀ (R-1420) showed high mean performance for all the traits except number of leaves, fresh weight of plant and fresh weight of cane and the genotype G₂₄ (R-67-34) also recorded high mean performance for number of effective canes, basal stem diameter, fresh weight of plant, fresh weight of cane, fresh weight of fibre and dry weight of fibre. Among these four genotypes, R-1420 and R-67-34 are improved varieties while the other two are collection from Nalbari, Barkhata, Dist. Goalpara(SC-7) & Tergagaon, Kokrajhar(SC-12). There is scope for further improvement of these genotypes particularly the local collections. These four genotypes, viz. SC-12, R-1420, SC-7 and R-67-34 deserve consideration as parents in hybridization programme for crop improvement.

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RESISTANCE OF *LYCOPERSICON* GERMPLASM TO EARLY BLIGHT DISEASE

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In a study to find out the reaction of certain tomato genotypes to early blight, it was found that the genotypes IHR 1939, IHR 1816, IHR 1954 and IHR 1968 showed resistance at both seedling and adult plant stages. IHR 1817 had relatively low levels of resistance at seedling stage. Of these five resistant lines, IHR 1939 derived from *L. pimpinellifolium* displayed higher level of early blight resistance at both seedling (42.91 per cent CDI) and adult (37.86 per cent CDI) plant stages.

Key words : Tomato, *Lycopersicon esculentum*, resistance, early blight disease

Tomato (*Lycopersicon esculentum* Mill), one of the most important vegetable crops grown in many parts of the world, is infested by fungi, bacteria, viruses, nematodes and insects. One of the most destructive diseases of tomato in tropical and sub-tropical regions of India is early blight caused by *Alternaria solani* Sorauer. The disease severity affects the **kharif** season (June-September) crop., grown commonly in the states of Karnataka, Tamil Nadu, Maharashtra, Madhya Pradesh and West Bengal. High humidity and ineffective fungicides due to continuous heavy downpour complement disease severity. Even under irrigated conditions, susceptible F₁ hybrids can be severely damaged by early blight incurring a loss of about 50 to 80 per cent (Mathur and Shekhawat, 1986). Deploying disease resistant cultivars is preferred because it is considered to be the most economical from the growers point of view. Success of such an approach depends on the identification of stable resistant sources on one hand on its subsequent utilization in breeding on the other. Hence, a study was undertaken to find out genotypes resistant to the early blight disease.

Table 1. Number of tomato genotypes used in screening against *A. solani*

Sl.No.	Accession Number	Species/EC number/Donor No.	Sources
1	IHR 1949	<i>L. peruvianum</i> EC308447	AVRDC, Taiwan
2	IHR 1939	<i>L. pimpinellifolium</i> L4394	NBPGR, New Delhi
3	IHR 1816	<i>L. esculentum</i> NCEBR-1	Beltsville
4	IHR 1954	<i>L.e. var. cerasiform</i> L128	AVRDC, Taiwan
5	IHR 1946	<i>L. esculentum</i> L594	AVRDC, Taiwan
6	IHR 1946	<i>L. hirsutum</i> L3684	AVRDC, Taiwan
7	IHR 1972	<i>L. peruvianum</i> L734	AVRDC, Taiwan
8	IHR 1945	<i>L. hirsutum</i> L3683	AVRDC, Taiwan
9	IHR 1948	<i>L. peruvianum</i> L671	AVRDC, Taiwan
10	IHR 1973	<i>L. hirsutum</i> L1042	AVRDC, Taiwan
11	IHR 1966	<i>L. pimpinellifolium</i> L101	AVRDC, Taiwan
12	IHR 1817	<i>L. esculentum</i> NCEBR-2	Beltsville
13	IHR 1970	<i>L. hirsutum</i> L634	AVRDC, Taiwan
14	IHR 1961	<i>L. peruvianum</i> EC312339	AVRDC, Taiwan
15	IHR 1783	PI 128650	Royal Sluis, Netherlands
16	IHR 1952	<i>L.e. var. cerasiforme</i> L130	AVDC, Taiwan
17	IHR 1940	<i>L. pimpinellifolium</i> L4396	AVRDC, Taiwan
18	IHR 1818	<i>L. esculentum</i> EC23243	Beltsville
19	IHR 1944	<i>L. hirsutum</i> L3234	AVRDC, Taiwan
20	IHR 1950	<i>L. peruvianum</i> L438	AVRDC, Taiwan
21	IHR 1943	<i>L. hirsutum</i> L733	AVRDC, Taiwan
22	IHR 1749	PI 182844	AVRDC, Taiwan
23	IHR 1873	<i>L. esculentum</i>	Peto Seeds
24	IHR 1969	<i>L. peruvianum</i> L631	AVRDC, Taiwan
25	BWR 1	<i>L. esculentum</i>	IIHR, Bangalore
26	IHR 1967	<i>L. esculentum</i> L165	AVRDC, Taiwan
27	IHR 1974	<i>L. cheesmani</i> L 1696	AVDC, Taiwan
28	IHR 1820	<i>L. esculentum</i> EC232433	Beltsville
29	IHR 1951	<i>L.e. var. cerasiforme</i> L3682	AVRDC, Taiwan
30	IHR 1953	<i>L. e. var. cerasiforme</i> L129	AVRDC, Taiwan
31	IHR 1955	<i>L. e. var. cerasiforme</i> L131	AVRDC, Taiwan
32	IHR 1950	<i>L. peruvianum</i> L438	AVRDC, Taiwan
33	IHR 1880	<i>L.e. var. cerasiforme</i>	NBPGR, New Delhi
34	IHR 1975	<i>L. esculentum</i> L1951	AVRDC, Taiwan
35	IHR 1941	<i>L. pimpinellifolium</i> L674	AVRDC, Taiwan
36	Pusa Ruby	<i>L. esculentum</i>	IARI, New Delhi
37	IHR 1627	<i>L. esculentum</i> PI182778	NBPGR, New Delhi
38	Arka Saurabh	<i>L. esculentum</i>	IIHR, Bangalore
39	IHR 1956	<i>L. e. var. cerasiforme</i> L132	AVRDC, Taiwan
40	IHR 1942	<i>L. pimpinellifolium</i> L679	AVRDC, Taiwan
41	IHR 1951	<i>L. cnessmani</i> L3682	AVRDC, Taiwan
42	IHR 1947	<i>L. peruvianum</i> L669	AVRDC, Taiwan
43	IHR 1842	<i>L. esculentum</i> Manikit	NBPGR, New Delhi
44	IHR 1746	P 118241	AVRDC, Taiwan
45	IHR 1958	<i>L. pennelli</i> L132	AVRDC, Taiwan

MATERIAL AND METHODS

The material used in the present investigation comprised 45 tomato genotypes which include wild and related species of *Lycopersicon*. They were collected from the germplasm repository maintained at the Division of Vegetable Crops, Indian Institute of Horticultural Research, Hessarghatta, Bangalore. The list of the genotypes studied are presented in Table 1. Screening was done independently at seedling and adult plant stages during November 1991 to January 1992, and were further confirmed in *kharif* (June-September 1992) season. For screening at seedling stage, the genotypes were sown in seed pans filled with pot mixture drenched with 0.2 per cent Captaf before sowing to protect the seedlings from soil borne pathogens. Plants were inoculated with spore suspension of *A. solani* at the 3- leaf stage (one month old) and again after 3 days to meet sufficient inoculum load for the infection to take place inside a polythene cage with high humidity by maintaining water continuously in the trenches. For screening at adult plant stage, the seeds of each genotype was sown in a nursery beds (6m × 1m, 20cm ht). Transplanting was done when the seedlings were 40 days old, at a spacing of 90 cm between and 30 cm within the rows. The susceptible cultivars Arka Saurabh and Pusa Ruby were planted as infector rows along the border as well as after every fifth row. The pathogen inoculation was done 30 days after transplanting with a mechanical sprayer 3 to 4 hr (5-6 pm) before darkness. The severity of the damage was estimated on all the plants of each accession using three disease parameters viz., number of lesions per leaflet, lesion size and per cent defoliation. Five leaves were drawn randomly from each plant to count the number of lesions. Five lesions were selected randomly to estimate the diameter from each plant. Per cent defoliation was estimated from each plant using the modified method suggested by Horsfall and Barratt (1945).

Score	Description		
	Number of lesions per leaflet	Lesion diameter	Per cent defoliation
1	Symptomless leaflet	No lesions	0-10
2	1 or 2 (< 10% leaf area was necrotic)	< 0.2 cm	11-25
3	Numerous lesions (10-25% area was necrotic)	0.2 to 0.5 cm	26-50
4	< 50% leaflet area covered by necrotic spots (26-49% leaf area was necrotic)	> 0.5 to 0.75 cm	51-75
5	50-100% area was necrotic	> 0.75cm	> 75

While selecting the genotypes as resistance to early blight, a cumulative disease index (CDI) was calculated using the formula :

$$\text{CDI} = \frac{\sum \text{of individual ratings of the three disease parameters}}{\text{Maximum disease score} \times \text{Number of leaves sampled}} \times 100$$

The CDI of 45 genotypes screened were compared statistically using Duncan's Multiple Range Test (Gomez and Gomez, 1976).

RESULTS AND DISCUSSION

The results were based on pure spray of inoculum which consisted only of *A. solani* and was confirmed under microscope. A wide range in the reaction of different genotypes to *A. solani* was observed, but none of the genotypes exhibited complete resistant or near immunity. Complete resistance or near immunity was rarely observed in foliar diseases (Vanderplank, 1963) and in tomato, no immunity to early blight is known (Barksdale, 1971). Varying levels of resistance to early blight have been commonly observed among tomato genotypes (Andrus *et al.*, 1942). Andrus (1953) pointed out that low levels of resistance to certain disorders were often sufficient to mean the difference between a poor and a good crop, since a delay of a few hours in the build-up of inoculum can make the difference between susceptible and resistant plants with a market crop.

Among the 45 accessions of wild and related species of *L. esculentum* tested for resistance against *A. solani*, the following 12 accessions viz., IHR 1949 (*L. peruvianum* EC 308447), IHR 1939 (*L. pimpinellifolium* L 4394), IHR 1816 (*L. esculentum* NCE BR-1), IHR 1954 (*L. esculentum* var. *cerasiforme* L 128), IHR 1968 (*L. esculentum* L594), IHR 1946 (*L. hirsutum* L3684), IHR 1972 (*L. peruvianum* L 734), IHR 1945 (*L. hirsutum* 13683), IHR 1948 (*L. peruvianum* L671), IHR 1973 (*L. hirsutum* L 1082), IHR 1966 (*L. pimpinellifolium* L 101) and IHR 1817 (NEBR-2) possessed resistance to leaf lesions of early blight at seedlings stage. While 11 accessions viz., IHR 1816 (*L. esculentum* NCEBR-1), IHR 1961 (*L. peruvianum* EC 312339), IHR 1973 (*L. hirsutum* L1042), IHR 1954 (*L. esculentum* var. *cerasiforme* L128), IHR 1939 (*L. pimpinellifolium* L4394), IHR 1817 (*L. esculentum* NCEBR-2), IHR 1945 (*L. hirsutum* L3683), IHR 1968 (*L. esculentum* L594), IHR 1949 (*L. peruvianum* EC 308447), IHR 1948 (*L. peruvianum* L671) and IHR 1969 (*L. peruvianum* L631) exhibited resistance at adult plant stages. Resistance to early blight at both seedling and adult plant stages was noticed in IHR 1939, IHR 1816, IHR 1954 and IHR 1968. IHR 1817 had relatively low levels of resistance at seedling stage. The resistant line IHR 1939 derived from *L. pimpinellifolium* displayed higher level of early blight resistance at both seedling (42.91 per cent CDI) and adult (37.86 per cent CDI) plant stages. In the above mentioned five resistant lines, the observed levels of resistance helped to maintain foliage cover over the fruits until harvest even when inoculum potential was high, while susceptible lines were defoliated as and when they were infected, eventually exposing the fruits also to the pathogens.

Table 2. Reaction of tomato genotypes against *A. solani* at seedling stage

Sl. No.	Accession Number	Percent of disease index (PDI %)			Cumulative Disease Index (%)*
		Lesion No.	Lesion Size	Defoliation	
1	IHR 1949	42.28	44.59	26.55	42.91 k
2	IHR 1939	42.28	43.83	39.21	42.96 k
3	IHR 1816	42.65	49.58	39.21	45.91 jk
4	IHR 1954	46.87	48.37	39.21	47.34 ijk
5	IHR 1968	46.87	48.37	39.21	47.36 ijk
6	IHR 1946	48.08	48.48	50.75	48.37 hijk
7	IHR 1972	51.10	50.34	50.74	50.75 ghijk
8	IHR 1945	49.80	53.70	39.21	51.71 fghijk
9	IHR 1948	52.33	52.27	50.74	52.31 efghijk
10	IHR 1973	51.92	53.04	50.74	52.49 efghijk
11	IHR 1966	51.32	54.31	63.41	53.16 efghijk
12	IHR 1817	52.33	56.33	50.74	54.22 defghij
13	IHR 1970	55.91	60.64	39.21	57.58 cdefghij
14	IHR 1961	55.25	59.71	50.74	57.67 cdefghij
15	IHR 1783	54.32	61.99	63.44	58.63 cdefghi
16	IHR 1952	60.50	61.11	26.55	59.89 cdefgh
18	IHR 1818	59.71	62.69	50.74	60.93 cdefg
19	IHR 1944	61.72	60.17	63.41	61.10 cdefg
20	IHR 1950	55.96	66.86	63.41	61.23 cdefg
21	IHR 1943	61.52	61.11	50.75	61.23 cdefg
22	IHR 1749	60.17	61.99	63.41	61.23 cdefg
23	IHR 1873	57.58	65.85	63.41	62.40 cdefg
24	IHR 1969	66.59	58.47	63.41	62.40 cdefg
25	BWR 1	63.41	61.99	63.41	63.11 bcdef
26	IHR 1967	64.94	51.18	63.41	63.11 bcdef
27	IHR 1974	65.85	62.42	31.21	63.46 bcdef
28	IHR 1820	58.47	70.32	63.41	64.11 bcde
29	IHR 1951	63.84	66.39	63.41	65.04 bcd
30	IHR 1953	63.84	66.39	63.41	65.08 bcd

(Table contd. on next page)

Sl. No.	Accession Number	Percent of disease index (PDI %)			Cumulative Disease Index (%)*
		Lesion No.	Lesion Size	Defoliation	
31	IHR 1955	66.94	65.39	39.21	65.15 bcd
32	IHR 1950	95.85	64.57	63.41	65.08 bcd
33	IHR 1880	63.84	66.31	63.41	65.41 bcd
34	IHR 1975	65.32	64.35	63.41	65.41 bcd
35	IHR 1941	67.99	64.35	50.75	65.57 bcd
36	Pusa Ruby	65.39	65.39	63.41	65.68 bcd
37	IHR 1627	65.09	66.62	63.41	65.80 bcd
38	Arka Saurabh	65.39	65.39	63.41	65.97 bcd
39	IHR 1956	67.42	67.42	63.41	66.29 bc
40	IHR 1942	65.85	69.09	63.41	67.61 bc
41	IHR 1951	67.42	70.23	50.70	68.18 bc
42	IHR 1947	66.47	73.12	63.41	69.65 bc
43	IHR 1842	70.59	77.44	63.41	75.54 b
44	IHR 1746	89.96	89.96	89.96	89.95 a
45	IHR 1958	89.96	89.96	89.96	89.95 a

*Significant test based on Duncan's multiple range test at 5%.

Table 3. Reaction of different tomato genotypes against *A. solani* at adult stage of the plant

Sl. No.	Accession Number	Per cent disease index (PDI %)			Cumulative Disease Index (%)*
		Lesion No.	Lesion size	Defoliation	
1	IHR 1816	33.43	36.85	39.21	35.94 l
2	IHR 1961	33.43	38.04	39.21	36.36 l
3	IHR 1973	33.19	41.53	26.55	36.52 l
4	IHR 1954	33.43	39.21	39.21	37.14 l
5	IHR 1939	40.96	36.85	26.55	37.86 l
6	IHR 1817	49.00	39.79	50.75	39.21 kl
7	IHR 1945	39.21	39.21	39.21	39.21 jkl
8	IHR 1968	30.64	40.38	50.75	39.21 jkl
9	IHR 1972	49.00	39.79	50.74	39.21 jkl
10	IHR 1972	46.12	42.69	50.74	39.21 jkl
11	IHR 1748	38.04	40.37	50.74	40.14 ijkl
12	IHR 1969	39.21	42.83	26.55	40.24 ijkl
13	IHR 1943	35.65	42.68	50.74	40.24 ijkl

(Table contd. on next page)

Sl. No.	Accession Number	Percent of disease index (PDI %)			Cumulative Disease Index (%)*
		Lesion No.	Lesion Size	Defoliation	
14	IHR 1947	40.38	40.38	39.21	40.24 ijkl
15	IHR 1946	42.68	40.38	39.21	40.24 ijkl
16	IHR 1880	38.04	40.38	50.75	40.25 ijkl
17	IHR 1873	44.98	42.69	26.55	42.39 hijk
18	IHR 1940	40.38	42.69	50.75	42.39 hijk
19	IHR 1783	46.12	40.38	39.21	43.42 jhij
20	IHR 1941	43.83	42.69	50.75	43.94 jhij
21	IHR 1875	41.54	42.69	63.41	43.94 jhij
22	IHR 1942	42.69	43.83	50.75	43.94 jhij
23	IHR 1955	43.83	42.68	50.74	43.94 jhij
24	IHR 1956	44.98	40.38	43.41	44.46 fghi
25	IHR 1952	44.99	44.98	39.21	44.46 fghi
26	IHR 1957	47.27	44.98	39.21	44.46 fghi
27	IHR 1950	46.12	44.98	50.75	46.29 fgh
28	IHR 1944	44.98	44.98	63.41	46.52 fgh
29	IHR 1970	50.74	43.83	39.21	46.53 fgh
30	IHR 1949	51.92	46.12	26.55	47.04 fgh
31	IHR 1946	50.74	43.83	50.74	47.56 efg
32	IHR 1942	49.58	46.12	50.75	48.14 efg
33	IHR 1953	49.58	51.92	63.41	49.19 def
34	IHR 1966	51.92	46.13	50.75	49.19 def
35	BWR-1	53.11	44.98	63.41	50.23 cde
36	IHR 1818	53.11	47.27	50.75	50.23 cde
37	IHR 1951	59.32	48.42	39.21	52.34 bcde
38	IHR 1820	51.92	53.12	63.41	53.42 bcd
39	Pusa Ruby	43.41	46.12	43.41	54.92 abcd
40	IHR 1958	63.41	48.42	50.74	54.92 abcd
41	Arka Saurabh	63.41	46.12	63.41	55.10 abc
42	IHR 1974	59.32	51.92	63.41	56.20 abc
43	IHR 1967	56.76	56.76	63.41	57.35 ab
44	IHR 1627	59.32	56.76	63.41	58.49 ab
45	IHR 1950	63.41	55.53	63.41	59.65 a

*Significant test based on Duncan's multiple range test at 5%.

The availability of sources of resistance to early blight in wild and related species have been reported by several workers. Accessions of *L. hirsutum*, *L. peruvianum* and *L. cheesmanii* have been reported to possess resistance to

early blight (Locke, 1949; Barksdale, 1969; Gardner, 1984, 1988; Maiero *et al.*, 1990; Kalloo, 1991). Resistance to early blight has also been observed in the cultivated species, *L. esculentum*, (Andrus *et al.*, 1942; Reynald and Andrus, 1945; Lodha, 1977; Barksdale and Stoner, 1977; Kalloo and Banerjee, 1991).

The resistant lines identified in this study viz., IHR 1939, IHR 1816, IHR 1954 and IHR 1968 can be used in future breeding programme to produce F₁ tomato hybrids having resistance to early blight or can be used to isolate resistant genotypes with better yield and other morphological features from the segregating generations of the crosses involving these resistant lines.

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POTATO GENETIC RESOURCES IN INDIA

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Potato (*Solanum tuberosum*) originated in Peru-Bolivian region, was introduced in India long back towards the beginning of 17th century from Europe. After the establishment of CPRI, Shimla in 1949, potato germplasm collection, conservation, evaluation, documentation and utilization received greater impetus. This paper reveals systematic efforts made by the CPRI in collecting, evaluation and development of potato varieties for consumption etc. Conservation efforts were also highlighted.

Key words : Potato, genetic resources, collection, evaluation, conservation documentation, utilization

Potato belongs to the family *Solanaceae* and the large genus *Solanum*, which contains about 2000 species, out of which nearly 235 are tuber bearing (Hawkes, 1990). These are confined mainly to the Andean region of south America. The ploidy level of potato species varies from 2X to 6X with 73 per cent of these being diploids, 4 per cent triploids, 15 per cent tetraploids, 2 per cent pentaploids and 6 per cent hexaploids (Hawkes, 1990). The commonly cultivated potato belongs to the species *S. tuberosum* L. ($2n = 4x = 48$) which has two subspecies viz. *ssp. tuberosum* adapted to long days and *ssp. andigena* adapted to short days. Besides these, six primitive species viz., *S. ajanhuiri* (diploid), *S. phureja* (diploid), *S. stenotomum* (diploid), *S. chaucha* (triploid), *S. juzepckjukii* (triploid) and *S. curtilobum* (pentaploid) are also under cultivation, but are restricted to the high Andes from central Peru to central Bolivia.

The cultivated potato is believed to have originated near lake Titicaca basin in Peru-Bolivian region (Simmonds, 1976; Ross, 1986). It was introduced in India from Europe towards the beginning of 17th century, about 40 years after its introduction in Europe. By the end of nineteenth century, potato cultivation spread throughout the country (Pushkarnath, 1976). After establishment of the Central Potato Research Institute (CPRI) in 1949 at Shimla, the potato germplasm collection, conservation, evaluation, documentation and utilization, became regular activities of the CPRI.

COLLECTION EFFORTS

The work on collecting variability in potato was initiated in 1940s with the help of the State Departments of Agriculture and about 400 indigenous lines were collected. Of these 16 varieties were identified as known exotic cultivars, while the rest were grouped into 16 distinct morphotypes whose original identity could not be established (Table 1). These cultivars represented some of the earliest introductions or their clonal variants and were termed as *desi* varieties (Pal and Pushkarnath, 1951; Pushkarnath, 1964). Morphologically, these varieties resemble *ssp andigena* (Swaminathan, 1958; Sinha and Pushkarnath, 1964). With the introduction of high yielding potato varieties, much of the earlier variability was lost over the

Table 1. Old indigenous (*desi*) and exotic potato varieties in India

Indigenous Varieties	Exotic Varieties
Agra Red	Ally
Chamba Red	Arran counsal
Coonoor White	Ben Cruachan
Coonoor Red	Craig's Defiance
Darjeeling Red Round	Runbar Cavalier
Desi	Great Scot
Dhantauri	Italian White Round
Gola type A	Late Carman
Gola Type B	Magnum Bonum
Gola type C	Majestic
Phulwa	Northern Star
Phulwa Purple Splashed	President
Red long Kidney	Raeburn's Gregor Cups
Sathoo	Red Rock
Shan	Royal Kidney
Silbilati	Up-to-Date

Source : Pushkarnath (1964).

period of time, some genetic variability, however, still exists in remote and difficult areas of the country. Attempts were, therefore, made during 1983-92 to collect this variability through surveys. A total of 621 samples were collected (Table 2). These were studied for various morphological characters and grouped into 125 distinct morphotypes (CPRI, 1992-93). These are now being fingerprinted by protein electrophoresis to eliminate duplicates, if any.

Since potato is not native to India, one cannot expect much genetic variability in the material available within the country. Acquisition of exotic germplasm from different countries has, therefore, been a continuing activity of the CPRI. This activity has been accelerated after establishment of the

International Potato Centre (CIP) at Lima, Peru in 1972, which has a large collection of potato germplasm. The collection at CPRI now has over 2,500 accessions, consisting mostly of cultivated species (*tuberosum* and *andigena*) and some of the wild or semi-wild species (Table 3). These germplasm accessions have been imported from 30 countries based on requirements of various potato improvement programmes in India.

GERMPLASM CONSERVATION

At CPRI, the available germplasm is being maintained by three methods, (i) *in vivo* clonal propagation, (ii) *in vitro* clonal propagation, and (iii) as true seeds. *In vivo* clonal propagation is done in glasshouses at Shimla and as duplicate sets in fields at Kufri and Jalandhar. All *tuberosum* and a part of *andigena* accessions are being maintained and multiplied by this method to facilitate their evaluation for adaptability in different agro-climatic regions as well as for resistance/tolerance to various biotic and abiotic stresses. A part of accessions belonging to *andigena* and wild species are being maintained in true seed form. True seeds for short term storage are maintained at CPRI at 10-15°C and for long term storage in cold modules at the National Bureau of Plant Genetic Resources, New Delhi. True seeds are produced by selfing and/or sib-mating. Sib-mating is often resorted to in the case of diploid species most of which are self-incompatible. Only a part of the germplasm is being maintained *in vitro*. Till date about 700 *tuberosum* accessions have been conserved in this form. It is proposed to conserve all the material *in vitro* as facilities and protocols are developed for cryopreservation of the meristem tips or axillary buds.

GERMPLASM EVALUATION

Evaluation of the available germplasm is a continuous process at CPRI, Shimla and its regional station located in different parts of the country. In the early stages of potato research in India, evaluation of a large number of European varieties was undertaken to identify cultivars adapted to temperate long day growing conditions in the hills and sub-tropical short day conditions in the plains. Simultaneously, attention was paid to identify suitable parental lines for Indian potato breeding programmes. The germplasm accessions were thus evaluated for economic characters like resistance to late blight (CPRI 1991-92; Gopal and Singh, 1993), bacterial wilt (Chakrabarti *et al.*, 1992; Nagesh *et al.*, 1993), wart (Singh and Gopal, 1990; Singh and Gopal, 1994), nematodes (CPRI, 1983), potato tuber moth (CPRI, 1992-92), powdery scab (Dutt and Pushkarnath, 1960), charcoal rot (Paharia *et al.*, 1976), hopper burn (CPRI, 1995-96) and viruses (CPRI, 1991-92; Garg and Gopal 1994), besides maturity, tuber dormancy (Joseph and Gopal, 1994), tuber drymatter and protein content (Gaur and Gupta, 1981), etc. The results of evaluation have been compiled

and presented in the catalogues of potato germplasm (*ssp. tuberosum*) collection (Gaur *et al.*, 1984; Gopal *et al.*, 1992).

Table 2. Indigenous potato variability collected during explorations in India (1983-92)

Year	Months	Duration of survey (days)	State	Districts surveyed	No. of samples collected
1983-84	November-March	130	UP	Farukhabad	20
1985	November	5	UP	Uttarkashi	18
1986	March	18	UP	Azamgarh, Barabanki, Ballia, Basti, Deoria, Faizabad, Gonda, Gorakhpur, Jaunpur, Lucknow, Raibareli, Sultanpur, Varanasi	160
1986	August-September	10	HP	High hills of Shimla	41
1986	November	11	Assam	Kokrajhar and Nawgaon	10
			Meghalaya	Jawai and Khasi Hills	16
1986	December	5	Assam	Karbi, Anglong, Nawgaon	11
			Meghalaya	East Khasi hills and jaintia hills	9
1987	February	20	Bihar	Begusarai, Bhojpur, Darbhanga, Gopalganj, East Champaran, Gaya, Khagaria, Madhubani, Muzaffarpur, Nalanda, Patna, Purnea, Ranchi, Rohtash, Saharsa, Samastipur, Saran, Sitamarhi, Siwan	125
1988	February-March	22	Bihar	Bhagalpur, Devgarh, Dumka, Gonda, Kishanganj, Munger, Sahibganj	23
			W. Bengal	Barrackpore, Birbhum, Cooch Behar, Hooghly, Jalpaiguri, Midnapore, Siliguri	30
1988	October-November	22	HP,UP	Kinnaur, Shimla, Uttarkashi	55
1991	September	18	HP	Rampur, Kinnaur	55
1992	November	7	HP	Chamba	38
Others*			HP	Kullu	2
			HP	Kinnaur	11

*Samples received from NBPGR Regional Station, Shimla (HP)

Table 3. Potato germplasm collection maintained at CPRI (1997)

Material	No. of accession				No. of donar countries	
	Tuber	<i>In vitro</i>	True seed	Total		
<i>Tuberosum</i>						
Cultivars/parental lines						
Indian						
Cultivars bred at CPRI	24	19	-	24		
Old indigenous cultivars	16	8	-	16		
Parental lines	11	1	-	11		
Indigenous samples	86	67	-	86		
Exotic	1156	638	-	1156	30	
<i>Andigena</i>	1028	-	200	1028	2	
Wild semi-cultivated sps.	50	-	175	187	2	
				(32 species)		

The germplasm accessions found promising for various characters have also been studied for their combining ability (Gaur *et al.*, 1983, 1985, 1993; Gopal, 1996a, 1996b; Kaushik *et al.*, 1996; Pandey and Gupta, 1997). A list of good general combiners for various characters is given in Table 4. Poor combiners, which may not be used in the breeding programmes, are also listed.

Flowering and fruiting behaviour of potato is important both in variety improvement as well as in raising crop from true potato seed. Germplasm accessions have been studied for these characters also (Gopal, 1994). Out of 676 accessions of cultivated ssp. *tuberosum* from 25 countries studied under natural long days (12-14 h) at Kufri, the majority (58.3%) bloomed profusely, whereas, 20.4% did not bloom at all. The time taken for flowering ranged from 6 to 15 weeks with majority (66.5%) of accessions blooming within 8 to 9 weeks of planting. The duration of flowering ranged from 1 to 10 weeks with the majority of accessions blooming for 1 to 4 weeks only. Twenty three per cent of the flowering accessions were completely male sterile. No berry setting was observed in 31.8% of the flowering accessions. Premature bud abscission was the major cause of sterility.

Table 4. General combining ability of some germplasm accessions

Character	General combining ability		
	Good	Average	Poor
Tuber Yield	CP 2000(1-1062), CP 2110 (CFK 69.1), CP 2334, (F-6) (AL-575), CP 2346 (F-6), CP 2370 (Muziranzara), CP 2378, (Poos. 16), Katahdin, K. Jyoti, K. Badshah, K. Bahar, EX/A 680-16, EX/B 687	CP 2407 (Montsama), CP 2417 (MEX 750838), K. Jeevan, K. Kundan, K. Khasigaro, K. Dewa, Up-to-date, EX/A 679-10	CP1710 (Kerr Pondy), CP 2132 (Tollocan), CP 2351 (Tobique), CP 2401 (CIP 702867)
Tuber Number	CP 2378 (Poos. 16), CP 2413 (Piratini), K. Kuber, K. Khasigaro, K. Dewa, EX/A680-16, EX/A 723, EX/A-687	CP 2346 (F-6), CP 2351 (Tobique), CP 2401 (CIP 702867), CP 2417 (MEX 750838), Dekama, Up-to-date, K. Jeevan, K. Sheetman, K. Kundan	CP 1710 (Kerr Pondy) CP 2334 (AL-575), CP 2370 (Muziranzara), CP 2407 (Montsama), CP 2132 (Tollocan), CP 2416 (MEX 750826), Katahadin, K. Jyoti. K. Badshah, K. Bahar
Average tuber weight	CP 2334 (AL-575), Katahbin, K. Jyoti, K. Badshah, K. Bahar, EX/A 680-16	CP 2407 (Montsama), CP 2416 (MEX 750826), CP 2417 (MEX 750838)CP 2346 (F-6), CP 2370 (Muziranzara), CP 24378 (Poos. 16), Dekama, Up-to-date, K. Jeevan, K. Kundan, EX/B 687	CP 2401 (CIP 702867), CP 2413 (Piratini), CP 2132 (Tollocan), CP 2351 (Tobiqu), K. Sheetman, K. Kuber, K. Khasigaro, EX/A 679-10, EX/A 723
Tuber dry matter	CP 2346 (F-6), CP 2370 (Muziranzara), CP 2378 (poos 16), CP 2416 (MEX 750826), CP 2417 (MEX 750383)	CP 2334 (AL-575), CP 2407 (Montsama), CP 2413 (Piratini)	CP 2351 (Tobique), CP 2401 (CIP 702867)
Resistance to late blight	CP 1673 (Dr. McIntosh), CP 2030 (G. 6246), CP 2333 (AL 624), CP 2378 (Poos.16)	CP 2011 (CIP 676082), CP 2370 (Muzranzara), CP 2381 (CFI 69.1), Desiree	CP 2013 (Atzimba), CP 2110 (CFK 69.1), Dekama, K. Badshah
Resistance to early blight	EX/A 680-16	CP 2132 (Tollocan)	CP 1710 (Kerr Pondy), EX/A 723

For characterisation of various accessions, observations have been recorded for morphological characters like tuber skin colour, tuber shape, eye depth, tuber flesh colour, flower colour etc. For this purpose, descriptors of the

International Board for Plant Genetic Resources (now IPGRI), are used. The information on these characters for ssp. *tuberosum* (Gopal *et al.*, 1992) and ssp. *andigena* (Unpublished) accessions has been compiled.

DOCUMENTATION

The information on passport data, morphological characteristics and reaction to various biotic and abiotic stresses of *tuberosum* germplasm has been published from time to time in the form of germplasm catalogues. The list of catalogues published is given below:

1. Pal, B.P. and Pushkarnath, 1951. Indian potato varieties. ICAR, New Delhi. Misc. Bull. 62, 63 p.
2. Pushkarnath, 1964, Potato in India-Varieties. ICAR, New Delhi. 466p.
3. Gaur, P.C., P.C. Misra and N.M. Nayar, 1984. Catalogues of Potato Germplasm Collection group Tuberosum, CPRI, Shimla, 38 p.
4. Gopal, J., R.K. Birhman and C.L. Khushu, 1992. Inventory of potato germplasm (group Tuberosum) collection, CPRI, Shimla. 47p.

The institute is presently in the process of publishing a similar catalogue on group Andigena. The entire data available is being computerised in readily retrievable form.

UTILISATION OF GERMPLASM

The available germplasm is being utilised in various breeding programmes at the CPRI. This has resulted in release of 29 improved varieties of potato. The parentage of these varieties show that in 9 varieties both the parents are of Indian origin (Table 5), 12 varieties have one parent of Indian origin and

Table 5. Cultivars developed using both parents from indigenous germplasm

S. No.	Cultivar	Year	Parentage
1.	Kufri Safed	1958	Phulwa (clonal selection)
2.	Kufri Red	1958	Darjeeling Red Round (clonal selection)
3.	Kufri Sindhuri	1967	Kufri Red × Kufri Kundan
4.	Kufri Neelamani	1968	Kufri Kundan × 134-D
5.	Kufri Chandramukhi	1968	Seedling 4485 × Kufri Kuber
6.	Kufri Badshah	1979	Kufri Jyoti × Kufri Alankar
7.	Kufri Megha	1988	SLB/K 31 × SLB/273
8.	Kufri Jawahar	1996	Kufri Neelamani × Kufri Jyoti
9.	Kufri Sutej	1996	Kufri Bahar × Kufri Alankar

one of exotic origin (Table 6) and 8 varieties have both the parents of exotic origin (Table 7). The exotic cultivars that have figured more frequently as parents in the release of Indian varieties are Adina, Craigs Defiance, Ekishiraju, Katahdin and Up-to-Date, and parental lines obtained from late Dr. William Black of UK.

Table 6. Cultivars developed using one parent from indigenous germplasm and one from exotic germplasm

S. No.	Cultivar	Year	Parentage
1.	Kufri Kisan	1958	Up-to-Date <i>timex</i> Sd.16
2.	Kufri Jeevan	1968	M 109-3 × Seedling-698-D
3.	Kufri Khasigaro	1968	Taborky × Seedling-698-D
4.	Kufri Naveen	1968	3070d (4) × Seedling 392-D
5.	Kufri Alankar	1968	Kennebec × ON-2090
6.	Kufri Chamatkar	1968	Ekizhirazu × Phulwa
7.	Kufri Sheetman	1968	Craigs Defiance × Phulwa
8.	Kufri Deqa	1973	Craigs Defiance × Phulwa
9.	Kufri Bahar	1980	Kufri Red × Gineke
10.	Kufri Lalima	1982	Kufri Red × Ag-14 (Wis × 37)
11.	Kufri Swarna	1985	Kufri Jyoti × (VTn) ² 62.33.3
12.	K. Ashoka	1996	EM/C 1021 × CP 1468

Table 7. Cultivars using both parents from exotic germplasm

S. No.	Cultivar	Year	Parentage
1.	Kufri Kuber	1958	(<i>S. curtlobum</i> × <i>S. tuberosum</i>) × <i>S. andigenum</i>
2.	Kufri Kumar	1958	Up-to-date × Katahdin
3.	Kufri Kundan	1958	Ekishirazu × Katahdin
4.	Kufri Neela	1963	Katahdin × Shamrock
5.	Kufri Jyoti	1968	3069 (4) × 1814a (1)
6.	Kufri Muthu	1971	3046(1) × M 109-3
7.	Kufri Lauvkar	1972	Serkov × Adina
8.	Kufri Shera	1983	Ultimus × Adina

In recent years, there has been a shift in the choice of parents in favour of Indian cultivars and parental lines. Whereas, the first batch of cultivars released during 1950-59 and mainly exotic varieties in their parentage, those released during 1960- 69 often involved one indigenous variety as one of the parents. At present, the choice of parents falls more often on newly bred

Indian cultivars and Indian parental lines. Thus, the cultivars **Kufri Badshah**, **Kufri Swarna**, **Kufri Jawahar** and **Kufri Sutlej**, have improved Indian cultivars in their parentage.

Wild species *S. verrucosum* and *S. microdontum* have been used as donors of durable resistance (horizontal) to late blight (Sharma *et al.*, 1982; Birhman *et al.*, 1991). Similarly, *S. chacoense* has been used to provide resistance to charcoal rot (Upadhyay *et al.*, 1977). Resistance to cyst nematodes in variety **Kufri Swarna** has been derived from *S. vernei*. In most of these programmes, dihaploids of *ssp. tuberosum* have been used as a bridge to transfer resistance to cultivated potato. Another programme worth mentioning is the development of parental lines possessing immunity of PVY and PVX at triples or quadriplex levels. Attempts are also being made to combine durable resistance to late blight with immunity to viruses.

FUTURE THURST

The CPRI is already recognised as the National repository for potato germplasm collection. The present collection is modest but is the best in South East Asia. This collection is proposed to be augmented to serve entire South Asian region. Efforts are being made to improve quarantine facilities to handle large import of germplasm. Infra-structural facilities are also being strengthened to maintain large collection in *in vitro*. Greater attention needs to be paid to *Solanum tuberosum ssp. andigena* which is adapted to short days and is thus more suitable for sub-tropical plains. Development of improved parental lines of *andigena* for various agronomic characters like tuber colour, tuber shape, eye depth, tuber size etc. is important if *andigena* is to be exploited extensively in the breeding programmes. Such lines also need to be evaluated for their general combining ability. In Indo-Gangetic plains which is the major potato growing region in India, potato is one of the crops in a multiple cropping system. This, and the economic considerations often require early planting of the crop when the ambient temperatures during germination and growth phase are high. Hopperburn and mites also pose serious problem to this crop. Need is, therefore, being felt to evaluate germplasm accessions for adaptability to these conditions. There is also need to extensively evaluate the germplasm for resistance to bacterial wilt and potato tuber moth which are major problems of the crop in mid hills and the plateau region. Characterisation of accessions for specific genes in terms of their allelic constitution is also required to be done. Work on DNA fingerprinting needs to be accelerated to have a catalogue for monitoring genetic integrity of germplasm collection from time to time, in the light of WTO and TRIPS.

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PATTERN OF GENETIC DIVERSITY AND VARIABILITY IN TOMATO*

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Fourty four genotypes of Tomato (*Lycopersicon esculentum* Mill.) which includes bacterial wilt resistant; tolerant and susceptible lines were evaluated for variability and magnitude of genetic divergence using Mahalanobis D^2 analysis. Genetic coefficient (GCV) variation of was substantial for weight of the fruits per plant and for number of fruits per plant. The GCV was moderate for number of secondary branches and low for other characters. The D^2 analysis grouped all accessions into 11 clusters. Source of the genotypes had no relation with genetic diversity. High yielders with resistance to bacterial wilt were grouped into close cluster. Average fruit weight per plant; number of fruits per plant; survival per cent; contributed much for clustering and genetic divergence. A number of genotypes with resistance to bacterial wilt have been identified for further improvement of the crop.

Key words : Tomato, genetic diversity, variability

Tomato (*Lycopersicon esculentum* Mill.) is grown over 2,90,279 hectares in India producing around 46,03,446 tonnes of fruits. It occupies significant position among vegetables because of its varied utility as raw and ripe fruits for **salads** and as vegetable for cooking. It is also used to make juices, puree, paste, cocktail, ketchup, soup, canned tomato and tomato concentrate. Considering the antiquity of cultivation, it is presumed that domestication of tomato took place in Mexico, however the Andean zone is likely to be the centre of origin of wild tomato. The productivity of tomato in India is 1,58,500 kg/ha against 2,39,130 kg in the Netherlands, 188571 kg/ha in U.K. and 1,50,000 in Belgium. However, this crop suffers from diseases like bacterial wilt, fusarium wilt, late and early blight, fruit rot etc. In the Andaman and Nicobar Islands which have congenial climatic conditions for the development and spread of diseases, bacterial wilt causes the maximum damage (Ramesh and Ansari 1993). Tomato production in these islands can be increased only

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if bacterial wilt resistant lines are used in breeding programme to select superior genotypes. An attempt has been made to study the variability and magnitude of genetic diversity in bacterial wilt resistant lines screened by Sharma *et al.* (1994) at the Central Agricultural Research Institute, Port Blair, India.

MATERIALS AND METHODS

The material for the present investigation comprised 44 accessions collected from various sources. The 44 accessions were planted in a randomized block design with three replications spaced of 50×50 cm apart between the rows and the plants. Each row was 3.5m long and 3 such rows were taken for each treatment. Recommended agronomic practices were followed in raising the crop. Observations on five randomly selected plants for 13 traits were recorded. Multivariate analysis (Mahalanobis, 1936; Rao, 1952) was done on mean values for computing the genetic divergence between accessions and the D^2 values thus obtained were used for clustering the accessions using Tocher's method. The Wilk's lambda test criterion was used for testing the significance of genotypes.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the accessions for 11 of the 13 characters studied. The range, mean and coefficient of variability are presented in Table 1. The highest GCV of 123.58 per cent was recorded for weight of fruits per plant followed by number of fruits per plant (78.23%). The GCV was moderate for number of secondary branches and variability was slow for other characters. This is in agreement with Kale *et al.* (1988) and Kumar *et al.* (1980). Based on D^2 values, the accessions were grouped into eleven clusters (Table 2). Cluster I has been formed with 19 accessions, cluster II comprised six accessions, cluster IV, IX and X had 2 accessions each, cluster V had three and other four cluster had one each. The accessions LE 79, 88BWR5, 83-211, Pusa Ruby, EC 165393, 88BWR 1, CI 9d-0-0-3-6 and 84 BWR 14 are the lines which had long distance from the rest. The cluster wise mean values for the thirteen characters are presented in table 3. In general, cultivars in cluster 1 were low yielders alongwith accession in cluster XI. Highest yielding accessions were in cluster VI, VII, VIII and IX (Table 3). Cluster IX and IV had large fruited accessions. Percentage of survival over 80 per cent was higher in the accessions in cluster X, VIII, V and in cluster VII. Accessions in cluster VI and IX had 70 per cent survival. Other accessions in the other clusters had moderate to low survival per cent because of bacterial wilt (Table 3). Number of primary and secondary branches were higher in the genotypes falling in cluster VIII.

Table 1. Genetic parameters of 12 metric characters of tomato

Character	Range		Mean	PCV	GCV
	Min.	Max.			
Days to flower	15.33	26.33	23.14	8.76	6.86
Plant height (cm)	22.77	61.00	43.25	29.00	20.73
Plant spread (cm)	25.67	68.93	47.92	27.00	16.83
No of primary branches	1.00	513.00	2.94	45.24	38.18
No of secondary branches	1.00	7.23	2.60	58.81	54.55
Wt of fruit/plant (gm)	5.50	782.34	225.36	138.23	123.58
No of fruits/plant	2.07	67.46	12.65	115.85	105.73
Av. fruit weight (gm)	1.73	78.19	18.34	88.86	78.23
Size of the fruit (cm)	1.27	4.57	2.88	30.23	23.56
No of locules/fruit	2.00	5.19	2.95	37.60	21.18
T.S.S (%)	3.23	7.93	4.96	24.52	19.60
Acidity	2.70	7.13	4.00	25.25	21.15

Table 2. Formation of clusters and accessions included in each cluster

Cluster Number	No. of Strains	Accession number / varieties of entries
I	19	LE 256, LE 259, LE 330, LE 337, LE 345, LE 915, LE 592, EL 12966, PKM 1, LE 522, 714-1-72, LE 528, EL 37234, 512, LE 721, LE 537, LE 514, Arka Shorab Punjab Shukara
II	6	LE 323, LE 427, LE 168704, LE 96, 84BWR3, KT-1
III	6	BT-1, LE 314, LE 354, EC 165395, LE 593, 13004/P
IV	2	84BWR-6, 88 BWR-1
V	3	84 BWR-1, c19d-0-03-6, EC 165393
VI	1	C19-0-0-3-6
VII	1	88 BWR-5
VIII	1	83-211
IX	2	84 BWR 14, LE 79
X	2	84 BWR-7, c15955-223-D4-2-2-0
XI	1	Pusa Ruby

The genetic divergence (Table 4) was maximum between cluster VI and X (5564.45), I and VI (5443.99) followed by between cluster I and VII (4516.67) I and VIII (4500.21), I and IX (4327.05) and III and VI (4229.58) (Table 4). Selecting such divergent genotype for hybridization might result in better segregants and higher heterotic response. However, it is always better to cross

Table 3. Cluster means for 13 characters in tomato

Cluster	No. of geno- types	Days to flower	Plant height (cm.)	Plant spread (cm)	No. of primary bran- ches	No. of Secun- dary bran- ches	No. of fruits per plat	Wt. of fruits per plant (gm)	Aver- age fruit weight (gm)	Size of the fruit (cm)	No. of locules per fruit	T.S.%	Acidity	Percent survival
I	19	19.98	40.81	44.06	2.20	1.65	5.41	44.95	9.35	2.44	2.59	5.11	3.95	32.78
II	6	19.33	43.73	46.98	3.27	3.52	27.22	368.91	17.00	2.80	3.30	5.59	4.23	51.90
III	6	23.93	39.99	43.09	3.09	3.02	11.76	194.43	17.51	2.94	3.01	4.83	4.57	39.79
IV	2	24.50	43.39	47.10	4.08	3.30	5.37	296.08	51.72	2.36	4.47	4.37	3.67	54.29
V	3	23.77	36.35	56.89	3.43	2.90	32.78	369.97	17.17	2.89	2.59	4.99	4.93	80.95
VI	1	22.17	42.60	59.50	4.32	4.35	25.80	770.50	26.84	3.57	3.57	3.79	5.30	71.43
VII	1	23.17	56.44	57.90	3.52	3.95	21.34	632.58	29.87	3.57	3.33	4.50	4.57	80.71
VIII	1	21.00	61.37	68.90	5.00	4.30	29.38	479.45	16.33	3.30	2.60	4.53	4.33	85.71
IX	2	23.00	35.40	39.30	4.40	2.10	78.00	609.80	78.18	4.13	3.30	4.17	3.17	71.43
X	2	22.67	57.67	59.60	3.00	3.60	17.51	450.46	26.13	3.43	2.60	4.78	3.23	95.71
XI	1	23.33	50.43	51.60	3.17	3.20	1.00	22.08	28.05	2.03	2.53	4.67	4.43	52.86

Table 4. Intra and inter-cluster divergence D^2 values in 44 genotypes of tomato

[illegible]

parents having high to moderate genetic divergence with high to medium survival per cent combined with high yields. EC 165395, 88 BWR1, 84 BWR14 CL5955-223-D₄-2-20, 84 BWR7, 88 BWR5, 84BWR6 and LE 79 considering high mean value alongwith high to moderate genetic distance were promising accessions. These may be crossed in several combinations or in a complete diallel fashion to achieve high yields combined with resistance to bacterial wilt. In tomato, D² analysis showed that genotypes possessing similar characteristics were grouped together even though, they were from different sources. Hence geographic diversity had no relation with genetic diversity. Perhaps selection to bacterial wilt resistance alongwith higher yields must have been the cause for the clustering. The genetic architecture of such population could be the result of prolonged selection by various natural and artificial forces. Successful use of D² analysis to assess the relative combination of different components of yield to the total divergence and to determine the nature of forces operating at intra and inter cluster levels have been emphasised by various workers in tomato (Patil and Bojappa, 1988; Kalloo, 1984; Skebe and Benne, 1989).

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PHALSA (*GREWIA ASIATICA* L.) GERMPLASM COLLECTION FROM ANDHRA PRADESH

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Seventy eight accessions of phalsa (*Grewia asiatica* L.) were collected from parts of Andhra Pradesh. Considerable variability in fruit and plant morphological characteristics is recorded. Ranga Reddy, Mahboobnagar and Medak districts have larger area under phalsa in comparison to other areas. Few promising lines for various traits were also collected.

Key words: Phalsa, *Grewia asiatica* L., genetic diversity, collection

Phalsa (*Grewia asiatica*, L.) is indigenous to India and is mainly cultivated for its small drupaceous fruits having medicinal value (Watt, 1972). It has wide adaptability and is suitable for arid zone horticulture. About 40 species of *Grewia* are reported to occur in India which are valued for their bark fiber, edible fruits (Wlth India, 1966). The fruit is a rich source of calcium, iron, minerals, carotene and nutritively highly placed (Gopalan *et al.*, 1971). It is reported to be cooling, digestive, tonic, aphrodisiac and also credited with curing inflammations, heart and blood disorders and urinary troubles. The root and bark are used in strangury, gleet, gonorrhoea, diarrhoea and dysentery. The leaves are used as an application to pustular eruptions and buds are also prescribed by native practitioners (Kirtikar and Basu, 1984). Hence, an exploration was undertaken in parts of Andhra Pradesh to augment genetic diversity of phalsa.

MATERIALS AND METHODS

Exploration was under taken in parts of Hyderabad, Ranga Reddy, Medak, Nizamabad, Mahboobnagar and Nalgonda districts in Andhra Pradesh during May, 1995. Farmers' field was taken as unit area and random samples from populations and biased samples of the elite material were collected. Samples were also collected from farmers' stores and market. Morphological observations of plant and fruits were recorded during exploration. Ten fruits for each accession were randomly collected for recording observations on quantitative

characteristics. The collected germplasm is being maintained and evaluated at Indian Institute of Horticultural Research, Bangalore.

RESULTS AND DISCUSSION

A total of 78 accessions were collected from 45 sampling sites (Table 1) possessing variability in habit (shrub/tree), leaf curl (inward/outward), shape (cordate/ovate) and size (medium to large), stem colour (grey/black), fruit shape, pulp colour (green/pink/white), seed colour (pink, yellow, white), shape (spherical/flat) seeds per fruit (1-3), taste (sweet, sour), quality and yield. The range, mean standard deviation and coefficient of variation (CV%) of quantitative characteristics are given in Table 2. A genotype (S-4581) collected from Ranga Reddy district appeared to be promising for high yield (fruit length 10.5mm; thickness 12.3mm; pulp colour-pink; 10-fruit weight 9.2g). Generally the ripe fruit has short storage life of 24-48 hours only (Gangwar and Tripathi, 1972) but it was observed that the fruits collected during the survey from tall growing trees had better storage life.

Table 1. District-wise sampling of Phalsa germplasm made during the survey

Name of species	District	No. of Accessions sampled
<i>Grewia asiatica</i> L.	Hyderabad	3
	Mahaboobnagar	17
	Medak	15
	Nalgonda	8
	Nizamabad	1
	Ranga Reddy	31
<i>Grewia</i> spp.	Medak	3
	Total	78

Table 2. Range, mean, standard deviation and CV% of quantitative characteristics of Phalsa germplasm

Character	Range	Mean	SD	C.V.%
Fruit thickness (mm)	5.9-13.1	10.6	1.54	14.5
Fruit length (mm)	6.1-10.6	9.1	1.14	12.6
10-Fruit weight (g)	2.2-9.4	6.5	2.50	38.3
100 Seed weight (g)	2.6-8.6	4.8	1.10	23.2
Seed thickness (mm)	3.1-6.9	5.4	0.54	10.0

In three accessions (S-4561, S-4562, S-4606), there appears to be an interesting correlation between the increase in leaf breadth and leaf area and

uniformity in fruit size at ripening with white pulp. Out of the germplasm collected, 16 accessions appeared to be elite genotypes having superior yield attributing characters and two accessions as highly drought resistant (S-4585, S-4605). Most of the genotypes have flat and spherical seeds except the line (S-4565) which has flat seeds, a desired character.

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COLLECTING JACKFRUIT GERMPLASM IN WESTERN GHATS

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A joint crop specific exploration and collection trip for jackfruit was conducted in parts of Western Ghats lying in states of Kerala, Karnataka and Tamil Nadu and a total of 95 accessions comprising 'koozha' (18), 'navarikka' (3), 'varikka' (59) 'rudraksha varikka' (2), 'rudraksha koozha' (2), wild (2) others (7) were amassed. Evaluation of these genotypes were undertaken and data presented. Distribution pattern of the species has also been enumerated.

Key words : Jackfruit, germplasm, variability, diversity, wild, cultivated, Collection

Jackfruit (*Artocarpus heterophyllus* L.) of the family Moraceae is distributed in the Indo-Malayan region. It is one of the most important fruit trees of South Asia, especially India. Immature and mature fruits are used as vegetable and are pickled. Flakes of mature fruits are used for making chips, 'papad' and ripe fruits for table purpose. In Kerala, it is used for sweet meat preparation known as 'chakkavaratti'. Fruits can be preserved as jam, jelly, etc. Flakes, seeds, sterile flowers, skin and core are used as important source of pectin. Seeds from mature fruits are also used as vegetable. Sometimes it is roasted and eaten as a delicacy. Jackfruit leaves, fruit rinds, bracts, etc. are used as cattle feed. It also yields good timber and is of great demand in Kerala.

Jackfruit has a very wide distribution in tropical semi and evergreen forest areas in Western Ghats. Its cultivation is continuous in western coast with high rainfall upto Konkan and sporadic in other areas with low rainfall. In western ghats, it is cultivated upto 1500m and has tremendous diversity. Two wild species with edible fruits, viz., *A. lackoocha* and *A. hirsutus* also occur there. It is highly heterozygous and is generally propagated through seed in the region. The planted seedlings, therefore, very rarely exhibit similar qualities of the mother plant and hence there is a strong belief among the locals that

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quality in planted jackfruit depends greatly on the man who planted it. High rate of natural crossing has resulted in rich variability in fruit morphology, quality and other characters. Deforestation in western ghats and indiscriminate felling of cultivated trees for timber has resulted in considerable loss of genetic variability in the crop. An attempt has been made in the past only to assemble the germplasm of commercial 'Varikka' variety of Jackfruit by the KAU under an ICAR ad-hoc scheme (Anon, 1983). Hence, an attempt was made to survey and collect entire variability of both cultivated and wild jackfruit in parts of Western Ghats lying in Kerala, Tamil Nadu and Karnataka in 1987. The results of the exploration trip and the variability collected are presented in this paper.

MATERIALS AND METHODS

An exploration tour was undertaken in May-June 1987 in parts of north Kerala and adjoining areas of Karnataka and Tamil Nadu (Fig. 1). Collection sites included commercial farms, forest areas, backyards of houses and government farms. Trekking in forest areas was done for wild forms. A single fruit was collected from each genotype encountered in the mission. Observations were made on morphological characters of fruits and seeds and data are presented in comparison to that available for 175 'Varikka' types (Anon, 1983).

RESULTS AND DISCUSSION

Jackfruit occurs in Western Ghats upto an elevation of 1500 m. The trees are planted in coffee, tea and cardamom plantations for shade. In most of these plantations, natural populations of jackfruit are also left out in selective felling of forest trees prior to establishment of crops. In most of the areas, the cultivation of jackfruit is very widespread and each homestead had one to a few trees depending upon the available area.

A wide variability in cultivated forms were observed. At the Horticultural Research Station, Burliar, a plantation of selected jackfruit from different states was established in 1948. 'Velipala' a type collected from the forest is regarded as possible ancestor to the jackfruit. Wild trees with fruits at four locations in Kerala were medium to very large in size, bearing relatively smaller fruits with numerous small, pointed spines on thicker rinds. Flake density was low and seed to flesh ratio was also low. The peduncles are easily separated from the fruits. The wild forms collected seem to be apparently more primitive than 'Velipala'. Broadly speaking, in the case of cultivated types, there are 'koozha' and 'varikka' forms, the former having soft, musky and slimy flakes and latter with hard and firm flakes. Fruit stalks are easily detachable in koozha and

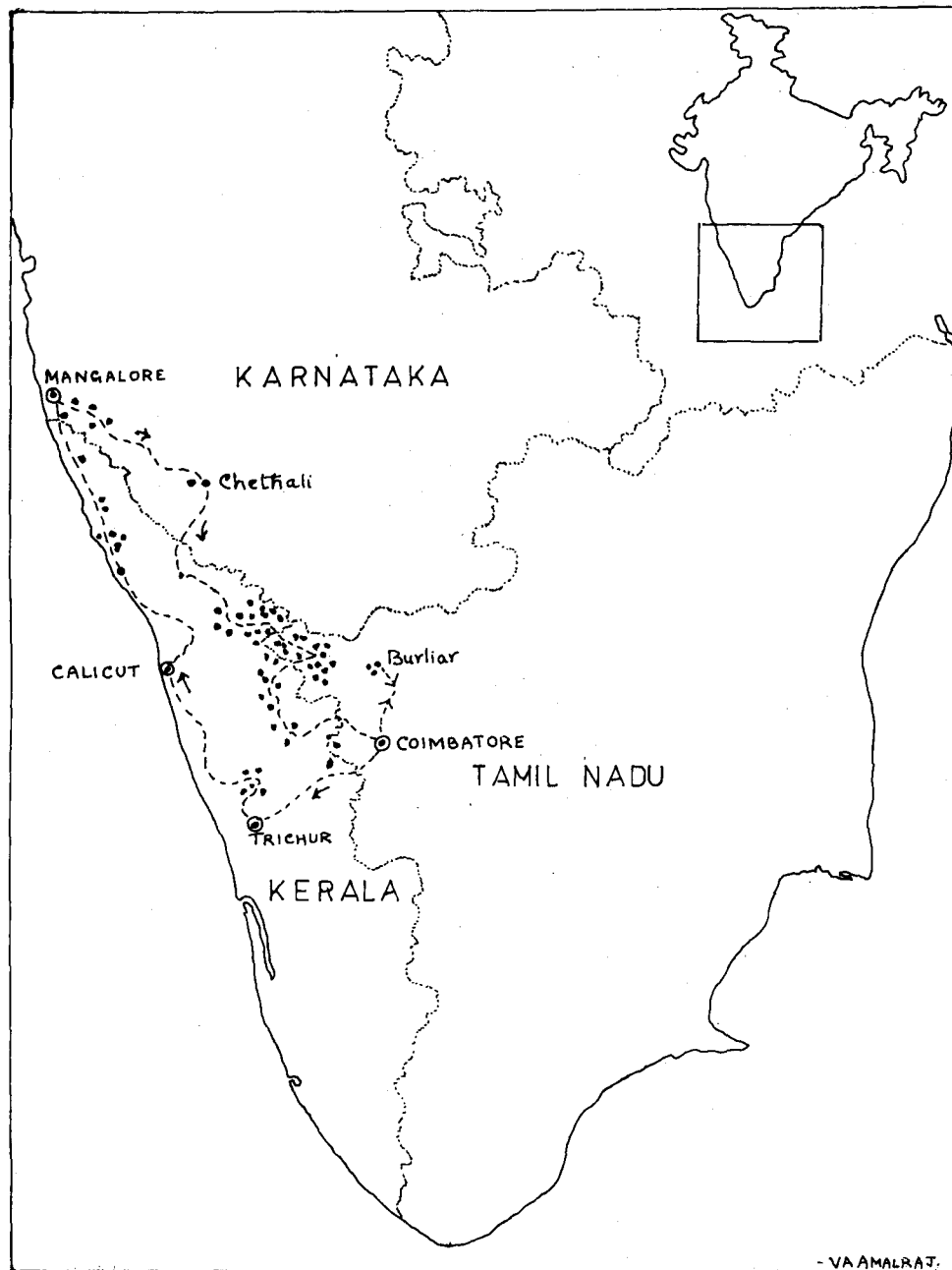


Fig. 1. Route map showing exploration sites for collection of jackfruit germplasm from western ghat

Table 1. Fruit and seed characters of jackfruit collections

Characters		Wild	Koozha	Navrikka	Varikka	Rudraksha koozha	Rudraksha varikka	ICAR project
No. of collections		2	18	3	59	2	2	175
Fruit length	R	32.0-37.0	28.0-68.0	32.0-58.0	23.0-72.0	28.0-30.0	21.0-28.0	22.0-84.0
	M	34.5	45.0	46.0	46.0	29.0	24.5	38.0
Fruit weight	R	2.2-3.5	2.0-25.4	4.0-9.0	1.5-39.0	2.0-4.1	2.5-3.9	1.6-25.1
	M	2.9	8.4	7.5	10.4	3.6	3.2	9.7
Fruit circumference	R	40.0-50.0	30.0-120.0	60.0-75.0	62.0-96.0	54.0-66.0	35.0-44.0	13.0-102.6
	M	45.0	52.0	68.0	73.0	60.0	40.0	41.5
Rind thickness	R	2.4-1.8	1.0-3.0	1.3-2.0	1.5-3.0	0.8-1.0	0.8-1.0	0.4-3.1
	M	2.1	2.0	1.8	1.9	0.9	0.9	1.5
Core length	R	23.0-24.0	13.0-15.0	16.0-38.0	12.0-56.0	13.0-14.0	0	11.0-61.0
	M	23.5	27.0	29.0	29.0	13.5	20.0	31.0
Core width	R	4.5-5.0	4.5-12.0	6.0-9.0	3.5-12.0	5.0-6.5	-	3.2-14.0
	M	4.8	6.4	7.3	6.8	5.7	4.5	6.8
Flake length	R	3.7-5.0	4.2-8.5	5.0-5.7	3.5-10.5	5.0-7.0	4.5-5.0	3.2-12.5
	M	4.4	6.1	5.4	6.7	6.0	4.7	6.2
Flake circumference	R	6.0-6.1	6.0-13.0	8.0-9.2	4.0-13.0	9.0-13.0	8.0-10.0	-
	M	6.1	9.0	8.7	9.2	11.0	9.0	-
Weight of flake	R	4.6-7.0	7.0-34.0	7.6-14.0	6.4-41.6	1.4-1.9	-	10.5-55.0
	M	5.8	17.0	10.8	19.0	17.0	23.0	27.8
Weight of a seed	R	4.6-5.0	5.0-15.4	7.0-11.0	3.4-13.4	6.2-7.0	3.0-8.4	1.2-14.2
	M	4.8	7.6	8.6	7.6	6.6	7.3	6.8
Seed length	R	-	2.7-4.5	2.3-4.0	2.0-5.0	2.4-3.5	3.5-4.3	2.4-11.0
	M	3.0	3.5	3.8	3.2	2.9	3.9	3.6
Seed width	R	-	1.2-3.0	2.0-2.3	1.2-3.0	1.4-2.0	2.0-2.2	1.3-9.0
	M	2.4	2.1	2.2	1.9	1.7	2.1	5.4

R = range

M = mean

the reverse is true in varikka. A third group known as 'navarikka' or 'pazhamvarikka' as reported by a farmer has soft and musky fruits but with persistent peduncles. This form has probably a hybrid origin from 'koozha' and 'varikka' types. This type is also known as 'vellaran'. The most strikingly different type is known as 'rudraksha' or 'thamara' in which fruits are nearly

spherical with thin rinds and spreading spines. In this, based on the firmness, of flesh both 'koozha' and 'varikka' forms exist. Very rarely an extremely sweet and tasty type known as 'thenvarikka' form also occur. In the present trip only two such collections were obtained. Due to the fine texture and sweetness of the flesh, mostly 'varikka' types are preferred. Colour of fruits is light yellow in wild forms, 'rudraksha' and 'navarikka' types. It varies from white to deep yellow and reddish in Koozha, light yellow to brownish yellow in 'Varikka' and whitish yellow in 'rudraksha varikka'. Density of flakes per unit volume was low in wild, high in 'koozha' and 'varikka', medium to high in 'rudraksha koozha' and low to medium in 'rudraksha varikka'.

A total of 95 samples were collected comprising wild (2), 'koozha' (18), 'navarikka' (3), 'varikka' (59), 'rudraksha koozha' (2), 'rudraksha varikka' (2) and others (7). The results of detailed observations on 12 quantitative characters of fruits and seeds of the above collections in comparison with range and mean of various characters in the case of 175 accessions collected by the ICAR project on varikka jackfruit at KAU, Thrissur are presented in Table 1. Generally heaviest fruits are noticed in 'Varikka' and the smallest in wild and in 'Rudraksha' types. 'Navarikka' and 'Rudraksha' have large and heavier seeds. Colour and quality of the flakes also changes within major varieties.

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DISTRIBUTION AND VARIATION IN MULBERRY GERMPLASM

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A total of 183 mulberry germplasm resources have been collected through 13 explorations covering 38 districts in 13 states and one union territory to assess their variability. The wild collections of *Morus serrata* were confined to North West India. *M. laevigata* and *M. alba* are available mostly in cultivated forms. The natural resources of *M. laevigata* in North East had a wide variation. The natural genepool reserves of *M. laevigata* with large tree population at Lamia bay, Doomarnalli, Havelock and John Lawrence Islands (Andamans) are identified and reported for the first time which serve as new locations of mulberry resources availability. The extent of variation in the developed genepool reserves at Central India and introduced European mulberry varieties in tea/coffee estates in Kerala in South India were identified. The variability of the *Morus* germplasm collected, its scope of utilization and necessity for long term conservation have been stressed.

Key words : *Morus*, exploration, variability, conservation

Mulberry (*Morus* sp.) is the only food plant of silkworm (*Bombyx mori* L.). The natural distribution of the genus has considerably changed because of its extensive cultivation for silkworm rearing in tropical, sub-tropical and temperate zones, most of it to the north of equator and ranging from 50° North latitude to 10° South latitude (Yokoyama, 1962). Vavilov (1926) while reviewing the centres of origin of crop plants placed the genus *Morus* in "China-Japan" region which includes East China, Korea and Japan. Hooker (1885) and Brandis (1906) have reported 4 species viz., *M. indica*, *M. alba*, *M. serrata* and *M. laevigata* occurring in India. Parkinson (1923) reported the occurrence of *M. laevigata* from Andaman and Nicobar Islands. Gamble and Fischer (1957) in the Flora of Madras Presidency recorded 2 *Morus* species viz., *M. alba* and *M. indica*. Nair (1977) documented the occurrence of *M. serrata* from Bushahr Himalayas. Kanjilal *et al.* (1940) enumerated 3 species from Assam and North East viz., *M. serrata*, *M. laevigata* and *M. acidosa*.

Survey and exploration of mulberry genetic resources were undertaken in Central Himalayas (Balakrishnan and Ramesh, 1989), North eastern India

(Jain and Kumar, 1989), North-western Himalayas (Dhar and Ashan, 1989) and Central India (Omachan, 1976). Osmoston (1927) and Dandin *et al.* (1993; 1995) reported the distribution of *M. indica*, *M. serrata* and *M. laevigata* in forest flora of Kumaon region and Northeastern India respectively. Sreekumar *et al.* (1995) have extensively explored for mulberry resources in Kerala and collected 134 accessions from 525 locations, mostly from house- hold and cultivated gardens/estates.

Mulberry is mainly cultivated for sericultural purposes. It is also exploited for multipurpose utilization of its fruits, timber in furniture making and branches for basket weaving, fire wood besides medicine. The wide spread incidence of shifting agriculture or *jhum* cultivation is rapidly eroding the forest habitats especially in Northeastern India and mulberry is threatened with wide spread destruction thereby necessitating an urgent need to survey and collect the potential mulberry resources from natural habitat, and the primitive and obsolete varieties (Sanjappa, 1989). Further, forestry resources are getting destroyed to convert land for agricultural use and urbanization (Chauhan and Thakur, 1995). Systematic documentation however, on the distribution of mulberry resources availability in India is meagre. Hence, exploration and survey were planned to identify the locations of availability of mulberry resources either under natural habitat or in cultivated forms and in different parts of the country so that long term conservation strategy could be suggested.

MATERIALS AND METHODS

In order to plan the survey and exploration throughout the country, published literature and herbarium records of Botanical Survey of India at Shillong, Dehradun, Port Blair, Pune and Coimbatore, Forest Research Institute herbarium at Dehra Dun, the Institute of Forest Genetics and Tree Breeding herbarium at Coimbatore, the State Forest Research Institute herbarium at Itanagar and the North-eastern Hill University herbarium at Shillong were consulted which indicate that the genus *Morus* is naturally distributed in the Sub-Himalayan regions upto an altitude of 2100 m with climate varying from temperate to sub-tropical and extending between Indus and Brahmaputra rivers. Thus, to expedite the process of exploration in different regions, 4 teams were formed to cover the various geographical regions of the country in two different seasons every year viz., spring (February to April) when natural flowering occurs accompanied by sprouting of buds and autumn (September to October). The regions covered are indicated in Fig. 1.

On locating the mulberry resources in natural habitats, following data were recorded uniformly by all teams : bark colour, leaf characters such as lobation, texture, shape, margin, surface and size (l × b), phyllotaxy, internodal

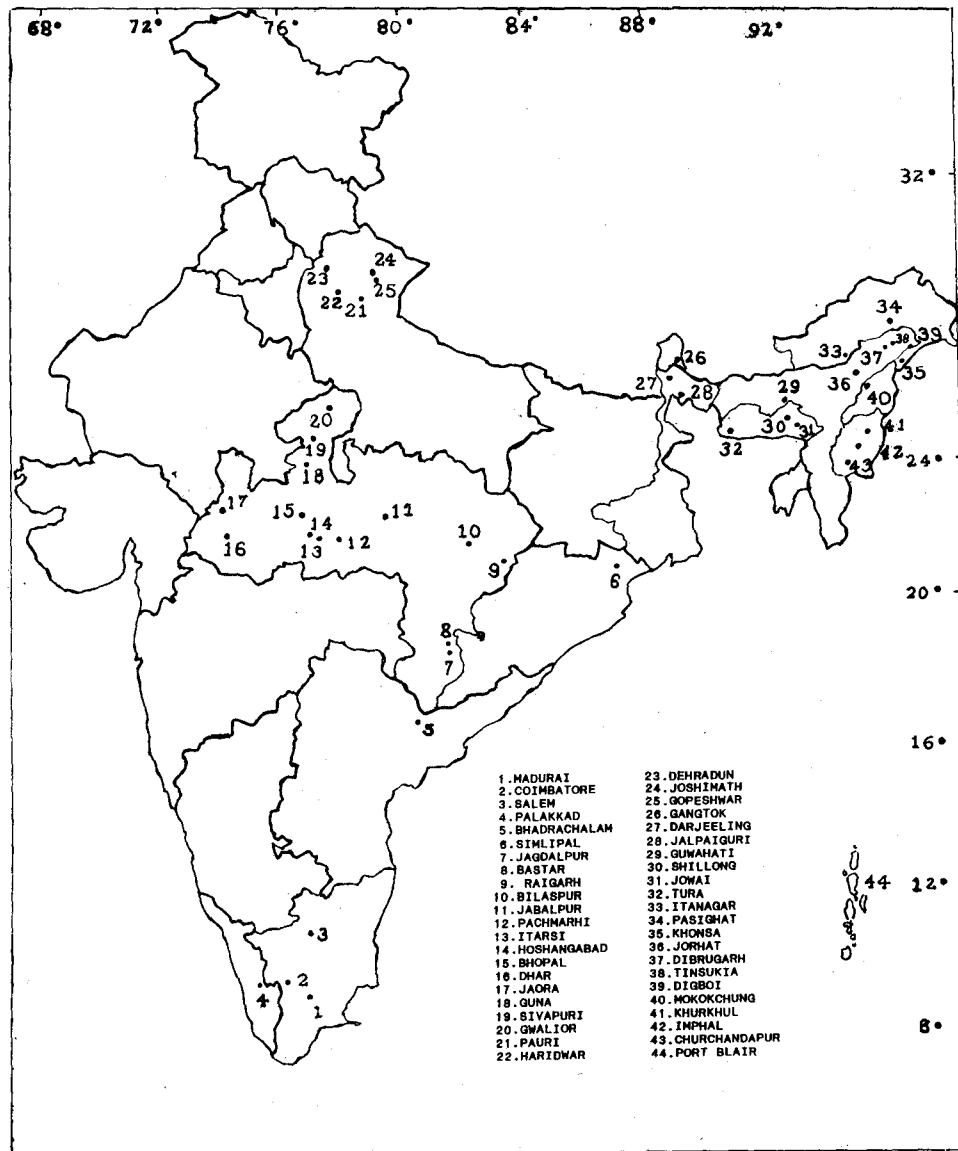


Fig. 1. Exploration sites for collection of *Morus* spp. in India

distance, sex, catkin length, fruit length. A portion of the shoot with leaves, inflorescence and fruits were collected and herbarium specimens made. The plants were sampled based on distinct morphological variability. Sufficient cuttings were collected having 4-5 dormant, healthy buds/cutting for further propagation through grafting/cutting to ensure survival and later transplanted from nursery to field gene bank for *ex situ* conservation.

RESULTS AND DISCUSSION

Distribution of mulberry resources

The explorations so far conducted revealed that 2 species under natural conditions i.e., *Morus laevigata* and *M. serrata* are available whereas under developed genepool, mostly *M. laevigata* is represented. Cultivated forms observed belonged to *M. indica* and *M. alba*. *M. laevigata* is widely distributed in different regions having no specificity of plants growing in particular types of soil or forest. In North-western India, it is found in natural habitats in Dehra Dun (30.19°N and 78.03°E), Hardwar (29.58°N and 78.09°E) and Laxman-Jhula (Pauri-Garhwal, 30.08°N and 78.48°E). In Andaman and Nicobar Islands (11.40°N and 92.44°E), wild trees of this species were observed along streams in the moist deciduous forest of Doormanalli and littoral forest of Lamia bay growing in close proximity from the sea (100 m). Wild form of *M. laevigata* was recorded earlier in Andaman by Parkinson (1923). Its availability has also been recorded by Vasudeva Rao (1986) but no specimen was examined. In North-eastern India, exploration in Sikkim was conducted for the first time as earlier explorations undertaken in North-east did not include Sikkim (Jain and Kumar, 1989; Dandin *et al.* 1995). Natural distribution of *M. laevigata* trees were observed in Eastern Himalayan wet temperate forests of namely, Rhenock, Tarpin (East Sikkim, 27.3°N and 88.51°E), Manring, Turung, Sipshu (South Sikkim 27.2°N and 88.39°E), June, Chakung and Phuncheybong (West Sikkim, 27.1°N and 88.12°E).

Naturally occurring but scattered *M. laevigata* trees were observed in West Bengal in Eastern sub-montane semi-evergreen forests of Lava and Alghara situated in Kalimpong (27.02°N and 88.34°E). It also occurs in sub Himalayan secondary wet mixed forests of Murthy and Imdong in Jalpaiguri (26.30°N and 88.50°E). In Assam, it is found to occur in forested areas of mixed deciduous type in Pengaree, Dibrunadhi near Digboi (27.22°N and 94.34°E). In Meghalaya, trees of this species were located in tropical evergreen forests of Umpling, Nongpoh (Ribhoi district 25.54°N and 91.54°E), Sung Valley, Mynso and Jowai (25.26°N and 92.14°E). In Manipur, *M. laevigata* trees with dissected leaves were observed in Khurkhul and unlobed leaves in Churachandpur and the forest type in this region was tropical semi-evergreen.

In Arunachal Pradesh, trees were scattered in tropical semi-evergreen forests of Drupong and Harmutty (27.02°N and 93.38°E). The occurrence of this species in North-east have also been reported by Jain and Kumar (1989) and Dandin *et al.* (1995). In Central India, trees of *M. laevigata* are grown for its sweet fruits which have a good market value. Thus, developed genepool reserves of this species were located in tropical moist deciduous forests of Jaora (23.40°N and 75.10°E), Dhar (22.32°N and 75.24°E), Shivpuri (25.26°N and 77.39°E), Gwalior (26.12°N and 78.09°E), Bilaspur (22.03°N and 82.12°E), Pachamarhi (22.29°N and 78.26°E), Jabalpur (23.10°N and 71.59°E) and Raigarh (21.53°N and 83.28°E). In South India, Yadav and Pavan Kumar (1996) identified population of *M. laevigata* trees in Yercaud, Shevaroy hills, (11.44°N and 78.11°E). So far this developed genepool seems to be the largest with the trees in slopy terrain over a two km radius covered with deciduous semi-evergreen vegetation.

M. serrata resources were found to be distributed in natural habitats of North-western India in Salna (700 m), Urgam valley, Joshimath (30.33°N and 79.35°E) and Chakrata (30.42°N and 77.52°E) situated at an altitude of 2200m. The mulberry tree of Joshimath is perhaps the oldest and almost 1220 years old (Rau, 1967). This species grows in association with oak, pines and conifers. Watt (1891) reported that this species is found at higher elevations between 1200 to 2750 m in North-west growing in association with oak (upto 1800 m). Dandin *et al.* (1993) have reported their distribution in Rajouri, Sundarbani, Poonch and Batote regions of Jammu Division; Kangra, Chamba, Nahan and Kullu districts of Himachal Pradesh and Garhwal Himalayas of Uttar Pradesh at an elevation of 1100 to 2200m.

M. alba, a deciduous, monoecious tree is cultivated in Punjab, North-west Himalayas and western Tibet ascending to 3350 m. Watt (1891) and Parkar (1956) are of the opinion that this species is indigenous to China and extensively cultivated throughout the plains of India and in Himalayas upto an elevation of 3300 m. It is also grown as a roadside and as avenue tree. In the present report, a tree belonging to this species was located in Surari Garhwal, (30.08°N and 78.48°E) at an altitude of 1365 m. This area was earlier covered under forest. In Central India a developed genepool of *M. alba* was observed in Guna (24.39°N and 77.18°E).

M. indica is commonly distributed in the sericultural areas extending from temperate to sub-tropical Himalayas from Kashmir to Sikkim ascending to 2100 m. Presently most of the cultivated forms belonging to this species are commonly distributed in Uttar Pradesh, West Bengal, Sikkim, Assam, Meghalaya, Arunachal Pradesh, Karnataka, Tamil Nadu, Kerala and Andhra Pradesh. Trees of this species are found growing in the backyards for utilization as firewood and timber. Thus, in Sikkim small trees of these species are found growing in the backyards in Sipshu and Budong. In West Bengal small trees

are found growing along the road sides and backyards in Jhorpukhari (Kalimpong), Mangalbari, Farabari and Churaimahal (Jalpaiguri) as also fringe areas of forest in Lataguri and Nagarkhata (Jalpaiguri). This species was observed growing in the backyard as a medium size tree in Tingrai near Tinsukia and Pengaree off Digboi. In Madhya Pradesh, the Forest Department have planted trees of this species in Katghora as part of social forestry programme. The present survey undertaken indicated that the distribution of natural resources of *M. indica* might have become rare due to widespread introduction of improved varieties and intensive farming practices.

In South India, the Britishers selectively introduced female mulberry varieties from Europe/Australia in tea estates of Coonoor and Munnar mainly for their ornamental value. Some of these varieties are selectively cultivated by sericulturists in Marayoor and Guhanathapuram. In Kerala, mulberry resources are commonly found growing in backyards of houses.

Variability

A total of 183 mulberry resources have been collected from different parts of the country (Table 1) representing four species. The variability in

Table 1. Mulberry resources collected during explorations (1993-98)

	North-East India	North-west India	Central India	South India	Andaman & Nicobar Is.	Total
<i>M. laevigata</i>	33	4	8	4	2	51
<i>M. serrata</i>	-	12	-	-	-	12
<i>M. indica</i>	32	8	5	-	-	45
<i>M. alba</i>	-	2	2	-	-	04
Unidentified	5	20	-	46	-	71
Total	70	46	15	50	2	183

M. laevigata resources collected from different parts of the country are presented in Table 2. The leaf is unlobed to different lobations with dissected leaves observed in a collection from Khurkhul (Manipur). The leaf shape is mostly wide ovate but narrow ovate leaf was also observed in a collection from Jowai (Meghalaya). The leaf surface is usually rough in Northeastern collections and smooth in Northwestern and Central Indian collections. Very big sized leaves (32.6×26.8 cm) were observed in *M. laevigata* trees occurring in Andamans as compared to mainland forms where the leaf size varied from 15×11 cm to 22×15 cm (L $\times$ B). The internodal distance varied from 4.0 to 10.9 cm.

Table 2. Comparative characteristic features of *M. laevigata* collected from different regions of India

Sl. No.	Characters	North-West India	North-East India	Central India	South India	Andaman & Nicobar Is.
1.	Bark colour	Brown, Grey, Greenish-grey, grey blackish	Pale brown, Grey brown	Grey brown	Brown/ Grey brown	Grey white
2.	Leaf location	Lobed, Unlobed dissected	Lobed, Unlobed dissected	Lobed, Unlobed	Unlobed	Unlobed
3.	Leaf Texture	Coriaceous	Coriaceous	Coriaceous	Coriaceous	Coriaceous, Membranous
4.	Leaf shape	Wide ovate, ovate, long ovate, ovate lanceolate	Widely ovate, ovate, narrow ovate	Wide ovate, ovate	Ovate	Ovate, widely ovate
5.	Leaf margin	Serrate	Serrate	Serrate	Serrate	Fine serrate
6.	Leaf surface	Smooth, rough	Rough very rough	Smooth, Rough	Rough	Slightly rough
7.	Leaf size (L × B cm)	15×11 - 18×12	22×11 - 22×15	15 × 12	-	22.6 × 22.1 to 32.6 × 26.8
8.	Phyllotaxy	1/2	1/2	1/2	1/2	1/2
9.	Internodal distance (cm)	6.0-7.0	4.0-8.5	5.0-7.0	4.0-7.0	4.9-10.9
10.	Sex	Male, Female	Male, Female	Female	Female	-
11.	Catkin length (cm)	4.0-7.0 (M) 7.0-9.0 (F)	6.0-7.10.0(M) 7.0-11.0 (F)	5.5-9.8 (F)	5.0 (F)	-
12.	Fruit length (cm)	7.0-12.0	7.5-12.0	6.0-18.5	-	-

Most of the trees were dioecious and female. Trees with male catkins were observed only in Northwestern and northeastern India. The fruit length exhibited variation ranging from 7.0 to 18.5 cm and exceptionally long fruits (18.5 cm) was observed in collections from Central India.

M. serrata resources were collected from natural habitats only from Northwestern region. The bark colour varied from red to dark brown with

heterophyllous leaves and mixed phyllotaxy rank such as 1/2 and 1/2, 1/3. The leaf surface was smooth to rough. The leaf margin was serrate. The leaf texture varied from chartaceous to coriaceous. The leaf size (L × B) varied from 15.0 cm × 10.0 cm to 20.5 cm × 20.0 cm. The internodal distance varied from 3.0 cm to 7.0 cm. The flowers were compactly arranged in catkins which were dioecious male.

Besides locating the naturally occurring tree mulberry resources, few morphologically distinct genotypes belonging to *M. indica* and *M. alba* were also collected. The rest of the collections are cultivated forms and growing in the backyard. The leaves varied from homophyllous to heterophyllous. The leaf lobation varied from one lobed to multi-lobed. Leaf base was cordate/truncate/retuse. Leaf margin was serrate/crenate/dentate. Leaf apex varied from acute to acuminate condition. Leaf surface was smooth/slightly rough/scabrous. Leaf texture was mostly chartaceous and few were coriaceous. The inflorescence was male/female, rarely mixed. Most of the cultivated forms had long styles and bifid erect to spreading stigmas. Few profuse fruiting varieties were also observed and collected in Central and Northeastern India.

Utilization of the resources

M. laevigata has good adaptability being distributed in diverse climatic conditions, forest and soil types including littoral habitat of Andamans. Because of its wide genetic base, characteristic features like big wide ovate leaves, long sized fruits and adaptability to diverse environments including saline habitats, it could be utilized in mulberry improvement programme. But due to constraints like sexual incompatibility, little success could only be achieved through conventional breeding programme. Hence, it is imperative to resort to biotechnological approaches like protoplast fusion in order to evolve superior hybrids by utilizing *M. laevigata* resources from diverse habitats.

M. serrata has limited adaptability having evolved in isolation and confined only in forested areas of Northwestern India. The leaves are hairy and usually not used for silkworm rearing. But there is scope to exploit the disease and frost resistant characters through biotechnology.

Among the cultivated forms collected, "Satin" variety belonging to *M. indica* is widely cultivated in Khasi and Jaintia hills of Meghalaya for rearing *bivoltine* silkworm races. It is characterised by glossy and coriaceous leaves and can straight away be introduced after initial evaluation. A few profuse fruiting varieties collected from Central and Northeast India can be exploited in breeding programmes. Further, Britishers introduced female mulberry varieties in tea estates of Coonoor and Munnar for utilizing the fruits in wine making. Some of these varieties are selectively cultivated by sericulturists in

Marayoor and Guhanathapuram areas for seed cocoon rearing resulting in good yield.

Because of shifting agriculture commonly practised in North-eastern India and also due to utilization of forest areas for agricultural purpose, there is considerable denudation of forested areas where wild trees of *M. laevigata* and *M. serrata* are available. Further, there is wide spread damage to mulberry trees especially in Sikkim, Meghalaya, North-west and Central India where the trees are exploited for various economic uses and no sustained efforts were made to propagate the resources. Only in Arunachal Pradesh, the State Govt. has enacted special legislation act to protect *M. laevigata* resources and it is an offence to cut or damage a tree. The developed genepool reserve of *M. alba* in Guna (Madhya pradesh) also deserves similar attention towards to *ex situ* conservation. As a part of conservation of biodiversity programme both in natural and developed conditions, necessary steps are required to be adopted for protecting the mulberry germplasm in *in situ* as also in *ex situ* conditions as these constitute valuable resources needed for future crop improvement programmes.

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PRETREATMENT FOR REMOVING SEED COAT IMPERMEABILITY IN *CORCHORUS* SPECIES

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The effect of different pre-treatments to reduce the seed coat imposed dormancy in the two species of *Corchorus* viz. *olitorius* and *capsularis* were studied. Results indicated that the two species exhibited significant differences in their response to various treatments. For *olitorius*, the best overall response was obtained when seeds were subjected to hot water treatment, the optimum durations being 65°C for 30 minutes (80%) and 80°C for 3 minutes (79%). On the other hand, concentrated acid treatment and mechanical scarification using fine sand paper provided the most rapid and effective methods for breaking seed coat imposed dormancy (96% germination as against 13%) in *capsularis* seeds. Besides, the effects of sub-zero storage at -20°C for one year, and application of dry heat at 65°C for 24 hrs were also studied and the results discussed.

Key words : *Corchorus capsularis*, *C. olitorius*, scarification, sub-zero storage, dry heat, hard seed

Jute, now the most important long vegetable fibre has attained commercial importance since 19th century. 95 per cent of world's jute is produced in India and Bangladesh and is one of the cheapest amongst the textile fibres. Jute is obtained from two species of *Corchorus* belonging to family Tiliaceae. *Corchorus* has about 40 species but only two are commercially important and cultivated i.e. *olitorius* and *capsularis*.

While testing the seeds of *Corchorus* species received from the Central Research Institute for Jute and Allied Fibers (CRIJAF), Barrackpore for long term storage in the National Gene bank, NBPGR, it was observed that a several accessions of both the species exhibited hardseededness ranging from 80-96 per cent. Hardseededness is an adaption allowing seeds to remain dormant for various periods of time before imbibing water and germinating. Variations in the degree of individual seeds are of significant ecological benefit to the species since they thereby multiply their chances of establishment (Serrato-Valenti *et al.*, 1989). In agriculture, hardseededness can be disadvantageous, the lack of simultaneous germination preventing the establishment of uniform stand of seedlings (RiggioBevilaqua *et al.*, 1985). This problem needs considerable attention especially in genebanks because it can not only seriously interfere with the results of the germination tests designed to assess the

viability of accessions but also can reduce the amount of precious seed which emerges when sown for regeneration, multiplication or other purposes. Treatments applied to break this dormancy are highly specific and no one type is universally accepted because even within a genus, distinct differences in the seed coat dormancy have been observed for several species of crop plants (Bhattacharya and Saha, 1990; Lopez and Aviles, 1988; Todaria and Negi, 1992). The present study was undertaken to evaluate the efficacy of various physico-chemical treatments in breaking the seed coat impermeability of *Corchorus* seeds.

MATERIALS AND METHODS

One accession each of *Corchorus olitorius* (OIN 124) and *Corchorus capsularis* (CIN 169) exhibiting maximum hardseededness of 92 and 88 per cent respectively were subjected to the following treatments in order to break the seed coat impermeability :

- (a) **Acid scarification** : Seeds were immersed in concentrated sulphuric acid for 5, 10, 15, 20, 25, 30, 40 and 50 minutes and rinsed several times in running tap water.
- (b) **Hot water treatment** : Seeds were subjected to hot water treatment by varying immersion time and temperatures. The time temperature combinations selected are given in Table 2.
- (c) **Mechanical scarification** : Seeds were placed between two sheets of fine and coarse sand paper and gently rubbed for 2 minutes.
- (d) **Storage at sub-zero temperature** : Seeds were packed in trilayered aluminium foil packets and stored for one year at -20°C .
- (e) **Dry heat treatment** : Seeds were subjected to dry heat at 65°C for 24 hours in a forced draught air oven.

The data were subjected to statistical analyses in randomized complete block design using MSTATC software.

RESULTS AND DISCUSSION

Various treatments (chemical, enzymes, pressure, scarification, freezing, radiation etc), that force hard seeds to germinate have been known for many years. Early methods have been reviewed by Rolston, 1978. Concentrated sulphuric acid (Hopkins, 1923) and mechanical scarification (Hughes, 1915) have been widely used with considerable success on many species. The results of the present study indicated that among all the methods tested, hot water treatment in the case of *C. olitorius* and sulphuric acid scarification along with

sand paper scarification in the case of *C. capsularis* were the most effective pretreatments for breaking coat imposed dormancy. Significant differences existed between genotypes and treatments and genotypes over treatments. Scarification with acid for 15-40 minutes did on the average result in more germination than either shorter or longer periods in *C. capsularis* (96% as against only 13% in the control). In *C. olitorius* acid treatment could raise the germination percentage to a maximum of 54-57 per cent when treated for 15-20 minutes. Shorter durations were less effective and longer durations were detrimental resulting in significant increase in the number of decayed seedlings (Table 1). The efficacy of sulphuric acid treatments have been reported by

Table 1. Effect of concentrated sulphuric acid on the germination of *Corchorus* species

Duration (Min)	Normal			Abnormal			Hard			Dead		
	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean
5	66.0	11.0	38.5	4.0	4.0	4.0	23.0	79.0	51.0	7.0	6.0	6.5
10	79.0	21.0	50.0	0.0	6.0	3.0	17.0	63.0	40.0	4.0	9.0	6.5
15	96.0	55.0	75.5	0.0	12.0	6.0	0.0	20.0	10.0	4.0	13.0	8.5
20	96.0	57.0	76.5	0.0	19.0	9.5	0.0	12.0	6.0	4.0	12.0	8.0
30	95.0	29.0	62.0	1.0	33.0	17.5	0.0	13.0	6.5	3.0	24.0	13.5
40	96.0	23.0	56.5	0.0	27.0	13.5	0.0	10.0	5.0	4.0	41.0	22.5
50	82.0	17.0	49.5	5.0	12.0	8.5	0.0	0.0	0.0	13.0	71.0	42.0
Control	12.0	5.0	8.5	4.0	0.0	2.0	80.0	95.0	87.5	4.0	0.0	2.0
Mean	77.8	27.5	52.1	1.8	14.1	8.0	15.0	36.5	25.8	5.4	22.0	13.7
CD	5%		1%	5%		1%	5%		1%	5%		1%
(V)	1.28		1.73	1.14		1.54	1.11		1.51	0.89		1.70
(T)	2.56		3.46	2.28		3.08	2.23		3.01	1.78		2.40
(V) × (T)	3.63		4.89	3.23		4.35	3.16		4.26	2.52		3.00

Horn and Hill (1974) in *Lupinus cosentine*, Tomer and Promila (1991) in *Vigna mungo*, Singh *et al.* (1985) in *Lens esculentus*, Rao *et al.* (1985) in *Atylosia platycarpa* and Cheema and Qadir (1973) in *Acacia senegal*. Concentrated sulphuric acid causes rapid desiccation of the seed coat resulting in the fragmentation of the integuments thus allowing the passage of moisture to the embryo (Duran and Tortosa, 1985). Treatments lasting for more than the optimal durations i.e. 15-40 minutes in *C. capsularis* and 15-20 minutes in *C. olitorius* resulted in death and decay of seeds and seedlings probably due to the acid finding its way into the embryo, thereby causing injury.

As for the hot water treatment, best response was shown by *C. olitorius* seeds where 80 and 79 per cent germination could be achieved by treating the seeds at 65°C for 3 min. respectively. For *C. capsularis* hot water treatment was slightly inferior to acid or sand paper scarification and the best combination of time and temperature was 75°C for 15 minutes which produced 92 per cent normal seedlings. Species specificity to a given treatment has already been reported by (Aveyard, 1986; Clemens *et al.*, 1977). The results reveal that with increasing temperatures, shorter exposures became sufficient to render seeds permeable. Longer exposures at higher temperatures resulted in heat impairment of germinability (Table 2). This could be due to thermal inactivation or damage to the embryo.

Table 2. Effect of hot water treatment on the germination of *Corchorus* species

Treat- ment	Dura- tion	Normal			Abnormal			Hard			Dead		
		C.	C.	Mean	C.	C.	Mean	C.	C.	Mean	C.	C.	Mean
Temp °C	Minu- tes	caps.	olit.		caps.	olit.		caps.	olit.		caps.	olit.	
65	30	40.0	80.0	60.0	17.0	0.0	8.5	27.0	12.0	19.5	17.0	8.0	12.5
70	30	25.0	74.0	49.5	20.0	5.0	12.5	23.0	9.0	16.0	31.0	11.0	21.0
75	15	92.0	68.0	80.0	0.0	5.0	2.5	4.0	25.0	14.5	4.0	2.0	3.0
75	30	17.0	48.0	32.5	43.0	16.0	29.5	12.0	1.0	12.0	29.0	4.0	26.5
80	3	81.0	79.0	80.0	9.0	4.0	6.5	5.0	3.0	9.0	5.0	4.0	4.5
80	5	47.0	65.0	56.0	31.0	11.0	21.0	10.0	9.0	9.5	12.0	15.0	13.5
80	10	27.0	30.0	28.5	21.0	39.0	30.0	4.0	0.0	2.0	47.0	31.0	39.0
Control	-	13.0	4.0	8.5	4.0	0.0	2.0	81.0	96.0	88.5	2.0	0.0	1.0
Mean	-	42.7	56.0	49.3	18.1	10.0	14.3	20.7	22.0	21.4	18.3	11.8	15.1
CD		5%		1%	5%		1%	5%		1%	5%		1%
(V)		1.15		1.55	0.94		1.26	0.99		1.33	1.14		1.53
(T)		2.30		3.09	1.86		2.51	1.97		2.67	2.28		3.06
(V) × (T)		3.25		4.38	2.64		3.55	2.79		3.75	2.22		4.34

Mechanical scarification by scraping the seed coat or rubbing over sand paper to create an abrasive force has been a very common method of treating seed coat dormancy for small lots of seeds. Duran and Tortosa (1985) in *Sinapis arvensis*, and Mitter *et al.* (1993) in *Psoralea corylifolia*, have emphasized the efficacy of this method for breaking coat impermeability (Table 3).

Table 3. Effect of some physical treatments on the germination of *Corchorus* species

Treatment	Normal			Abnormal			Hard			Dead		
	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean	C. caps.	C. olit.	Mean
Fine scarification	96.0	75.0	85.5	0.	14.0	7.0	0.0	5.0	2.5	4.0	6.0	5.0
Coarse scarification	50.0	71.0	60.5	27.0	19.0	23.0	5.0	6.0	5.5	18.0	5.0	11.5
Dry heat	49.0	58.0	53.5	11.0	9.0	10.0	28.0	25.0	26.5	13.0	7.0	10.0
Storage at -20°C	46.0	6.0	26.0	4.0	0.0	2.0	46.0	94.0	70.0	4.0	0.0	2.0
Control	12.0	5.0	8.5	4.0	0.0	2.0	80.0	95.0	87.5	4.0	0.0	2.0
Mean	50.6	43.0	46.8	9.2	8.4	8.8	31.8	45.0	38.4	8.6	3.6	6.1
CD at	5%		1%	5%		1%	5%		1%	5%		1%
(V)	1.07		1.46	1.16		1.59	1.95		1.29	0.87		1.19
(T)	1.69		2.31	1.84		2.51	1.51		2.06	1.37		1.86
(V) × (T)	2.39		3.26	2.60		3.55	2.12		2.93	0.94		2.64

Besides the above mentioned treatments, which were highly effective in breaking seed coat dormancy of jute species, storage at -20°C for one year as well as dry heat application were tried in the present study. There was a partial response of *C. capsularis* to sub-zero treatment which resulted in 46 per cent germination as against 13 per cent in the control whereas it was totally ineffective for *C. olitorius*. On the other hand subjecting the seeds to dry heat for 24 hrs. evoked equal response of both the species and resulted in 48 and 58 per cent germination in *C. capsularis* and *C. olitorius* respectively.

From the results obtained in this study, it is very clear that the two species of *Corchorus* respond in a significantly different manner with regard to various treatments used for breaking seed coat dormancy. Also the results clearly advocate the use of hot water treatment for *C. olitorius* and acid or sand paper scarification for *C. capsularis* as effective methods to overcome this problem.

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GENETIC DIVERGENCE IN GLADIOLUS

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The genetic divergence analysis of 60 varieties of gladiolus for 20 developmental characters showed grouping of varieties into 12 clusters. Based on cluster means, characters such as spike length, no. of florets per spike, no. of florets opening at first, no. of florets remaining open at a time, no. of capsules forming per spike and the seeds set per capsule, no. of daughter corms & cormels produced per plant, and diameter of foremost floret were major factors of differentiation among these 60 varieties. The varieties producing more no. of corms and cormels, spike length and no. of florets per spike can thus be utilized for hybridization for making improvement in these characters in this crop.

Key words : Gladiolus, divergence, genotype, variability

Gladiolus occupies fourth place in the international cut flower trade hence is grown in each country on the globe for cut flower and garden display. The improvement in this crop was very much limited due to limited germplasm but with the introduction of exotic and indigenous varieties the avenues have opened in our country. Therefore, the present study was undertaken to gather the information on genetic divergence among existing varieties, and the factors influencing genetic divergence.

MATERIALS AND METHODS

The material for the present investigation consisted of 60 varieties of gladioli, 57 exotic belonging to America, Europe, Australia and USSR, and 3 indigenous. These were subjected to multivariate analysis using D^2 statistics. They were grown at Naggar Farm of IARI Regional Station, Katrain, Kullu Valley (H.P.) during 1988 and 1989 seasons (April to November), in randomised block design with three replications, maintaining a distance of 40 cm from row to row and 20 cm from plant to plant. Each entry consisted of two rows and data were recorded on 12 plants per replication for the characters as mentioned in Table 3.

The data were subjected to multivariate analysis using Mahalanobis' generalized distance D^2 . The 20×20 dispersion matrix was used for simultaneous

use for testing significance of difference in the character means using Wilk's criterion (1952) and the varieties were grouped into clusters according to the Tocher's method adopted from Rao, (1952)

RESULTS AND DISCUSSION

The analysis of plant means revealed significant differences at 1% level between 60 varieties of gladioli for all the 20 characters. Maximum variation was observed for spike length, no. of florets per spike, no. of florets remain open at a time, no. of capsules per shoot, no. of seeds per capsule, no. of cormels produced per plant and 10-cormel weight. The multivariate analysis revealed that the 60 varieties could be grouped in 12 clusters (Table 1). The varieties included were 29 in cluster I, 10 in cluster II and five in cluster III.

Table 1. Name of varieties included in twelve clusters of gladioli

Cluster	No. of genotypes falling in each cluster	Name of genotypes
I	29	American Beauty, Smoky Lady, Vladimir Vasiliev, Ruby pattern, Camel tone, Rose Royal, Redeem, Rose Time Steamboat, Barlew, Heady Wine, Ratna's Butterfly, Setting sun, Salmon Queen, Gambier Pearl, Vicki Lin, High Style, Spring Song, Howard, Ivy Agnes, Coppertone, Bush Ballad, High Hopes, Tall Timber, Wind Song, Red Softglow, Tiger Flame, Rose Memento, Legend, Green Willow
II	10	Himprabha, Cardinal, Miss America, Ecstasy, Sylvia, Cygnet, Ultima, Coral Beauty, Katrain Local, Green Lilac
III	5	Blue Lilac, Spectacular True Love, Beauty Crest, Peter Pears, Ripples
IV	4	Littlest Angle, Garnet, Sugar Babe, Little Mo
V	4	Gillian, Green Finch, Gambier Dainty, Ave
VI	2	Nugget, Melody
VII	1	Lady Fayre
VIII	1	White Oak
IX	1	Royal Jubilee
X	1	Psittacinus Hybrid
XI	1	Australian Fair
XII	1	Kawaliar

Clusters IV and V comprised four varieties in each while the cluster VI had two varieties. Rest of the clusters i.e. VII, VIII, IX, X, XI and XII were having one variety in each. Most varieties in cluster I were of exotic origin but they

The inter and intra-cluster distances D^2 among 12 clusters presented in Table 2 revealed that lowest intra-cluster distance was observed for cluster III

[illegible]

($D^2 = 70.52$) and maximum ($D^2 = 144.47$) for cluster V. clusters I, II and IV had relatively moderate to high D^2 values (79.50, 86.42 and 84.71, respectively), indicating that the varieties were relatively more diverse genetically. Similar expectations also emerged from the inter-cluster distances which were maximum among clusters XII and IX ($D^2 = 508.24$) and minimum between clusters XI and X ($D^2 = 47.73$).

The character mean of varieties in 12 clusters are given in Table 3. The mean values of these clusters expressed a wide range among the varieties of different clusters. Cluster I was distinguished by members having less durability of spike while with average number of days taken by the florets open at first. Cluster III having five members was characterised with more number of days taken by the florets to open at first. However, the varieties included in cluster V were having more durability of the first flower, more number of florets remaining open for longer days, more spike durability and larger polar and equatorial diameter of daughter corms. The clusters with only one entry had distinct characteristics, e.g. cluster X had tallest height of the plant and less number of shoots per planted corm, cluster IX had more number of leaves per shoot, more number of days for first flower, more durability of first floret and of the whole spike with more number of side spikes formed per shoot, cluster VIII was characterized for largest flower diameter, more number of florets remaining open at a time with more number of florets per spike, more number of capsules per shoot, more number of seeds per capsule and maximum weight of one daughter corm.

Earlier studies with 39 varieties conducted by Negi *et al.* (1982) had also indicated that the selection of varieties based on the characters namely weight of cormels produced per plant, number of cormels produced per plant and the weight of daughter corms produced will be very effective for the improvement of this crop. Though the exotic genotypes responded poorly for some of the characters but these are good sources for increasing flower diameter, durability of foremost floret and the number of florets opening at a time. These can help directly to achieve the goal of increasing the number of cormels per corm, etc. Some of the characters which change with the change of environment like height of the plant, capsule and seed setting and corm formation can also help to improve the economy of this crop. In this way more number of florets with good quality and size appear when the total height of the plant is increased and thus it becomes more remunerative.

In the past gladiolus remained neglected and improvement through breeding in this crop was not very much effective for improving the characters like number of corms and cormels per plant, number of florets per spike and the number of florets remaining open at a time due to limited genetic stock. The recent introductions have opened the way for improvement through hybridization. The cluster comprising only one variety with specific trait could

Table 3. Cluster mean values for twelve clusters in gladiolus

	Characters*																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
I	107.81	88.26	6.75	1.53	94.85	11.77	3.46	1.76	5.50	15.35	13.21	4.97	10.18	0.51	2.44	4.59	1.59	39.19	50.74	4.50
II	102.56	79.57	6.46	1.77	91.26	10.66	3.35	1.69	4.64	15.51	13.64	6.99	17.51	0.45	1.98	3.84	1.60	23.60	43.54	4.70
III	104.23	80.08	6.27	1.99	83.79	10.63	3.53	2.05	5.39	15.27	13.36	6.80	13.58	1.02	2.48	4.40	1.89	34.87	37.11	3.72
IV	98.64	75.81	6.39	1.60	87.80	8.06	3.27	1.98	5.85	17.17	13.02	9.50	17.95	0.96	2.74	4.44	1.59	35.45	30.40	5.18
V	112.82	90.15	7.17	1.48	386.57	12.19	3.67	1.70	5.97	15.30	13.55	5.57	9.67	0.62	4.12	5.17	1.84	49.53	37.44	4.23
VI	100.52	70.25	6.50	1.83	85.70	9.23	3.50	1.53	5.40	17.03	14.66	12.40	18.75	0.53	2.25	4.25	1.84	31.36	31.03	4.65
VII	114.67	82.00	7.13	1.60	83.07	11.20	3.00	2.80	5.80	14.27	13.27	1.07	8.87	1.13	2.93	4.43	1.53	21.23	20.27	3.50
VIII	137.27	94.27	8.67	1.07	107.53	13.67	3.33	2.07	7.53	20.27	15.53	12.87	36.83	0.00	2.70	5.17	1.07	52.20	80.57	4.37
IX	128.53	91.70	8.93	1.07	128.60	12.07	4.00	2.00	4.00	16.73	18.13	11.53	9.40	2.00	2.30	3.63	1.00	24.37	7.40	17.20
X	146.67	106.00	8.00	1.13	116.93	10.20	3.00	1.40	4.67	16.60	17.67	6.80	2.47	1.00	2.33	4.33	1.20	35.57	30.83	15.17
XI	144.73	107.27	7.53	1.47	112.20	8.10	2.93	1.80	3.93	17.13	18.00	6.07	1.00	0.40	2.33	4.70	1.40	44.20	9.27	19.03
XII	82.12	58.87	5.93	2.60	81.73	7.07	2.00	1.00	2.00	8.80	13.33	3.93	16.73	1.07	2.07	4.10	2.07	25.93	111.83	4.93

*1. Height of the plant, 2. Spike length, 3. Number of leaves per plant, 4. Number of shoots per plant, 5. Days to flowering, 6. Diameter of foremost floret, 7. Durability of foremost floret, 8. Number of florets open at first, 9. Number of florets remain open, 10. Number of florets per spike, 11. Durability of whole spike, 12. Number of capsules per shoot, 13. Number of seeds per capsule, 14. Number of side spikes per shoot, 15. Polar diameter of daughter corns, 16. Equatorial diameter of daughter corns, 17. Number of daughter corns per plant, 18. Weight of one daughter corn, 19. Number of cornels produced per plant, and 20. 10-cornel weight.

be used in hybridization programme for exploiting hybrid vigour. The highly divergent groups are likely to produce new genotypes with desired characters on crossing.

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Short Communication

GENETIC DIVERGENCE IN FORAGE COWPEA

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Key words : Genetic divergence, cowpea, forage

Cowpea (*Vigna unguiculata* L. Walp) is a legume grown for vegetable, fodder or pulse in the tropics and sub-tropics. Further, the clustering of forage cowpea accessions on the basis of genetic divergence may provide the basis for selection of suitable parents to be used in hybridization programme. Therefore, the present study was undertaken on these aspects using multivariate statistical technique, for some fodder attributes in cowpea.

A total of 280 diverse genotypes (49 genotypes, *viz.*, IL 3939 to IL 3988 from Delhi, 81 genotypes, *viz.*, IL 93 to IL 174 from Punjab and 150 genotypes, *viz.*, IL 1520 to IL 1670 from Gujrat) of fodder cowpea along with 3 check varieties were studied in an augmented block design. Each plot consisted of one row of 4m length; spacing between and within rows were 60 and 15 cm, respectively. The crop was raised by adopting standard cultural practices. Observations were recorded on 5 competitive plants for 10 quantitative traits, *viz.*, days to 50 per cent flowering, plant height (cm), number of branches/plant, branch length (cm), leaf number/plant, fresh leaf weight (g), fresh stem weight (g), dry leaf weight (g), dry stem weight (g) and leaf/stem ratio. All the metric traits were analysed in augmented block design (Petersen, 1985). This analysis gave adjusted mean value, on which principal component analysis as given by Hotelling (1933) and Mardia (1971) was applied, to transform the interdependent variables into a set of independent variables. Further, these principal component scores were used for non-hierarchical euclidean cluster analysis (Beale, 1969; Spark, 1973). For assigning appropriate number of cluster F-test was applied. The analysis was carried out using SPAR1 package.

Correlation matrix of adjusted mean values was used to transform all the quantitative traits into a single index of similarity in the form of principal components, which yielded into 10 eigen vectors and eigen roots. Further, the

maximum eigen root value 3.43 was obtained by eigen vector 1 and followed by 2.08, 1.11, 0.91, 0.67, 0.52, 0.51, 0.35, 0.27, and 0.16 respectively, for rest of the vectors. The first four principal components accounted for 34.29 per cent, 20.76 per cent, 11.125 per cent and 9.12 per cent of the variation. Thus, cumulative percentage of total variation reflected that more than 75 per cent variation was explained by first four principal components and rest by others.

The cluster analysis was initiated with 8 principal component scores, grouped 280 accessions into a convenient grouping of 10 non-overlapping clusters with like genotypes within clusters for different attributes. Further, F-test showed that 10 clusters (F ratio significant at 5% probability) were most suited. The maximum number of genotypes fell in cluster number 5 (61 genotypes), while cluster number 10 was solitary. The average inter- and intra-cluster distances are presented in Table 1. The intra-cluster distances ranged from 0.00 to 3.01. Maximum cluster distance (8.13) was found between cluster 8 and 9 followed by 5 and 8 (7.53). The minimum distance was observed between cluster 1 and 9 (1.97). The observed distances showed the genetic diversity among and within the clusters and clustering is useful to identify the diverse genotypes.

Table 1. Average inter and intra-cluster distances in forage cowpea

Cluster No.	1	2	3	4	5	6	7	8	9	10
1	(1.6480)									
2	2.670	(2.131)								
3	2.984	3.615	(1.7500)							
4	4.808	3.647	3.235	(2.640)						
5	2.156	3.664	3.635	5.592	(1.681)					
6	3.057	2.410	4.432	4.511	2.932	(1.926)				
7	2.531	2.768	2.598	3.824	2.944	2.959	(2.064)			
8	7.264	5.105	7.349	5.434	7.534	5.043	5.859	(3.014)		
9	1.967	4.048	2.548	5.231	2.264	4.242	2.559	8.128	(1.595)	
10	6.179	5.458	4.404	5.130	6.367	5.130	6.004	4.755	6.860	(0.000)

Values in parentheses shows intra-cluster distances

The relative superiority of different attributes is presented in the Table 2. The potential genetic donor for fresh leaf weight, fresh stem weight, dry leaf weight and dry stem weight fell into cluster number 8 (IL 102, IL 114, IL 1540, IL 1610, IL 1614, IL 3983 and IL 3987); for tallest plant height cluster number 2 (IL 107, IL 119, IL 140, IL 171, IL 1580, IL 1588, IL 1636, IL 1665,

IL 1669, IL 1669, IL 3966, IL 3984 and IL 3986); for leaf/stem ratio cluster number 4 (IL 143, IL 174, IL 1589, IL 3939, IL 3952 and IL 3980).

Table 2. Cluster mean for various traits in forage cowpea

Character	1	2	3	4	5	6	7	8	9	10
1	55.12	142.92	6.93	223.85	59.93	88.92	181.60	17.07	38.70	0.44
2	71.00	183.33	8.78	230.97	107.00	152.89	287.39	26.03	62.92	0.45
3	48.49	163.35	8.38	160.12	62.95	161.83	166.59	23.61	22.88	1.08
4	49.17	163.75	9.63	190.23	98.62	264.63	261.35	44.84	77.36	1.24
5	87.52	106.25	7.40	188.04	66.95	66.06	135.76	15.00	32.76	0.49
6	87.65	101.48	8.89	244.46	121.14	132.04	260.60	28.19	68.63	0.43
7	51.46	124.52	10.20	157.71	107.82	133.61	208.55	21.59	43.40	0.53
8	82.00	136.23	12.26	203.20	265.80	246.11	486.86	46.95	101.85	0.47
9	49.21	126.63	6.81	147.59	54.73	76.08	125.60	12.35	23.03	0.60
10	88.00	83.30	8.00	293.00	115.30	183.30	431.60	37.50	100.22	0.34

1 = Days to 50 % flowering, 2 = Plant height (cm), 3 = Number of branches/plant, 4 = Branch length (cm), 5 = Leaf number/plant, 6 = Fresh stem weight (g), 8 = Dry leaf weight (g), 9 = Dry stem weight (g), 10 = Leaf/stem ratio

Therefore, the studies help in grouping of genotypes into clusters and selection of desired genotypes from a particular cluster for further utilization in hybridization programme.

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Short Communication

STABILITY PARAMETERS IN RAINFED WHEAT

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Key words ; Wheat, stability, rainfed situation

Wheat (*Triticum* sp.) is a sensitive crop to the vagaries of environment, and the yield fluctuates with variations in environments. Hence, a study was conducted to assess genotype $\times$ environment interactions and stability of 20 genotypes at Dharwad under rainfed cropping system.

Twenty genotypes of wheat selected from National Drought and Heat Tolerance Observation Nursery (NDHTON), were tested over three years (1993-94 to 1995-96) in randomised block design with plot size of 3m $\times$ 4 rows. All the recommended agronomic practices were followed to raise good crop. Data on grain yield/plot (g) was recorded and used for statistical analysis for stability parameters (Eberhart and Russell, 1966). The differences were highly significant among the genotypes for grain yield/plot (Table 1). The environment (linear) was significant, indicating that environments differ markedly and thereby satisfying the requirement of stability analysis. Significant genotype $\times$ environment (linear) interaction indicated genotypic differences for regression over environmental means (Table 1) and that genotypes behaved differently in different environments during three years of study.

Table 1. Analysis of variance of stability for grain yield of 20 genotypes wheat in rainfed ecosystems

SOURCE	D.F.	M.S.
Varieties	19	4240.4*
Environments	2	60855.4*
Variety $\times$ Environment	38	2533.2*
ENV + (Var. $\times$ ENV)	40	5449.3*
Environ (Linear)	1	121710.8*
Var $\times$ environ (Linear)	19	3890.0*
Pooled deviation	20	1117.6*

* = probability at 0.05 level.

For grain yield/plot, Sujata and Bijata Yellow with higher mean value (293.67 and 237.5), unit value (1.37 and 1.53) and non-significant S^2d value suggests that these genotypes are stable over three years in all the environments tested. Also, genotypes such as C-306 and NI-8223 with higher means (230.5 and 270.0) with significant b values (-0.33 and 2.86) and non-significant deviations from S^2d values may perform better in a favourable environment. RS-491 and RS-626 showed relatively better means with low b values (0.23 and 0.65) indicating their better performance in poor environments (Table 2).

Table 2. Estimates of stability parameters (mean, b and s^2d) for grain yield per plot(g) in wheat under rainfed condition.

Sl.No.	VAR	SOURCE	MEAN	b	S^2d
1	A-9-30-1	NDHTON	193.0	0.33	9.3
2	C-306	"	230.5	-0.33^{**}	672.4
3	Hindi-62	"	173.2	0.61	253.2
4	Sujata	"	293.7	1.37	469.7
5	CM-59	"	233.3	1.32	117.9
6	Narmada-4	"	170.0	1.11	2628.9
7	NI-8223	"	270.0	2.86^{**}	63.2
8	Pissi-local	"	198.8	0.01	61.3
9	K-8027	"	188.0	1.10	867.6
10	Kharchia-65	"	200.5	1.11	131.2
11	Hyb-65	"	172.5	0.14	2816.1
12	B-Yellow	"	237.5	1.53	23.8
13	AKW-407-1	"	204.5	1.43	528.9
14	AKW-1057	"	191.2	1.32	61.4
15	RS-491	"	214.2	0.23	654.9
16	RS-628	"	132.3	-0.11	5711.8
17	RS-626	"	258.0	0.65	1748.3
18	21(s)Ad	"	210.33	1.91	3183.5
19	DT-20	"	212.67	1.63	532.9
20	HI-8351	"	188.17	1.77	558.5
Population Mean = 208.61			SEm $\pm$ = 23.6	SEm $\pm$ OF B = 0.42	

* $P = 0.05$, ** $P = 0.01$

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Short Communication

EVALUATION OF LENTIL GERMPLASM FROM NORTH WESTERN HIMALAYA

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Key words : Lentil, yield, variance, interaction, evaluation, germplasm

Lentil (*Lens culinaris*) is considered to be one of the oldest food crops of mankind. The major lentil-growing countries of South-Asia are India, Nepal, Bangladesh, Pakistan and Myanmar. As a part of efforts to strengthen lentil breeding programme, the investigation under report was conducted to identify promising donors having consistently superior performance under North-Western Himalayan conditions.

A set of fifty lentil genotypes, comprising material collected from hills as well as from other agro ecological regions of the country, was evaluated in a randomized block design with three replications during the rabi seasons of 1991-92, 1992-93 and 1993-94. The data were recorded on (i) days to 50 per cent flowering, (ii) plant height (cm), (iii) number of pods per plant, (iv) days to maturity, and (v) grain yield (kg/ha). The data was subjected to pooled analysis of variance (ANOVA). The results of pooled ANOVA (Table 1) indicated that 'year' was a source of significant variation for all the characters except for the number of pods per plant. However, the genotype mean squares were significant for all the characters thereby indicating that the set of genotypes chosen had significant variation within it. The 'year $\times$ genotype' interaction was significant only for the three characters viz., days to 50 per cent flowering, days to maturity and grain yield. This indicated that different years did cause differential effects on various genotypes with respect to these three characters.

Observations of such a phenomenon made 'instability of yield' as one of the important production constraints (Bahl *et al.*, 1993) in lentil. The analysis further revealed the presence of wide range of variability with respect to different characters (Table 1). Also top five highest yielding genotypes, on the basis of three years average, were identified and are listed in Table 2.

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Table 1. Pooled ANOVA for yield and its components in lentil over three years

	Days to 50% flowering	Plant height (cm)	No. of pods per plant	Days to maturity	Yield (kg/ha)
A. Mean squares					
Year	298.6**	54.1**	214.6	1652.4**	760143.1**
Genotype	241.4**	37.6**	922.9**	376.3**	432334.1**
Year × Genotype	29.4**	6.1	47.6	135.4**	89963.8**
Error	3.9	10.6	140.1	3.2	41305.5
B. Other parameters					
Mean	114.9	27.8	55.2	165.8	555.4
Standard error of mean	1.97	3.25	11.84	1.78	202.9
Critical difference at 5% level	3.16	5.21	18.9	2.86	324.85
Range	104 (PML 8803) to 128 (VL-4)	22.7 (VL 119) to 31.7 (DPL 05)	37 (301) to 85 (VL 115)	158 (VL 107) to 179 (T-36)	209 (NP 6565) to 1131 (VL-4)

Table 2. Performance of some promising genotypes evaluated during 1991-92 to 1993-94

Sl. No.	Days to 50% flowering	Plant height (cm)	No. of pods per plant	Days to maturity	Yield (kg/ha)
VL 103	125	28.0	71.4	179	966.2
VL 105	122	27.6	54.0	177	930.8
VL 108	121	24.3	49.9	176	909.7
VL 4	128	29.2	76.4	179	1131.4
VL 109	118	29.9	53.3	178	919.8

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Short Communication

LETTUCE (*LACTUCA* SPP.) : AN UNDERUTILIZED CROP

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Key words: *Lactuca*, lettuce collections, domestication, dormancy, oilseed, origin, wild progenitor

Lettuce (*Lactuca* spp.) is the world's most important and widely-consumed leafy salad vegetable. It represents a large genus of the Asteraceae (Compositae) family ($x = 8,9,17$) which includes approximately 100 species of annual and perennial plants and is allied with other genera, such as chicory (*Cichorium intybus*) and dandelions. They occur most abundantly in the temperate regions of the old world. The common cultivated salad lettuce, *Lactuca sativa*, is one of the four species with 9 pairs of chromosomes (i.e., $2n=18$), the other three being *Lactuca serriola*, *L. virosa*, and *L. saligna*. The latter three species have now become obsolete and are rarely cultivated. All four species are native to the Mediterranean basin and are interfertile with each other thus facilitating exchange of desirable genes among them for breeding purposes. Despite its cultivation under varied conditions it remains largely an underutilized crop.

Origin of salad lettuce

Three main theories have been advanced concerning the origin of cultivated lettuce (Damania, 1975). 1. It was domesticated from wild forms of *L. sativa*, 2. That it arose as a result of a natural cross between *L. sativa* and *L. serriola*, and 3 from hybridization among several species. The latter theory is based on cytological and genetical evidence put forward by Lindquist (1960). However, the most commonly accepted theory of domestication of *Lactuca sativa* is that it evolved as a natural selection from its closest wild progenitor, *L. serriola*, which is a prickly biennial of the temperate regions (Purseglove,

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1968). *Lactuca sativa* originated in the eastern Mediterranean about 7000 years ago, most likely in Egypt when the climate of that part of northeastern Africa was not as dry as it is today. Lettuce was a common oilseed crop in Upper Egypt as far back as 4500 B.C. as depicted by rosettes of a tall, large vegetable with subulate leaves painted on the walls of tombs at Thebes (2500 B.C.). The presence of latex in primitive lettuce also marked the plant as a fertility symbol (Damania, 1975). Unfortunately, the available illustrated record found in ancient monuments is not complemented by dry or carbonized remains of leaves or seed of this crop in Egypt. Keimer (1924) informs us that early agriculture in Upper Egypt included lettuce as a seed crop for its edible oil and was being used in that country as such as recently as 1964. Subsequently, other refined edible oils more economically extracted from ground nuts, sunflower, olive, and maize have taken over throughout the Mediterranean.

Early human selection for nonshattering seed heads, late flowering, non-prickly leaves, decrease in latex content, and hearting character (the tendency of leaves to congregate in layers in a heart shaped head) is said to have led to its domestication as a leafy salad vegetable (Ryder and Whitaker, 1976). Salad lettuce was brought to the New World following Columbus's voyage in 1492 and by 1565 it was being grown abundantly in Haiti and the Caribbean. A seedsman catalog published in 1806 lists 16 cvs. already being offered in America (Hedrick, 1919). Among the cultivated types there is extensive variation of forms but four main groups have been recognized, viz., asparagus, cabbage, cos, and curled lettuces (Purseglove, 1968). Around 6500 years ago lettuce was transported to Greece and subsequently spread throughout the Roman Empire and was known to Hippocrates, Aristotle, and Pliny. The Moors in Spain developed several varieties, especially in Artdalucia, when that region was under Arab domination. In Syria and Palestine lettuce was widely grown and consumed in the river valleys during the Byzantine period. Lettuce reached China around the 7th century A.D. where a special cultivar (cv.) of the asparagus type (*L. serriola* f. *integrifolia*) was developed and reported by Fuchs in 1543 from Sinkiang. The local name of this cv. is 'usum' or 'on-sen'. According to Vavilov (1992) this form of lettuce is practically unknown in South West Asia. Domesticated *L. indica* is also grown in China and Japan and later introduced to Java and parts of Malaysia. Its leaves are usually boiled and eaten with chopsticks as a vegetable in chinese cooking. The cultivated vegetable lettuce exhibits a close relationship to a group of other *Lactuca* species. Its closest wild relative, *L. serriola* (prickly lettuce), which is found all over the Mediterranean region and the Near East, has colonized large areas as a weed much outside these territories. For instance, following the highly successful post Columbus colonization of the New World, *L. serriola* has become a proliferate weed in North America.

U.S. Plant explorer collects unique lettuce germplasm in Egypt

P.F. Knowles, a plant scientist working on oilseed crops in the Department of Agronomy at the University of California, Davis (UC Davis), USA, travelled to Upper Egypt in 1958 to collect safflower (*Carthamus tinctorius*) and other oilseed crop genetic resources for his research. He was made aware of the oilseed producing lettuces of Egypt when he happened to visit the Plant Breeding Station at Giza (near Cairo) and met Mustapha Serry who was in-charge of the Oil Crops Section at that time. During the discussions Serry mentioned that the Station had a sample of an obsolete form of *Lactuca sativa* which was being grown sporadically in Upper Egypt for its large seeds from which edible oil was extracted. Sensing an opportunity for collection of germplasm potentially useful for crop improvement in the U.S., Knowles requested and received a subsample (collector's No. K1020, PI 250020) of the seeds of these plants from the Station nursery. The seeds of this particular sample contained 30 per cent edible oil and the plants did not show any disease symptoms.

Samples of the obsolete lettuce form, which turned out to be *Lactuca serriola*, were cultivated exclusively for their relatively large seeds, and since the leaves are prickly and full of latex and bitter to taste this form is unpalatable as salad. Nevertheless, such germplasm had been known to possess resistance to several diseases (especially downy mildew and mosaic virus) which affect the normal salad lettuce crop in Europe, North America, and Australia. Due to its complete compatibility with cultivated lettuce, *L. serriola* accessions have been used to make crosses resulting in cvs. such as, "Calmar" and "Valverde". Prickly lettuce is reportedly also been utilized for improvement of iceberg type lettuce in California which produced 3 million tons of this crop valued at approximately a billion dollars in 1995.

The seeds of a prickly lettuce *L. serriola* (collector's No. K 1058), reportedly grown in Upper Egypt for its oil in the same manner as safflower, were obtained from the warehouse of El Haq Menoufi el Said at Kena. This lettuce sample together with samples of safflower and other crops collected in Egypt was brought to the U.S. on 13 August 1958 where it entered the New Crops Research Branch of the Crops Research Division of US Department of Agriculture (USDA) at Beltsville, Maryland.

The entire collection from Egypt was subsequently evaluated for disease resistance and it was discovered that the prickly lettuce sample collected at Kena, which was given the number PI 251245, possessed resistance to lettuce mosaic virus. The resistance was located on a recessive allele named *mo*. Consequently, crosses with lettuce cvs. were made and the desirable gene was transferred to four lettuce cvs. grown in the western U.S., viz., Vanguard 75, Winterset, Autumn Gold, and Salinas 88 (Ryder, 1979) resulting in huge financial savings to the farmers. This valuable sample (PI 251245) and others

have been multiplied and are now conserved in the USDA *Lactuca* Germplasm Collection (LGCS), Salinas, California, which is the largest and most diverse collection of defined and characterized accessions of this genus in the world with over 10,000 samples. The accessions were also duplicated for safety, at the Western Regional Plant Introduction Station (Table 1), Pullman, Washington (McGuire et al., 1993). It is assumed that the samples Knowles collected in 1958 are no longer cultivated and possibly extinct. Hence his collection is very valuable for future breeding efforts.

Table 1. Number of *Lactuca* accessions at the USDA Regional Plant Introduction Station, Pullman, Washington (1995)

Species	Number	Species	Number
<i>L. altaica</i>	1	<i>L. serriola</i>	159
<i>L. dregeana</i>	1	<i>L. serriola</i> f.	
<i>L. indica</i>	1	<i>L. integrifolia</i>	1
<i>L. livida</i>	1	<i>L. undulata</i>	1
<i>L. perennis</i>	5	<i>L. viminea</i>	1
<i>L. quercina</i>	1	<i>L. virosa</i>	17
<i>L. saligna</i>	16	<i>Lactuca</i> spp. (unidentified)	7
<i>L. sativa</i>	1,037		
<i>L. sativa</i> var. <i>capitata</i>	5		
		Total	1,254

High-temperature dormancy in lettuce seeds

The optimum soil temperature for germination of lettuce seeds ranges between 25 to 29°C (Damania, 1975). Genes from such wild and obsolete type of lettuce germplasm such as the *L. virosa* is known to have been used to overcome high temperature seed dormancy problems which, in the past, led to scarcity of this leafy vegetable during the hot summer months since salad lettuce seed rarely germinate when soil temperature is above 29°C (Damania, 1986). The cv. Vanguard is the only known derivative of the difficult cross between *L. sativa* and *L. virosa*. Crosses with *L. saligna* will provide resistance to the cabbage looper. Dried latex from *L. virosa* provided the drug lactucarium (Purseglove, 1968).

Lettuce germplasm collections

In USA, in addition to the collections at Salinas, California, and Pullman, Washington, UC Davis also maintains a sizable *Lactuca* collection. This collection was established in 1948 and includes mostly research and breeding material. Other major collections of this vegetable crop are located at: Center for Genetic Resources (CGN), Wageningen, the Netherlands; Horticultural Research

International (HRI), Wellesbourne, England; N.I. Vavilov Institute of Plant Industry (VIR), St. Petersburg, Russia; Research and Plant Breeding Institute for Vegetables, Olomouc, Czech Republic; and the Horticultural Sciences Department, Cornell University, New York, USA. It must be noted that, although *Lactuca* originated in the eastern Mediterranean, all the major genetic resources collections are located in the western hemisphere's major consumer countries.

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Short Communication

GENOTYPIC AND PHENOTYPIC VARIABILITY IN DAHLIA (*DAHLIA VARIABILIS*)

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Key words : Dahlia, variability, phenotype, genotype

The present study was undertaken to find out the extent of genetic variability by determining the magnitude of genotypic coefficient of variation, heritability estimates and genetic advance of the nine quantitative characters in dahlia. Twenty three dahlia varieties were evaluated at IARI Regional Station, Katrain, Kullu Valley during gladiolus growing season (April to November 1988 and 1989) in RBD replicated thrice, using the variety Avalanche as control. Seven plants per replication were planted providing an area of 75 × 60 cm per plant, whereas data were recorded on 5 plants per replication for the characters mentioned in Table 1. Standard statistical procedures were adopted for the calculation of genetical constants as described by Burton, 1952; Burton and De Vane (1953), Keller and Linkens (1955), Kneebone (1958) and Frakes *et al.* (1961). Heritability in broad sense was calculated according to formula suggested by Hanson *et al.* (1956). Genetic advance was calculated by the formula as suggested by Lush (1949) and Johnson *et al.* (1955) with 5 per cent selection intensity. The data were analysed with the aid of the computer at IASRI, New Delhi.

The differences among the varieties were significant for all the characters. There was a wide sense of phenotypic variability for all these characters. Significant treatment differences were discernible at 1 per cent level. The estimates of phenotypic (σ^2_{ph} , genotypic σ^2_g) and error ($\sigma^2_{e/N}$) variances of varietal means (Table 1) indicated the variances to be high for flowers per plant, flower weight and shoots. The gcv ranged from 4.23 for flower diameter to 27.57 for flowers per plant (Table 1). The highest gcv was observed for flowers per plant followed by shoots per plant and spread. The components with low gcv were flower diameter, days to first flower and durability of one flower. Heritability in broad sense ranged from 54.15 per cent for days to first flower to 98.60 per cent for flower diameter. Most of the characters

possessed high heritability. The important ones being flower weight, length of floral stalk, flowers per plant, durability of one flower, and shoots per plant. High heritability estimates were helpful in making selection of superior genotypes on the basis of phenotypic performance of quantitative characters.

Table 1. Phenotypic and environmental variability and estimates of genotypic coefficient of variation, heritability and genetic advance in dahlia

	Characters	Range	mean	σ^2_{ph}	σ^2_g	σ^2_e	gcv	Heritability	Genetic advance as % of mean
1.	Plant height	72.6-148.4	11.13	19.01	16.84	2.17	8.81	78.49	34.17
2.	Shoots/plant	1.0-4.33	2.04	40.51	36.73	3.78	17.08	82.21	1.40
3.	Days to 1st flower	102.6-129.7	114.41	7.83	5.76	2.07	5.30	54.15	1.00
4.	Durability of one flower	5.13-9.40	7.72	16.03	14.94	1.09	5.82	86.82	2.22
5.	Flowers/plant	12.3-147.1	52.06	78.01	72.98	5.03	27.57	87.51	73.23
6.	Flower diameter	4.6-21.8	13.84	35.75	35.50	0.25	4.23	98.60	10.05
7.	Length of floral stalk	12.3-30.6	21.48	26.36	24.78	1.48	8.97	88.41	10.31
8.	Flower weight	3.5-49.0	24.59	59.47	59.00	0.47	7.49	98.41	29.65
9.	Plant spread	36.11-99.9	68.23	25.99	23.63	2.36	10.83	82.63	30.19

The estimates of genetic advance expressed as percentage of mean showed a wide range from 1.00 for days to first flower to 73.23 for flowers per plant. Thus the highest genetic advance was expressed by flowers per plant followed by plant height, plant spread and flower weight. Durability of one flower and shoots per plant showed lower estimates, and the percentage of genetic advance was poorest for days to first flower. However, Johnson *et al.* (1955) reported that heritability estimates along with genetic gain is more useful than the heritability value alone in predicting the resultant effect for selecting the best individual.

Flower weight and flowers per plant had very high genetic advance together with high heritability, which indicates that high heritability obtained in these characters is probably due to additive gene effects (Panse, 1957). Durability of one flower and shoots per plant possessed high heritability but low genetic advance indicating that high heritability for these characters may likely be due to non-additive gene action (Panse, 1957). Selection of individual plants for flowers per plant, flower diameter and flower weight might therefore be effective.

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CONSERVATION OF ZINGIBERACEOUS PLANTS IN ORISSA

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Key words : Conservation, Zingiberaceous plants

Species belonging to the family Zingiberaceae are of considerable economic importance. Turmeric (*Curcuma domestica*), mango ginger (*Curcuma amada*), ginger (*Zingiber officinale*), small cardamum (*Elettaria cardamomum*) and large cardamum (*Amomum subulatum*) are very important spices. These are also used in pharmaceutical and cosmetic industries. *Alpinia* oil has uses in perfumery, pharmaceutical, food and flavouring industries. In tribal areas plant parts of some Zingiberaceous species are used as carminative and an antidote to snakebites. Pharmaceutical studies in Zingiberaceous plants show that ginger rhizomes are effective for intestinal disorders (Krishnamurty and Sreenivasamurthy, 1956) and salivary secretion for stimulating the vasometer and respiratory centres (Ally, 1961), for relaxing the tracheae and ileal smooth muscles (Reiter and Brandt, 1985) and for lowering serum and hepatic cholesterol levels (Gujral *et al.*, 1978). Recent investigations also indicate that pungent principles of ginger rhizomes, such as gingerols and shagaols, have pharmacological actions (Shoji *et al.*, 1982, Suekawa *et al.*, 1984, 1986). In addition, antioxygenic effect of the rhizomes on food has been found (Du Bois and Tressler, 1943; Sethi and Aggarwal, 1952; Chipault *et al.* 1955, 1956, Kihara and Ingue, 1962; Fujio *et al.*, 1969).

There are some other species in Zingiberaceae family which have uses in pharmaceutical, dyes, cosmetics, condiments, food and flavouring industries as the rhizomes contain steroid, diosgenin, saponins, flavonoids, phenolics, iridoids, alkaloids and tannins. Zingiberaceous plants are available predominantly in South-East Asia. Ginger is cultivated in many tropical and subtropical countries. Major exporting countries are India (over 15,000 tonnes), Australia, Nigeria, Fiji, Taiwan and China (Turris *et al.*, 1987). In peninsular Malaysia about 22 genera and nearly 200 species of Zingiberaceae have been identified for conservation purpose and a Zingiberium has been developed at the Department of Biology, University of Pat, Malaysia (Ahmad and Rahman, 1991). Zhong Yi (1991) organised a Zingiberaceae workshop at Prince of Sangkla university.

In India the germplasm from Maharashtra, Kerala, Andhra Pradesh, Orissa and North-Eastern Hilly states have been exploited by ICAR, CSIR, State institutes and R & D activities. Agrotechnology and the method for extraction of oleoresin, curcumin etc. have been standardised. Orissa is considered as a major centre of Zingiberaceous plants. Orissa, University of Agriculture and Technology, Bhubaneswar has a research centre in Pottangi (High Altitude Research Station) where work is going on mostly on ginger, turmeric and cardamom.

It seems that only a small fraction of the genetic & cytoplasmic diversity available in the germplasm of Zingiberaceous crops have entered the parentage of the present day advanced varieties. Hence there is an urgent need to collect and evaluate the germplasm for every crop. Intensive basic studies would be essential on adaptation mechanism of genotypes to moisture, diseases, soil and climatic stresses and on the biochemical and cytogenetical basis of their resistance to the biotic and abiotic factors so that the planned transfer of useful genes into the advanced varieties would be possible. For better yield the cultivars have to be up graded and the agrotechnology for each crop be standardised and at the same time the suitable crops should also be popularised. Considering the importance of this family the study has been undertaken in Regional Research Laboratory, Bhubaneswar. The study includes the germplasm collection and improvement aspects (quantitative and Qualitative). Collections were made from Nandankanan, Pottangi, Kashipur, Patia, Dhenkanal, Saptasajya, Astarang and Sorishiapada areas of Orissa. Besides, the *Cardamom sp.* was also procured from Calicut, Kerala. Twenty species were identified and some were locally known as Krishna kedar, Garuda keder, Basu keder and Ram keder (having tribal medicinal use in snakebite) are maintained in the research garden at Regional Research Laboratory. Some identified species grown here are *Alpinia calcarata*, *Zingiber cassumunar*, *Curcuma montana* & *Zingiber rubens*. Two improved varieties of ginger (**Suravi** and **Suprava**) and four varieties of turmeric (Armoor, Rama PTS-14 and Surama) were collected from Pottangi, HARS Koraput.

Introduction and cultivation of local turmeric ginger, *Curcuma amada* Parashukedar were started in 1994. Its plant height, tiller number, yield and chlorophyll content of leaf were recorded and hydrodistillation of root, rhizome and leaf of turmeric, ginger, *A. calcaratas*, *Z. cassumunar* and *C. amada* were done and the oil percentage were calculated.

Zingiber officinale (Ginger)

Two experiments were conducted on ginger. One on the intercropping with cinnamon and another in the field. Yield data showed the poor growth

of ginger and the oil percentage was recorded in rhizome (0.38 % in fresh), traces in roots and no oil in the leaf. Oil content and oleoresin of an improved variety of ginger (**suparva**) was 0.75 per cent (dry wt. basis) and 7 per cent respectively. Oleoresin of local ginger was 6 per cent.

***Curcuma longa* (Turmeric)**

Turmeric plantation was done on 18th June 1994 and harvested during the month of January 1995. Rhizome yield varied from 210- 325 g/plant and per hectare yield was 11.74 t. Maximum oil content (1.32%) was recorded in dry leaves of turmeric and it varied from 0.812 to 1.85% and followed by rhizome (0.95% dry), and root (0.83% dry). The ratio of dry leaf to rhizome and root was 3:17:1 oil content and oleoresin of four improved varieties of turmeric were as follows; for Rasmi : 3 per cent and 11.1 per cent Ranga : 2.66 per cent and 8.7 per cent Rama : 2.77 per cent and 11.1 per cent and for Surama : 3.3 per cent and 15.1 per cent respectively. Oleoresin of local turmeric was 10 per cent.

***Curcuma amada* (Mango ginger)**

Curcuma amada plantations were done on 11th June 1994 and harvested on 3rd June 95. Rhizome varied from 310-560 g/plant and the plot yield indicated 30.45t/ha. In *C. amada* rhizome oil content was maximum (0.34% dry) followed by root (0.08%) but in leaf it was in traces. Oleoresin content was 7.4%.

Zingiber cassumunar

In *Z. cassumunar* highest oil content was recorded in rhizome (1.05% dry) followed by root (0.94% dry) but no oil was found in leaf.

Alpinia calcarata

In *A. calcarata* highest oil percentage was recorded in root and it varied from 0.25-0.28% followed by rhizome (0.17- 0.25%) leaf (0.07 - 0.10%) and found traces in stem (Rath *et al.* 1994). Except ginger, turmeric, *C. amada*, *Z. cassumunar* and *Alpinia* showed a good yield in the lateritic soil of Bhubaneswar. All the plant parts produced aromatic oils on hydrodistillation except the leaves of ginger and *Z. cassumunar*. The identification of chemical composition of the oils are yet to be studied. Considering the growth, biomass, oil yield and oleoresin content of Zingiberaceous plants in the introductory trials turmeric, *C. amada*, *Z. cassumunar* and *Alpinia calcarata* provided scope for further investigation to establish its economic potential. The future phytochemical investigation will be useful for industrial use of these oils. The

identification of unknown species may help in getting new sources of raw materials for food, beverage, cosmetics and pharmaceutical products.

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Short Communication

COLLECTION AND CHARACTERIZATION OF POMEGRANATE GERMPLASM FROM HIMACHAL PRADESH

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Key words : Pomegranate, germplasm, diversity, promising genotypes

The pomegranate (*Punica granatum*) is said to be indigenous to Iran and is also grown to some extent in India (Patil and Karale, 1985). It is one of important arid fruit crops of commercial significance. Rich genetic diversity occurs in parts of Himachal Pradesh (Solan, Sirmaur, Shimla districts) due to natural crossing and perpetuation through seed (Gammie and Patwardhan, 1929). The variability in landrace/forms is prevalent in diverse agro-ecological conditions from very high to low rainfall areas. Undulating topography of the terrains has diversified the nature of native variability tremendously. Several factors including deforestation and natural calamities pose great threat to its survival. Therefore, the exploration was undertaken to collect the pomegranate variability from this region.

Regions surveyed and sampling strategies

An exploration was undertaken in collaboration with Department of Fruit Breeding, YSPUH&F, Nauni, Solan during the month of August, 1994 for collection of pomegranate germplasm. The areas covered include parts of district Sirmaur, Bilaspur, Solan and Shimla of Himachal Pradesh (Fig 1) representing varying soil, edaphic factors and cropping systems. Random as well as biased sampling (Sinha, 1981) were followed for gene pool sampling and to collect information (Arora, 1981) on the crop diversity and exploration route. Data on five randomly picked fruits in each genotypes were recorded for fruit length (cm), fruit diameter (cm), average fruit weight (g), aril length (cm), aril breadth (cm), total soluble solids and other characteristics (Table 1). The mature cuttings were collected and being propagated at the Department of Fruit Breeding, Dr Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan for further evaluation and maintenance of germplasm.

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Table 1. Fruit characteristics of pomegranate germplasm collected from Himachal Pradesh August, 1994

NIC Numbers	Size	Shape	Fruit Characteristics Surface colour	Calyx	Rind thickness	Aril boldness	Aril colour- ration	Fruit length (cm)	Fruit diam- eter (cm)	Fruit weight (g)	TSS (Brix)	Aril length (cm)	Aril breadth (cm)
NIC-23343	Small	Pear	Golden	Fully open	Thin	Bold	> 50%	4.36	4.20	44.33	11.20	0.85	0.59
NIC-2334	Medium	Round	Light yellow	Slightly open	Thick	Medium	20%	4.44	4.64	57.67	11.20	0.90	0.54
NIC-23345	Medium	Round	Yellow green	Open	Thick	Bold	> 90%	4.45	4.49	58.60	12.40	0.87	0.61
NIC-23346	Small	Flatten	Deep red	Open upwards	Thick	Bold	> 50%	4.71	4.10	48.77	13.10	0.85	0.61
NIC-23347	Medium	Round	Light green	Close	Thick	medium	Nil	5.05	4.56	56.97	9.90	0.85	0.52
NIC-23348	Medium	Guava	Golden yellow rough surface	Semi opened	Thick	Medium	> 90%	4.03	3.86	46.55	12.30	0.73	0.48
NIC-23349	Medium	Round	Light green, red blushed	Slightly open	Thick	Medium	> 20%	4.99	4.71	68.94	13.07	0.86	0.53
NIC-23350	Medium	Pear	Golden yellow, red stringed	Slightly open	Very thick	Bold	Nil	4.65	4.11	58.83	13.00	0.75	0.53
NIC-23351	Medium	Round	Light green, light red blush	Small open	Thin	Medium	> 10%	4.59	4.66	60.33	11.33	0.80	0.61
NIC-23352	Medium	Round	Yellow, slightly rough	Open outwards	Thick	medium	> 20%	4.98	4.88	86.20	14.27	0.88	0.63
NIC-23353	Small	Round	Deep red blush	Open outwards	Thin	Bold	25%	4.00	3.84	50.33	9.40	0.79	0.52
NIC-23356	Medium	Round	Light green, rough surface	Open	Thin	Bold	> 50%	4.72	4.81	67.50	10.53	0.87	0.57
NIC-23357	Small	Round	Golden	Slightly open	Thin	Bold	Nil	4.42	4.37	50.00	12.53	0.90	0.57

(Table 1 contd.)

Table 1. contd.

NIC-23358	Small	Round	Light red, smooth	Slightly open	Thin	Bold	Nil	4.62	4.86	61.67	12.47	0.91	0.63
NIC-23359	Medium	Oval	Light yellow, slightly bluish	Close	Thick	Medium	Nil	5.00	4.73	55.43	12.87	0.99	0.61
NIC-23360	Large	Flatten	Light red, smooth surface	Open	Thin	Bold	Nil	5.63	5.23	84.33	11.53	0.88	0.61
NIC-23361	Small	Round	Golden, slightly surface	Slightly open	Very thick	Bold	20%	4.15	4.11	58.83	15.50	0.82	0.63
NIC-23362	Small	Guava	Golden yellow, rough	Fully open	Thick	Medium	> 90%	4.71	4.33	40.66	13.27	0.84	0.58
NIC-23363	Medium	Pear	Golden yellow, red bluish	Open upwards	Thin	Bold	> 90%	5.13	4.89	71.67	14.83	0.96	0.61
NIC-23364	Medium	Guava	Dull yellow, rough surface	Open towards	Very thick	Small	Nil	5.29	4.52	64.83	9.20	0.80	0.54
NIC-23365	Medium	Round	Light yellow, smooth surface	Open upwards	Thick	Medium	> 20%	4.99	4.65	60.43	12.30	0.87	0.58
NIC-23367	Medium	Round	Golden yellow	Open	Thin	Small	> 90%	4.61	4.76	68.50	13.97	0.94	0.63
NIC-23368	Small	Round	Light green, rough surface	Open	Thin	Medium	Nil	3.48	3.76	47.50	14.17	0.74	0.50
NIC-23369	Small	Pear	Light red, slightly rough	Small open	Thin	Small	> 20%	4.14	3.94	60.00	13.40	0.84	0.57
NIC-23370	Small	Round	Light yellow, smooth surface	Open upwards	Thick	Bold	> 10%	4.52	4.21	59.83	15.67	0.79	0.58

(Table 1 contd.)

Table 1. contd.

NIC-23371	Medium	Flatten	Light red, smooth surface	Open	Thick	Bold	> 40%	4.51	3.92	44.33	11.57	0.86	0.53
NIC-23372	Small	Flatten	Golden, deep red bright blush	Fully open	Very thick	Bold	20%	3.74	3.73	40.17	13.00	0.84	0.61
NIC-23373	Medium	Round	Pale yellow	Fully open	Thin	Medium	40%	5.26	4.60	68.27	15.73	0.87	0.60
NIC-23374	Small	Round	Golden, deep red blush	Slightly open	Thick	Medium	Nil	4.13	3.80	36.17	12.27	0.77	0.40
NIC-23375	Medium	Oval	Light red	Medium close	Thick	Medium	> 10%	4.41	4.05	41.92	13.10	0.80	0.64
NIC-23376	Medium	Round	Deep red, smooth surface	Fully open	Thick	Bold	> 50%	4.49	4.20	58.83	15.50	0.82	0.63
NIC-23377	Small	Oblong	Pale yellow slightly rough	Fully open	Thick	Bold	> 50%	3.81	4.03	38.83	12.03	0.91	0.59
NIC-23378	Medium	Round	pale yellow, light red blush	Close	Thick	Bold	Nil	4.90	5.03	38.83	12.03	0.91	0.59
NIC-23379	Medium	Round	Light green, bright	Slightly open	Thin	Bold	> 90%	4.98	4.88	62.33	13.53	0.74	0.53
NIC-23380	Large	Round	Golden	Open	Thin	Bold	> 90%	5.17	5.59	111.67	12.73	0.90	0.60
NIC-23382	Medium	Round	Light green slightly rough	Slightly open	Very thick	medium	> 10%	4.60	4.53	60.94	11.77	0.77	0.54
NIC-23386	Large	Oval	Light green, slightly rough	Close inwards	Thick	Bold	> 20%	5.38	5.67	89.67	12.90	0.87	0.54

(Table 1 contd.)

Table 1. contd.

NIC-23387	Small	Guava	Light green, light red blush	Fully open	Thin	Small	> 90%	3.60	3.43	51.70	13.80	0.84	0.65
NIC-23388	Large	Pear	Pale yellow, red streaks	Slightly open	Very thick	Bold	> 90%	5.64	4.85	74.83	11.53	0.86	0.53
NIC-23389	Large	Round	Light yellow	Slightly open	Thin	Bold	> 50%	5.16	4.51	61.50	14.60	0.79	0.57
Range	Minimum							3.49	3.43	36.17	9.20	0.73	0.40
	Maximum							5.64	5.67	111.67	15.50	0.99	0.64
Mean								4.64	4.45	197.06	12.73	0.84	0.57
S.E.m								0.12	0.12	2.98	0.45	0.01	0.01
C.D. at 5%								0.03	0.03	0.82	0.12	0.002	0.002

Extent of variability

Fourty distinct genotypes of pomegranate identified based on the fruit morphological characteristics are located in Solan (20), Sirmaur (15), Shimla (4) and Bilaspur (1) districts of Himachal Pradesh. Pomegranate diversity was more concentrated in Solan, Sirmaur and part of Shimla districts because of semi arid climate and red laterite soil which may be suitable for its growth. Most of old plants in forest were seedling origin and considerable variability in morphological characters exhibited including the TSS content (Table 1). It was also observed that the seedling trees were less susceptible to diseases, insects and had also longer life. The fruit length varied from 3.48 cm (NIC-23368) to 5.64cm (NIC-23388); fruit diameter from 3.43 cm (NIC-23387) to 5.67cm (NIC-23386); fruit weight 36.17g (NIC-23374) to 11.67g (NIC-23380); TSS from 9.20 (NIC-23364) to 15.50 (NIC-23376); aril length 0.73 cm (NIC-23348) to 0.99 cm (NIC-23359) and aril breadth 0.40 cm (NIC-23374) to 0.64 (NIC-23375).

Promising collections

Genotype (NIC-23387) sampled from road side near Falcon restaurant, Kandaghat, Solan bear small size, guava shape fruit, surface light green with light red blushed, calyx fully developed, early maturing and having less infestation of fruit fly. The genotypes NIC-23380, NIC-23388 were also observed to e promising for large to extra large fruit size, smooth to rough fruit surface with deep red colour alongwith very attractive pink flesh. The forest zone of Narang (Sirmaur district) and Basantpur (Shimla district) possesses natural vegetation of pomegranate needs fine grid survey for the collection of landraces/genotypes variability.

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Short Communication

**VARIATION IN KERNEL CHARACTERS OF SEEDLING *
WALNUT TREES (*JUGLANS REGIA* L.) OF DIFFERENT AGES**

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Key Words : Walnut, variation, kernel characters

The kernel characters are of great economic importance in walnut. Kernels of walnut vary from relatively thin to very plump forms. It is desirable to have kernel which fill the nut cavity and should not be so tight that it becomes difficult to extract them from the nut. A well filled nut with some space remaining between the kernel and the shell is preferred.

The kernel characters are becoming increasingly important in view of the fact that in the international markets, increasing quantities of produce is going as kernel rather than in shell nut (Forde, 1975). Walnut in India is mostly grown in hilly areas and to transport the produce to main markets, involves heavy transportation cost. To overcome this, emphasis should be given to marketing of kernels instead of shell nut. Keeping in view the significance of the kernel characters in the present day marketing, it is essential to select walnut seedlings not only on the basis of nut characters but also on kernel characters. With these objectives, the studies were undertaken to study variation in kernel characters of seedling walnut trees of different ages. The present studies were conducted in 1995 and 1996 in Jaunaji area of district Solan in Himachal Pradesh (India) which is located at latitude 30°50'N and 77°08'E and elevation from 1400 to 1600 meters above mean sea level. Of a total population of 500 seedling walnut trees, 125 were selected on the basis of preliminary information obtained from the growers in different villages. The detailed observations were recorded on these 125 seedling trees which were scattered in 15 villages.

Data on kernel characters were recorded (UPOV, 1988). Thirty nuts were sampled from all sides of the tree for recording data for each tree. Data of metric characters were analysed statistically (Panse and Sukhatme, 1957).

RESULTS AND DISCUSSION

The data on kernel characters *viz.* - percentage, weight, length, width and breadth are presented in Table 1.

Table 1. Variation in kernel characters of different seedling walnuts of different ages

Kernel characters	Mean	Range	Coefficient of variation	Standard deviation	Standard error	Critical differences
Age Group 1 (Upto 20 years)						
Percentage	39.18	26.27-68.17	21.78	8.53	1.27	2.57
Weight (g)	4.15	2.34-6.31	19.99	0.83	0.12	0.25
Length (cm)	2.62	1.62-3.31	14.36	0.37	0.06	0.11
Width (cm)	1.93	1.04-3.25	15.74	0.30	0.04	0.09
Breadth (cm)	2.24	1.12-3.17	16.85	0.38	0.06	0.11
Age Group 2 (21-40 years)						
Percentage	38.05	20.67-59.24	19.63	7.47	1.11	2.25
Weight (g)	4.01	2.58-6.13	21.40	0.86	0.13	0.26
Length (cm)	2.59	1.72-3.11	12.38	0.32	0.05	0.10
Width (cm)	1.87	1.26-2.41	14.75	0.28	0.04	0.08
Breadth (cm)	2.30	1.12-2.99	18.21	0.42	0.06	0.13
Age Group 3 (above 40 years)						
Percentage	36.63	11.51-49.55	16.54	6.06	1.05	2.15
Weight (g)	4.10	1.38-6.26	23.17	0.95	0.16	0.34
Length (cm)	2.47	1.83-3.10	11.84	0.29	0.05	0.10
Width (cm)	1.91	1.19-2.59	15.12	0.29	0.05	0.10
Breadth (cm)	2.27	1.29-2.98	16.39	0.37	0.06	0.13

As far as ease to kernel removal is concerned, six trees had easily extractable nuts. Forty six tree were placed under easy, 45 under medium, 23 under difficult and 5 were under very difficult category. Intensity of colour was also studied; the kernel colour was dark in the nuts of 23 trees, very

dark in 7 trees, medium in 60 and very light colour in 35 trees. Kernel taste and flavour was adjudged by a panel of judges and depending upon the score out of 10 marks, the trees were categorised poor (5.5 and less), fair (5.6-7.0) and good (above 7.0). The kernels of 16 trees were having poor, 58 pair and 51 were of good quality in respect of taste and flavour.

The kernel characters vary considerably among 125 seedling walnut trees studied. The kernel percentage in the present studies ranged from 11.51 to 68.17, whereas the values were reported from 28.84 to 64.33 per cent by Chauhan and Sharma (1979) and 24.08 to 52.65 per cent by Sharma and Chauhan (1980). The kernel weight ranged from 1.38 to 6.31 g in the present study whereas Rathore (1984) reported to vary from 1.2 to 4.6 in an elevation study of 22 walnut accessions. Similar variation was also reported by many workers in respect of kernel characters (Nauriyal *et al.*, 1970; Motiyal and Gilkar, 1970; Barton 1979; Komanich, 1980; Pandey and Sinha, 1984; Thakur, 1993). This variation in the present studies and as reported by earlier workers may be due to genetic differences in the make up of these seedling trees. Moreover, most of these characters are polygenically controlled and are greatly influenced by the environmental factors which are prevailing in different areas where such studies were conducted.

It revealed from present studies that the age of the tree has some influence, although it was inconsistent and inclusive in the present case. However, kernel percentage was diminished with the increase of age of the tree. Similarly Nenyukhim (1972) reported that the population of different ages showed the species to be very polymorphic. There was a clear tendency for the number of large nuts, weight and thickness of shell to diminish with the age.

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PLANT GERMPLASM REGISTRATION NOTIFICATION*

The germplasm registration recently introduced by the Indian Council of Agricultural Research (ICAR), being implemented by the National Bureau of Plant Genetic Resources (NBPGR), provides a mechanism of getting valuable plant genetic resources recognised for its claimed attributes, provided adequate evidence for such claim is available and it has been characterised for its distinctive traits. The seed, propagules and specimen plants of registered germplasm are conserved in the National Gene Bank for long term. The source and donor of each registered germplasm is accorded due recognition by way of this registration. The responsibility of the distribution of registered germplasm to the user community lies with the donor scientist/institution. The germplasm Registration Committee of the ICAR in its first meeting held on October 27, 1997 at NBPGR approved the registration of seven germplasm lines out of the 93 proposals received. The details on the germplasm lines registered are summarised below :

INGR 97001 is a leafletless, powdery mildew resistant, high yielding, dual purpose pea (*Pisum sativum* L.) designated as **Jayanti (HFP 8712)**. This variety was developed jointly by R.K. Yadav, V.P. Singh, R.K. Chowdhary, B.P.S. Malik, Y.S. Tomar and Mehar Singh at Pulses Section, Department of Plant Breeding, CCS HAU, Hisar by crossing Aparna with PG3. INGR 97001 was approved on the recommendations of crop specialists and registered by ICAR committee on Plant Germplasm Registration in a meeting held on 27th October 1997.

INGR 97002 is a dwarf, leafletless, powdery mildew resistant pea (*Pisum sativum* L.) designated as **Uttra (HFP 8909)**, developed jointly by R.K. Yadav, V.P. Singh, R.K. Chowdhary at Pulses Section, Department of Plant Breeding, CCS HAU, Hisar. INGR 97002 is a result of crossing EC1109185 with HFP4 and was approved on the recommendations of crop specialists and registered by ICAR committee on Plant Germplasm Registration in a meeting held on 27th October 1997.

INGR 97003 is a pentafoolate mung bean (*Vigna radiata* L. Wilczek) designated as **Pentafoolate** with five small leaflets. The variant is of academic and practical importance. It was developed jointly by V.P. Singh, R.K. Yadav and R.K. Singh at Department of Genetics, CCS, HAU Hisar. INGR 97003 is result of hybridisation between LM696 and ML33 followed by selection in segregating generation. INGR 97003 was approved and recommended for

*Communicated by Director, NBPGR, New Delhi 110 012

registration by ICAR committee on plant Germplasm Registration in a meeting held on 27th Oct. 1997.

INGR 97004 is first genetic male-sterile line of cotton (*Gossypium arboreum* L.) designated as **a-GMS 1 DS-5**. This genetic stock is stable and usable for economic hybrid seed production of diploid cultivated cotton. Gene symbol is designated as $ams_1\ ams_1\ 1$ (recessive gene pair) for male sterile condition and $aMs_1\ ams_1$ for fertile heterozygous gene pair. The original male sterile single plant was identified in Desi Cotton (*G. arboreum* L.) var *DS-5* of race *bengalense* by V.P. Singh, B.P.S. Lather and R. Kumar at CCS HAU, Hisar. INGR 97004 was approved by crop specialists and recommended for registration by ICAR committee on plant Germplasm Registration in a meeting held on 27th Oct. 1997.

INGR 97005 is a heat and drought tolerant germplasm of wheat (*Triticum aestivum* L.) designated as **Hindi 62** and identified by Genetic Resources Unit of DWR Karnal. INGR 97005 was approved on the recommendations of crop specialists and registered by ICAR committee on Plant Germplasm Registration in a meeting held on 27th October 1997.

INGR 97006 is a genetic stock of mustard (*Brassica juncea*) designated as of **CMS Trachy (Restorer)**, with restorer gene and recombinant mitochondrial genome. The restorer gene is in heterozygous condition and the mitochondrial genome is derived from the somatic hybrid *Trachystoma ballii* + *B. juncea*. This stock was jointly developed by P.B. Kirti, Shyam Prakash, S.R. Bhat, V. Dinesh Kumar and V.L. Chopra at NRC on Plant Biotechnology, IARI, New Delhi. INGR 97006 was approved on the recommendations of crop specialists and registered by ICAR committee on Plant Germplasm Registration in a meeting held on 27th October 1997.

INGR 97007 is a cytoplasmic male sterile line of mustard (*Brassica juncea*) designated as **CMS Trachy**, carrying recombinant mitochondrial genome derived from the somatic hybridization of *Trachystoma* and *Brassica juncea* followed by repeated back crossing of the somatic hybrid with *Brassica juncea* cv Pusa Bold. The CMS line was developed at NRC on Plant Biotechnology, IARI New Delhi by P.B. Kirti, Shyam Prakash, V.L. Chopra and T. Mohapatra. INGR 97007 was approved on the recommendations of crop specialists and registered by ICAR committee on Plant Germplasm Registration in a meeting held on 27th October 1997.

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