

Improvement in Pearl Millet Grain and Stover Yields through Hybridization between Indian and African Germplasm under Arid Zone Conditions

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(Received: 24 October 2011; Revised: 10 July 2012; Accepted: 13 July 2012)

Pearl millet (*Pennisetum glaucum*) is valued for both grain and stover in arid and semi-arid regions. This study was designed to measure the magnitude of improvement for grain and stover yields in crosses between Indian landrace-based populations and African composites. Twenty crosses produced from four landrace populations and five elite composites were evaluated for four seasons under rainfed conditions of arid zone. Improvement in crosses was measured as percent increase (referred to as heterosis) in cross performance over landrace parent. There was differential expression of heterosis for different traits. Heterosis in individual crosses was between +32% to -6% for grain yield, +62% to -14% for stover yield and +48% to -10% for biomass. Positive heterosis for biomass resulted into positive heterosis for both grain and stover yields. Contradictory contribution of heterosis for harvest index on grain yield and stover yield heterosis was observed. Only those crosses that had a combination of high heterosis for biomass with no negative heterosis for harvest index resulted into positive heterosis for grain and stover yields.

Key Words: Arid zone, Drought, Heterosis, Landraces, Pearl millet, *Pennisetum glaucum*

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] grain forms the staple diet of human and its stover is the basis of ration for large ruminants in crop-livestock farming systems of arid and semi-arid regions of north western India and Sub-Sahara Africa where other cereal crops, such as maize or sorghum are not cultivable. These regions are highly prone to drought of unpredictable intensity and duration and have native soils with low fertility in addition to having high temperatures and greater evaporative demand during the crop season. Such climatic and adaphic conditions result into extremely stressful crop growing environments and render arable cropping a risky proposition especially in northwestern India.

As a strategy to minimize the risk of crop failure under prevalent harsh environmental conditions, drought resilient pearl millet landraces are conventionally grown by farmers. However, this strategy is likely to be at the cost of harvestable yields in more favourable years, as landraces often lack sufficient yield potential to fully exploit improved levels of inputs (Yadav *et al.*, 2004; Yadav and Bidinger, 2007; Yadav 2008). On the other hand, exotic germplasm originating from better-endowed environments, despite having a much higher yield potential, which is better expressed in favourable environment, does not have sufficient adaptation to

stress conditions to provide better yields than adapted germplasm under arid zone environments (Kelley *et al.*, 1996; Yadav and Weltzien, 2000; Christinck, 2002; Bidinger *et al.*, 2006). Thus these two groups of material with differential adaptation pattern to contrasting environmental conditions are complimentary to each other. Hence genetic diversification of Indian landraces through introgression of appropriate germplasm from African regions has been suggested as a strategy to diversify the Indian pearl millet germplasm (Yadav and Bidinger, 2007; Yadav *et al.*, 2005; Prestrel and Weltzien, 2003) in order to amalgamate the drought tolerance of landraces and high yield potential of exotic materials. The guiding principal in this approach would be the magnitude of improvement over landraces in crosses between two groups of material. The present study was therefore undertaken to quantify the degree of improvement in crosses between Indian landraces and African composites under arid zone environments with respect to grain and stover productivity and to understand how heterosis in these traits is affected by heterosis in biomass and harvest index under arid zone conditions.

Materials and Methods

This study used four landrace-based populations from northwestern India and five very diverse elite composites developed mainly from African genetic material (Table 1). Landrace populations were chosen to represent

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Table 1. Origin details of Indian landrace-based populations and elite exotic populations used in the study

Parental populations	Origin
Landraces-based populations	
Jakharana	A dual-purpose landrace from eastern Rajasthan with long, cylindrical and thin panicles with a slight curved panicle
BarPop	Bred by inter-mating five selected, typical landraces from the Barmer district of Rajasthan
ERajPop	Bred from 30 S ₁ progenies from four early maturing landraces (IP 3188, IP 3228, IP 3246 and IP 3464) from Rajasthan and improved by several cycles of recurrent selection
WRajPop	Bred from 13 selected, representative landrace accessions from North-western India and subjected to several cycles of improvement through recurrent selection
Exotic composites	
Smut Resistant Composite (SRC)	Composite bred from interpopulation crosses of Smut Resistant Composite (SRC) and intervarietal composite (IVC) which was developed by random mating 79 varietal crosses involving African and Indian germplasm.
Early Smut Resistant Composite (ESRC)	Composite developed by selecting for earliness in the initial bulk of SRC
Medium Composite (MC)	This composite is based on crosses of elite non-Togo material from ICMP 89410 with elite bold seeded early composite. This has African, Indian and Togo germplasm (Iniadi) in its parentage
Early Composite (EC)	Developed by random mating EC II, ICMV 87901, ICMV 87902 and ICMV 87119
Bold Seeded Early Composite	It is a composite mainly based on Iniadi landrace germplasm from Togo and Ghana

a gradient from elite landrace-based populations to unimproved types. Jakharana, a dual-purpose landrace from eastern Rajasthan, represented the improved type of landrace in terms of productivity and disease resistance. BarPop, on the contrary, represented unimproved typical landrace population from western Rajasthan. ERajPop and WRajPop were made from a small number of carefully selected landrace accessions from Rajasthan, with WRajPop having a geographic focus and ERajPop having a maturity focus. Five exotic elite composites were based on early- to medium-maturing Togo and non-Togo material from Africa (Table 1).

Four landrace populations were crossed using hand pollination with each of five elite populations to produce 20 crosses. In each population, at least 100 plants were used in attempting each cross in order to sample variation from parental populations. These crosses together with nine parental populations were evaluated for their performance at the Central Arid Zone Research Institute, Jodhpur under rainfed conditions of rainy seasons, during 1999-2003 (except 2002 when season was lost due to failure of rains) in Randomized Block Design with three replications. Each entry was grown in four rows at a spacing of 60 cm in 4 m long row. The plots were over sown with a tractor-drawn planter and then thinned to a plant-to-plant spacing of 15 cm within

two weeks of sowing. Trials received 20 kg/ha N and 8 Kg/ha P₂O₅ at sowing and an additional 20Kg/ha N was top dressed 3-4 weeks after sowing. Weeds were controlled with two manual weedings.

Flowering was recorded on plot basis as number of days taken from sowing to the emergence of stigma in the main shoot panicle of 50% plants in a plot. All the panicles from entire plot were harvested at maturity and were dried for two weeks before weighing and threshing. Both grain and dry stover weights were recorded on plot basis. To obtain total biomass, dry panicle weight and stover weight were added. The harvest index was calculated as ratio of grain to biomass and was expressed in percentage.

Data of all traits were subjected to both individual environments and across-environment analysis of variance. Heterosis was calculated as percent increase/decrease in the performance of cross over its landrace populations which is the relevant comparison for the question of increasing grain and stover productivity over currently available farmers' open-pollinated cultivars as it measured the potential exploitable gain in productivity of crosses over traditional landraces. Effect of heterosis for biomass and harvest index on grain yield heterosis and stover yield heterosis was studied through correlation analysis.

Results and Discussion

Environmental and genotypic effects

The four growing seasons had a considerable variation in grain productivity ranging from 32 g m⁻² to 216 g m⁻² covering full range in expected grain yields under rainfed conditions of arid zone. Thus the results obtained in this study would be applicable in a range of environmental conditions of arid zone.

The mean squares due to genotypes were highly significant for all traits. For grain and stover yields and total biomass, genotypes sums of squares (SS) could account for only up to 10% of fraction of total SS. Genotypes, however, accounted for 24% and 43% of variation for days to flower and harvest index, respectively. This observation also explains the historical reason for manipulating crop duration and biomass partitioning rather than grain yield *per se* to enhance the pearl millet productivity in arid zone, though the higher grain at the cost of stover has little relevance for arid zone (Bidinger *et al.* 2006).

Magnitude of heterosis in crosses

Within genotypes, mean squares due to parental populations and their crosses were significant for all traits suggesting that there occurred adequate genetic differences both within populations and crosses for all the measured traits. These effects were further modified by environments as indicated by significant interaction of each component with environment.

There was differential expression of heterosis for various traits (Table 2). Mean heterosis ranged from 17% for stover yield to 0.3% for harvest index. Heterosis estimates for pearl millet in the literature vary widely, depending upon the type of parental materials used and the type of crosses from which heterosis was estimated (Virk, 1988). Highest heterosis estimates (>100%) are based on single cross hybrids made with highly inbred parents (Virk, 1988) which are often very low yielding due to inbreeding depression. However, estimates of grain yield heterosis (hybrid vs. pollinator) of topcross hybrids made with non-inbred Indian and African population parents are in the order of 20–40% (Mahalakshmi

Table 2. Mean heterosis (%) across four seasons for grain yield, stover yield, biomass, harvest index and days to flower in twenty crosses between four Indian landraces and five African elite populations

Cross (landrace x elite population)	Heterosis (%) over landraces for				
	Grain yield	Stover yield	Biomass	Harvest index	Time to flowering
Jakharana x SRC	32.25 **	51.30 **	41.89 **	-5.01	2.29
Jakharana x ESRC	20.43 *	62.31 **	48.37 **	-8.19	2.99
Jakharana x MC	5.05	37.84 *	22.63 *	-13.15 *	3.35
Jakharana x EC	3.36	24.38	14.58	-3.99	-0.35
Jakharana x BSEC	14.21	22.35	17.84	4.49	-0.53
BarPop x SRC	-6.38	18.29	12.1	-10.3	5.62 *
BarPop x ESRC	-4.15	7.32	5.4	-9.02	4.92 *
BarPop x MC	-12.95	3.35	-1.03	-14.99	6.85 **
BarPop x EC	-3.23	17.38	9.8	-11.49	6.15 *
BarPop x BSEC	17.95	14.94	15.41	8.46	0.35
ERajPop x SRC	36.35 **	20.42	21.94 *	1.82	5.97 *
ERajPop x ESRC	21.64 *	21.13	26.85 *	-0.17	8.58 **
ERajPop x MC	9.36	13.73	10.09	-1.04	7.84 **
ERajPop x EC	-3.61	18.66	11.49	-5.54	6.16 *
ERajPop x BSEC	8.65	-0.71	2.67	11.81	0.19
WRajPop x SRC	13.55	2.31	3.93	14.85	-0.7
WRajPop x ESRC	13.06	17.63	17.79 *	3.63	1.74
WRajPop x MC	2.79	1.45	2.39	13.92	-0.7
WRajPop x EC	4.78	1.16	-0.09	5.85	-2.43
WRajPop x BSEC	11.02	-14.45	-10.2	23.81 *	-2.61
Mean	9.21	17.00	13.69	0.29	2.78

*, ** significant at P<0.05 and 0.01, respectively

et al., 1992; Yadav *et al.*, 2000; Bidinger *et al.*, 2005). These are comparable to mean grain yield heterosis estimates derived from population crosses Prestrel and Weltzien, 2003; Ouendeba *et al.*, 1993). Level of heterosis observed in the present study thus compared well with those reported in literature in crosses between open-pollinated non-inbred materials; though average level of heterosis was low mainly because of positive and negative heterosis values balanced each other out (Table 2). Individual cross heterosis was positive, though not necessarily significant, in the most of crosses for grain yield, stover yield and biomass. In contrast, heterosis was positive in only half of the crosses for harvest index and in one-fourth of crosses for days to flower.

Mean grain yield heterosis was positive (9%) and there was significant and positive grain yield heterosis in four crosses (Table 2). The best combination was ERajPop x SRC, with an overall yield heterosis of +36%. The other three combinations had a heterosis of +20% to +32%. These data indicated that it is possible to identify crosses of landrace and exotic population with useful levels of positive heterosis for grain yield. All four crosses that had positive and significant heterosis for grain yield also had positive significant heterosis for biomass. However the converse was not true. Out of six crosses that had significant heterosis for biomass, only four had a positive heterosis for grain yield. Of the remaining two, high biomass heterosis in cross Jakharana x MC was accompanied by significant negative heterosis for harvest index. While in other cross *viz.*, WRajPop x ESRC, the moderate level of heterosis for biomass came with no heterosis for harvest index. Thus positive heterosis of grain yield was not exclusive due to biomass heterosis but also depended upon heterosis for harvest index. Only those crosses that had a combination of high heterosis for biomass with no negative heterosis for harvest index only resulted into positive heterosis for grain yield. The role of heterosis for biomass and harvest index was more critically examined by studying the relationship of grain yield heterosis with heterosis for biomass and harvest index. Variation in grain yield heterosis was accounted for by biomass and harvest index heterosis by 36% and 11%, respectively (Fig. 1), both contributing positively to grain yield heterosis.

The overall heterosis for stover yield was positive (17%) ranging from +62% (Jakharana x ESRC) to -14% (WRajPop x BSEC) (Table 2). All but two crosses showed positive heterosis for stover yield, three of them

showing significant heterosis over landraces. Positive heterosis for stover yield was strongly associated for positive heterosis for biomass (Fig. 1). The variation for biomass heterosis accounted for 92% of variation in stover yield heterosis. However, higher heterosis for harvest index resulted into negative heterosis for stover yield ($r^2 = 33\%$). These data suggested that improving harvest index might not be a viable strategy in breeding for arid zone areas where pearl millet stover is as important as grain, especially in drought years (Kelly *et al.*, 1996). In contrast, the major gains in grain yield of pearl millet in favourable areas have been achieved through greater partitioning of biomass to grain, rather than increasing the overall biomass (Ouendeba *et al.*, 1993). This is one of main reasons of low adoption of improved cultivars of pearl millet in arid zone of India despite their large scale adoption elsewhere (Kelley *et al.*, 1996; Christinck, 2002) as there is often a trade-off between high grain yield and stover yield in modern cultivars.

Individual cross heterosis for biomass was positive in most of crosses with mean heterosis being 14% (Table 2). Negative heterosis was uncommon occurring only in two crosses. This magnitude of improvement in biomass is very encouraging as previous genetic studies suggest that the improvement of biomass productivity by conventional plant breeding, without extending crop duration, is likely to be slow, especially under marginal conditions. For example, Rattunde and Witcombe (1993) reported average gains in biomass after three to four cycles of recurrent selection for improved grain yield in four populations of only 2.3% per cycle measured under terminal stress conditions. These increases translated to a 2.5% gain in grain yield and 0.5% gain in stover yield per cycle. Such results would be expected physiologically, as growth rate or biomass productivity is a not a simple genetic trait, but the result of the interaction of many underlying, complex factors (canopy development, radiation interception, radiation use efficiency, respiration rate, etc.). The varying effects of stress on the individual components of overall biomass productivity further complicate attempts at genetic improvement of biomass productivity in marginal environments. Growth rate/biomass productivity in pearl millet appears to be governed mainly by non-additive gene effects (Lynch *et al.*, 1995; Gupta and Phul, 1981) and heritabilities for biomass productivity are modest (Rattunde *et al.*, 1989). Thus exploiting heterosis appeared more effective and rapid way to improve biomass yield in pearl millet under

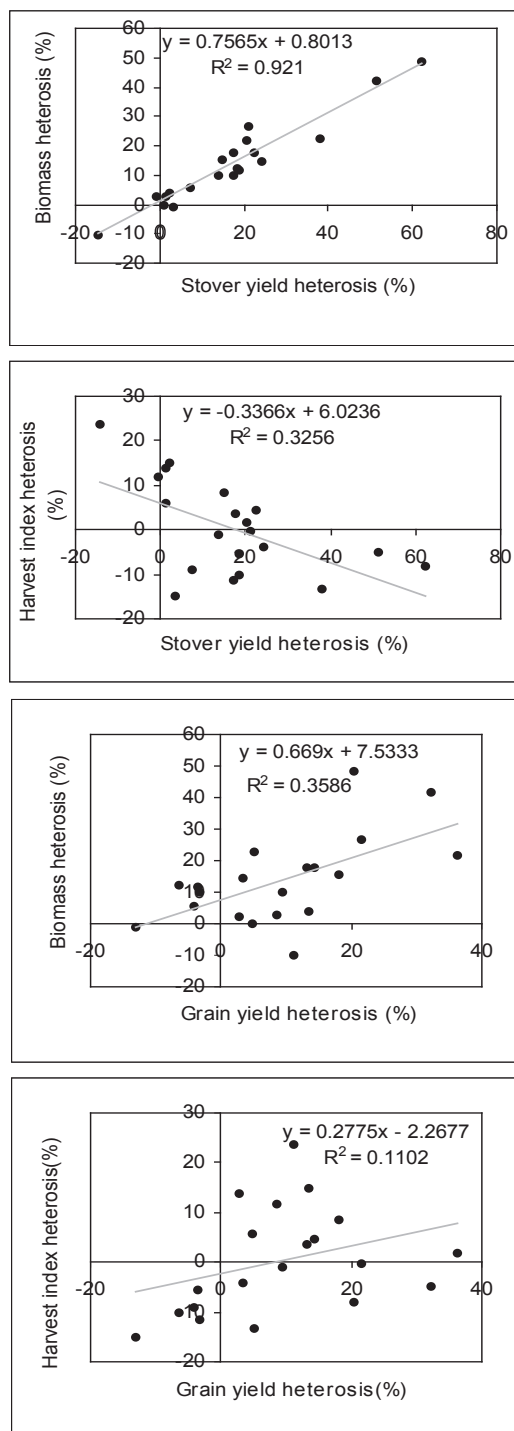


Fig. 1. Heterosis for grain and stover yields of pearl millet as influenced by biomass and harvest index heterosis

marginal conditions of arid zone. Heterosis estimates obtained in the present study are similar to biomass heterosis observed in topcross hybrids produced by crossing male-sterile lines with landrace pollinators (Yadav *et al.*, 2000). The partitioning of this extra biomass

of hybrids to either grain or stover was controlled by the harvest index of the seed parent, resulting in differential heterosis for either grain or stover yields, depending upon the seed parent used.

Contradictory contribution of harvest index on grain yield and stover yield as observed in this study raises an important point. Improvement of grain yield in arid regions has to come without any adverse effect on stover yield as pearl millet stover is valued as important feed for ruminants in arid regions. Sale of animals and animal products is often the major source of household cash income in severe drought years (Hall *et al.*, 2004). The practical and more realistic strategy thus would be to enhance biomass yield maintaining the existing levels of harvest index. The data presented here clearly showed that this objective is possible to achieve as one-third of the crosses had positive and significant heterosis for biomass with all but one of them having non-significant heterosis for harvest index (Table 2). However, the biomass improvement has to be made without extending the crop duration to a great extent as increasing duration makes the crop more vulnerable to the end-of-season drought (Sastri *et al.*, 1982; van Oosterom *et al.*, 1995; van Oosterom *et al.*, 1996). Though half of the crosses had significant positive heterosis for days to flower, the magnitude of heterosis in these crosses was in the range of 5-8% which effectively means 2-3 days of additional flowering time in these crosses (with 40-45 days of flowering time) which might be of little practical value considering the magnitude of improvement in biomass and finally in grain and stover yields.

Two crosses (Jakharana x SRC and Jakharana x ESRC) which had a positive grain yield heterosis also exhibited positive heterosis for stover yield (Table 2). This is clearly a reflection of their better adaptation to arid zone conditions and of their ability to provide both enhanced grain and stover yields over landraces. This probably explains the reasons of introgression of modern cultivars into local landraces by some farmers in arid zone of north western India in order to enhance diversity within their landraces (Yadav *et al.*, 2009) and to increase the adaptive range of their seed stocks (Christinck, 2002).

The results of the present study showed that crosses between landraces and elite materials offer good opportunities for exploiting heterosis in arid zone environments. However, not all cross combinations had same benefit. Most importantly, the data clearly

demonstrated that it is possible to identify crosses made with adapted landraces and exotic populations that are statistically superior to the landrace populations both for stover and grain yield and expression of heterosis in biomass is most critical to enhance both grain and stover productivity.

Acknowledgements

This work was done under AP Cess Project (28-1/2000 FFC) funded by the Indian Council of Agricultural Research.

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Delineation of Navara Punja - a Unique Germplasm in *Oryza sativa* cv. Navara Complex in Kerala, India using Morphological and SSR Markers

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(Received: 26 December 2011; Revised: 12 July 2012; Accepted: 19 July 2012)

The diversity analysis among the indigenous medicinal rice germplasm of Navara (*Oryza sativa* L. cv. Navara) using morphological, biochemical and molecular parameters showed genetic polymorphism in this landrace. Germplasm characterization has been attempted using 35 qualitative and 48 quantitative traits and it revealed distinct variation for 6 vegetative and 10 reproductive qualitative traits. Analysis of variance for 48 quantitative traits showed significant variation ($P < 0.05$) for six traits within accessions viz. endosperm elongation ratio, number of leaves (40th day), leaf width, flag leaf width, panicle length and spikelet distance. Cluster analysis using qualitative and quantitative traits grouped Navara punja as a separate cluster. Protein (40.7mg/g) and total free amino acid content (2.06mg/g) was significantly high in accessions of Navara punja when compared to other ecotypes of Navara landraces and released varieties. High degree of polymorphism was exhibited by 27 SSR markers among Navara races. Unique bands of molecular weight 207.2bp were amplified from RM20 which delineated Navara punja from other Navara races. Results showed existence of a unique genotype in Navara germplasm namely Navara punja apart from Navara golden yellow and Navara black.

Key Words: Morphological evaluation, Navara germplasm, Navara punja, Nutritional traits, SSR

Introduction

Many of the Indian rice varieties have known medicinal properties which have been traditionally used in Ayurveda, Unani and by traditional healers for generations. India depends on this crop as a common man food and is also considered sacred in religious ceremonies in temples. In Kerala, the southernmost state in India, among the indigenous germplasm for medicinal rices, Navara is important as it is traditionally cultivated for ayurvedic medicine due to its properties in alleviating rheumatism and neural disorders (Sreejayan *et al.*, 2005). As per GI (Geographical Indication) registry, 2008, registration for this rice landrace was obtained as “Navara” by the Navara rice farmer’s society, Palakkad, Kerala and hence the epithet “Navara” (Yasodharan, 2008) is used in describing the landrace.

As most farmers are shifting to other cultivars of rice, availability of Navara is diminishing and the germplasm is becoming endangered. It is therefore necessary to collect, preserve and characterize Navara for increasing awareness among the people on the importance of this landrace.

Traditionally Navara rice has been classified as black and golden yellow on the basis of its glume color (Leena Kumary, 2004). Sreejayan *et al.* (2003)

classified Navara into 4 ecotypes viz. long yellow (Kuttanadan), short yellow (Palakkadan), intermediate yellow (Vadakkan) and short black (Wynadan). Apart from these landraces, Navara punja is a rare medicinal landrace found only in certain parts of northern Kerala especially Kannur and Kasaragod districts. Local farmers of this area consider this landrace as more superior to other Navara races.

Studies including morphological evaluation and SSR markers were carried out to characterize and analyze the genetic relationship of Navara germplasm with other traditional rice landraces (Mariet *et al.*, 2010). Though many attempts have been made to study the Navara germplasm in different perspectives (Menon and Potty, 1997, 1999, 2005; Sreejayan *et al.*, 2003, 2005; Jiji *et al.*, 2007; Sanal Kumar *et al.*, 2008, 2010) the existence of Navara punja, a unique race, in this complex has not been revealed till date. In this background, a biosystematic approach in studying the germplasm using morphological, biochemical and molecular traits has been undertaken to characterize and delineate Navara punja as a separate entity in Navara germplasm complex.

Materials and Methods

Germplasm of Navara along with three released cultivars

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viz. PTB-35 (Annapurna; PTB-20 X IR8), PTB-50 (Kanchana; Pavizham (HS) X IR36) and PTB-39 (Jyothi: PTB-10 X IR8) was procured from different agroecosystems of Northern Kerala. Locations were mapped using GPS and the germplasm was evaluated under organic farming in Randomized Block Design in triplicates for five consecutive seasons. In each season, data of five plants selected at random from each replicate was recorded and the average data from each season was analyzed. Germplasm characterization has been attempted using 35 qualitative and 48 quantitative traits following Standard Evaluation System for rice (IRRI, 2002). Qualitative and quantitative traits were classified into 155 and 121 sub traits respectively and their presence or absence was scored as 1 or 0. Data analysis has been carried out using NTSYS pc version-2.02i (Numerical Taxonomy and multivariate System) and SPSS-13.0 for qualitative and quantitative traits respectively. Analysis of variance (One-way ANOVA) was performed for 48 quantitative traits using SPSS 13.0. Biochemical analysis for primary metabolites viz. protein (Lowry *et al.*, 1951), total free amino acids (Lee and Takahashi, 1966), starch and total carbohydrates (Hedge and Hofreiter, 1962) were carried out to find variability in nutritional traits among Navara germplasm.

Young leaves of 20-day-old seedlings of various Navara races were used for genomic DNA isolation following the CTAB method (Doyle and Doyle, 1990). SSR analysis was carried out in order to determine the genetic uniqueness among different ecotypes of Navara complex. Twenty seven SSR markers (Ocimum Biosolutions, USA) were used for SSR analysis to find level of polymorphism among landraces.

Touchdown PCR (Applied Biosystems, USA) was performed for SSR analysis. PCR amplification profile has initial denaturation step of 95°C for 5min. It was followed by ten cycles of 94°C for 30 sec, 65°C for 30 sec and 72°C for 30sec with 10°C decrease in temperature per cycle. This was followed by 30 cycles of 94°C for 30 sec, 56°C for 30 sec and 72°C for 60 sec. Final extension was carried out at 72°C for 20 min and was held at 4°C. Amplified DNA fragments were subjected to electrophoresis with marker DNA of known molecular wt. (100-500bp) in 2.8% agarose gel at 6V/cm using 1X TAE buffer and Ethidium Bromide (0.5 µg/ml) was used for staining. Gel was viewed and photographed using gel documentation system (Syngene G-Box, USA). Data analysis was carried out using NTSYS-pc version 2.02i and Jaccard's similarity co-efficient generated were used in constructing dendrogram with UPGMA (Unweighted Pair Group of Arithmetic averages).

Results

The characterization and evaluation of the Navara germplasm at morphological, biochemical and molecular levels presented distinct variations and the results showed the delineation of Navara punja as a separate entity in Navara germplasm complex.

Locations from where the germplasm has been procured have been marked using GPS and the passport information is given in Table 1.

Morphological Characterization

Characterization of the germplasm for 35 qualitative traits revealed distinct variation for 6 vegetative and 10 reproductive traits. Erect leaves, partly exerted panicle,

Table 1. Passport information of germplasm analyzed

Sl. No.	IC Number/ other ID	Cultivar name	Regions explored	District	State	Latitude	Longitude	Altitude
1	539968	Navara black	Chitur	Palakkad	Kerala	10°41.534'	76°43.186'	289ft
2	539983	Navara golden yellow	Kolazhi	Thrissur	Kerala	10°59.319'	76°54.785'	642ft
3	86475	Navara black with awn	NBPGR regional station	Thrissur	Kerala	10°59.319'	76°54.785'	642ft
4	539998	Navara golden yellow	Thrikkaripur	Kasaragod	Kerala	12°08.055'	75°10.094'	274ft
5	557561	Navara punja	Morazha	Kannur	Kerala	11°59.259'	75°21.140'	152ft
6	557562	Navara punja	Morazha	Kannur	Kerala	11°59.259'	75°21.140'	152ft
7	557564	Navara punja	Kanul	Kannur	Kerala	11°59.620'	75°21.377'	160ft
8	557587	Navara black	Maruthur	Palakkad	Kerala	12°03.275'	75°15.693'	206ft
9	557588	Navara golden yellow	Malakakkattil	Palakkad	Kerala	12°03.275'	75°15.693'	206ft
10	PTB 35	Annapurna	Pattambi	Palakkad	Kerala	12°03.275'	75°15.693'	206ft
11	PTB 50	Kanchana	Chittur	Palakkad	Kerala	10°41.591'	76°43.275'	361ft
12	PTB 39	Jyothi	Pattambi	Palakkad	Kerala	10°41.591'	76°43.275'	361ft

golden yellow glume and light brown seed coat are the traits which showed variation in Navara punja (IC557561, IC557562, and IC557564). Negligible variations were also observed in collar color, blade color, apiculous color, internode color, coleoptile color, early plant vigor and root hairiness. Cluster analysis using UPGMA generated dendrogram with one base cluster dividing the germplasm into three clusters at 63% similarity (Fig.1). Jaccard's co-efficient of similarity ranged between 0.52 and 0.92. Navara black (IC539968 and IC557587) formed first cluster showing a similarity of 70%, whereas second cluster had all the released varieties (PTB35, PTB50 and PTB39). All the Navara punja accessions viz. IC557561, IC557562, and IC557564 formed third cluster. IC557561 and IC557564 presented a similarity of 90%, but IC557562 had only 82% similarity with these two accessions. Navara punja ecotypes showed 62% similarity with Navara black (IC539968 and IC557587), whereas it showed 70% similarity with IC539983 (Navara golden yellow) and 67.5% with IC557588 (Navara golden yellow). Genotype IC86475 (Navara black with awn) clustered separately at 52% and had the least similarity co-efficient with other cultivars.

Dendrogram generated based on 121 sub-traits of 48 quantitative characters revealed 2 major clusters at a similarity coefficient of 0.50 (Fig. 2). Jaccard's co-

efficient of similarity ranged between 0.37 and 0.83. Cluster I was subdivided into two sub clusters and the first sub cluster included two accessions of Navara black (IC539968 and IC557587). Navara golden yellow (IC539983 and IC557588) and Navara punja (IC557561, IC557562, and IC557564) formed second sub cluster. Second major cluster grouped released varieties (PTB-35, PTB-50, PTB-39) and Navara black with awn (IC86475). In first sub cluster, IC539968 presented a similarity of 67% with IC557587 and the similarity coefficient of IC539983 with IC557588 was 61%. Navara punja showed 50% similarity with Navara black, Navara black with awn and released varieties. But similarity coefficient of Navara punja with Navara golden yellow was 56%. Among Navara punja accessions, similarity coefficient of IC557561 and IC557562 was 83% and that of IC557564 with other two accessions was 70%. Genotype IC86475 (Navara black with awn) presented a similarity coefficient of 50% with other cultivars.

Analysis of variance (One-way ANOVA) for 48 quantitative traits has been carried out and significant variation ($P < 0.05$) was recorded for six traits within accessions viz. endosperm elongation ratio, number of leaves (40th day), leaf width, flag leaf width, panicle length and spikelet distance. Among Navara cultivars, Navara punja showed maximum mean values for

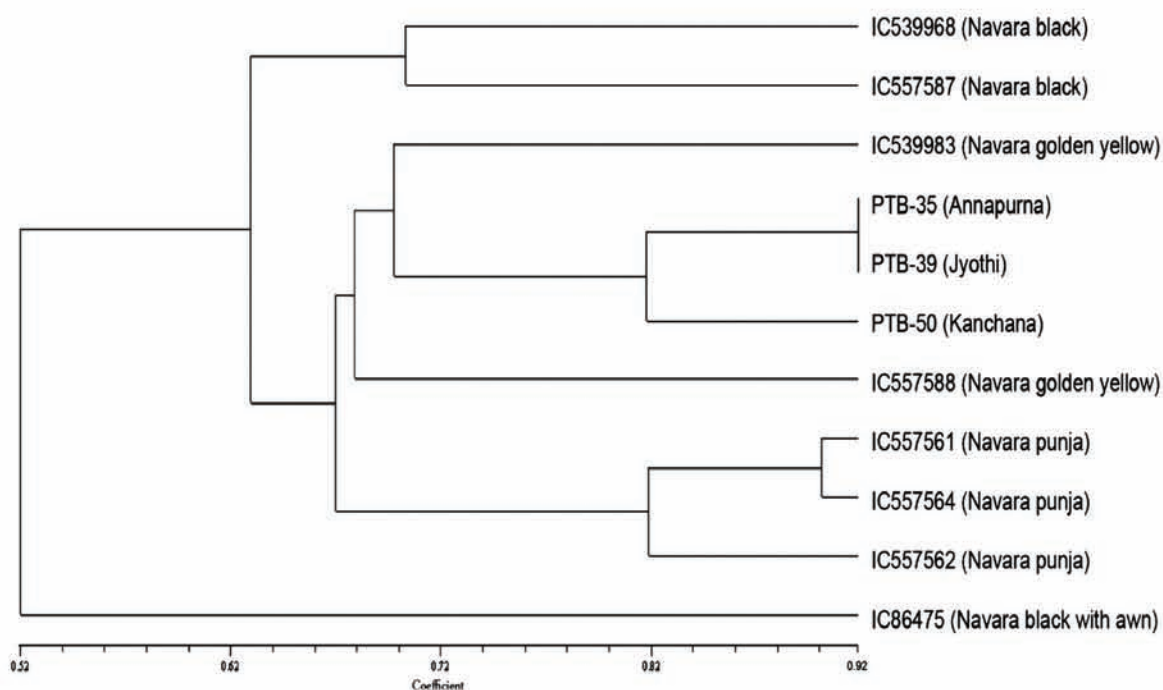


Fig. 1. Dendrogram generated from qualitative traits

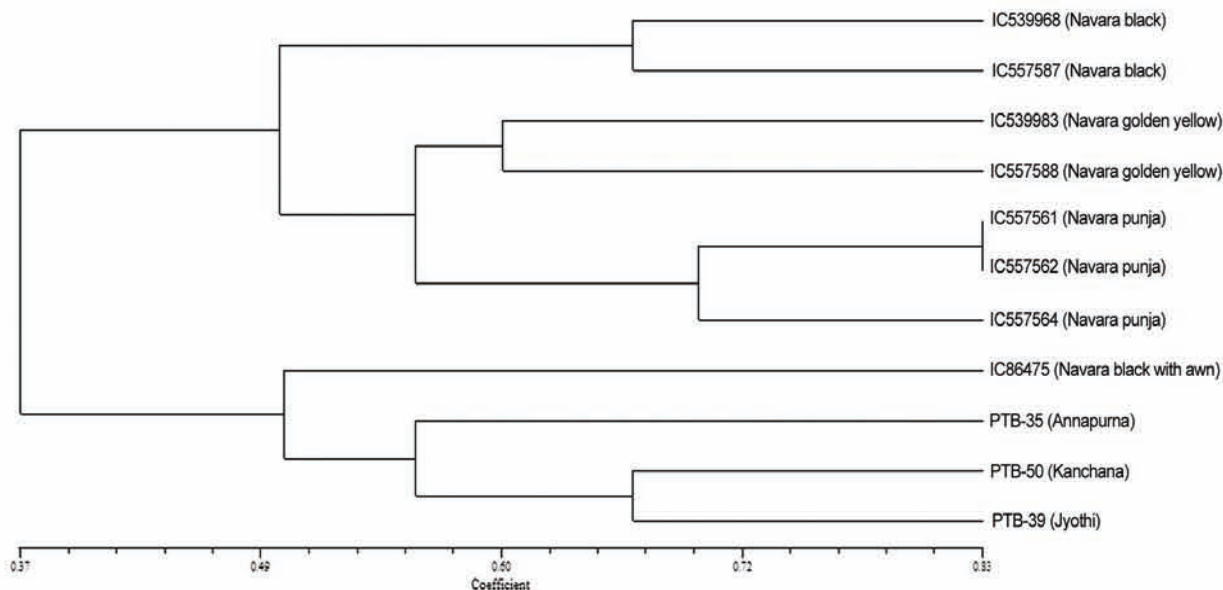


Fig. 2. Dendrogram generated from quantitative traits

elongation ratio, widening ratio, flag leaf length, ligule length, culm diameter, days to 50% flowering, days to 100% flowering, days to maturity and panicle length. These traits also showed significant variation among these cultivars (Table 2).

Quantification of Primary Metabolites

Estimation of primary metabolites viz. protein, total free amino acids, total carbohydrate and starch among different Navara accessions also showed distinct variation (Table 2). Protein (40.7mg/g) and total free amino acid content (2.06mg/g) was significantly high in accessions of Navara punja when compared to other ecotypes of Navara landraces and released varieties. Relative increase of total carbohydrate and starch content (742.35mg/g and 187.14mg/g respectively) was observed in released varieties than medicinal rice, Navara.

SSR Analysis

Genetic diversity across 11 rice genotypes was analyzed using twenty seven SSR markers. RM 28050, RM 257, RM 337, RM 168 and RM 20 grouped Navara punja as a distinct landrace. RM 20 (Chr.12, p) was the only SSR marker displaying unique bands (Mwt: 207.2bp) for all the three Navara punja accessions (IC557561, IC557562 & IC557564) (Fig. 3). In Navara punja accessions, SSR markers RM 208, RM 210, RM 190, RM 225, RM 518 and RM 212 generated bands for IC557561, whereas RM 282 produced unique bands for IC557562 and RM

535, RM 6100, RM 611, RM 167 for IC557564. Two hundred and forty eight bands were generated from 27 SSR markers and average number of bands obtained per marker was 9.92. Markers exhibited a polymorphism of 63.36% (Table 3). Diversity among genotypes was assessed using UPGMA analysis.

In the present study, SSR analysis showed Navara landrace and released rice varieties as genetically different. Dendrogram generated based on SSR markers revealed 2 major clusters as given in Figure 4. Each cluster was sub divided into two clusters at similarity co-efficient of 0.11. Jaccard's co-efficient of similarity varied from 0.03 to 0.40. In cluster I, sub clusters comprised of Navara black (IC539968 and IC557587) and released varieties (PTB-39 and PTB-50). Similarity coefficient of Navara punja, IC557562 and IC557564 was 20% and that of IC557561 with other two accessions was 19%. Genetic distance was found to be least for IC 86475 (Navara black with awn) and IC557588 (Navara golden yellow). Thus SSR markers helped in revealing genetic diversity within three ecotypes of Navara landrace.

Discussion and Conclusion

Distinct variation observed in morphological traits viz. erect leaves, partly exerted panicle, golden yellow glume and light brown seed coat can be used as markers in identifying Navara punja among other ecotypes of Navara. Similar studies for identifying Navara genotypes have been reported by Sanal Kumar *et al.* (2010).

Table 2. Variability in quantitative traits and primary metabolites

Serial No	Traits	Navara black			Navara golden yellow			Navara punja				Released varieties				Standard error	Significant variation
		IC539968	IC86475	IC557587	Average	IC539983	IC557588	Average	IC557561	IC557562	IC557564	Average	PTB-35	PTB-50	PTB-39	Average	
1	Seed length(mm)	7.85	7.32	7.75	7.64	7.5	6.5	7.02	6.61	6.62	7.02	6.75	8.07	7.58	6.87	7.51	.03523 .000
2	Seed breadth(mm)	1.52	1.85	1.77	1.71	1.51	1.58	1.55	1.62	1.46	1.61	1.56	1.59	1.77	1.77	1.71	.03523 .264
3	Seed Length-breadth ratio (mm)	5.22	4.23	4.53	4.65	4.87	4.14	4.51	4.11	4.54	3.81	4.15	5.12	4.32	4.03	4.49	.12414 .250
4	Endosperm length before boiling (mm)	7.08	6.31	6.44	6.61	6.16	6.4	6.28	6	5.92	6.34	6.08	7.02	6.44	5.97	6.48	.06176 .000
5	Endosperm length after boiling (mm)	8.18	7.38	7.32	7.62	7.12	6.78	6.95	6.98	7.08	7.36	7.14	7.36	7.08	7.02	7.15	.06452 .000
6	Elongation ratio (mm)	1.15	1.17	1.14	1.15	1.16	1.06	1.11	1.17	1.19	1.16	1.17	1.05	1.11	1.18	1.11	.01129 .047
7	Endosperm width before boiling (mm)	1.33	1.5	1.32	1.38	1.27	1.38	1.33	1.32	1.08	1.3	1.23	1.28	1.5	1.42	1.4	.03285 .315
8	Endosperm width after boiling (mm)	1.68	1.9	1.8	1.79	1.64	1.75	1.69	1.7	1.52	1.7	1.64	1.74	1.78	1.83	1.78	.03018 .334
9	Widening ratio (mm)	1.27	1.26	1.36	1.3	1.29	1.26	1.27	1.28	1.41	1.31	1.33	1.36	1.18	1.30	1.28	.01823 .312
10	Sterile lemma length (mm)	7.88	7.39	7.76	7.67	7.7	6.6	7.18	6.69	6.62	7.04	6.78	8.1	7.64	6.68	7.47	.09348 .000
11	Sterile palea length (mm)	7.34	7.02	7.32	7.22	7.34	6.18	6.76	6.32	6.32	6.54	6.39	7.53	7.32	7.68	7.16	.08340 .000
12	Percentage germination	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0.000 0.000
13	Day of completion of germination	4.4	4.2	4.4	4.3	4.6	4.2	4.4	4.4	4.4	4.4	4.4	4	4.2	4.4	4.2	.06703 .966
14	Germination speed	23	24	23	23.3	24	24	24	23	23	23	23	25	24	23	24	.06703 .917
15	Radicle length (cm)	2.92	3.95	2.44	3.13	1.49	2.62	2.06	1.56	2.36	1.53	1.82	3.39	3.91	4.85	4.05	.16322 .000
16	Plumule length (cm)	6.53	5.09	3.01	4.87	1.13	3.27	2.2	2.49	2.48	1.85	2.27	4.4	3.87	5.91	4.73	.26216 .000
17	Vigor Index	652.6	508.6	300.6	487.3	176	326.6	251.3	248.6	247.8	184.6	227	440.4	387.2	591.2	472.9	25.9883 .000
18	1 st leaf length (cm)	2.93	3.69	2.45	3.02	2.0	2.74	2.37	3.12	3.65	2.98	3.25	2.78	3.19	3.32	3.09	.12181 .207
19	1 st leaf breadth (cm)	0.21	0.22	0.19	0.21	0.19	0.17	0.18	0.27	0.29	0.18	0.24	0.21	0.28	0.29	0.26	.00774 .000
20	Height upto 1 st leaf (cm)	4.99	4.72	7.56	5.75	2.73	4.69	3.71	5.29	6.09	5.23	5.53	4.43	4.53	3.54	4.17	.22536 .000
21	No. of leaves on 40 th day	3.79	3.75	4.05	3.86	3.63	3.92	3.78	4.09	3.96	4.03	4.03	4.05	4.03	3.95	4.01	.03326 .088
22	Seedling ht on 40 th day (cm)	29.95	31.5	32.51	31.32	32.96	31.84	32.37	25.8	23.51	28.72	26.01	18.5	16.9	26	20.47	.99332 .307
23	Leaf length (cm)	31.95	38.15	28.31	32.8	30.26	33.64	31.95	36.8	36.51	30.72	34.68	33.52	26.9	28.89	29.77	1.11928 .513
24	Leaf width (cm)	0.49	0.87	0.53	0.63	0.64	0.62	0.63	0.73	0.65	0.59	0.66	0.8	0.76	0.66	0.74	.02400 .387
25	Culm No on 60 th day	4.06	7.45	3.79	4.27	4.93	4.36	4.65	5.05	4.49	4.98	4.84	4.39	4.96	4.86	4.74	.24359 .156
26	No of tiller on 60 th day	3.13	6.39	2.72	4.08	3.8	2.69	3.24	4.09	3.26	3.99	3.78	2.97	3.95	3.81	3.57	.24270 .070
27	No. of effective tiller on 60 th day	2.44	2.77	2.48	2.56	2.87	2.39	2.63	2.95	2.68	2.59	2.74	2.6	3.23	2.57	2.8	.15421 .877

Table 2. continued

Serial No	Traits	Navara black			Navara golden yellow			Navara punja			Released varieties				Standard error	Significant variation		
		IC539968	IC86475	IC557587	Average	IC539983	IC557588	Average	IC557561	IC557562	IC557564	Average	PTB-35	PTB-50			PTB-39	Average
227	No. of effective tiller on 60 th day	2.44	2.77	2.48	2.56	2.87	2.39	2.63	2.95	2.68	2.59	2.74	2.6	3.23	2.57	2.8	.15421	.877
228	Culm length before flowering (cm)	32	33.4	41.98	35.77	44.14	40.35	42.25	29.97	27.27	34.55	30.59	21.11	20.91	19.65	20.56	1.83319	.080
229	Flag leaf length (cm)	23.42	28.69	23.49	25.2	25.98	26.39	26.19	29.06	28.70	24.66	27.47	24.92	23.51	17.76	22.06	.90083	.125
230	Flag leaf width (cm)	0.68	0.92	0.57	0.72	0.74	0.61	0.66	0.81	0.73	0.64	0.73	1.02	0.85	0.88	0.92	.02858	.020
231	Ligule length (cm)	0.62	0.88	1.02	0.84	1.08	1.07	1.07	1.09	1.49	1.21	1.26	1.33	0.6	1.14	1.12	.06786	.041
232	Culm diameter (mm)	2.52	3.65	1.86	2.68	1.38	3.01	2.2	2.84	2.61	2.74	2.72	2.31	2.88	4.28	3.16	.18311	.061
233	Days to heading	79	90	61	77	71	67	69	77	81	78	79	97	98	97	97	1.46689	.076
234	Days to flowering	83	94	65	81	75	72	74	82	85	83	83	103	105	103	104	1.46144	.054
235	Days to 50% flowering	87	97	67	84	79	75	77	87	89	90	89	110	112	109	110	1.53711	.012
236	Days to 100% flowering	92	104	76	91	85	82	84	92	96	95	94	121	122	121	121	1.62607	.020
237	Days to maturity	122	131	116	123	115	123	119	127	131	128	129	151	154	150	152	1.25837	.006
238	Panicle length (cm)	13.4	14.6	13.8	13.9	14.1	11.3	12.7	19.9	18.5	15.8	18.1	13.74	15.2	15.5	14.8	.51981	.007
239	No. of primary branches	4.15	5.19	4.38	4.57	4.36	4.3	4.33	5.03	5.2	4.98	5.07	3.39	6.03	3.98	4.46	.10343	.000
240	No. of Panicle	3.74	3.52	4.69	3.98	2.62	3	2.81	3.45	3.80	4.03	3.76	2.36	2.95	2.44	2.58	.11120	.000
241	Spikelet distance(cm)	0.56	0.57	0.51	0.55	0.53	0.53	0.53	0.59	0.57	0.50	0.55	0.56	0.47	0.50	0.51	.00811	.067
242	Total seeds per/panicle	47.2	63.34	56.21	55.58	41.14	50.59	45.86	58.46	60.12	56.64	58.4	63.52	63.41	62.72	63.2	3.15487	.711
243	Sterile seeds per/panicle	22.61	25.87	24.67	24.38	16.48	18.27	17.38	21.04	20.65	17.65	19.78	28.72	25.41	25.32	26.48	1.53357	.912
244	% panicle sterility	48.4	40.72	42.54	43.88	41.01	35.01	38.01	40.8	36.43	37.24	38.15	45.42	43.76	43.29	44.16	2.34273	.802
245	Fertile seeds/per panicle	24.59	37.47	31.54	31.2	26.66	32.33	29.5	37.42	39.47	38.99	38.62	34.8	37.99	37.4	36.73	2.63302	.859
246	% panicle fertility	51.54	59.24	57.45	56.08	59.08	54.88	56.98	59.2	63.57	62.73	61.83	54.57	56.23	56.7	55.8	2.20597	.880
247	Single plant yield (g)	8.08	8.96	8.05	8.36	9.15	8.02	8.58	9.85	9.24	10.17	9.75	8.52	7.22	9.36	8.36	.13410	.000
248	Hundred seed weight (g)	1.52	2.02	1.51	1.68	1.33	1.44	1.39	1.55	1.27	1.39	1.4	1.61	1.71	1.77	1.7	.03125	.000
Biochemical analysis																		
1	Protein(mg/g)	29.66	23.61	37.24	30.17	39.1	38.05	38.57	41.31	40.84	39.82	40.65	28.	26.	27.51	27.6	.73313	.996
2	Total free amino Acids(mg/g)	1.83	1.05	0.64	1.17	0.88	1.95	1.41	2.06	2.07	2.06	2.06	1.8	0.36	0.52	0.89	.08258	1.000
3	Starch(mg/g)	149.45	145.35	70.13	121.6	102.59	128.33	115.46	123.59	92.22	145.59	120.4	187.44	162.83	211.16	187.44	5.08784	1.000
4	Total carbohydrates (mg/g)	657.63	564.57	338.58	520.26	471.67	544.77	508.22	500.46	538.71	647.13	562.1	665.45	777.23	784.37	742.35	15.81776	.998

Table 3. SSR markers and bands obtained for Navara Punja

SSR Marker	Chromosome	Position	Total No. of Amplicons	No. of Poly-morphic bands	% poly-morphism	IC number	Molecular weight of band	Rf value		
RM 212	Chr.1	Q(148.7cm)	10	8	80	IC557561	189.29	0.345		
RM 208	Chr.2	Q(186.4cm)	9	4	44.44	IC557561	299.9	0.429		
RM 535		Q(195.7cm)	10	7	70	IC557564	114.13	0.576		
RM 282	Chr.3	P(100.6cm)	9	7	77.77	IC557562	145.95	0.614		
RM 168		Q(171.2cm)	11	6	54.54	IC557562	93.61	0.504		
						IC557564	84.79	0.516		
RM 518	Chr.4	P(25.5cm)	11	7	63.63	IC557561	156.68	0.768		
RM 317		Q(118.3cm)	10	7	70	IC557561	163.41	0.479		
						IC557562	68.29	0.474		
RM 611	Chr.5	P	5	5	100	IC557564	546.6 131.25	0.264 0.442		
RM 225	Chr.6	P(26.2cm)	10	7	70	IC557561	124.99	0.625		
RM 190		Q(7.4cm)	9	5	55.55	IC557561	105.64	0.630		
RM 337	Chr.8	P(1.1cm)	14	11	78.57	IC557561 IC557564	181.4, 151.16 62.79	0.452, 0.482 0.470		
RM 210		Q(90.3cm)	6	5	83.33	IC557561	163.41	0.544		
RM 201	Chr.9	Q (81.2cm)	11	6	54.54	IC 557561 IC557564	104.69 84.78	0.332 0.340		
RM 257		Q(66.1cm)	11	8	72.72	IC557561	122.22	0.548		
						IC557564	05.56	0.562		
RM 6100	Chr.10	Q	11	5	45.45	IC557564	139.62	0.574		
RM 167	Chr.11	P(37.5cm)	10	7	70	IC557564	70.31	0.449		
RM 20	Chr.12	P(3.2cm)	11	7	63.63	IC557561				
RM 28050								IC557562	207.2	0.529
								IC557564		
		P	9	7	77.77	IC557561 IC557564	163.48 51.58	0.430 0.442		

Quantitative traits also showed distinct variation in Navara punja apart from other Navara landraces. Navara punja showed variation in flag leaf width, ligule length, culm diameter and panicle length from other cultivars. Days to 50% flowering, days to 100% flowering and days to maturity are also more in Navara Punja than other two Navara races.

Cluster analysis of qualitative and quantitative morphological traits revealed the existence of three forms of Navara viz. Navara black, Navara golden yellow and Navara punja. Dendrogram generated by cluster analysis revealed Navara punja as a separate entity. The similarity coefficient within accessions of Navara punja also showed variation revealing phenotypic variability even within this ecotype. Thus qualitative and quantitative analysis

of morphological data delineates Navara punja from other Navara ecotypes.

Quantification of primary metabolites revealed that Navara Punja has high protein and amino acid content compared to other Navara landraces and released varieties. Navara punja and other Navara landraces were also characterized by low starch and total carbohydrate content compared to released varieties. Maximum amount of free amino nitrogen and incorporation of amino acids, in rice grains with high protein content was reported by Lourdes *et al* (1970).

Analysis of SSR profiles showed similarity in dendrogram generated from morphological traits. Navara germplasm was found to be genetically different from released varieties as the genetic distance between them

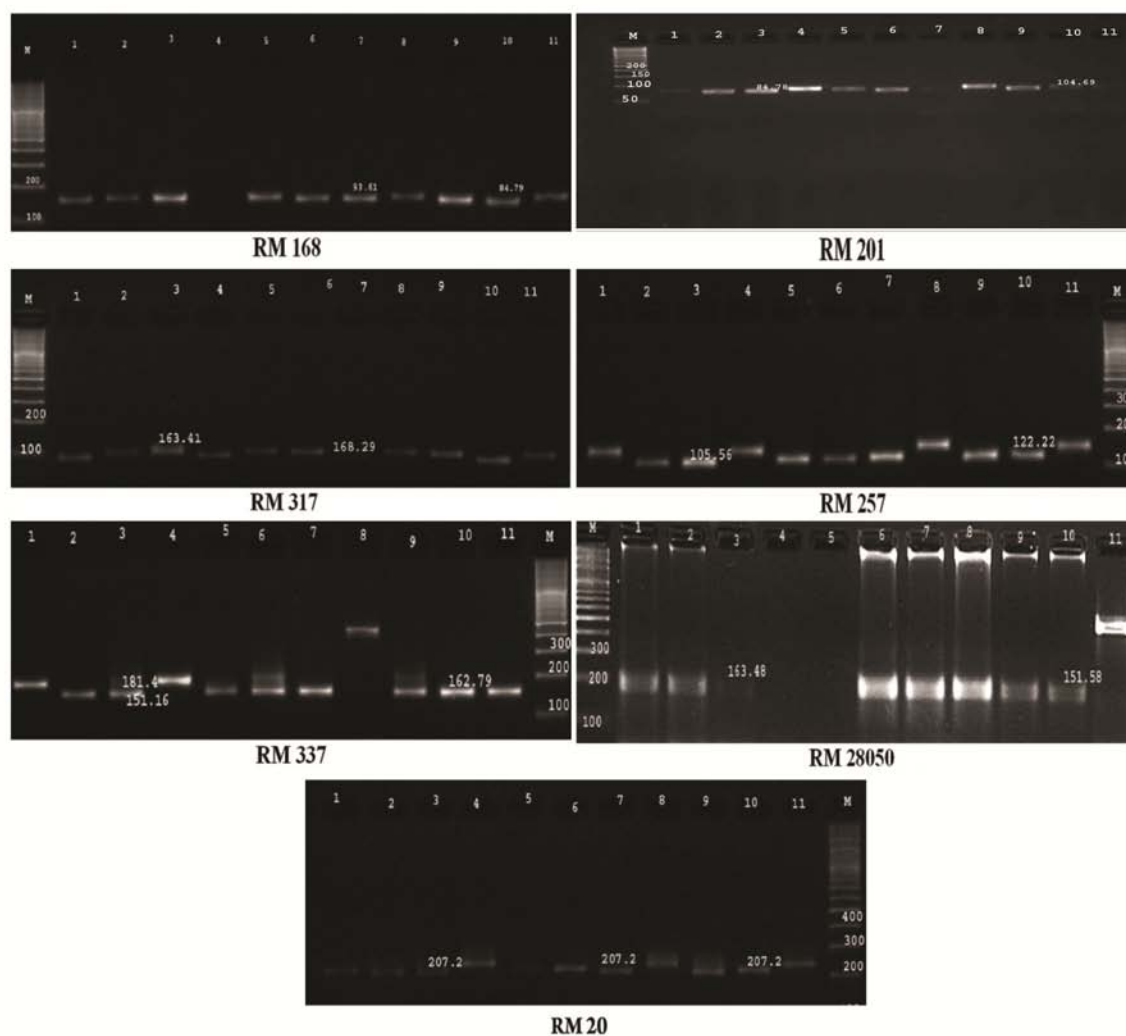


Fig. 3. SSR profile for differentiating *Oryza sativa* cv. Navara punja. Lane 1-Navara black (IC539968); Lane 2-Navara golden yellow (IC539983); Lane 3-Navara punja (IC557561); Lane 4-Annapurna (PTB-35); Lane 5-Navara black with awn (IC86475); Lane 6-Navara golden yellow (IC557588); Lane 7-Navara punja (IC557562); Lane 8-Kanchana (PTB-50); Lane 9-Navara black (IC557587); Lane 10-Navara punja (IC557564) and Lane 11-Jyothi (PTB-39)

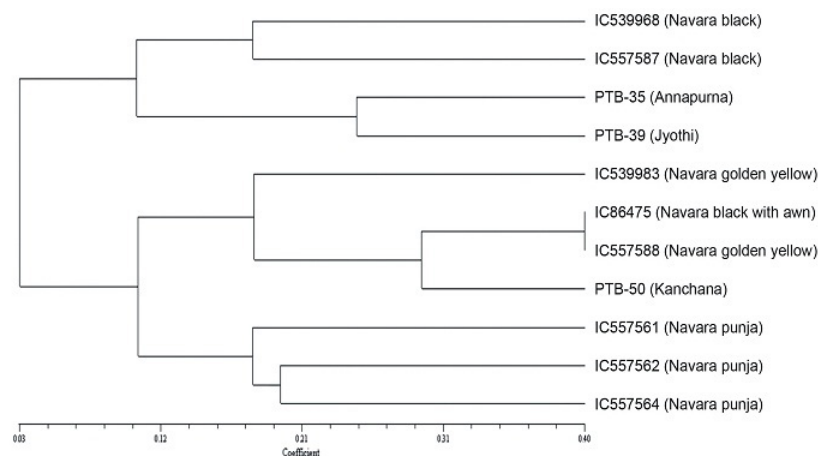


Fig. 4. Dendrogram generated based on SSR markers

was high. Allelic frequencies of Navara landraces also showed clustering of Navara landraces into three different entities. The unique bands exhibited by RM 20 for the three accessions of Navara punja suggest the utilization of this marker for the characterization of Navara punja. Similarity coefficient within Navara punja accessions was observed to be varying. SSR markers viz. RM 208, RM 210, RM 190, RM 225, RM 518 and RM 212 was found to be specific to IC557561, whereas RM 282 was specific to IC557562, and RM 535, RM 6100, RM 611, RM 167 for IC557564. Thus it reveals that genetic variability exist even within Navara punja. Similar work has been carried out by Sreejayan *et al.* (2005) in Navara landraces using molecular markers viz. SSR where Navara was clustered into three different morpho types and varieties forming a distinct group. The unique bands observed for Navara punja accessions and clustering of Navara punja into a separate group confirm delineation of Navara punja as a distinct morphotype among the Navara land race.

Acknowledgements

The first two authors thank Dean, School of Environmental Sciences, Mahatma Gandhi University and Dr. P.K.K. Nair, Director, ERRC, for technical support. Sincere gratitude to Dept. of Botany, B.A. College of Agriculture, Anand Agricultural University, for providing facility in carrying out molecular work. The first author is grateful to MG University, Kottayam, Kerala, for the Research fellowship granted.

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Identification of Diverse Sources of Multiple Disease Resistance in Wheat

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(Received: 8 June 2012; Revised: 26 August 2012; Accepted: 28 August 2012)

Wheat germplasm, numbering 6, 319 available with NBPGR, New Delhi, was evaluated at multilocations during 2004-05 to 2008-09 (five crop seasons) against major diseases of wheat under hot spot and artificially epiphytotic conditions. The diseases were: the three rusts, foliar blight and Karnal bunt. Based on this, the accessions of germplasm were identified as having multiple disease resistance. These diverse sources are available in National Genebank of NBPGR, New Delhi, and can be utilized in the breeding programme for providing durable or sustainable resistance.

Key Words: Diverse sources of resistance, Foliar blight, Karnal bunt, Multiple disease resistance, Rusts of wheat, *Triticum aestivum*, Wheat

Introduction

Wheat (*Triticum* spp.) is the second most important cereal crop after rice in India and a key crop of green revolution and the post-green revolution era. The wheat production touched its peak during 2010-11 crop season, with an all time high production of 85.93 mt (Anonymous, 2011) in comparison to 12.3 mt during 1964-65 (Tandon and Rao, 1986). The backbone of the Indian wheat programme is the breeding for disease resistance, especially for rusts. Cultivation of resistant varieties is the most eco-friendly and economically viable method for combating the diseases or the pests. New and diverse sources of resistance are very important for inclusion in the breeding programme. Hence, there is always a search for such sources of resistance against the major diseases and pests.

The major diseases of wheat in India are rusts, namely, leaf or brown rust, stripe or yellow rust and stem or black rust, Karnal bunt and leaf blight. Other diseases, like powdery mildew, head scab, foot rot, flag

smut and hill bunt are the diseases of limited importance, due to their distribution in some limited areas (Joshi *et al.* 1988). Sources of resistance to various diseases in wheat, have been identified and enlisted in various publications (Sharma *et al.* 2002; Singh, *et al.*, 2001, 2004). The National Bureau of Plant Genetic Resources (NBPGR), New Delhi, has about 30,000 germplasm of wheat and its wild species in National Genebank, local land races, indigenous and exotic materials with diverse backgrounds. It was decided to evaluate this germplasm at multilocations with the purpose of enlisting their disease level as well as to identify the sources of resistance against the major diseases to utilize them in the wheat breeding programme. With this objective, genotypes were evaluated at multilocations under hot spot and inoculated conditions against the three rusts (black, brown and yellow), Karnal bunt and foliar blight.

Material and Methods

Germplasm supplied by the NBPGR, New Delhi, which was censerved in National genebank, was planted at

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multilocations for evaluation against the three rusts, viz., leaf or brown rust (*Puccinia triticina* Eriks. & Henn.), stripe or yellow rust (*Puccinia striiformis* West.), stem of black rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn); Foliar blight or spot blotch (*Bipolaris sorokiniana* (Sacc.) Shoem) and Karnal bunt (*Tilletia indica* Mitra, syn. *Neovossia indica* (Mitra) Mundkur). In all, 6319 germplasm lines were evaluated during four crop seasons (2004-05 to 2008-09) at multilocations. The seeds of the accession numbers given here, are available in the genebank at NBPGR, New Delhi.

The germplasm was planted at the following locations during 2004-05 (1500 entries), 2005-06 (1660 entries), 2006-07 (1041 entries), 2007-08 (1018 entries) and 2008-09 (1100 entries).

For yellow or stripe rust	Ludhiana, Pantnagar, Karnal
For brown or leaf rust	Ludhiana, Pantnagar, Varanasi, Faizabad, Vijapur, Powarkheda, Pune, Dharwad, Karnal
For black or stem rust	Vijapur, Powarkheda, Pune and Dharwad
For Karnal bunt	Ludhiana
For Foliar blight	Varanasi, Faizabad

The wheat germplasm was subjected to artificial inoculations of virulent pathotypes/strains or isolates of the pathogens at their respective hot spot locations for ensuring that there are no escapes while identifying the resistant genotypes (Sharma *et al.*, 2002). The procedure followed for each of the diseases is as follows:

Rusts

The inoculum of virulent and predominant pathotypes maintained under controlled conditions at DWR, Regional Research Station, Flowerdale, Shimla, H. P. and also at Rust Laboratory, Mahabaleshwar (Maharashtra) were used for inoculation. Following are the important pathotypes of three rusts used for artificial inoculation:

Stem rust: 11(79G31), 40 A (62G29), 42 (19G35), 122(7G11), 117-6 (37G19)

Leaf rust: 12-2(1R5), 77-2 (109R31-1), 77-5(121R63-1), 104-2(21R55)

Stripe rust: K (47S102), P (46S103), L (70S69), 13 (67S8), 46S119 and 78S84

Inoculation procedure: The initial inoculum in the form of uredospores of the most virulent and prevalent pathotypes of a rust was inoculated on 30 days old wheat seedlings of susceptible cultivars, like Agra Local,

Sonalika or Mahabaleshwar?, HD 2329, Kharchia 65, WL 711, PBW 343, grown under polythene tunnels in the month of October for inoculum multiplication. The inoculation was done by rubbing the inoculum on leaves, sprays and syringe inoculation in the afternoon. Proper humidity and temperature conditions are provided to make inoculation successful and further multiplication of uredospores. The fresh uredospores collected with the help of spore collector from these plants were used for inoculation in the fields. Inoculation in the field was done by spraying of suspension of uredospores prepared in water by using TWEEN 80 spreader. Generally a knapsack sprayer was used for inoculation. Syringe inoculation was also done on border rows of susceptible varieties in the screening block. A line of susceptible check varieties was planted after every 20 lines of test entries in field as an infector besides planting on borders of each sub block in field to create maximum disease pressure of rusts. The pots having rust infected wheat plants were also kept in the field during the month of December and January. To help maximum sporulation and multiplication of the rusts, fields were irrigated after the inoculations.

Disease scoring: The scoring of rusts was done after dough stage by taking both severity of disease on plant parts denoted by per cent area covered as well as kind of host response (R, MR, MS, S, X) as per modified Peterson scale (Joshi *et al.*, 1986). The coefficient of infection (CI) was calculated by multiplying the severity with the standard value of host response which is as follows:

Response	Numerical value
Resistant (R)	0.2
Moderately Resistant (MR)	0.4
Intermediate (X)	0.6
Moderately Susceptible (MS)	0.8
Susceptible (S)	1.0

Once CI of a location is calculated, an average CI (ACI) of multilocation data is computed. The highest rust score amongst locations along with ACI represents the rust reaction of a test entry. A variety is considered resistant if its ACI for a rust is less than 10.00.

Karnal bunt

Each entry was sown in one meter row. Recommended cultural practices were followed to grow the crop till

harvest. To determine the response of genotypes to Karnal bunt, earheads were injected with hypodermic syringe with adequate amount of inoculum (10,000 allantoids/ml water) at Zadok's crop growth stage 43-49 (Zadoks, *et al.* 1974). Five earheads were inoculated in each entry during evening hours. After inoculation, high humidity was maintained for proper development of disease. The disease incidence in the earheads was recorded at crop maturity and was calculated by reckoning the infected and the total number of grains (both diseased and healthy) of 5 earheads per entry. On the basis of the data, the entries showing response of upto 5 per cent infection were rated as resistant.

Leaf blight

One row of 1m length of each entry was planted and a row of a highly susceptible entry RAJ 4015 was repeat planted after every 20 test entries. The inoculations of pathogens were done right from the month of January at 15 days intervals till development of disease. The built up of disease was ensured by using regular irrigations. The recording of disease was done in 0-9 double digit scale. The right hand side digit of score represents the per cent blighted area of flag-1 leaf, whereas the left side digit indicates the score of blight on flag leaf. The score (0-9) was as follows:

0:-No blight, **1:-**Up to 10% leaf area blighted, **2:-**11-20% leaf area blighted, **3:-**21-30% leaf area blighted, **4:-**31-40% leaf area blighted, **5-41:-**50% leaf area blighted, **6:-**51-60% leaf area blighted, **7:-**61-70% leaf area blighted, **8:-**71-80% leaf area blighted, **9:-**>80% leaf area blighted.

Categorization of entries

Following range of scores (average) were used to identify the resistant and moderately resistant entries at dough stage:

Highly resistant: Av. score range 00-13, Highest score up to 35; *Resistant:* Av. Score range 14-35 (With highest score up to 57).

Results and Discussion

Based on the multilocation data over the years, the following multiple disease resistant genotypes were identified.

Stem, leaf and stripe rusts: IC128654, IC128649, IC128638, IC128639, IC128642, IC128656, IC128555, IC128592, IC128619, IC279333, IC128647, IC128520,

IC128643, IC310106, IC128521, IC128179, IC128524, IC128590, IC128624, IC310124, IC128631, IC128652, IC128587, IC145276, IC128564, IC145811, IC128525, IC128594, IC128692, IC128650, IC128553, IC128637, IC145636, IC128507, IC145780, IC128629, IC321153, IC145602, IC128457, IC128526, IC145808, IC145331, IC63954, IC63955, IC111659, IC111667, IC111668, IC111670, IC111686, IC111687, IC111688, IC111691, IC111692, IC111693, IC111694, IC111701, IC111731, IC111771, IC111783, IC111787, IC111888, IC111892, IC111905, IC111912, IC111918, IC 111919, IC31982, IC47044, IC73591, IC73593, IC75313, IC75314, IC82194, IC260877, IC321981, IC416080, IC416082, IC416083, IC416084, IC416087, IC416088, IC416089, IC416092, IC416094, IC416098, IC416102, IC416106, IC416107, IC416108, IC416112, IC416113, IC416281, IC427210, IC138364, IC138426, IC138432, IC138438, IC138477, IC138478, IC138479, IC138504, IC138521, IC138524, IC138618, IC138625, IC138626, IC145882, IC145884, IC145916, IC145951, IC145977, IC252370, IC252392, IC252407, IC252420, IC252423, IC252430, IC252431, IC252432, IC252433, IC252438, IC252439, IC252441, IC252443, IC252444, IC252445, IC252448, IC252450, IC252453, IC252455, IC252456, IC252457, IC252458, IC252459, IC252469, IC252472, IC252477, IC252490, IC252497, IC252499, IC252520, IC252541, IC252542, IC252547, IC252591, IC252611, IC252629, IC252641, IC252650, IC252673, IC252676, IC252678, IC252686, IC252694, IC252706, IC252710, IC252723, IC252725, IC252767, IC252818, IC252819, IC252892, IC252983, IC335670, IC335671, IC335683, IC335704, IC335707, IC335716, IC335717, IC335737, IC335742, IC335746, IC335750, IC24177, IC260849, IC260877, IC279320, IC279321, IC279875, IC281566, IC290022, IC290025, IC290039, IC290046, IC290057, IC290058, IC290065, IC290070, IC290087, IC290095, IC290096, IC290098, IC290150, IC290154, IC290157, IC290162, IC290168, IC290173, IC290175, IC290176, IC290177, IC290178, IC290182, IC290184, IC290186, IC290191, IC290196, IC290197, IC290208, IC290215, IC290217, IC290221, IC290222, IC290226, IC290227, IC290231, IC290238, IC290241, IC290242, IC290243, IC290244, IC290258, IC290261, IC290262, IC290264, IC290280, IC290281, IC290298, IC290299, IC290302, IC290305, IC290309, IC290311, IC290314, IC290316, IC290325, IC290326, IC290326, IC290327, IC290329, IC290342, IC310120, IC310124, IC316100, IC36901 and IC535341.

Stem and leaf rusts: IC128561, IC145810, IC145808, IC128654, IC145806, IC145769, IC128649, IC128638, IC128456, IC310117, IC128639, IC128642, IC128656, IC310124, IC128552, IC145253, IC128594, IC128566, IC128692, IC145748, IC128614, IC128624, IC128496, IC128555, IC128650, IC145809, IC145801, IC128592, IC145696, IC128689, IC145797, IC128553, IC128201, IC128250, IC145828, IC145692, IC128619, IC128617, IC128663, IC145275, IC279333, IC128631, IC128209, IC128196, IC128570, IC128647, IC128652, IC321157, IC145541, IC128263, IC128610, IC128565, IC145501, IC128536, IC128190, IC128541, IC128678, IC145638, IC128645, IC128549, IC128637, IC128520, IC128693, IC128195, IC128567, IC279314, IC145813, IC128643, IC128568, IC145635, IC145341, IC128558, IC145636, IC145778, IC128202, IC128595, IC145416, IC128551, IC128616, IC145538, IC128697, IC128560, IC128554 and IC145768, IC128197, IC128185, IC145822, IC145415, IC128564, IC145816, IC145257, IC128694, IC128525, IC310106, IC128587, IC128167, IC128181, IC128507, IC128547, IC128538, IC128495, IC128640, IC128171, IC128526, IC145780, IC128521, IC145804, IC279229, IC128247, IC128696, IC145262, IC145335, IC128569, IC128179, IC145334, IC128588, IC145286, IC128524, IC145796, IC128457, IC145642, IC128609, IC145798, IC145276, IC145683, IC321160, IC128571, IC128157, IC145781, IC128550, IC128528, IC128458, IC128497, IC145331, IC128590, IC128625, IC145784, IC145703, IC128629, IC128682, IC145753, IC145293, IC128186, IC145281, IC145282, IC128466, IC128464, IC145800, IC128193, IC145285, IC145682, IC321154, IC128499, IC145602, IC128557, IC145811, IC279335, IC128546, IC145825, IC321153, IC128662, IC145436, IC111954, IC111930, IC111944, IC111828, IC111736, IC111807, IC75356, IC73589, IC111767, IC73578, IC73582, IC111735, IC111884, IC75340, IC75352, IC75354, IC75348, IC73585, IC75343, IC111715, IC82404, IC75251, IC111714, IC75334, IC111883, IC111779, IC73581, IC111708, IC111939, IC111785, IC75346, IC73498, IC73588, IC111941, IC111763, IC29049, IC75250, IC75316, IC111860, IC111786, IC82394, IC75336, IC111893, IC111882, IC75355, IC28960, IC111876, IC111794, IC111688, IC111717, IC26740, IC29000, IC82355A, IC111784, IC47517, IC253015, IC35125, IC35117, IC36854, IC111916, IC111864, IC111719, IC111886, IC111705, IC75358, IC111940, IC73576, IC111915, IC118713, IC262365, IC279314, IC279321, IC279327, IC279335, IC279480,

IC279604, IC279642, IC279709, IC279864, IC279866, IC279871, IC279876, IC279879, IC279883, IC281558, IC319810, IC321871, IC322026, IC361695, IC372646, IC372657, IC372660, IC372666, IC397523, IC397922, IC415839, IC415945, IC415948, IC415950, IC415954, IC415967, IC415974, IC415975, IC415977, IC415979, IC415981, IC415983, IC415985, IC415986, IC415991, IC415993, IC415998, IC416001, IC416004, IC416007, IC416017, IC416018, IC416019, IC416029, IC416033, IC416036, IC416055, IC416064, IC416091, IC416093, IC416097, IC416099, IC416100, IC416101, IC416103, IC416104, IC416105, IC416109, IC416110, IC416111, IC416117, IC416122, IC416124, IC416125, IC416126, IC416127, IC416129, IC416130, IC416131, IC416133, IC416134, IC416138, IC416139, IC416140, IC416141, IC416142, IC416143, IC416144, IC416145, IC416146, IC416147, IC416148, IC416150, IC416151, IC416152, IC416153, IC416156, IC416163, IC416164, IC416166, IC416167, IC416171, IC416172, IC416173, IC416174, IC416179, IC416181, IC416182, IC416184, IC416186, IC416187, IC416188, IC416190, IC416191, IC416197, IC416198, IC416201, IC416205, IC416207, IC416208, IC416209, IC416216, IC416232, IC416235, IC416236, IC416237, IC416238, IC416254, IC416274, IC416276, IC416277, IC416279, IC416280, IC416284, IC416286, IC138395, IC138397, IC138401, IC138404, IC138406, IC138407, IC138408, IC138410, IC138422, IC138424, IC138427, IC138428, IC138429, IC138433, IC138434, IC138437, IC138440, IC138441, IC138444, IC138486, IC138487, IC138488, IC138556, IC138609, IC138616, IC138637, IC138639, IC138641, IC145950, IC145956, IC145957, IC145958, IC145966, IC145971, IC145972, IC145980, IC252348, IC252351, IC252352, IC252353, IC252369, IC252374, IC252381, IC252382, IC252385, IC252396, IC252400, IC252408, IC252409, IC252414, IC252419, IC252424, IC252434, IC252435, IC252436, IC252437, IC252440, IC252442, IC252446, IC252447, IC252449, IC252451, IC252452, IC252454, IC252460, IC252461, IC252467, IC252470, IC252471, IC252473, IC252488, IC252491, IC252493, IC252498, IC252506, IC252508, IC252512, IC252516, IC252526, IC252532, IC252536, IC252540, IC252550, IC252551, IC252554, IC252565, IC252571, IC252593, IC252608, IC252610, IC252618, IC252620, IC252621, IC252623, IC252626, IC252628, IC252632, IC252635, IC252640, IC252643, IC252645, IC252648, IC252654, IC252660, IC252663, IC252665, IC252666, IC252668, IC252679, IC252680, IC252681, IC252682, IC252684, IC252687, IC252688,

IC252692, IC252695, IC252699, IC252702, IC252704, IC252708, IC252718, IC252726, IC252727, IC252731, IC252753, IC252755, IC252768, IC252775, IC252806, IC252834, IC252836, IC252854, IC252861, IC252886, IC252888, IC252893, IC252927, IC252947, IC252948, IC252951, IC252952, IC252953, IC252961, IC252973, IC252974, IC253014, IC335697, IC335706, IC335709, IC260878, IC279688, IC279864, IC290037, IC290040, IC290041, IC290043, IC290051, IC290055, IC290056, IC290072, IC290081, IC290082, IC290084, IC290086, IC290091, IC290153, IC290156, IC290165, IC290169, IC290179, IC290180, IC290181, IC290183, IC290188, IC290192, IC290194, IC290195, IC290199, IC290205, IC290211, IC290212, IC290214, IC290216, IC290225, IC290228, IC290233, IC290245, IC290272, IC290279, IC290296, IC290297, IC290300, IC290303, IC290304, IC290310, IC290318, IC290322, IC290324, IC290327, IC290332, IC290334, IC290336, IC290337, IC290338, IC290339, IC290340, IC310106, IC310127, IC313156, IC313157, IC315921, IC316086, IC316088, IC317422, IC321875, IC535212, IC535305 and IC535459.

Stem and stripe rusts: IC128654, IC128649, IC128638, IC128639, IC128642, IC128656, IC128555, IC128592, IC128619, IC279333, IC128647, IC128520, IC128643, IC310106, IC128521, IC128179, IC128524, IC128590, IC128657, IC145305, IC128644, IC145479, IC128648, IC145478, IC311078, IC279866, IC145587, IC128624, IC128545, IC128634, IC145304, IC128579, IC310124, IC128631, IC128652, IC128587, IC145349, IC145452, IC145330, IC145313, IC79037, IC145705, IC82195, IC145571, IC128573, IC145306, IC145706, IC128591, IC145563, IC208901, IC145567, IC145595, IC145593, IC145565, IC145568, IC145276, IC145564, IC145569, IC128564, IC128523, IC145431, IC145811, IC128525, IC128594, IC128692, IC128650, IC128553, IC128637, IC145636, IC128507, IC145780, IC128629, IC321153, IC145453, IC145779, IC128636, IC128461, IC128574, IC128172, IC145265, IC128575, IC145299, IC381144, IC128589, IC279886, IC145294, IC145248, IC128641, IC145612, IC313151, IC145425, IC145594, IC145540, IC381179, IC145602, IC128457, IC145329, IC145704, IC145443, IC145442, IC128526, IC145808, IC145331, IC128251, IC145570, IC128448, IC145685, IC145473, IC145430, IC145591, IC145417, IC128462, IC145312, IC128174, IC128384, IC145787, IC145302, IC145562, IC128440, IC111648, IC111652, IC111660, IC111664, IC111669, IC111683, IC111689, IC111690, IC111695, IC111697, IC111698, IC111699, IC111700, IC111702,

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Leaf and stripe rusts: IC128654, IC128649, IC128638, IC128639, IC128642, IC128656, IC128555, IC128592, IC128619, IC279333, IC128647, IC128520, IC128643, IC310106, IC361692, IC128521, IC128179, IC128524, IC145528, IC128590, IC128624, IC145820, IC310124, IC128631, IC128652, IC128593, IC128587, IC145812, IC145276, IC128564, IC145811, IC128525, IC128594, IC128692, IC145818, IC128650, IC128553, IC128637, IC145636, IC279877, IC128507, IC145780, IC279324, IC128629, IC321153, IC145602, IC128457, IC128526, IC145808, IC128453, IC128527, IC145331,

Leaf and Stripe rusts: IC41589, IC36751, IC36747, IC36723, IC112006, IC111921, IC111757 and IC111713, IC138507, IC138511, IC145909, IC252402, IC252425, IC252427, IC252428, IC252537, IC252796, IC321977, IC321982, IC415940, IC415966, IC416081, IC416085 and IC416095, IC260935, IC266764, IC279564, IC279877, IC281564, IC290038, IC290050, IC290076, IC290088, IC290094, IC290097, IC290146, IC290163, IC290185, IC290190, IC290193, IC290204, IC290213, IC290256, IC290259, IC290312 and IC316085.

Leaf Blight, Stem Rust, Leaf Rust and Stripe Rust: IC145780, IC82194, IC111692, IC260849, IC279320, IC290261, IC290262, IC290264, IC290299, IC290309, IC290314, IC290316 and IC316100.

Leaf blight, stem rust and stripe rust: IC145780, IC145779, IC82194, IC111692, IC260849, IC260919, IC260930, IC260967, IC260972, IC266831, IC279320, IC290018, IC290075, IC290089, IC290261, IC290262, IC290264, IC290299, IC290309, IC290313, IC290314, IC290316, IC290317, IC316100 and IC321162.

Leaf blight, leaf rust and stripe Rust: IC145780, IC82194 and IC111692, IC260849, IC279320, IC290076, IC290088, IC290185, IC290261, IC290262, IC290264, IC290299, IC290309, IC290312, IC290314, IC290316 and IC316100.

Leaf blight, stem rust and leaf rust: IC145798, 145780, IC82194, IC28960, IC111692,

IC138404, IC138408, IC138429, IC260849, IC279320, IC290084, IC290261, IC290262, IC290264, IC290299, IC290309, IC290310, IC290314, IC290316, IC290318, IC290322, IC290337, IC310106 and IC316100.

Karnal bunt, stem rust, leaf rust and stripe rust: IC128619, IC128642, IC128647, IC128643, IC128624, IC128507, IC128564, IC128637, IC128592, IC128654, IC128639, IC128521, IC128590, IC128525, IC128587,

IC128652, IC128638, IC128656, IC128555, IC128526, IC128631, IC279333, IC310124, IC47044, IC63954, IC63955, IC75314, IC111670, IC111771, IC111783, IC321981, IC416082, IC416083, IC416084, IC416089, IC416092, IC416102, IC416112, IC416113, IC427210, IC24177, IC260849, IC279321, IC290065, IC290096 and IC290196.

Stem Rust, Leaf Rust and Karnal Bunt: IC128181, IC128186, IC128197, IC128201, IC128202, IC128250, IC128496, IC128499, IC128507, IC128521, IC128525, IC128526, IC128538, IC128546, IC128547, IC128554, IC128555, IC128561, IC128564, IC128566, IC128567, IC128568, IC128570, IC128571, IC128587, IC128590, IC--128592, IC128619,

IC128624, IC128625, IC128631, IC128637, IC128638, IC128639, IC128642, IC128643, IC128647, IC128652, IC128654, IC128656, IC128662, IC128663, IC128697, IC145257, IC145275, IC145334, IC145341, IC145501, IC145538, IC145642, IC145683, IC145748, IC145769, IC145781, IC145796, IC145797, IC145798, IC145801, IC145809, IC145810, IC145816, IC279229, IC279314, IC279333, IC310117, IC310124, IC321157 and IC321160. IC111670, IC82394, IC75356, IC75352, IC75348, IC75343, IC75340, IC75336, C 75316, IC75314, IC75251, IC75250, IC73589, IC73588, IC73582, IC73581, IC73578, IC73576, IC73498, IC63955, IC63954, IC47044, IC35117, IC111954, IC111940, IC111893, IC111882, IC111794, IC111785, IC111784, IC111783, IC111779, IC111771, IC111670, IC111767, IC111735, IC111708 and IC111705, IC279864, IC279879, IC372646, IC397922, IC415945, IC415954, IC415977, IC415981, IC415983, IC415985, IC415986, IC415993, IC416018, IC416019, IC416029, IC416033, IC416093, IC416099, IC416103, IC416104, IC416122, IC416124, IC416133, IC416147, IC416148, IC416151, IC416156, IC416163, IC416164, IC416174, IC416179, IC416184, IC416186, IC416190, IC416191, IC416197, IC416198, IC416232, IC416236, IC416237, IC416274, IC416276, IC416279, IC416286, IC279688, IC290086, IC290156, IC290205, IC290297, IC290322, IC290334 and IC535459.

Stem rust, stripe rust and Karnal bunt: IC128172, IC128507, IC128521, IC128525, IC128526, IC128545, IC128555, IC128564, IC128574, IC128579, IC128587, IC128590, IC128592, IC128619, IC128624, IC128631, IC128634, IC128637, IC128638, IC128639, IC128641, IC128642, IC128643, IC128647, IC128652, IC128654, IC128656, IC128657, IC145304, IC145306, IC145430,

IC145442, IC145443, IC145452, IC145453, IC145479, IC145564, IC145568, IC145569, IC145612, IC145706, IC145779, IC145787, IC279333, IC310124, IC313151, IC381179, IC82195, IC128654, IC128638, IC128642, IC128656, IC128592, IC128619, IC128590, IC128631, IC128652, IC128587, IC128564, IC128525, IC128637, IC310124, IC279333, IC361692, IC128624, IC128555, IC128643, IC279324, IC128526, IC128647, IC145812, IC128507, IC128521, IC128593, IC128527, IC28936, IC35161, IC36705, IC36761, IC47044, IC63954, IC63955, IC63956, IC64224, IC64230, IC75224, IC75249, IC75314, IC75394, IC78991, IC79062, IC79087, IC79091, IC79111, IC82193, IC82323, IC82333, IC111669, IC111670, IC111683, IC111702, IC111771, IC111776, IC111783, IC112000, IC112037, IC112039, IC112041, IC112049, IC112051, IC112064, IC78989A, IC321985, IC416074, IC416072, IC427231, IC416075, IC416258, IC398115, IC398067, IC416161, IC397999, IC416273, IC416247, IC397830, IC416162, IC416219, IC397986, IC36747, IC41589, IC47044, IC63954, IC63955, IC75314, IC111670, IC111757, IC111771, IC111783 and IC112006. IC24175, IC24548, IC255632, IC260875, IC260876, IC260912, IC260942, IC266791, IC279317, IC279324, IC279480, IC279617, IC28086, IC28518, IC28544, IC290062, IC290319, IC30253, IC30275, IC30289, IC30291, IC30297, IC31278, IC317632, IC321152, IC36875, IC535193, IC535334, IC535335, IC535337, IC535339, IC535437, IC535473, IC535476, IC535478, IC535480, IC535504, IC535553, IC535556 and IC535559.

Karnal bunt, leaf rust and stripe rust: IC416081, IC416095, IC290038 and IC290322.

Leaf blight and Karnal bunt: IC145797, IC145779, IC145798, IC31979, IC36737, IC36739, IC73647, IC78981, IC82246, IC355872 and IC82190A.

Leaf blight and stem rust: IC138411, IC138419, IC138538, IC138551, IC138557, IC138587, IC138595, IC145871, IC145888 and IC252785.

Leaf blight and stripe rust: IC138512, IC138538, IC145871, IC145888 and IC252785.

Leaf blight: IC138458, IC138516, IC138591 and IC252784.

The germplasm, thus, identified as resistant contains a wide range of material, like those of exotic and indigenous origin, the local landraces, the Indian germplasm, etc. Thus, these are the diverse sources of resistance for the diseases in wheat. Most of these have not been utilized

for incorporating the disease resistance in the wheat breeding programme. These resistance sources carry resistance to more than one disease and hence are very useful for use in the breeding programme. Though, rust resistance gene postulation has not been done so far in these lines, it is expected that these diverse sources of resistance can provide durable or sustainable resistance over a period of time. It is recommended that these sources be utilized in the wheat breeding programme.

Acknowledgements

The scientists from various cooperating centres contributed to the evaluation of the material which was conserved and supplied by NBPGR, New Delhi, at their respective centres. Data compilation, analysis and report preparation was undertaken at DWR, Karnal.

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Canonical Discriminant Analysis for the Assessment of Genetic Variation in Soybean (*Glycine max* (L.) Merrill)

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(Received: 29 January 2011; Revised: 06 January 2012; Accepted: 12 June 2012)

For improvement of soybean, it is necessary to gain insight into the magnitude of variability present in the species. The study was conducted to assess sources of genetic and phenotypic variability in 62 soybean varieties. Seventeen morphological, agronomical and quality characters were measured. The multivariate data set was analyzed by Canonical Discriminant Analysis (CDA) in combination with a clustering procedure. In this analysis, the first four canonical varieties were significant and, number of pods/plant was the most differentiating traits among the varieties. The canonical roots clustered the varieties into eighteen groups on the basis of the differentiating traits. CDA effectively analyzed the genetic variation and identified the traits that could better describe the variation among soybean genotypes. Cluster analysis was successful in differentiating the varieties into similar subgroups on the basis of the measured traits.

Key Words: Canonical discriminant analysis, Cluster, Soybean

Introduction

Soybean (*Glycine max* (L.) Merrill) is one of the most important crops in the world today by virtue of its richness in balanced protein and oil. However, overall improvement in yield, oil and protein content in soybean remains a perpetual task to be accomplished by the plant breeders. This can be achieved either by selecting superior genotypes or to be utilized as parents for the development of future cultivars through hybridization, from the variability existing in the available genepool. However, in Indian soybean varieties, a narrow genetic base has been observed (Chung and Singh, 2008; Pushpendra *et al.*, 2008), whereas, now-a-days breeding programmes use soybean improved cultivars in hybridization to create genetic variability. The use of related wild species is at minimum bringing about a very low impact on broadening of genetic base in soybean. Hence knowledge of genetic divergence in the available cultivars of soybean has an immense importance and in tune with immediate need in the selection of parents to be used in hybridization programme for obtaining desirable genetic combination.

An insight into the magnitude of variability present in crop species is of utmost importance, as it provides the basis for effective selection. Genotypic variation is the component of variation that is due to the genotypic

differences among individuals within a population or among populations within a species, and is the main concern of a plant breeder. Genetic variation may be measured in several ways. With univariate analyses, each variable is analyzed separately allowing for substantial overlapping of results to occur. Univariate statistical techniques such as analysis of variance do not explain how accessions differ when all measured variables are considered jointly. In Canonical Discriminant Analysis (CDA), a multivariate statistical technique, all independent variables are considered simultaneously in the differentiation of cultivars. This approach results in a more powerful comparison of populations than can be achieved with univariate analysis, provided the variables are correlated. Canonical discriminant analysis can separate among-population effects from within population effects by maximizing discrimination among populations when tested against the variation within populations (Riggs, 1973; Tai, 1989). Canonical variate analysis is discussed by Anderson (1958) has been frequently used in discriminating populations belonging to diverse genetic and geographic origin. It also serves as a pictorial presentation of the configuration of various groups. The information obtained from CDA can then additionally be used to group the accessions-populations into the smaller subgroups that are more similar to each other (Khattree and Naik, 2000). This CDA have been used in

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the assessment of genetic variation in tall fescue (*Festuca arundinacea* Schreb) (Vaylay and Santen, 2002) and hairy vetch (*Vicia villosa* Roth) (Yeater *et al.*, 2004).

Our objectives were to use the canonical discriminant analysis to study the genetic variation and selection of parents for further hybridization.

Materials and Methods

The experimental material consisted of 62 Indian varieties of soybean (Table 2). They were planted in a single row plot of three meter length with spacing of 60 × 10 cm in a Completely Randomized Block Design with two replications, at the Crop Research Centre of GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The observations were recorded on five randomly selected competitive plants. The agronomical characters were days to initiation of flowering, days to 50 per cent flowering, days to maturity, flowering span, reproductive phase, basal node height (cm), basal pod height (cm), plant height (cm), number of primary branches/plant, number of nodes/plant, number of pods /plant, number of seeds/pod, number of seeds /plant, grain yield/plant (g), 100-seed weight (g). In addition to agronomic characters two quality characters were also included in this study *viz.*, oil content (%) and protein content (%). Observations were subjected to CDA as discussed by Andersen (1958). The goal of this analysis is to arrive at cluster of accessions that display small within-cluster variation relative to the between-cluster variation.

Results and Discussion

Canonical discrimination is obtained by the ratio of variance among accessions to the variance within accessions (Rencher, 1992).

The extent of diversification, expressed as percentage contribution of first four canonical variate (Table 1) is the linear combination of the independent variables (characters) and is orthogonal to the other. A critical perusal of this table indicated that 34.40% of the total genetic diversity present in the genotypes was accounted by the first four canonical variates. All the four vectors contributed almost equally to total variation. Sum of all other variates contributed 65.60% of the total genetic variation. Therefore, the pre dominant axis of variation essentially remains in the sum of all other variates, playing a considerable role in further divergence. Other canonical variates also played a major part in determining

total genetic diversity present in 62 varieties of soybean. This result is in agreement with the report of Shukla (1996). This may be due to the inclusion of much more diverse varieties and characters in this study.

The coefficients attached to the different characters in the first four canonical roots (vectors) are also shown in Table 1. The maximum importance of number of pods/plant followed by days to initiation of flowering and number of primary branches/plant in the primary differentiation between populations is reflected in the corresponding coefficients of the first canonical vectors. Similarly, 100-seed weight, days to initiation of flowering, number of pods/plant, basal pod height and grain yield /plant are reflected in their respective coefficients in the second canonical vectors indicating their relative importance in the secondary differentiation. In the third canonical vectors, protein percentage was of maximum importance followed by number of pods/plant and reproductive phase. Grain yield/plant, reproductive phase, number of primary branches/plant, 100-seed weight and plant height are reflected in their corresponding coefficients in the fourth canonical vectors indicating their relative importance in the further differentiations.

Table 1. Coefficients of first four canonical vectors in different soybean varieties

Character	Canonical vector			
	1	2	3	4
Days to initiation of flowering	0.458	-0.607	0.042	-0.061
Days to 50% flowering	0.175	-0.132	0.096	0.013
Days to maturity	0.113	-0.018	0.205	0.120
Flowering span	0.141	-0.101	0.251	-0.115
Reproductive phase	0.120	0.052	0.392	0.293
Basal node height	0.023	-0.267	0.027	0.082
Basal pod height	0.038	-0.349	-0.346	0.013
Plant height	0.302	-0.110	0.147	0.202
Number of primary branches/plant	0.393	0.156	0.247	0.278
Number of nodes/plant	0.044	0.145	-0.081	0.036
Number of pods/plant	0.566	0.352	-0.427	-0.223
Number of seeds/pod	0.280	0.089	-0.035	0.098
Number of seeds/plant	0.214	0.138	-0.331	-0.040
Grain yield/plant	0.023	0.340	-0.007	0.492
100-seed weight,	-0.067	0.936	-0.040	0.228
Oil content	0.046	-0.025	0.055	0.065
Protein content	0.109	0.273	0.472	-0.631
λ	60.080	58.830	57.230	55.670
%	8.920	8.730	8.490	8.560

Number of pods/plant appeared to be the most important in creating differentiation based on canonical variates. This was in line with the results obtained earlier in soybean by Das *et al.*, (2000); Ganesamurthy and Seshadari (2002) and Kayande and Patil (2009).

The mean value of the varieties for first two canonical roots (Z_1 and Z_2) is given in Table 2. The relative deposition of varieties in two dimensional space in Z_1 (Y-axis) and Z_2 (X-axis) (Fig. 1) shows the genetic divergence among the 62 varieties of soybean. The relative distribution of varieties reflected the broad genetic diversity among the genotypes. Based on the

graph, 62 varieties were grouped into eighteen clusters (Table 3). Cluster I comprised on fifteen varieties while the Cluster II comprised of nine varieties. Cluster III and IV had eight and six varieties respectively. Cluster V had five varieties while Cluster VI, VII and VIII comprised three varieties each. Cluster XV had two varieties and remaining ten clusters were mono-genotypic. It was observed that the genotypes of different geographical origin were grouped together and the genotypes with same origin were included in different clusters. Since Cluster I comprised of varieties from nine different geographical areas. On the contrary, the varieties belonging to the same

Table 2. Mean value of the varieties for first 2 canonical roots (Z_1 and Z_2)

S. No.	Varieties/ genotypes	Developed/ released	Value		S. No.	Varieties/ genotypes	Developed/ released	Value	
			Z_1	Z_2				Z_1	Z_2
1	Alankar	Pantnagar	12.72	6.91	32	MACS 58	Pune	10.86	4.67
2	Ankur	Pantnagar	12.13	4.83	33	MAUS 2	Prabhani	10.59	4.09
3	Bragg	Pantnagar	10.91	5.24	34	MAUS 32	Prabhani	10.9	3.96
4	Birsa Soya-1	Ranchi	10.09	4.44	35	MAUS 47	Prabhani	11.22	5.59
5	Co 1	Coimbatore	10.69	4.21	36	Monetta	Prabhani	10.45	4.98
6	Co 2	Coimbatore	11.37	4.9	37	NRC 2	Indore	11.33	4.8
7	GS 1	Gujarat	11.56	4.23	38	NRC 12	Indore	11.48	5.94
8	Hardee	Karnataka	10.12	4.59	39	NRC 37	Indore	10.82	2.69
9	Himso 1563	Palampur	11.04	5.82	40	NRC 7	Indore	11.69	6.44
10	Improved Pelican	Karnataka	11.37	3.2	41	PS 1024	Pantnagar	11.19	5.61
11	Indira Soya 9	Raipur	10.36	3.96	42	PK 1029	Pantnagar	12.05	5.93
12	JS 2	Jabalpur	9.71	5.4	43	PK 262	Pantnagar	10.53	4.83
13	JS 335	Jabalpur	11.35	5.41	44	PK 308	Pantnagar	11.42	4.36
14	JS 71-05	Jabalpur	11.07	7.43	45	PK 327	Pantnagar	11.7	4.77
15	JS 72-280	Jabalpur	10.79	5.37	46	PK 416	Pantnagar	11.82	5.37
16	JS 72-44	Jabalpur	10.76	4.01	47	PK 471	Pantnagar	12.23	6.51
17	JS 75-46	Jabalpur	10.28	4.26	48	PK 472	Pantnagar	13.47	5.91
18	JS 76-205	Jabalpur	10.29	5.11	49	PK 564	Pantnagar	11.93	5.96
19	JS 79-81	Jabalpur	10.74	4.09	50	Punjab 1	Ludhiana	12.04	3.57
20	JS 80-21	Jabalpur	11.39	3.29	51	PUSA 16	New Delhi	10.39	4.23
21	JS 90-41	Jabalpur	9.69	5.06	52	PUSA 20	New Delhi	12.48	4.99
22	Kalitur	Bangalore	11.78	4.08	53	PUSA 22	New Delhi	11.5	4.73
23	KB 79	Bangalore	9.4	5.3	54	PUSA 24	New Delhi	10.32	4.73
24	KHSb 2	Karnataka	9.03	5.62	55	PUSA 37	New Delhi	11.2	4.2
25	Lee	Pune	11.28	3.99	56	PUSA 40	New Delhi	12.73	4.87
26	MACS 124	Pune	10.83	4.27	57	Samrat	Jabalpur	9.28	5.15
27	MACS 13	Pune	11.2	4.95	58	Shilajeet	Pantnagar	11.65	5.76
28	MACS 330	Pune	7.51	7.85	59	Shivalik	Pantnagar	11.25	4.72
29	MACS 450	Pune	10.71	4.54	60	SL 295	Ludhiana	12.26	6.56
30	MACS 57	Pune	12.35	4.31	61	T 49	Kanpur	11.42	3.56
31	MACS 754	Pune	10.23	4.25	62	VLS 47	Almora	12.3	5.14

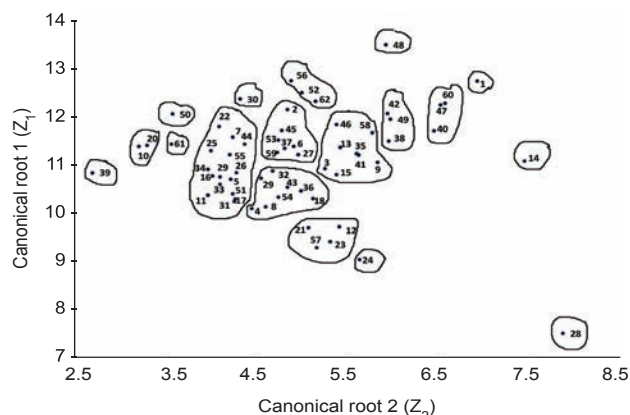


Fig. 1. Two dimensional presentation of divergence of genotypes of soybean using the first two canonical vectors as co-ordinate

geographical area of location fell into different clusters viz., varieties developed at Pantnagar have been fallen into nine different clusters. The clustering pattern of the accessions showed that geographical diversity was not related with genetic diversity. Sharma (2000), Gawande *et al.*, (2002), Tyagi and Sethi (2011) and Patil *et al.*, (2011) reported that there exists no association between genetic diversity and geographical diversity.

The variety PK 472 forming a separate Cluster (IX) had maximum mean values for number of primary branches/plant (5.60), number of pods/ (101.30) and oil percentage (22.86). Alankar variety also had maximum mean values for number of seed/plant (159.90) and grain yield/plant (18.92g). Likewise JS 71-05 had maximum mean value for protein percentage (43.23). Thus, variety PK 472, Alankar and JS 71-05 holds great promise as a parent to obtain promising hybrids and create further variability for these characters.

Based on the genetic divergence analysis and cluster mean value (Table 3), it would be possible to point out some potential combinations, subject to the condition that environment maintain the relative expression of characters with regard to the genotypes. The potential combinations based on the canonical analysis were found to be NRC 37 × MACS 330, NRC 37 × JS 71-05, PK 472 × MACS 330, PK 472 × NRC 39, PK 472 × KHSb 2, T 49 × PK 472, T 49 × PK 471, T 49 × MACS 330, Samart × T 49, Samart × PK 472, NRC 37 × Alankar and Alankar × T 49. These combinations should result in maximum hybrid vigour and highest number of useful segregants during the process of selection in the genotypes of soybean.

Table 3. Clustering pattern of cultivars on the basis of genetic divergence

Cluster group	Varieties	Number
I	GS -1, JS 72-44, Indira Soya 9, PK 308, JS 79-81, PUSA 16, Lee, Co 1, JS 75-46, PUSA 37, MAUS 2, MACS 754, MAUS 32, MACS 124, Kalituri	15
II	Ankur, Co 2, MACS 13, MACS 450, MACS 58, NRC 2, PK 327, PUSA 22, Shivalik	9
III	Bragg, Himso 1563, JS 335, JS 72-280, MAUS 47, PS 1024, PK 416, Shilajeet	8
IV	Birsa Soya-1, Hardee, JS 76-205, Monetta, PK 262, PUSA 24	6
V	JS 2, JS 90-41, KB 79, Samrat	4
VI	NRC 12, PK 1029, PK 564	3
VII	PUSA 20, PUSA 40, VLS 47	3
VIII	NRC 7, PK 471, SL 295	3
IX	PK 472	1
X	Alankar	1
XI	JS 71-05	1
XII	MACS 330	1
XIII	KHSb 2	1
XIV	NRC 37	1
XV	Improved Pelican, JS 80-21	2
XVI	T 49	1
XVII	Punjab 1	1
XVIII	MACS 57	1
TOTAL		62

It is concluded that significant genetic diversity was observed among the cultivars and, canonical discriminant analysis could identify the genetic variation and the most influential traits affecting genetic variations among the genotypes. Numbers of pods/plant and 100-seed weight were identified as the most effective traits in creating diversity amongst cultivars.

Acknowledgment

The authors thankfully acknowledge the Directorate of Research, GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand for the encouragement and help rendered during the course of this investigation.

Table 4. Cluster mean values value of the varieties for different characters

Characters																		
S. No.	Cluster group	Days to flowering initiation	Days to 50% Flowering	Days to Maturity	Flowering span	Reproductive phase	Basal node height (cm)	Basal pod height (cm)	Plant height (cm)	No. of primary branches/ plant	No of nodes/ plant	No of pods / plant	No of seeds / pod	No. of seeds / plant	Grain yield/ plant (g)	100 seed weight (g)	Oil content (%)	Protein content (%)
1	I	52.90	57.67	123.50	11.77	68.80	1.71	13.79	69.43	3.59	14.60	42.75	1.77	66.17	5.88	9.35	20.30	37.02
2	II	49.28	56.72	123.39	10.94	71.78	1.66	13.91	71.39	3.59	15.76	54.40	1.87	88.77	8.84	10.23	20.67	39.59
3	III	49.69	53.56	122.00	10.63	73.81	1.57	14.11	65.83	3.95	15.01	50.78	1.93	85.93	9.80	11.62	20.15	40.14
4	IV	50.17	53.83	123.08	10.75	74.58	1.71	12.77	65.78	2.53	13.82	32.82	1.89	49.28	5.69	11.95	20.70	39.48
5	V	46.50	46.75	121.25	10.00	78.63	1.42	12.59	67.38	2.43	15.13	17.78	1.57	24.80	2.80	10.68	20.37	40.17
6	VI	53.50	52.17	122.50	11.00	75.50	1.75	12.32	73.37	3.97	14.20	62.20	1.90	104.37	13.80	13.55	20.79	40.05
7	VII	41.75	55.67	125.50	11.17	75.00	1.57	15.95	81.67	3.50	15.83	84.00	1.98	139.63	14.35	10.88	20.93	39.26
8	VIII	52.50	52.33	122.17	11.17	74.83	1.63	11.25	73.17	3.53	14.73	66.20	1.90	121.73	17.62	14.43	21.24	39.54
9	IX	49.50	58.00	124.00	15.00	74.5	1.66	10.30	70.30	5.60	15.20	101.30	1.88	105.90	17.25	11.62	22.86	39.2
10	X	55.50	59.50	120.50	10.00	65.00	1.23	7.85	53.00	4.80	15.10	83.60	2.00	159.90	18.92	11.89	20.79	39.55
11	XI	45.00	50.00	121.00	11.00	76.00	1.28	3.55	42.60	4.00	10.00	52.70	1.39	61.20	6.68	10.37	21.41	43.23
12	XII	21.00	25.00	79.00	9.00	58.00	1.00	5.85	34.00	1.40	10.50	1.40	1.00	1.40	0.10	10.17	18.62	40.69
13	XIII	44.00	48.50	122.00	10.00	78.00	1.80	8.60	50.00	2.00	10.60	5.00	1.42	7.90	1.00	13.75	20.75	40.43
14	XIV	53.50	59.00	122.50	12.50	69.00	2.60	16.60	74.70	2.90	15.30	41.60	1.89	53.60	4.77	9.17	21.54	37.28
15	XV	60.25	65.00	125.25	11.75	65.00	1.75	17.97	81.00	3.10	15.55	43.60	2.08	86.00	7.84	9.72	20.56	38.63
16	XVI	61.50	67.00	124.00	12.50	62.50	1.75	9.85	89.90	2.80	12.30	41.80	1.88	79.40	6.14	7.78	17.63	40.89
17	XVII	58.00	65.50	121.50	16.00	63.50	1.93	15.15	87.40	4.90	17.10	48.20	1.90	90.00	9.98	9.74	20.45	39.02
18	XVIII	57.00	60.50	119.50	11.00	62.50	1.80	1.73	73.30	5.20	19.30	80.90	1.87	138.20	12.16	8.95	20.36	38.51

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Malt Quality Evaluation of Exotic Barley Germplasm Grown in Northern Hills: A Non-Traditional Malt Area

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(Received: 02 June 2011; Revised: 11 July 2012; Accepted: 18 July 2012)

Barley (*Hordeum vulgare* L.) cultivation in recent past has got boost in India due to its industrial use in malting and brewing. The areas like northern hills having relatively cooler temperatures during grain development phase with longer duration are considered suitable for malt barley production. However, it is believed that malt quality gets adversely affected by the occurrence of rains during maturity of the crop in the hills. Thirty germplasm cultivated at Hawalbagh, Almora, Uttarakhand were analyzed for malt traits. Though these were not bred for malt barley but the malt quality was found highly desirable for a number of malt traits suggesting that hills can be promising areas for malt barley cultivation.

Key Words: Barley, Germplasm, Hills, *Hordeum*, Malt

Introduction

Barley (*Hordeum vulgare* L.) is one of the important cereal crops of northern hills of India comprising the states of Himachal Pradesh, Jammu and Kashmir and Uttarakhand, particularly in marginal and fragile lands as well as in higher hills. It is the staple food crop in the tribal areas of hills where it is also used in preparation of the local beverages in addition to food and cattle feed. Barley is predominantly grown under rainfed conditions in northern hills and farmers use very low inputs (Verma *et al.*, 2005, Kant, 2006). During past few years the winters have become warmer in hills and drought is becoming a frequent phenomenon. Therefore, most of the farmers now prefer to grow barley over other crops as it supposed to be drought tolerant (Verma *et al.*, 2005). Although, this gives some yield even under drought like conditions but, that's not very profitable in absence of good market. However, if malt quality barley can be grown in hills and procured for use in malting and brewing industry the cultivation of barley will become a profitable preposition.

During recent years barley cultivation in India has got a boost due to its use as industrial raw material for malting and brewing. The minimum quality standards of barley grain and malt have been finalized (Table 1) as desirable limits to classify any barley variety as malt type in India (Verma *et al.*, 2005). As such, malt quality depends on combination of a number of grain and malt

traits and not on any single trait because of differential requirements of the brewing and non-brewing malt by these industries. Many of these traits are though genetic in nature but the environmental effects are also significant. The areas of Haryana, northern Rajasthan, western UP and southern Punjab with sandy soils and shorter vegetative phase with grain development under relatively lower temperature, have been identified suitable for malt barley cultivation (Verma and Nagarajan, 1996). The released cultivars if grown under optimum management conditions in these areas produce very good quality grain. However, in India, barley doesn't get equivalent grain filling period with mild temperatures like Europe and other countries which grow better malting quality barley. In northern plains hardly 30 to 35 days after anthesis are available for grain development and then there is sudden rise in temperature causing the forced maturity (Verma *et al.*, 2005). However, in Northern hills the available period for grain development ranges from 40 to 50 days and temperature are not so high during maturity and the crop matures naturally. Therefore, apart from the traditional areas of malt barley, northern hills can also be a potential area for production of good quality malt barley owing to these highly suitable climatic conditions. There is a general understanding and belief that the malt barley do not perform well under hills condition as the crop normally experience rainfall during maturity which affects the malt quality adversely (Kant, 2006).

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Table 1. Pedigree of the germplasm tested for malt quality

Sl. No.	Accessions	Pedigree / Cross
Two-rowed barley		
1.	VB 0701	Roho//Alger/Ceres362-1-1/3/Kantara/4/Bowman
2.	VB0705	Mo.B1337/WI2291//Moroc9-75
3.	VB 0708	PRTL/BICHY2000//MSEL
4.	VB 0709	SICH84.80/MSEL//INCI
5.	VB 0710	Akrash//WI2291/WI2269/3/WI2291/WI2269//WI2291/Bgs
6.	VB 0711	Viringa'S//Hml-02/ArabiAbiad*2
7.	VB 0712	WI2291/Roho//WI2269/3/WI2291/Bgs//Hml-02
8.	VB 0713	WI2291/Roho//WI2269/3/WI2291/Bgs//Hml-02
9.	VB 0714	Alpha/Durra//ICB-101912
10.	VB 0718	EC-532636
11.	VLB 111	LAMOLINA 94/PETUNIA 1
12.	VLB 113	L.P/OXBOW/MSEL
Six-rowed barley		
13.	VB 0702*	15 th HBSN-16
14.	VB 0703*	MJA/BRB2//QUINA/3/PETUNIA 2
15.	VB 0704	Akrash//WI2291/WI2269/3/WI2291/WI2269//WI2291/Bgs
16.	VB 0706	Lignee640/Lignee527//Lignee527/Rhn
17.	VB 0707	CHUAN 1/3/SLLO/ROBUST//QUINA/4/CEN-/2*CALI92
18.	VB 0715	TOCTE/3/MJA/BRB2//QUINA/4/CIRU
19.	VB 0716	WI2291/Roho//WI2269/3/Arta
20.	VB 0721	BOLDO/MJA//CABUYA/3/CIRU
21.	VLB 94	DL237/VLB 58
22.	VLB 102	TOCTE/TUBO//SHYRI
23.	VLB 104	P.STO/3/LNRIAN/UWA80//LIGNEE640/4/BLLU/5/PETUNIA 1
24.	VLB 107	ISBONO4-27 (BF 89IM-592)
25.	VLB 108	LINAZA-BAR/JAZMIN/5/CEN-B/3/LBIRAN/UNA8271//GLORIA- BAR/ COME-B/4/SEN
26.	VLB 109	CABUYA/3/CLN-B/80.5138//GLORIA-BAR/COPAL/4/CIRU
27.	VLB 110	GOB91DH/ALELI/3/ARUPO/K8755//MORA
28.	VLB 1(C)	NP 109/HBL 62
29.	VLB 56 (C)	Morocco/ VLB 1
30.	VLB 85(C)	HBL 348/VLB 49

* Hull-less barley

Materials and Methods

The present study was undertaken with a view to examine whether the malt quality traits really get adversely affected by the climatic conditions of northern hills. One hundred and seventy six exotic barley germplasm were selected during *rabi* 2005-06 from different International nurseries viz., IBON06-LRA-C, 15th HBSN, IBON-MRA, 13th EMBSN, IBON-06-LRA-M, 28th IBYT, IBYT-06-LRA-C and 33rd IBON during field day at NBPGR, New Delhi as well as DWR, Karnal. These were evaluated during *rabi* 2006-07 at VPKAS, experimental farm, Hawalbagh for agronomic suitability and disease resistance. Grain samples of 30 barley germplasm were selected for malt quality analysis. These including 27

exotic germplasm and three prevalent checks, chosen for grain yield, were grown in station trial, state varietal trial and coordinated IVT during 2007-08 season at experimental farm, Hawalbagh of *Vivekananda Parvatiya Krishi Anusandhan Sansthan* (Vivekananda Institute of Hill Agriculture), Almora, India (29° 36'N and 79° 40' E and 1250 m amsl) under rainfed conditions. All the recommended package of practices was followed. The temperature and rainfall during the period is given in Fig. 1. None of these germplasm has been bred for malt quality. The malt quality analysis was done at quality laboratory, Directorate of Wheat Research, Karnal, India during 2009. The observations on following malt traits were recorded.

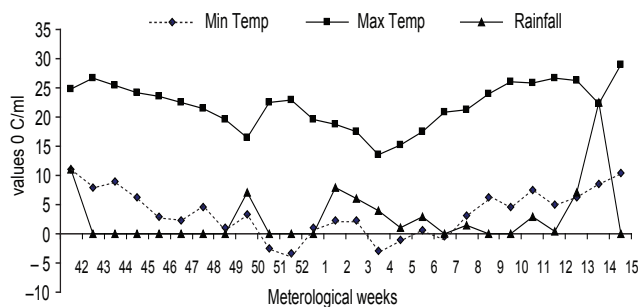


Fig. 1. Meteorological data during the period at Hawalbagh

1. **Malt yield (MY) %:** The malt yield with acceptable range of malt friability should be taken into consideration.
2. **Hot water extract (HWE %):** is one of the most important malting quality traits for the industry and is measured in per cent on fine grind dry weight basis as per the EBC-Analytica IV, 2003 after mashing the grounded malt in mashing bath. It is the extract of soluble components from the malt. It should be around 80% as per standard.
3. **Malt friability (Fb %):** The physical quality of malt is measured by malt friability and homogeneity. The friability meter is a device whose role is to physically disintegrate the grain of malt and to separate its friable constituents from the hard constituents. More a malt is friable, better will it be disintegrated. The whole grain percentage permits to examine the homogeneity of the share (http://www.e-malt.com/specifications/en_friability.htm). It was measured as per EBC-Analytical, 2003. The acceptable limit is 60% in India and 80% at international level.
4. **Malt homogeneity (Hg%):** measured as per cent homogeneous malt using sample retained in malt friability meter mesh during friability analysis and passing this fraction on Sortimat for sieve analysis, as per EBC-Analytica IV, 2003. The non-homogenous fraction is that, which is retained on the 2.2 mm sieve and rest was considered as homogeneous malt (Verma *et al.*, 2008).
5. **Diastatic power (DP):** measured in degree linter value ($^{\circ}\text{L}$) as the total enzymatic activity of the amylases in malt samples as per Institute of Brewing (IOB) Method. Its desirable limit is 90-100 $^{\circ}\text{L}$.
6. **Sachharification time (min):** The total time of transformation of the starch into sugar at the time of the brewing is measured. The time is verified by

the disappearance of blue coloration of the iodine in presence of starch. A good malt saccharifies in less than 10 minutes (correct enzymic action), a longer duration is caused by a bad disintegration of the starch (<http://www.e-malt.com>). More than 5 S times is undesirable.

7. **Wort filtration rate (F rate):** The rate of wort filtration on the standard Whatman No. 1 filter papers, measured as amount of wort (ml/hr) passes through filter paper in one hour duration, as per EBC-Analytica, 2003.
8. **Wort Colour:** Wort colour was measured using EBC Analytica, 2003. The value between 2.0 to 2.5 is desirable.
9. **Grain filling period:** has been calculated by deducting the days to 50% heading from days to 75% maturity.

Results and Discussion

Though there are various malt parameters important in barley but the hot water extract (HWE) is the trait which is paramount (Wright, 2000) and the price of malt is mainly dependent on its HWE values, apart from few other traits like *diastatic* power, friability and homogeneity *etc.* The malting quality is the optimum combination of several grain and malt traits. Since the main purpose of this study was to find out the effect of environmental conditions on malt quality, therefore, the observations were recorded only on malt traits. For comparison the germplasm were grouped into two-rowed and six-rowed. Generally the six-rowed barley is considered to have higher enzyme content, more protein, less starch and a thicker husk than two-rowed barley. The higher level of *diastatic* enzymes makes six-rowed barley desirable for conversion of adjunct starches during mashing (<http://www.maltcompany.com/malt.htm>). The brewing industry does not prefer the malt with very high *diastatic* power and this kind of malt is preferred for malt based energy drinks and confectionaries.

Among the two-rowed strains VB 0710 has number of malt quality traits *viz.*, HWE (80.2), Hg (99.5), Fb (93.1), DP (105) and F rate (285) (Table 2). It has a grain filling duration of 42 days almost one week longer than the plains. The other strain VB 0709 has HWE (81.0), Fb (97.3), Hg (99.3), F rate (265) and grain filling duration 53 days but it has high DP (122). Out of 12, three more strains VB 0701, VB 0705 and VB 0708 have more than 80% HWE. The average HWE of this

set of germplasm was 78.64 and average DP was 105. All the strains showed very high Fb% as well as Hg%. The high wort filtration rate is desirable for the brewing industry. Seven strains VB 0709, VB 0710, VB 0712, VB 0714, VB 0718, VLB 111 and VLB 113 showed F

rate more than 250 ml/h (Table 2).

Out of 18 six-rowed strains VB 0706 has HWE (79.0), Fb (81.5), Hg (98.1), DP (105), F rate (265) and 44 grain filling days whereas, VB 0715 has HWE (78.5), Fb (96.0), Hg (99.8), DP (105), F rate (310) and 46 grain

Table 2. Malt quality traits of two-rowed barley grown at Hawalbagh, Almora

Accessions	MY (%)	HWE (%)	Fb (%)	Hg (%)	D.P. (°L)	S.Time	F.Rate (ml/hr)	WC (EBC)	Heading (days)	Maturity (days)	GF (days)
VB 0701	88.2	83.2	90.6	99.0	83	5	105	2.5	130	173	43
VB 0705	90.7	80.2	83.3	95.5	125	5	150	2.5	110	163	53
VB 0708	88.6	85.2	95.9	99.1	105	5	170	3.0	117	165	48
VB 0709	83.9	81.0	97.3	99.3	122	5	265	2.5	113	166	53
VB 0710	84.7	80.2	93.1	99.5	105	5	285	2.5	128	170	42
VB 0711	85.3	77.0	83.1	97.6	105	5	235	2.5	137	174	37
VB 0712	86.2	78.0	88.5	97.8	100	5	290	2.5	124	169	45
VB 0713	84.3	75.0	70.7	91.8	125	5	230	2.5	133	170	37
VB 0714	84.4	78.7	97.1	99.8	111	5	310	2.0	136	170	34
VB 0718	83.2	71.0	84.2	97.9	105	5	255	2.5	133	171	38
VLB111	86.8	75.0	96.4	99.8	80	5	300	2.5	126	166	40
VLB113	86.6	79.0	95.1	99.8	95	5	310	2.5	124	167	43
Mean	86.1	78.6	89.6	98.1	105.2	5	242.1	2.5	126	169	42.8
Range	83.2-90.7	71.0-85.2	70.7-97.3	91.8-99.8	80-125	-	105-310	2-3	110-137	163-174	34-53
STDEV	2.2	3.8	8.0	2.4	14.6	0.00	67.5	0.2	8.8	3.0	6.2
Desirable limit		>80%	>60%	>90%	80-120 °L	≤ 5.0	>250	2.0-2.5			

Note: Bold one indicate the desirable values

Table 3. Malt quality traits of six-rowed barley grown at Hawalbagh, Almora

Accessions	MY (%)	HWE (%)	Fb (%)	Hg (%)	D.P. (°L)	S.Time	F.Rate (ml/hr)	WC (EBC)	Heading days	Maturity days	GF (days)
VB 0702	77.7	83.5	78.4	98.1	91	5	120	2.5	130	170	40
VB 0703	82.7	85.5	79.1	98.7	71	5	110	2.5	124	166	42
VB 0704	88.2	80.7	67.9	86.7	83	5	175	2.5	139	175	36
VB 0706	87.3	79.0	81.5	98.1	105	5	265	2.5	125	169	44
VB 0707	88.6	81.0	74.0	93.6	105	5	220	3.0	122	163	41
VB 0715	81.9	78.5	96.0	99.8	105	5	310	2.5	122	168	46
VB 0716	87.4	78.3	86.3	99.3	87	5	275	2.5	134	172	38
VB 0721	79.8	75.5	94.7	99.5	119	5	260	3.0	136	176	40
VLB 56	85.3	73.8	82.3	97.3	111	5	80	3.0	149	195	46
VLB 102	75.8	73.3	72.1	94.4	91	5	165	3.0	151	194	43
VLB 85	77.6	76.5	68.2	92.5	74	5	85	2.5	127	171	44
VLB104	83.4	78.7	94.1	99.1	74	5	145	2.5	148	195	47
VLB107	84.9	78.0	68.8	93.9	77	5	275	3.0	150	196	46
VLB108	81.1	79.0	96.2	99.8	67	5	150	2.5	152	192	40
VLB1	82.1	71.8	74.5	95.9	91	5	275	2.5	141	184	43
VLB109	89.3	77.0	88.9	99.4	95	5	330	2.5	127	171	44
VLB110	83.0	73.5	90.0	99.3	95	5	300	2.0	126	167	41
VLB94	85.3	75.0	91.8	98.5	77	5	320	2.5	152	195	43
Mean	83.4	77.7	82.5	96.9	89.9	5.0	214.4	2.6	136	179	42.4
Range	75.8-89.3	71.8-85.5	67.9-96.2	86.7-99.8	67-119		80-320	2-3	121-152	163-196	36-47
STDEV	4.00	3.60	10.10	3.5	15.0	0.00	85.5	0.27	11.5	12.2	2.9
Desirable limit		78%	>60%	>90%	90-130 °L	≤ 5.0	>250	2.0-2.5			

Note: Bold one indicate the desirable values

filling days. Malt Fb and Hg showed very high values for all the accessions. In addition, eight more strains had high HWE (> 78%) and two more strains have F rate > 250 (Table 3). The average grain filling period in both the groups is more than 42 days ranging from 34-53 days (Table 2 & 3). The mean maximum temperature ranged from 13.5 to 28.9 °C and minimum temperature from -2.9 to 10.4°C. From mid march to mid april around 33 mm rainfall was received (Fig. 1).

The encouraging results from the present study are suggestive that northern hills can be a promising area for malt barley production. The climatic conditions are more congenial for its production and high malt quality can be obtained in hills as compared to plains. The cultivation of malt barley in the hills will not only provide good quality malt barley leading to establishment of new malting and brewing units to utilize the locally produced malt barley, but will also provide premium

prices to the farmers. More employment can be generated and migration of rural youth can also be checked.

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Influence of Seed Size on Germination and Early Seedling Growth in Indian Mustard (*Brassica juncea* L.)

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(Received: 22 November 2010; Revised: 14 July 2011; Accepted: 27 March 2012)

Indian mustard (*Brassica juncea* L.) accounts for about 66% of the total germplasm holdings of rapeseed-mustard group of oilseed crops in the country. Conservation of good quality seeds of a germplasm accession is a prerequisite for its long-term viability and use in crop breeding programme. Seed size in Indian mustard influenced the loss of germination during storage. In the present investigation the effects of seed size on oil and protein content of seed, seed germination and seedling growth were studied during 2008-09 with 4 varieties and an advanced breeding line (Kranti, Pusabold, Pusa Jaikisan, Varuna, and BPR-549-9) of Indian mustard. Oil content varied from 36.4-38.9%, 39.0-42.6% and 39.0-43.8%, respectively, for small, medium and large group of seeds. Seed size had significant and positive correlation with root length ($r=0.655^*$), dry weight ($r=0.894^{**}$), root to shoot ratio ($r=0.879^{**}$) and vigour index ($r=0.938^{**}$). Seedlings dry weight, vigour index, root length and root to shoot ratio increased with an increase in seed size thereby suggesting that the seeds after grading should be conserved in the gene bank.

Key Words: *Brassica juncea* L., Seedling vigour index, Germination, Seed size, Germplasm, Conservation

Introduction

Rapid seedling establishment is an important requirement for successful crop production in dryland farming systems. Seed size, as a characteristic of seed quality, influences seedling growth and establishment. Seedling establishment and speed of emergence influence the time required for seedling to reach the autotrophic phase. Most investigators have reported a positive relationship between seedling vigor, improved stand establishment and higher productivity of cereal crops with plants originating from large seed compared to those grown from smaller seed. Amico *et al.* (1994) concluded that higher vigor that occurred in larger seed is due to the larger food reserves in these seeds. They also noted a positive linear relationship between seed weight and emergence in the field. Rapeseed-mustard is an important group of oilseed crops in India having more than 14, 000 germplasm accessions (Anonymous, 2009). Indian mustard (*Brassica juncea* L.), among these crops account for nearly 66 % of the total germplasm holdings in the country (Anonymous, 2007). Conservation of germplasm is an important aspect of crop genetic resource management programme. Kant and Tomar (1995) reported that seed size in Indian mustard also influenced seed germination. Furthermore, the rate of dry matter transfer and depletion of nutrients from the cotyledons is dependent on the size

of the seed (Naidu and Narayanan, 1981) thus influencing seedling development. Therefore, conservation of good quality seeds of a germplasm accession is a prerequisite for its long-term viability, early seedling establishment, vigorous and healthy crop growth for higher yield and use in crop breeding programme. Grading of seeds is an effective method for eliminating seed of weaker seeds. In the present investigation an attempt was made to assess the effects of different grades of seeds on oil, protein content, seed germination and seedling growth of Indian mustard.

Materials and Methods

The present experiment was carried out during 2008-09 in laboratory with 4 varieties and an advanced breeding line of Indian mustard (Kranti, Pusabold, Pusa Jaikisan, Varuna and BPR-549-9). Grading of seeds was done by passing a random sample through a series of 3 sieves of different pore sizes and seeds were categorized in to three groups, viz., small ($< 2 \text{ mm}^2$), medium (2 mm^2) and large (4 mm^2). The oil and protein content of different groups were analyzed using a pre-calibrated NIR Analyzer (Dick John Instalab 600) while a random sample of 1000-seed was weighed with a digital electronic balance (Precisa). The pure seed fraction is poured onto the working table, mixed well, and divided with a spatula into the

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same number of equal parts as replicates. Each part is mixed well again and the replicates counted at random. The moist filter paper was lined in Petri dishes (9-cm diameter) and seeds were placed on top of the paper. The seeds in Petri-dishes were allowed to germinate in B.O.D incubator at a temperature of $25 \pm 1^{\circ}\text{C}$ and 55-60% relative humidity. The uniform temperature was maintained throughout the germination period. Seedlings were exposed to light for eight hours in every 24 hour as per rules (ISTA, 1985). At the first count (3rd day), the normal seedlings were removed and recorded and final count was taken on 7th day. The experiment was repeated thrice. Root dry weight was divided by shoot dry weight to work out the root to shoot ratio. Seedling vigour index was computed as the product of seedling dry matter and seed germination (Abdul-Baki and Anderson, 1973) and expressed in percent. Water imbibition of different groups was recorded on 20 seeds each during 2-12 hours of seed soaking and computed as follows:

$$\text{IR} = \frac{W_2 - W_1}{W_1} \times 100;$$

Where, IR = W_1 = Initial weight of seeds and W_2 = Weight of imbibed seeds.

Analysis of variance was conducted considering the data in factorial completely randomized design (Gomez and Gomez, 1984).

Results and Discussion

Analysis of variance revealed significant genotypic differences for all the characters except seed germination while seed size significantly affected all the characters investigated except seed germination and protein content. Water imbibition, 1000-seed weight, protein content, seedling dry weight and vigour index were significantly affected by interaction of variety x seed size.

Oil and Protein Content

Different groups of seeds had significantly different 1000-seed weight. Varuna showed maximum seed weight (2.94 g) within small seed group. The seed weight was highest for the genotype Pusa Jaikisan in the medium and BPR 549-9 in the large seed group (Table 1). Seed weight varied from 1.49 (Kranti) -2.94g (Varuna); 3.40 (Kranti) – 4.73g (Pusa Jaikisan) and 4.93 (Kranti)-6.54g (BPR-549-9), respectively, for small, medium and large seed group (Table 1). Oil content (%) also showed substantial variation among the genotypes and the groups.

The genotype Kranti and BPR 549-9 showed maximum (39.0%) oil content for smaller seeds while the genotype BPR-549-9 showed maximum oil content for medium (42.6%) and large (43.8%) seeds. Within the group oil content ranged from 36.4-39.0%, 39.0-42.6 and 39.0-43.8%, respectively, for small, medium and large seed group. The results suggested that higher oil content of large seeds might result in good seedling vigour as the seedling growth depends on the seed reserve during the initial growth stage as also suggested by (Naidu and Narayana 1981) in groundnut. Protein content (%) of the seeds did not differ significantly among the groups but genotypes had significant differences. The mean protein content was 20.1% for small, 20.2% for medium and 20.5% for large seeds (Table 1). Varuna and Pusa Jaikisan showed fairly consistent and higher protein content in all the groups of seeds. Since Indian mustard contains food reserve as oil, predominantly fatty acids, hence, limited variability existed for protein content and it seemed to be independent of seed size.

Water Imbibition and Germination

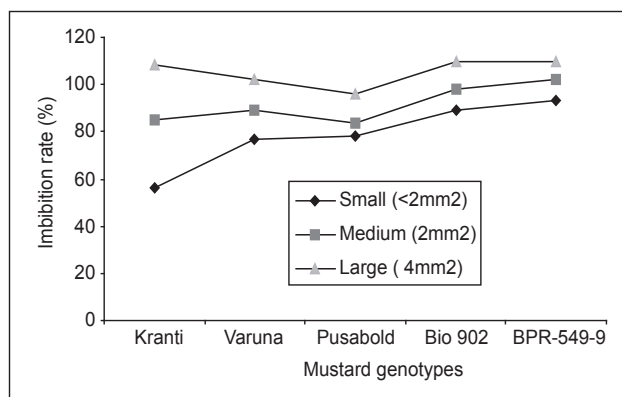
Water imbibition gradually increased from 2 to 12 hrs and was the highest in large seeds irrespective of the genotypes, ranging from 56.5% (Kranti) to 109.7% (Pusa Jaikisan) after 12 hours of seed soaking (Fig.1). The imbibition was 25.8(BPR 549-9)-62.3% (Pusa Jaikisan), 28.7 (BPR 549-9)-71.3% (Pusa Jaikisan), 37.0 (BPR 549-9)-88.4% (Pusa Jaikisan), 45.6 (Kranti)-105.0% (Pusa Jaikisan) and 48.0(Kranti)-107.9% (BPR 549-9), respectively, at 2, 4, 6, 8 and 10 hours of seed soaking. Among the groups, the range was 56.5 (Kranti)-93.1% (BPR 549-9), 78.5 (Pusa bold)-102.5% (BPR 549-9) and 89.1 (Pusa bold)-109.7% (Pusa Jaikisan, BPR 549-9), respectively, for small, medium and large seeds. The imbibition was 27.6 % higher in large seeds as compared to small seeds and the highest increase was recorded for the variety Kranti (58.9 %) at 12 hours of seed soaking. Pusa Jaikisan followed by BPR 549-9 showed the highest imbibition. The increased imbibition was also reflected in enhanced germination. The highest germination recorded for BPR 549-9 might be due to its better imbibition. The findings of the present investigation are in agreement with those earlier reports (Anonymous, 2008). There was no significant difference among the genotypes as well as different size of seeds for germination. The genotype BPR-548-9 showed maximum germination in all the groups varying from 94.5 to 97.2%. All the genotypes had > 90 % germination irrespective of the

Table 1. Effect of seed size on seed weight, oil, protein content, seedling growth and vigour index of Indian mustard

Genotype	1000-seed weight (g)			Oil content (%)			Protein content (%)			Germination (%)			Shoot length (cm)		
	Small	Medium	Large	Small	Medium	Large	Small	Medium	Large	Small	Medium	Large	Small	Medium	Large
BPR 549-9	1.75	4.46	6.54	39.0	42.6	43.8	18.3	19.6	19.8	94.5	96.0	97.2	3.70	2.70	2.20
Kranti	1.49	3.40	4.93	39.0	41.7	41.7	20.1	20.3	20.5	92.1	93.3	95.0	3.73	3.07	2.90
Pusa bold	2.47	4.68	6.34	38.3	40.8	41.3	19.3	19.5	19.9	93.5	96.6	94.7	4.20	4.10	3.60
Pusa Jaikisan	2.62	4.97	6.52	36.4	39.0	39.0	22.3	21.2	21.1	92.7	91.1	95.2	4.30	3.63	3.10
Varuna	2.94	4.10	5.91	38.8	40.1	40.0	20.3	20.7	21.3	90.8	92.2	94.7	4.20	3.90	3.00
CD (P = 0.05)															
Genotypes (G)	0.24			0.77			0.56			NS			0.56		
Groups (g)	0.19			0.59			NS			NS			0.44		
G x g interaction	0.42			NS ^a			0.97			NS			NS		

Contd.-----

Genotype	Root length (cm)			Dry weight / 5 seedlings (mg)			Root to shoot ratio			Vigour index (%)		
	Small	Medium	Large	Small	Medium	Large	Small	Medium	Large	Small	Medium	Large
BPR 549-9	12.30	13.20	14.20	12.30	20.47	29.23	3.37	4.97	6.67	1163.2	1971.2	2884.5
Kranti	10.20	10.30	11.20	11.53	17.60	18.67	2.73	3.43	3.87	1058.9	1643.0	1782.9
Pusa bold	11.27	12.90	13.80	11.83	18.87	28.10	2.80	3.13	3.83	1108.7	1828.1	2661.6
Pusa Jaikisan	10.00	10.30	11.70	15.63	20.83	29.60	2.33	3.57	3.90	1451.2	1899.6	2820.5
Varuna	9.57	10.20	11.60	11.13	16.50	22.43	2.70	3.40	3.93	1466.7	1520.6	2123.6
CD (P = 0.05)												
Genotypes (G)	1.44			1.48			0.77			179.5		
Groups (g)	1.11			1.14			0.60			139.0		
G x g interaction	NS			2.56			NS			310.9		

NS^a: Non-significant**Fig. 1. Effect of seed size on water imbibition of different mustard genotypes**

group. Dubey *et al.* (1989) and Kant and Tomar (1995) also reported reduced germination up to 8% of small seeds in Indian mustard

Seedling Growth

The seed size and shoot length appeared to have an inverse relationship as the shoot length was significantly reduced with increased seed size. The decrease in shoot

length was about 25% for large seeds over that of small seed. In the small size group, all the varieties had similar shoot length (Table 1). The varieties Pusa Bold, Pusa Jaikisan and Varuna in the medium group and all the varieties under large seed group exhibited significant differences in shoot length. Root length increased by about 9.3 and 14% for the medium and large seeds over that of small seeds. Genotype BPR 549-9 had the maximum root length in all the three groups varying from 12.3-14.2 cm. Genotypes Pusa bold and BPR 549-9 had significantly longer roots than the other varieties in small, medium and large seed groups (Table 1). The increase in root length with the seed size suggested that the large seeds might result in better crop establishment in Indian mustard. Kant and Tomar (1995) also reported significant increase in root and non-significant differences in shoot length in Indian mustard. However, Dubey *et al.* (1989) reported significant increase in root and shoot length of large seeds over small seeds. Seedling dry weight differed significantly among the groups and showed an increase of 39.7 and 89.8% for medium and large over the small seeds, respectively. There was further increase of 35.9% in seedling dry weight of large

seeds over the medium ones. Pusa Jaikisan followed by BPR 549-9 had significantly higher seedling dry weight than other genotypes in all the three groups (Table 1). The increase in dry weight of the seedling could be due to increase in root length as well as more dry matter accumulation in shoot and roots per unit length. Increase in seed size was also reflected in enhanced root to shoot ratio. The mean root to shoot ratio was 2.79, 3.70 and 4.44, respectively, for small, medium and large seeds. Genotype BPR 549-9 had the highest root to shoot ratio irrespective of the seed size (Table 1). High root to shoot ratio in early seedling development might result in better crop establishment.

Seedling Vigour Index

Since seedling vigour index was the product of germination and seedling dry weight, hence followed the similar pattern of change as that of seedling dry weight. It differed significantly among the groups and showed an increase of 41.8 and 96.4% for medium and large over the small seeds, respectively. Seedling vigor of large seeds was higher by 38.5% over that the medium seeds. Seedling vigour was significantly higher for the genotype BPR 549-9 followed by Pusa Jaikisan than other genotypes in large seeds (Table 1). The increase in seedling vigour was primarily due to more seedling dry matter with increase in seed size, as the germination did not differ significantly among the genotypes and group of seeds.

Correlation analysis revealed that seed size had no relationship with seed germination, oil and protein content. But positive and significant association of seed size was observed with root length ($r=0.655^*$), dry weight ($r=0.894^{**}$), root to shoot ratio ($r=0.879^{**}$) and vigour index ($r=0.938^{**}$). Sedighi *et al.* (2011) also observed similar trend of correlation in safflower. The results of the present investigation revealed that although seed germination was not affected significantly by seed size but root length, seedling dry weight, root to shoot ratio and seedling vigour index enhanced with increase in seed size which would result in early and fast emergence of the crop especially under limited moisture conditions.

Therefore, simple technique of seed grading could be valuable for the long-term conservation of the germplasm. However, there is a need to further study the effects of storage on germination and seedling development of different grades of seeds.

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Physico-chemical Characterization of Unexploited Mango Diversity in Sub-mountain Zone of Northern India

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(Received: 23 November 2011; Revised: 24 July 2012; Accepted: 28 July 2012)

In Punjab province of India, area under mango (*Mangifera indica* L.) fruit plantation in the state has declined drastically due to deforestation, population pressure, shifting to high remunerative cropping systems, reoccurrence of cold waves, developmental works, higher incidence of pests and diseases, etc. Hence, a survey was conducted for documentation about the extent of diversity found in the native landraces/strains of mango. Twenty eight elite strains enjoying local patronage were evaluated for table and sucking purposes, preparation of pickle/canning/beverages/amb leather on the basis of physical appearance and chemical attributes. Physico-chemical analysis of fruit samples revealed that variability found in indigenous mango population in various qualitative and quantitative attributes not only contributes to biological diversity, nutritional security and livelihood but can also be used for crop improvement. The present study highlights that it is the need and demand of Punjabi folklore to conserve and protect such biologically rich areas for the benefit of posterity.

Key Words: Biodiversity, *Mangifera indica*, Economic valuation

Introduction

India is traditionally world's largest producer of mango (*Mangifera indica* L.) contributing nearly 49.1% of the total global mango production from an area of 2.31million ha with an annual production of 15.0 mt. During 2009-10, almost \$ 9.8 million foreign exchange was earned from the export of fresh mango fruits and their value added products, i.e. mango pulp, pickles, jam, squashes, chutney, slice etc. Mango fruit is a rich source of vitamin A and C, potassium, β -carotene, amino acids, minerals and antioxidants; and also contain an enzyme showing stomach soothing properties. Mango originated in Indo-Malayan region stretching from India to the Philippines and Papua New Guinea. It belongs to family Anacardiaceae and comprises 69 species of genus *Mangifera*, which are distributed throughout the world (Kostermans and Bompard, 1993). It is domesticated in the Indian sub-continent dates back to at least 4000 years; however, importance to its plantation was given during the dynasty of Mughals.

Mango is highly cross-pollinated and heterozygous fruit crop, thus exhibits wide genetic variability in seedling population. Majority of cultivated mango varieties were developed through selection on the basis of fruit shape, colour, size, flavour, aroma, taste, time of maturity, juice

content, TSS/acid blend, etc. Presently, India harbours more than 1000 mango varieties/landraces in different diversity regions and represents the biggest mango germplasm in the world. In Punjab province of India, nearly 80% of total mango growing areas are confined to sub-mountain zone. In this region, old mango plantation predominantly from seedling origin are established naturally or propagated through selected stones from meritorious indigenous mango plants on the basis of fruit quality characteristics by local fruit lover during 19th and early 20th century. These are at present mostly growing along a strip of roads, riverbanks, undulated terrain in mountainous tracts, government revenue lands, mango groves etc., exhibit a wide range of variability in desirable horticultural traits like fruit shape, size, juice consistency, bearing regularity, fruit yield, tolerance/resistance to various biotic and abiotic stresses etc. (Navprem *et al.*, 2011).

Besides, enhancing biodiversity in natural habitat and providing nutrition security to local population, these seedling mangoes provide a wealth of variability for carrying out selections of desirable strains and ensure continuous supply of novel genetic material for future crop improvement (Singh and Jawanda, 1963). Likewise, Ravishankar *et al.* (2000) reported that knowledge of

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a diverse genetic gene pool is essential in designing future breeding strategies for sustainability in mango production. It is therefore, germplasm act as basis of variation for new assortment and necessary to conserve these precious genetic resources through collection of local indigenous germplasm. It is well documented that mango cultivars/strains/landraces/clones are developed from open-pollinated seedling progenies viz. 'Neldawn', 'Neldica', 'Heidi' and 'Ceriese' in South Africa (Marais, 1992); 'Manipur-I' and II mango clones in North-eastern region of India (Chadha and Yadav, 1996); 'Paiyur-1' from 'Neelum' mango cultivar (Yadav, 1997); 'Dashehari-51' from 'Dashehari' mango cultivar (Negi, 1997); 'Rumang' a chance seedling of 'Xiangmang' mango in China (Luo and He, 1996); 'Gangian Sindhuri' (Sharma *et al.*, 2006) and 'Ataulfo' from 'Manila' mango in Mexico (Galan Sauco, 2011). Rajwana *et al.* (2011) reported that most of the mango cultivars grown in Pakistan have been selected from the seedling population of 'Chaunsa' or hybrids developed by using it as one of the parents. Hence, the present survey was carried out to investigate the nature and assessment of genetic variability in mango seedling progenies for physico-chemical attributes.

Material and Methods

A survey of indigenous mango seedlings was carried out jointly by Punjab Agricultural University and Punjab Biodiversity Board, Chandigarh (India) for the evaluation of elite germplasm and to conserve in situ, in their wild habitats, where these can continue to adopt and grow along with their natural surroundings. Mango samples from more than twenty eight apparently phenotypically different mango varieties/landraces, locally popular for their high performance and good quality fruit as per the information provided by Department of Forests and Wildlife (Hoshiarpur), Department of Horticulture (Punjab) and feed back from local villagers etc., were selected before harvesting period. Fruits from marked trees were collected randomly at the time of their respective harvesting period and analysed for various physico-chemical traits in the laboratory. Average fruit and stone size, peel weight, stone weight, pulp weight, fruit weight, pulp/stone ratio, fruit colour, flavour and time of maturity were determined using standard methods. The juice was extracted from the pulp by straining through a muslin cloth and total soluble solids were noted with Bausch and Lomb hand refractometer and expressed in terms of degree brix and values were corrected at 20°C. Juice acidity was estimated by titrating 2 ml juice

against 0.1 N NaOH using phenolphthalein as indicator (AOAC, 1980). Total sugars, reducing sugars and non-reducing sugars were determined by volumetric method. The data was analysed as per the method by Gomez and Gomez (1984).

Results and Discussion

The data pertaining to physico-chemical attributes of elite mango strains along with common vernacular name indicating a great diversity (Table 1-3). Some interesting mango strains observed in the area are locally known as *Anda Dusehree* (flavour & taste resembled to a popular Indian table purpose mango variety 'Dashehari', but fruit shape was looked like egg), *Laddu Amb*, *Gola Ghassipur* and *Ber Amb* on the basis of fruit shape. In Punjabi folklore, native mango strains are called as '*Chhalli*' on account of their oblong shape and large fruit size (resembling a small sized corn cob). Attractive yellow fruit colour with red blush on the shoulders was observed in seven mango strains (*Anami Chhalli*, *Choe Sindhuri*, *Ghassipur di Chhalli*, *Laddu Amb*, *Mahantan di Laltain*, *Sindhuri Chusa*). Fruit colour ranged from yellowish to light yellow, deep chrome, greenish, spinach green and dark green in rest of selected mango strains. Fully coloured fruits are locally preferred and called as *Arru Amb* and *Pencil Amb*. These are preferred for sucking type of mangoes mostly due to thin and abundant juice content; soft flesh, coarse fibres and sell at higher price in the area.

Maximum fruit weight (380.4 g) and fruit length (12.52 cm) was found in strain *Jogiya Chhalli* collected from Government Orchard, Bhunga and percentage contribution of pulp, peel and stone in the fruit was 70.3, 16.0 and 13.7, respectively. Minimum average fruit weight of 60.1 g was recorded in *Ber amb* (which appeared like a ripe fruit of *Zizyphus* species). The highest fruit pulp weight (267.5 g) was also recorded in *Jogiya Chhalli*, followed by *Achhari Gola* (186.1 g), *Thudi Amb* (155.5 g), *Gola Desi* (153.2 g) and the lowest fruit pulp weight was recorded in *Ber Amb* (18.3 g). The average stone weight in different strains varied from 19.2 g to 64.5 g; being maximum in *Achhari Gola* and minimum in *Arru Amb* (tastes like a *Prunus persica*). Peel weight in strains- *Mahantan di Chhalli*, *Thudi Amb*, *Banta Amb No. 1* and *Jogiya Chhalli* ranged from 46.6 g to 60.8 g; however, it was the lowest (12.5 g) in *Kala Amb*. Higher pulp/stone ratio is a favourable physical character in mango and it varied from 0.94 in *Ber Amb* to 5.13 in

Table 1. Phenotypic characters of sucking mango varieties in district Hoshiarpur

Strains	Sample collection site	Fruit shape	Fruit colour	Time of fruit maturity	Pulp colour	Fruit taste	Flavour	Presence of fibres
Achari Gola	Inami Bagh	ovate oblong	Yellow	2 nd week of July	Yellow	sweet	Pleasant	Abundant short
Anami Amb	Inami Bagh	ovate	Yellow with red blush	4 th week of July	Yellow	very sweet	Pleasant	Absent
Anami Chhalli	Inami Bagh	oblong	Yellowish green	3 rd week of July	Creamish yellow	very sweet	Pleasant	Sparse short
Anda Dushehree	Inami Bagh,	ovate	Yellowish green	1 st week of July	Creamish	Sweet	Pleasant	Absent
Arru amb	Inami Bagh	round	Sindhuri yellow	2 nd week of July	Orange	Sweet	Pleasant	Scanty
Banita Amb No. 1	Village Darapur	ovate oblong	Yellowish green	2 nd week of July	Creamish	Sour	Pleasant	Abundant long
Banita Amb No. 2	Village Darapur	ovate oblong	Yellowish green	2 nd week of July	Yellow	Sour	Pleasant	Abundant long
Banita Amb No. 3	Village Darapur	round	Spinach green	3 rd week of July	Yellow	Sour	sonfia	Abundant long
Ber Amb	Inami Bagh	round	Deep chrome	1 st week of July	Yellow	very sweet	Sonfia	Scanty short
Bhagva Chhalli	Inami Bagh	ovate oblong	Yellowish green	1 st week of July	light yellow	very sweet	Pleasant	Scanty short
Chhalli No. 18	Village Daffar	oblong	Yellowish	2 nd week of July	Yellow	superb	Pleasant	Abundant long
Charan Achari	Ghassipur Orchard	ovate oblong	Greenish	2 nd week of July	Orange	Sour	Sonfia	Scanty
Choe Sindhuri	Ghassipur Orchard	ovate	Yellowish with red blush on shoulders	1 st week of August	Light yellow	Sour	Pleasant	Long all over
Ghassipur Amb	Ghassipur Orchard	ovate	Yellowish red tinge	2 nd week of July	Yellow	very sweet	Pleasant	Scanty
Gola Desi	Inami Bagh	round	Light yellow	2 nd week of July	Yellow	Sweet	Pleasant	Abundant short
Gola Ghassipur	Ghassipur Orchard	round	Yellowish green	2 nd week of July	Yellow	Sweet	Sonfia	Scanty short
Jogiya Chhalli	Govt. Orchid, Bhunga	ovate oblong	Yellowish	2 nd week of July	Orange	Sweet	Pleasant	Scanty
kala Amb	Govt. Orchid, Bhunga	ovate	Green	3 rd week of July	Yellow	Sweet	Pleasant	Absent
Laddu Amb	Ghassipur Orchard	round	Yellow with red blush	3 rd week of July	Orange	Sour	Pleasant	Much short
Mahantan di Chhalli	Village Daffar	oblong	Yellowish	2 nd week of July	Yellow	Sweet	Sonfia	Abundant long
Mahantan di laltrain	Village Daffar	ovate	Light yellow	3 rd week of July	Yellow	Sweet	pleasant	Much short
Pencil Amb	Inami Bagh	oblong	Yellow with apple blush	2 nd week of July	Cream	Sweet	Pleasant	Abundant short
Pirh wala Amb	Village Chohal (Road side)	ovate	Yellowish green	2 nd week of July	Creamish	very sweet	aromatic	Abundant short
Rasbhari	Village Daffar	oblong	Yellow	4 th week of July	Lemon	very sweet	pleasant	Abundant short
Shashi Amb	Village Chohal	oblong	Greenish yellow with reddish tinge	3 rd week of July	Orange	very sweet	Pleasant	Absent
Sindhuri Chusa	Adia Orchid, Hariana Town	oblong	Yellow with red blush	2 nd week of July	light yellow	very sweet	Pleasant	Sparse
Thudi Amb	Adia Orchard, Hariana Town	Oblong ovate	Greenish	3 rd week of July	light yellow	Sweet	Pleasant	Abundant short
Tota pari	Village Kukanate	ovate oblong	Greenish yellow	2 nd week of July	Orange	Very sweet	sonfia	Scanty

Table 2. Comparison of fruit size and weight in different sucking mango varieties in district Hoshiarpur

Strains	Fruit weight (g)	Fruit length (cm)	Fruit breadth (cm)	Pulp weight (g)	Pulp (%)	Peel weight (g)	Peel (%)	Stone weight (g)	Stone (%)	Pulp:stone ratio
Achari Gola	296.5	10.07	7.77	186.1	62.8	45.9	15.5	64.5	21.8	2.89
Anami Amb	99.8	7.22	4.59	39.8	39.9	27.2	27.3	32.8	32.9	1.21
Anami Chhalli	175.7	10.27	5.57	104.5	59.5	26.5	15.1	44.7	25.4	2.34
Anda Dushree	60.1	6.75	4.63	22.2	36.9	18.5	30.8	19.4	32.3	1.14
Arru amb	110.0	6.01	5.55	68.0	61.8	22.8	20.7	19.2	17.5	3.54
Banta Amb No. 1	212.7	9.09	6.58	103.2	48.5	55.6	26.1	53.9	25.3	1.91
Banta Amb No. 2	142.5	7.52	5.52	71.5	50.2	30.7	21.5	40.3	28.3	1.77
Banta Amb No. 3	138.0	7.43	6.04	65.5	47.5	32.7	23.7	39.8	28.8	1.65
Ber Amb	50.3	4.63	3.83	18.3	36.4	12.6	25.1	19.4	38.6	0.94
Bhagva Chhalli	185.2	10.04	5.59	122.5	66.1	25.5	13.8	37.2	20.1	3.29
Chhalli No. 18	110.4	9.29	5.24	46.1	41.8	27.1	24.5	37.2	33.8	1.24
Charan Achari	162.3	7.51	5.79	106.1	65.4	27.5	16.9	28.7	17.7	3.70
Choe Sindhuri	111.6	7.52	5.01	61.4	55.0	19.3	17.3	30.9	27.7	1.99
Ghassipur Amb	95.5	6.73	5.01	48.9	51.2	16.5	17.3	30.1	31.5	1.62
Gola Desi	220.2	8.01	6.52	153.2	69.6	27.3	12.4	39.7	18.0	3.86
Gola Ghassipur	170.7	7.22	6.26	96.5	56.5	39.5	23.1	34.7	20.3	2.78
Jogiya Chhalli	380.4	12.52	7.51	267.5	70.3	60.8	16.0	52.1	13.7	5.13
Kala Amb	64.6	6.09	4.55	29.0	44.9	12.5	19.4	23.1	35.8	1.26
Laddu Amb	97.5	6.03	5.09	50.5	51.8	20.5	21.0	26.5	27.2	1.91
Mahantan di Chhalli	163.2	9.51	5.60	67.2	41.2	46.6	28.6	49.4	30.3	1.36
Mahantan di laltain	142.9	7.20	5.53	64.5	45.4	33.9	23.2	44.5	31.3	1.45
Pencil Amb	119.7	7.53	5.04	75.8	63.3	19.0	15.9	24.9	20.8	3.04
Pirh wala Amb	99.1	6.50	5.25	51.4	51.9	17.2	17.4	30.5	30.8	1.69
Rasbhari	106.5	7.07	5.50	57.3	53.8	21.4	20.1	27.8	26.1	2.06
Shashi Amb	192.1	9.27	6.47	120.5	62.7	37.6	19.6	34.0	17.7	3.54
Sindhuri Chusa	90.6	7.21	4.54	53.4	58.9	17.1	18.9	20.1	22.2	2.66
Thudi Amb	248.5	11.57	6.56	155.5	62.6	48.1	19.4	44.9	18.1	3.46
Tota pari	120.9	7.52	5.01	63.5	52.5	23.3	19.3	34.1	28.2	1.86
C.V. (%)	49.4	22.5	16.1	64.4	18.2	44.0	22.5	32.5	25.2	44.8

Table 3. Physico-chemical attributes of different sucking mango varieties in district Hoshiarpur

Strains	Stone length (cm)	Stone breadth (cm)	TSS (%)	Acidity (%)	TSS/acid ratio	Total sugars (%)	Reducing sugars (%)	Non reducing sugars (%)
Achari Gola	8.60	4.52	15.2	0.51	29.8	10.30	3.63	6.34
Anami Amb	6.25	4.05	15.9	0.51	31.2	13.80	4.14	9.18
Anami Chhalli	9.18	3.74	15.2	0.51	29.8	12.14	3.41	8.29
Anda Dushehree	5.74	2.57	17.8	0.32	55.6	15.97	4.31	11.08
Arru amb	4.75	3.27	15.2	0.54	28.1	12.73	3.40	8.86
Banta Amb No. 1	6.58	4.23	13.9	1.28	10.9	10.09	2.23	7.47
Banta Amb No. 2	6.02	3.55	13.4	0.74	18.1	8.51	3.82	4.46
Banta Amb No. 3	5.50	3.64	14.2	0.96	14.8	11.20	2.99	7.80
Ber Amb	4.48	3.08	21.1	0.25	84.4	16.08	4.77	10.74
Bhagva Chhalli	9.41	4.26	15.9	0.51	31.2	14.10	3.20	10.36
Chhalli No. 18	8.15	4.25	19.1	0.38	50.3	14.92	5.33	9.11
Charan Achari	6.06	3.53	14.2	1.81	7.90	10.20	2.68	7.14
Choe Sindhuri	6.55	3.99	13.6	0.76	17.0	11.71	2.15	9.08
Ghassipur Amb	5.81	3.52	17.6	0.38	46.3	16.03	4.46	10.99
Gola Desi	7.25	4.22	14.2	0.45	31.6	11.56	4.00	7.18
Gola Ghassipur	5.44	4.07	12.4	0.83	14.9	8.62	2.95	5.39
Jogiya Chhalli	10.34	3.62	13.8	0.42	32.9	10.53	2.15	7.96
kala Amb	5.74	3.05	10.4	0.54	19.3	9.46	2.39	6.72
Laddu Amb	5.23	3.58	14.4	0.86	16.7	11.56	2.42	8.68
Mahantan di Chhalli	9.09	4.22	13.5	0.80	16.9	10.57	2.72	7.46
Mahantan di laltain	6.52	4.04	16.2	1.12	14.5	13.99	2.99	10.45
Pencil Amb	6.71	4.01	14.4	0.45	32.0	10.85	3.41	7.07
Pirh wala Amb	6.03	3.58	14.2	0.42	33.8	12.26	3.40	8.42
Rasbhari	5.87	4.21	17.5	0.44	41.7	12.90	3.27	9.15
Shashi Amb	8.57	4.08	15.8	0.38	41.6	12.17	3.90	7.86
Sindhuri Chusa	6.01	3.17	16.2	0.42	38.6	10.49	2.71	7.39
thudi Amb	10.02	4.56	14.0	0.53	25.9	11.56	2.64	8.47
Tota pari	5.88	3.99	17.6	0.45	39.1	13.78	3.20	10.05
C.V. (%)	23.9	12.6	14.2	53.9	53.1	17.6	24.6	19.7

Jogiya Chhalli. This attribute can be used for selection of varieties that has potentially to be exploited for juice and canning industry. Further, strains like *Charan Achari*, *Gola Desi* and *Banta strains No.1, 2 and 3* could be conserved and exploited for further used as pickle type of mangoes on account of their higher juice acid per cent, pulp/stone ratio, sour-sweet taste, almost roundish shape and medium to abundant fibres content. Fruit pulp per cent recovery next to strain *Jogiya Chhalli* was observed in *Gola Desi* (69.6) followed by *Bhagva Chhalli* (66.1) and minimum (36.4) in *Ber Amb*.

Besides, *Jogiya Chhalli*, higher in fruit length and oblong shaped mango strains was also found in *Thudi Amb*, *Anami Chhalli*, *Achari Gola* and *Bhagva Chhalli*. On the contrary, maximum fruit breadth was observed in *Achari Gola* and minimum fruit size in *Ber Amb*.

Strains-*Thudi Amb*, *Bhagva Chhalli*, *Anami Chhalli* and *Mahatan di Chhalli* had stone length of 10.02 cm, 9.41 cm, 9.18 cm and 9.09 cm, respectively. Although, fruit size and pulp/stone ratio of elite mango strains *Ber Amb*, *Anda Dushree* is uneconomical, but juice contained appreciably higher percentage of soluble solids and total sugars with sweet taste. Fruit weight showed significant positive correlation with fruit size, pulp weight, stone weight, peel weight, pulp content, pulp/stone ratio and stone size (Table 4). However, it exhibited negative significant correlation with fruit stone content. Significant negative correlations were also recorded for fruit weight, fruit breadth, pulp weight, peel weight, pulp/stone ratio with total sugars content of the fruit. Total soluble solids in juice showed significant positive correlation with total sugars (0.88) and reducing sugars (0.62), and negative

correlation with juice acid content (-0.47).

Variability in chemical attributes of fruits was also found among different mango strains (Table 2). The highest total soluble solids in juice were observed in *Ber Amb* (21.1%), and also possessed very sweet, aromatic, thin juice consistency and superb fruit taste. Brix per cent of the juice ranged from 12.4 to 13.8 in *Gola Ghassipur*, *Choe Sindhuri*, *Mahantan di Chhalli*, *Jogiya Chhalli* and *Banta Amb No. 1*. The Juice acid content (%) was maximum in *Charan Achari*, followed by *Banta Amb No. 1*, *Mahantan di laltain* and minimum in *Ber Amb*. TSS/acid ratio in different selected strains ranged from 7.9 in *Charan Achari* to 84.4 in *Ber Amb*. Total sugar per cent was estimated to be highest in *Ber Amb* followed by *Ghassipur di Chhalli* and minimum in *Banta No. 2*. Sweetness and taste of mango juice is mainly contributed by the presence of reducing sugars per cent and it was maximum in *Chhalli No. 18* values were 5.33 per cent. Non-reducing sugars per cent also showed considerable variability in different strains and it ranged from 4.46 to 11.08.

Old records, mentioned dated back to the early nineteenth century by Captain Montgomery in Hoshiarpur District Gazetteer (Anonymous, 1914) reported that a large number of mango varieties/strains/landraces were grown in the region. These include Panchpaya mango: large fruit, said to weigh five quarters (*panch pao*) of a kacha ser, equal to one pound avoirdupois; the *Kharbusa*: fruit average size, inside colour supposed to be like a musk melon (*kharbusa*); the *Kasumbila*: Small fruit, outer colour like safflower (*kasumba*); the *basantia*: small fruit, inner colour yellow (*basanill*); the *Pera*: small and very sweet, supposed to be in shape and taste like the sweetmeat pera; the *Dihalu*: large fruit, inside like curds (*dahi*), and not stringy; the *Marabla*: large fruit, sweet, with a small stone used principally for making preserves (*maraba*); the *Pathar*: fruit average size, supposed to be like a stone (*pathar*) in weight and hardness of its skin, keeps for a long time; the *Laler*: shape like a coconut: fruit, large and sweet; the *Bhadauria*: average size, ripens in the month of Bhadon (September), after other mangoes are over; the *Sandhuria*: average size so called on account of its red (*sandur*) colour; the *Kesari*: large fruit, colour saffron (*Kesar*); the *kela*: long fruit like a plantain (*kela*), with a large stone; the *Misri*: large fruit, sweetest sugar (*misri*); the *Jawainia*: the large fruit, smells like aniseed (*ajwain*); the *Shahatia*: large fruit, sweet as honey (*shahad*); the

Gora: large and brown like the bolls made up of cleaned cotton. The above species fetched the highest prices, especially the *Bhadauria* as being in the market when no other fruits are available in the market. The remainder fruits, which were less consideration are; *Saru*: small fruit, very quickly rots (*sorjala*); the *Harar*: small like the fruit of harar (*Terminalia chebula*); the *Dohki*: small with a strong taste of turpentine; the *Sufeda*: small and of a white colour; the *Rara*: small and sweet in size like the fruit of the bahera (*T. bellerica*); the *khala*: average size, bad colour and acid (*khata*) taste; the *kala*: average size, dark coloured skin even when ripe; the *Laichi*: small fruit, grows in clusters said to smell like cardamom (*ilaichi*); the *Dodhia*: small, white inside like milk (*dudh*); the *Chhali*: long fruit like maize cob; the *Kakra*: large long fruit, origin of name unknown.

None of mango seedlings except '*Sandhuria*' and '*Chhalli*' strains like characteristics were found during the present survey; indicating that the natural mango diversity has declined or vanishing in the region. In the present study, higher estimates for coefficient of variation with regard to various qualitative and quantitative characters indicated that a greater variability exist among different strains. There is an ample scope for crop improvement through direct selection of elite mango genotypes available in the different diversity regions. Variability in various physico-chemical attributes is due to inherent genetic capacity of different mango cultivars and also depends upon their phenotypic expression in a particular ecological zone (Singh and Chadha, 1981). Dash and Hota (1977) reported that soluble solids character in elite selected strains was highly heritable, therefore, strains possess higher TSS can be selected as donor or utilized as parent in hybridization programme. Navprem and Sharma (2007) evaluated sucking types of mangoes under sub mountane zone of eastern Punjab (India) conditions and reported a wide variation in respect of fruit shape, size, pulp colour, TSS, acidity, malformation etc.

It was noted that fruit colour ranged from attractive yellow with red blush on the shoulders, fully coloured, yellowish, light yellow, deep chrome and greenish among selected mango strains and these can be used as a donor source for developing coloured mango hybrid cultivars. Sharma and Majumdar (1989) revealed that red skin colour of the fruit is dominant and it has been governed by duplicate gene thereby showed various gradation of pink blush on the fruits in progeny population. The natural deep fruit pulp colour may be utilized for substitution of

Table 4. Correlation studies among different Physico-Chemicals attributes in mango

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0.83**	0.89**	0.98**	0.81**	0.85**	0.63**	-0.32	-0.70**	0.73**	0.68**	0.48**	-0.29	0.13	-0.29	-0.35	-0.32	-0.26
2	1.00	0.69**	0.79**	0.73**	0.73**	0.49**	-0.23	-0.55**	0.54**	0.89**	0.50**	-0.11	-0.02	-0.17	-0.11	-0.12	-0.07
3		1.00	0.84**	0.78**	0.83**	0.56**	-0.22	-0.68**	0.62**	0.49**	0.51**	-0.24	0.18	-0.33*	-0.33*	-0.26	-0.27
4			1.00	0.69**	0.74**	0.75**	-0.46**	-0.77**	0.83**	0.66**	0.39*	-0.28	0.07	-0.24	-0.34*	-0.30	-0.26
5				1.00	0.82**	0.23	-0.10	-0.27	0.23	0.62**	0.58**	-0.18	0.19	-0.31	-0.23	-0.21	-0.18
6					1.00	0.25	0.17	-0.50**	0.43**	0.55**	0.55**	-0.28	0.27	-0.35*	-0.35*	-0.39*	-0.23
7						1.00	-0.81**	-0.90**	0.92**	0.43**	0.25	-0.24	0.05	-0.24	-0.31	-0.24	-0.26
8							1.00	0.47**	-0.58**	-0.29	-0.06	0.11	0.11	0.06	0.13	0.03	0.15
9								1.00	-0.95**	-0.43**	-0.33**	0.28	-0.15	0.31	0.37*	0.33*	0.28
10									1.00	0.45**	0.20	-0.29	0.08	-0.23	-0.35*	-0.29	-0.28
11										1.00	0.54**	0.03	-0.18	0.04	0.05	-0.08	0.10
12											1.00	0.06	-0.01	-0.06	0.01	-0.21	0.11
13												1.00	-0.47**	0.85**	0.88**	0.62**	0.76**
14													1.00	-0.75**	-0.49**	-0.45**	-0.37*
15														1.00	0.76**	0.56**	0.64**
16															1.00	0.60**	0.92**
17																1.00	0.23
18																	1.00

1. Fruit weight 2. Fruit length 3. Fruit breadth 4. Fruit pulp weight 5. Fruit stone weight 6. Fruit peel weight 7. Fruit pulp (%) 8. Fruit peel (%)

9. Fruit stone (%) 10. Pulp/stone ratio 11. Stone length 12. Stone breadth 13. TSS (%) 14. Acidity (%) 15. TSS/acid ratio 16. Total sugars (%)

17. Reducing sugars (%) 18. Non-reducing sugars (%)

** Significant at $P < 0.01$ * Significant at $P < 0.05$

synthetic colour in preservation industry. Kumar (2000) reported that pulp colour of the fruit was not influenced by the environment and it was controlled by genetical make up. Fruits with good flavour and taste are in great demand in both domestic and international market, hence, mango seedlings population in the region will be further screened for the selection as strains in crop improvement. Presence of fine fibres are a necessity to protect the interior of a fruit from bruising and internal collapse during handling and shipping, however, abundance of fibre content are not acceptable to the consumer (Iyer, 1991). Hence, the existing mango seedlings population in the region not only adds to biological diversity but can also be utilized in different mango breeding programme for developing superior varieties.

On the basis of fruit maturity, these strains were classified into three groups i.e., early season, mid season and late season. Availability of mango fruits under north Indian conditions of Punjab commence from 1st fortnight of July to the end of August, consequently, late maturing strains fetch good market price because of their availability at fag end of the season. Mango fruits on the basis of fruit shape and size were classified as ovate, oblong, round and ovate-oblong. Wide variability was recorded in fruits for the presence of flavour, taste and aroma at the time of ripening; this can be exploited for identifying sucking, pickle and table purposes mango strains. Several workers also described the promising local mango seedling with respect to physico-chemical attributes under different agro-climatic conditions of India (Teotia and Singh, 1963; Rabbani and Singh, 1989; Parida and Rao, 1989; Navprem and Sharma, 2007). In the present survey, it was felt that demand for sucking and pickles type has been escalated in the region due to decrease in seedlings mango population.

During the survey, it was observed that indigenous mango seedlings population in the region is declining owing to poor management practices in general and occurrence of insects-pests and diseases in particular i.e. stem borer *Batocera rufomaculata* (de Geer), mango hopper *Amritodus atkinsoni* (Lethierry), mango mealy bug *Drosicha mangiferae* (Green), mango scale *Aspidiotus destructor* (Signoret), shoot borer *Chlumetia transversa* (Walker) and dieback (*Botryodiplodia theiobromae*). Efforts are being made to declare nearly 150 years old mango seedlings orchard known as 'Inami Bagh' spread over 12 acres at village Bassi Umar Khan Hoshiarpur as 'Biodiversity Heritage Site'

for *in situ* conservation and to prevent genetic erosion of rare indigenous mango plantation. Indigenous mango seedlings are presently conserved mainly due to religious beliefs, growing along strips of roads, railway lines, canals/drains and restriction imposed on felling of trees over the Shiwalik areas of Punjab under section 4 & 5 of the Land Preservation Act 1900. These studies showed that there exists a great variability among different mango seedling progeny and this can be exploited for the selection of elite genotypes in future after evaluating their performance.

Acknowledgements

The authors are thankful to Dr Jaspal Singh, Horticultural Development Officer, Bhunga (Hoshiarpur) and Dr Karnail Singh, Senior Statistician, Department of Plant Breeding & Genetics, Punjab Agricultural University, Ludhiana for their support and encouragement for the study.

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Genetic Variability for Morphological and Qualitative Traits in Cabbage (*Brassica oleracea* var. *capitata* L.)

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(Received: 25 September 2010; Revised: 15 March 2012; Accepted: 18 March 2012)

An experiment was conducted during the winter season of 2006-2008 to investigate the genetic variability for morphology and quality traits in 30 diverse cabbage genotypes. Wide range of variation was observed for all most all morphological and qualitative traits. The study showed high range for yield, days to maturity and leaf length. The highest estimates of PCV and GCV were for stalk length and low for leaf width. High estimates of heritability were noticed for yield while gross weight showed low heritability. Positive and significant association of yield was observed with all the characters except days to maturity and stalk length at both genotypic and phenotypic level. C-10 recorded the maximum amount of sulphur, carotenoids, ascorbic acid, iron, potassium, zinc, calcium and dry matter. Estimate of phenotypic coefficient of variation were higher than the genotypic coefficient of variation indicating that the apparent variation was not only due to genotypes but also due to environment. The genotypic correlation coefficient is higher than the corresponding phenotypic correlation coefficient for all the parameters. The dry matter had significant and positive correlation with all quality traits. Positive direct effect on the dry matter was the highest for sulphur followed by iron. Total carotenoids and potassium exhibited a negative direct effect on dry matter content but this negative direct effect was neutralized due high positive indirect effect through sulphur content on dry matter. Thus, these traits may be effectively be used as a selection criterion for screening potential genotypes in a breeding programme.

Key Words: Quality, Germplasm, Chapatti quality, Bread loaf volume, Bread quality

Introduction

Among the Cole crops, cabbage (*Brassica oleracea* var. *capitata* L. $2n = 2x = 18$) is one of the most important vegetable being grown in more than ninety countries throughout the world and consumed widely around the globe (Chiang *et al.*, 1993; Singh *et al.*, 2010). It belongs to the family Brassicaceae, which includes Brussels sprouts, broccoli, collards, cauliflower, knolkhol and kale. The cabbage head is best described as a single, large terminal bud comprising of tightly overlapping leaves attached to and enclosing most of the un-branched short stem. The different cultivated type of cabbage show great variation in respect of shape, size and colour of leaves as well as texture of the head (Singh *et al.*, 2006). The head shape ranges from pointed ellipsoidal to flattened drum heads. Spherical or nearly spherical heads are preferred. Foliage is either with or without waxy surface. Leaf texture may be smooth or savoy types. It is a rich source of protein comprising all essential amino acids, especially sulphur containing

amino acids, minerals such as calcium, iron, magnesium, sodium, potassium, phosphorus and antioxidants, which is reported to have anti-carcinogenic properties (Singh *et al.*, 2009, Ghebramlak *et al.*, 2004; Kopsell *et al.*, 2004). It is also rich source of ascorbic acid, carotene (pro. Vitamin A) and has high fiber content and calcium which reduce the risk of colon cancer. Improvement in any crop depends on the magnitude of genetic variability and the extent of transmission of characters from one generation to the next. The net head weight and its component characters are polygenic in nature, hence, influenced by the environmental factors. In spite of immense economic and medicinal importance, dry matter and total minerals content of the cabbage neglected traits in breeding programmes and practically very little information is available about the genetic variability of minerals in cabbage. Therefore, it is essential to partition the overall variability into its heritable and non-heritable components, which will enhance the precision of selection. Thus, the present study was conceived with objective to examine

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the magnitude and the direction of variability, inter-relationship and path analysis for minerals content and identify/developing superior genotypes for obtaining higher yield with good quality traits in cabbage.

Materials and Methods

The experimental materials comprised of 30 cabbage genotypes (Table 1). Each genotype was planted in a plot having 3.0×2.7 m area in a randomized block design with three replications. Thus, there were 25 plants in each plot planted at row and plant spacing of 60×45 cm. All the standard package of practices and plant protection measures were timely adopted to raise the crop successfully. Five randomly selected plants from each replication were utilized for recording observations and drawing sample for estimating quality parameters in the Laboratory of the Department of Applied Plant Science (Horticulture), BBAU, Lucknow during the winter season of 2006 to 2008. The ascorbic acid and total carotene were estimated as per method of Ranganna (1986); Sulphur through flame photometer (Chesnin

and Yien, 1951), potassium through spectrophotometer (Jackson, 1967) and calcium, iron and zinc through atomic absorption spectrophotometer. The mean values obtained from 2 years data were used for estimating the analysis of variance (Panse and Sukhatme, 1978). The genotypic and the phenotypic coefficients of variation were calculated by the formulae given by Burton (1951), heritability in broad sense and genetic advance as percent of mean were computed following the methods of Allard (1960) and Johnson *et al.* (1955), respectively.

Results and Discussion

Analysis of variance for eleven morphological traits revealed significant differences among the genotypes for all the traits under study. The estimates of genetic parameter of variability viz., phenotypic and genotypic coefficient of variation (PCV and GCV) along with heritability in broad sense (h^2) and genetic advance (GA) as percentage of mean for different characters are given in Table 2. The study showed high range for marketable yield (11.10 - 56.60 t/ha), days to maturity (71.28 - 110.53) and leaf length (15.95 - 46.02 cm). The highest estimates of PCV and GCV were for stalk length (PCV = 40.42, GCV = 39.21) followed by core length (PCV = 37.43, GCV = 36.02) and yield (PCV = 37.07, GCV = 36.87) and low for leaf width (PCV = 21.51, GCV = 21.12) followed by polar length (PCV = 16.85, GCV = 16.47) and days to maturity (PCV = 12.91, GCV = 11.50). Narrow differences between PCV and GCV gave evidence to the genotypes that the variability existing in them was mainly due to their genetic make up. High estimates of heritability was noticed for yield (98.90%) followed by leaf length (97.30%) and equatorial length (97.10%). Number of non-wrapper leaves, head weight, core length and stalk length showed moderate heritability estimates (Atter *et al.*, 2009). Days to maturity (79.40%) and gross weight (78.60%) showed low heritability estimates. High heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and were less influenced by environment. High percentage of genetic gain was observed for yield (75.54%) whereas it was low for days to maturity (21.10%) and polar length (33.16%). Hence, selection can bring worthwhile improvement in these traits.

The analyses of variance for eight quality traits revealed that mean square were highly significant for all genotypes. The extent of variability with respect to various characters in different diverse genotypes of cabbage

Table 1. Diverse genotypes of cabbage and their sources under study.

Genotypes	Sources
1923	IARI, New Delhi
C - 1	IARI, Katrain
C - 2	IARI, Katrain
C - 3	IARI, Katrain
C - 4	IARI, Katrain
C - 5	IARI, Katrain
C - 6	IARI, Katrain
C - 7	IARI, Katrain
C - 8	IARI, Katrain
C - 9	IARI, Katrain
C - 10	IARI, Katrain
C - 11	IARI, Katrain
C - 12	IARI, Katrain
C - 13	IARI, Katrain
C - 14	IARI, Katrain
C - 15	IARI, Katrain
C - 16	IARI, Katrain
C - 17	IARI, Katrain
EDH	IARI, New Delhi
Golden Acre	IARI, New Delhi
KK - 3	IARI, New Delhi
KK - 2	IARI, New Delhi
MR - 1	IARI, Katrain
Prem Nath	IARI, Katrain
Pride of India	IARI, Katrain
Pusa Agetti	IARI, New Delhi
Pusa Mukta	IARI, Katrain
Pusa Synthetic	IARI, Katrain
Red Cabbage - 2	IARI, Katrain
RRM	IARI, Katrain

Table 2. Estimates of genetic constants for different morphological and yield characters in some cabbage genotypes

Character	Range		Mean	Coefficient of variation		Heritability (%)	Genetic advance	Genetic gain (%)
	Min.	Max.		Phenotypic	Genotypic			
Days to maturity	71.28	110.53	86.96	12.91	11.50	79.40	18.36	21.10
No. of non – wrapper leaves	5.40	23.70	15.16	25.00	24.25	88.90	7.14	47.09
Core length (cm)	2.31	13.85	7.95	37.43	36.02	92.60	5.62	70.69
Stalk length(cm)	2.36	9.46	4.78	40.42	39.21	94.10	3.75	78.45
Leaf width (cm)	14.35	42.75	26.68	21.51	21.12	96.40	11.40	42.73
Leaf length (cm)	15.95	46.02	25.49	22.78	22.47	97.30	11.64	45.66
Equatorial length (cm)	12.10	31.10	20.05	24.19	23.84	97.10	9.71	48.42
Polar length (cm)	12.43	27.40	19.60	16.85	16.47	95.50	6.50	33.16
Gross weight (kg)	1.20	3.55	2.10	28.28	25.03	78.60	0.96	45.71
Head weight (kg)	0.49	2.33	1.24	32.23	30.13	87.40	0.72	58.06
Yield (t/ha)	11.10	56.60	24.78	37.07	36.87	98.90	18.72	75.54

Table 3. Estimates of genetic constants for different quality characters in some cabbage genotypes

Traits	Range		Mean $\pm$ SE (m)	Coefficient of Variation		Heritability (%)	Genetic advance	Genetic gain (%)
	Min.	Max.		Phenotypic	Genotypic			
Ascorbic acid (mg/100g)	9.75	39.95	21.40 $\pm$ 0.44	29.38	29.16	98.50	12.76	59.65
Calcium (mg/100g)	41.25	57.90	46.38 $\pm$ 0.56	7.54	7.25	92.30	6.65	14.34
Carotenoids (μ g/100g)	27.05	95.84	49.37 $\pm$ 0.63	25.52	25.42	99.30	25.76	52.18
Dry matter (mg/100g)	6.80	11.58	9.67 $\pm$ 0.36	12.80	11.64	82.80	2.11	21.82
Iron (mg/100g)	0.23	0.82	0.48 $\pm$ 0.03	26.86	24.29	81.80	0.22	15.83
Potassium (mg/100g)	196.25	296.65	234.35 $\pm$ 1.39	8.39	8.33	98.50	39.89	17.02
Sulphur (mg/100g)	22.15	75.30	41.91 $\pm$ 0.46	26.30	26.23	99.50	22.59	53.90
Zinc (mg/100g)	0.13	0.31	0.20 $\pm$ 0.01	18.08	14.07	60.50	0.05	25.00

measured in terms of general mean, range, coefficients of variation along with the amount of heritability in broad sense and expected genetic advance as percent of mean for eight quality characters are presented in Table 3. A wide range variation was observed for all most all the traits. C-10 recorded the maximum amount of sulphur (75.30), carotenoids (95.84), ascorbic acid (39.95), iron (0.82), potassium (296.65), zinc (0.31), calcium (57.90) and dry matter (9.67). However, absolute variability in different traits does not permit in deciding as to which character is showing the highest degree of variability, the relative values of phenotypic variance, genotypic variance and coefficients of variations (PCV and GCV). In the present investigation, the information obtained showed that the estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation meaning thereby that the apparent variation was not only due to genotypes but environment also influenced.

The phenotypic and genotypic coefficient of variation was higher for ascorbic acid (29.38 and 29.16) and lowest for calcium (8.29 and 8.16). These results indicated that higher magnitude of genotypic coefficient of variation for the above traits offer a better opportunity for improvement through selection. These results are in consonance with those of Singh *et al.* (2007) and Singh *et al.* (2009). The genotypic coefficient of variation provides help to measure the genetic variability in a character and accordingly, it is not possible to partition existing heritable variation in population based solely on this estimate. Burton and Devane (1953) suggested that genotypic coefficient of variation together with heritability estimates would give the best result of the amount of genetic advance to be expected from selection. High estimates of heritability (broad sense) were obtained for all the characters except zinc and dry matter. The heritability in broad sense ranged from (60.50 to 99.50). Higher values of heritability were obtained for sulphur

(99.50) while zinc (60.50) showed the lowest values of heritability which indicate that they were least affected by environment modification and selection based on phenotypic performance would be reliable. Ghebramlak *et al.* (2004) also reported higher heritability for all characters except zinc and dry matter.

The genetic advance as per cent of mean ranged between 14.34 and 59.65 %. High genetic advance was recorded for ascorbic acid (59.65%), sulphur (53.90%) and total carotenoids (52.90%). However, the heritability estimates along with genetic advance is more useful than heritability values alone for selecting individual. From this point of view, ascorbic acid and sulphur possessed greater estimates of genetic advance as per cent of mean coupled with high amount of heritability indicating that these traits are governed by additive gene action and continued selection would be helpful in modifying the selection procedure. The characters like zinc and dry matter showed low heritability with moderate to low genetic advance as per cent of mean indicated non-additive gene action and can be improved through multiple crosses. Singh *et al.* (2010) reported low heritability estimates for all the characters except sulphur and total carotenoids. Panse and Sukhatme (1978) expressed that if a character is governed by additive gene action, heritability and genetic advance both would be high. High estimates of heritability along with high genetic advance provide good scope for further improvement in advance generation if characters subject to mass progeny or family selection.

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Genetic Diversity in Rice Varieties of Singpho Community of Assam

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(Received: 03 March 2011; Revised: 27 November 2011; Accepted: 24 December 2011)

Genetic variation for thirty two qualitative and quantitative characters was studied in few rice accessions of Singpho community of Tinsukia district in Assam. The accessions showed maximum variation for grains/plant and seed yield/plant. Maximum Euclidean distance was found between variety Keteki Joha and Khawlung, and a close proximity was observed between Chengkhaw and Miatong. The utility of the landraces in rice breeding and variety conservation has been discussed.

Key Words: Assam rice, Genetic diversity, Landraces, Singpho community, Variability

Introduction

North East (NE) India including Assam is considered as one of the primary centres of origin of rice representing a rich source of genetic diversity and reservoir of valuable rice gene pool. Diverse agro-climatic conditions, migration and immigration of different ethnic groups through this region are considered responsible for such diversity (Pathak *et al.*, 1996). Among various ethnic tribes of Assam, Singpho community is one of the most important agrarian tribe in Upper Assam. They are of Mongolian origin, having their roots in South East Asia, with rice as a principal crop. Being largely neglected from modern developments with very limited penetration of modern high yielding varieties (HYVs), the rice varieties grown by this tribe are unique in nature with use as food and in wine making. The different rice accessions grown by them might provide new genes/alleles for yield and adaptation. So, a systematic collection and characterization is a necessary prerequisite to exploit the genetic potential of these varieties. Again, their characterization is more crucial under the regime of the Protection of Plant Varieties and Farmers' Rights Act. Therefore, the present experiment was undertaken to study the different genetic parameters and their association among different yield attributing traits in few traditional varieties of Singpho tribes as a part of the effort towards conservation, characterization and genetic improvement of rice grown by different tribes of NE India.

Materials and Methods

Nine accessions of rice were collected from different villages of Singpho tribes and they were selfed for several generations to maintain genetic purity. Additionally three

HYVs were included in this study for a comparison (Table 1). The experimental materials were transplanted in a Randomized Block Design (RBD) with three replications during *wet* season of Assam. Observations were recorded on the different morphological characters following International Union for Protection of New Plant Varieties guidelines (UPOV, 1985), and National guidelines (DRR, 2002), for DUS (Distinctiveness, Uniformity and Stability) test.

Analysis of variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) in broad sense and genetic advance (GA) as percentage of mean were calculated following the method of Singh and Choudhary (1985). The genotypic and phenotypic correlations were determined as per the method suggested by Johnson *et al.* (1955). Multivariate statistical methods namely cluster analysis was used to determine the genetic relationship of the 12 varieties. The genetic relationship as revealed by Euclidean distance was obtained through cluster analysis using unweighted pair group method using arithmetic average (UPGMA). For cluster analysis the SAHN module (Sokal and Sneath, 1963), which performs various clustering algorithms like Sequential Agglomerative Hierarchical and Nested clustering was used.

Results and Discussion

In the present experiment 12 rice varieties were characterized using 32 descriptor traits encompassing different grain and plant characters (Tables 2 and 3). The varieties were divided into two groups with respect to attitude of flag leaf at early observation, of which, varieties Khuntung and Ranjit belonged to semi erect

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Table 1. Rice varieties under investigation

Variety	Description
Miatong	Collected from village Maanmoumukh
Rongapikhi	Collected from village Pangna
Bogapikhi	Collected from village Pangna
Chengkhaw	Collected from village Maanmoumukh
Khawlung	Collected from village Maanmoumukh
Dumung	Collected from village Maanmoumukh
Kulapikhi	Collected from village Pangna
Khuntung	Collected from village Maanmoumukh
Dolkochi	Collected from village Pangna
Keteki Joha	High yielding variety
Aghoni Bora	High yielding variety
Ranjit	High yielding variety

group, while remaining varieties belonged to erect type. In late observation, the variety Rongapikhi belonged to erect type while the remaining varieties belonged to semi erect type. Erect leaves are associated with better dry matter accumulation and increased yield Sinclair and Sheehy, 1999). Leaf length was found higher in Singpho varieties as compared to the high yielding varieties. In general leaves are wider in Singpho varieties than those of HYVs with the highest leaf width in Khawlung.

Panicle traits such as spikelets/panicle, secondary branches/panicle, length and weight have the direct bearing on the grain yield in rice. In this present study, lowest panicle number/plant was found in Kulapikhi and Aghoni Bora while the highest was found in Keteki Joha. Two distinct types were observed in respect to panicle length of which the varieties Miatong, Rongapikhi, Chengkhaw, Dumung, Kulapikhi and Khuntung belonged to long group (26-30 cm) type and the remaining varieties belonged to medium group (21-25 cm). Regarding panicle secondary branching, the varieties Rongapikhi, Dumung, Kulapikhi and Keteki Joha belonged to the strong type of secondary branching while the remaining varieties belonged to weak type of secondary branching in the panicle. Attitude of secondary branching in the panicle also constituted a distinguishable character among the varieties. Varieties Rongapikhi, Chengkhaw, Khawlung belonged to semi erect type while varieties Miatong, Kulapikhi, Khuntung, Dolkochi and Ranjit belonged to semi-erect type while the remaining varieties belonged to semi erect to spreading type of secondary branching.

Regarding Stem length, highest stem length was found in singpho variety Khawlung while lowest was found in the high yielding variety Aghoni Bora. Stem thickness was also found higher in the singpho varieties than the high yielding varieties in the present experiment.

For tip colour of lemma, seven varieties showed brown tip colour of lemma, three varieties Chengkhaw, Dumung and Aghoni Bora showed yellowish and two varieties Kulapikhi and Khuntung showed purple tip colour of lemma. This character can be employed as diagnostic character for identification of rice varieties. Similarly for lemma palea colour, eight varieties were straw coloured, while two varieties (Rongapikhi and Khawlung) showed gold and gold furrows on straw background. Moreover, two varieties (Kulapikhi and Dolkochi) showed brown spot on straw coloured lemma palea. Awns were present only in Rongapikhi, Kulapikhi, Keteki Joha and Aghoni Bora. Among these, the variety Kulapikhi exhibited purple awn colour, while the other three varieties exhibited yellowish white colour awn. So, purple coloured awn can be considered as diagnostic marker for Kulapikhi.

Based on grain length, in the present investigation, varieties Bogapikhi, Dumung, Kulapikhi, Dolkochi, Keteki Joha and Ranjit belonged to the short type grain length while the remaining varieties belonged to medium type grain length. The varieties were categorized into two distinct groups based on decorticated grain length. Varieties Dumung, Dolkochi and Ranjit belonged to medium type, while the remaining varieties belonged to long type group of decorticated grain length. Three distinct groups were observed with respect to grain width. The varieties Rongapikhi, Keteki Joha belonged to narrow type of grain width while Miatong, Bogapikhi, Khawlung and Khuntung belonged to broad type and the remaining varieties belonged to medium type grain width. With respect to decorticated grain width three distinct groups were observed with respect to grain width in the present study. The HYV Keteki Joha belonged to narrow type while Chengkhaw, Khawlung, Dumung, Khuntung and Dolkochi belonged to broad type. Remaining varieties belonged to medium type decorticated grain width. Decorticated grain colour in all the varieties was white. The grain length/ grain width ratio ranged from 2.47 in Bogapikhi and Khuntung to 3.55 in Rongapikhi. Based on 1000-grains weight of rice varieties, grain weight was found highest in the variety Khawlung and lowest was found in the high yielding variety Keteki Joha. In the relationship between grain weight and the length to width ratio revealed that varieties with high grain weight showed lower for length to width ratio. Grain shape and size are important quality characters in determining market value of rice. Four distinct types

Table 2. Mean performance of different quantitative traits

Varieties	Length of the leaf blade (cm)	Width of the leaf blade (cm)	Plant height (cm)	Panicle length (cm)	Stem length (cm)	Stem thickness (cm)	Panicle number per plant	Time of heading (days)	Number of grains per Plant	Grain length (mm)	Grain width (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain length/decorticated grain width	1000 grain weight (g)	Yield/ plant (g)
Aghoni Bora	48.87	1.30	110.65	24.83	85.82	0.53	10.00	136.67	1318.67	2.80	3.36	7.20	2.40	3.00	25.30	33.37
Bogapikhi	58.78	1.27	160.62	25.07	135.55	0.41	13.67	130.00	847.00	7.87	2.47	6.27	2.50	2.51	22.56	19.13
Chengkhaw	64.55	1.31	175.40	27.20	148.20	0.47	11.33	127.33	903.67	8.83	3.03	6.63	2.67	2.49	25.11	22.70
Dolkochi	57.67	1.16	147.49	24.33	123.16	0.45	12.67	130.00	940.67	8.00	2.97	5.90	2.80	2.11	26.61	25.07
Dumung	67.67	1.29	172.78	28.92	143.87	0.50	12.67	129.67	807.33	8.37	3.00	5.90	2.60	2.27	24.89	20.08
Keteki Joha	43.83	1.12	129.46	23.43	106.03	0.40	18.33	136.00	1499.67	8.40	2.40	6.50	1.80	3.61	17.17	25.74
Khawlung	66.47	1.38	184.14	24.46	159.66	0.65	12.33	129.00	1018.67	9.13	3.43	6.43	3.03	2.12	32.90	33.50
Khuntung	61.35	1.25	162.03	28.72	133.32	0.46	13.00	133.00	780.33	8.57	3.47	6.87	2.87	2.39	31.16	24.30
Kulapikhi	60.18	1.18	166.02	28.31	137.71	0.48	9.67	131.67	983.33	8.00	2.90	6.60	2.50	2.64	23.39	23.00
Miatong	60.27	1.28	182.04	27.92	154.12	0.48	13.00	116.67	1027.33	8.53	3.23	6.63	2.37	2.81	26.05	27.44
Ranjit	56.05	1.13	135.12	24.32	110.8	0.40	13.67	128.33	974.33	8.03	2.83	5.53	2.43	2.28	19.34	18.84
Rongapikhi	65.63	1.17	176.03	27.33	148.70	0.42	13.33	135.00	1014.00	8.73	2.47	6.57	2.27	2.90	26.25	26.58
Mean	59.28	1.24	158.48	26.24	132.24	0.47	12.81	130.28	1009.58	8.49	2.97	6.42	2.52	2.59	25.06	24.98
C.V.	11.99	6.70	14.59	7.64	16.63	14.39	17.07	4.04	20.56	5.65	11.04	7.14	12.66	16.71	17.34	19.38
S.E.	0.76	0.016	0.91	0.23	0.96	0.01	0.34	0.34	20.49	0.04	0.04	0.03	0.04	0.03	0.01	0.54
C.D. 5%	2.23	0.046	2.68	0.68	2.81	0.02	0.99	1.01	60.12	0.11	0.10	0.10	0.11	0.09	0.04	1.57
C.D. 1%	3.03	0.06	3.64	0.92	3.82	0.03	1.35	1.37	81.71	0.14	0.16	0.14	0.15	0.12	0.05	2.13

Table 3. Performance of qualitative characters

Varieties	Flag leaf attitude (Early stage)	Flag leaf attitude (late stage)	Anthocyanin colouration of keel	Presence/absence of panicle secondary branching	Secondary branching	Attitude of the secondary branching	Panicle exertion	Lemma palea colour	Awn	Awn colour	Decorticated grain shape	Decorticated grain colour	Decorticated grain	Phenol test	Colour tip of lemma
Aghoni bora	Erect	Semi-erect	Absent	Present	Weak	Erect to semi-erect	Mostly exerted	Straw	Present	Yellowish white	Long slender	White	Absent	Positive	Yellowish
Bogapikhi	Erect	Semi-erect	Absent	Present	Weak	Erect to Semi-erect	Partly exerted	Straw	Absent	Absent	Long slender	White	Absent	Positive	Brown
Chengkhaw	Erect	Semi-erect	Absent	Present	Weak	Semi-erect	Mostly exerted	Straw	Absent	Absent	Long slender	White	Absent	Positive	Yellowish
Dolkochi	Erect	Semi-erect	Absent	Present	Weak	Semi-erect to spreading	Well exerted	Brown spot on straw	Absent	Absent	Short bold	White	Absent	Positive	Brown
Dumung	Erect	Semi-erect	Weak	Present	Strong	Erect to semi-erect	Partly exerted	Straw	Absent	Absent	Short bold	White	Absent	Positive	Yellowish
Keteki Joha	Erect	Semi-erect	Absent	Present	Strong	Erect to semi-erect	Well exerted	Straw	Present	Yellowish white	Long slender	White	Present	Negative	Brown
Khawlung	Erect	Semi-erect	Medium	Present	Weak	Semi-erect	Well exerted	Gold and golden furrows on straw background	Absent	Absent	Long slender	White	Absent	Positive	Brown
Khuntung	Semi-erect	Semi-erect	Absent	Present	Weak	Semi-erect to spreading	Well exerted	Straw	Absent	Absent	Long slender	White	Absent	Positive	Purple
Kulapikhi	Erect	Semi-erect	Strong	Present	Strong	Semi-erect to spreading	Well exerted	Brown spot on straw	Present	Purple	Long slender	White	Absent	Positive	Purple
Miatong	Erect	Semi-erect	Absent	Present	Weak	Semi-erect to spreading	Well exerted	Straw	Absent	Absent	Long slender	White	Absent	Positive	Brown
Ranjit	Semi-erect	Semi-erect	Absent	Present	Weak	Semi-erect to spreading	Well exerted	Straw	Absent	Absent	Medium slender	White	Absent	Positive	Brown
Rongapikhi	Erect	Erect	Absent	Present	Strong	Semi-erect	Mostly exerted	Gold and golden furrows on straw background	Present	Yellowish white	Long slender	White	Absent	Positive	Brown

Table 4. Variability of morphological characters

Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (broad sense) (%)	Expected genetic advance as % mean
Length of leaf blade	50.02	51.75	11.93	12.14	96.7	24.16
Width of leaf blade	0.01	0.01	6.58	6.94	90.1	12.87
Plant height	533.94	536.44	14.58	14.61	99.5	29.97
Panicle length	3.97	4.13	7.60	7.75	96.2	15.34
Stem length	482.49	485.25	16.61	16.66	99.4	34.12
Stem thickness	0.01	0.01	14.33	14.52	97.4	29.12
Panicle no./Plant	4.66	5.01	16.86	17.48	93.1	33.51
Time of heading	27.62	27.97	4.03	4.06	98.7	8.26
No. of grains/panicle	9.82	22.59	2.94	4.47	43.5	3.99
No. of grains/Plant	42663.93	43924.33	20.46	20.76	97.1	41.54
Grain length	0.23	0.23	5.63	5.68	98.3	11.50
Grain width	0.11	0.11	10.98	11.17	96.6	22.23
Grain length/grain width	0.14	0.15	12.94	13.18	96.5	26.19
Length of decorticated grain	0.21	0.21	7.12	7.18	98.4	14.55
Decorticated grain length/decorticated Grain width	0.19	0.18	16.67	16.79	98.6	34.09
1000 grain weight	18.88	18.88	17.34	17.37	100.0	35.71

of were observed among the rice varieties based on decorticated grain shape. Most of the Singpho varieties were long slender in shape, except two varieties (Dumung and Dolkochi) which showed short bold shaped grain. This character can be used in identification of the rice varieties. The present findings corroborated the findings of Borah (2002) indicating sufficient variation in grain characters in Assam rice. Aroma could not be detected in traditional varieties. In phenol test, all accessions showed positive results except Keteki Joha.

Two distinct groups were observed with respect to time of heading, of which varieties Rongapikhi, Kulapikhi, Khuntung, Keteki Joha and Aghoni Bora belonged to very late group (>131days) while the remaining varieties belonged to the late group (111-130 days).

Regarding yield/plant, in the present study it ranged from 18.84 g in Ranjit to 33.50 g in Khawlung. Though high yielding varieties have more yield than traditional varieties, but in this present investigation it was observed that traditional varieties may have some characters which may lead to higher yield than modern varieties. The height of rice plants is another decisive factor in grain yield potential. All the Singpho varieties were taller

than HYVs. Though the Singpho variety Khawlung was the tallest variety but it has highest yield, for which its highest grain weight and highest stem thickness may be attributed for.

In the present investigation, yield and yield attributing traits like number of grains/panicle, number of grains/plant, 1000-grain weight, stem thickness etc. revealed that varieties Khawlung, Miatong, Rongapikhi, Chengkhaw and Kulapikhi are few promising traditional varieties that could be utilized in the development of HYVs.

Variability among the characters

The analysis of variance revealed the existence of significant variation among the varieties for grain yield/plant and all other yield attributing characters. In case of morphological characters a comparison of the genotypic and phenotypic variances of the characters clearly revealed that there was a close correspondence between the two estimates for all the characters. A better comparison of the extent of genetic variation in the traits could be made from the estimates of genotypic and phenotypic coefficients of variations (Table 4). The maximum GCV was reflected for number of grains per plant followed

by yield/plant and seed weight. For these characters GCV estimates had a close correspondence with PCV estimates along with their high heritability estimates. The high estimates (>80%) of heritability for these characters also indicated considerable genetic variation and lower influence of environment in the expression of these characters

Length of leaf blade, plant height, stem length, stem thickness, panicle number/plant, number of grains/plant, grain length/grain width ratio, width of decorticated grain, decorticated grain length/ decorticated grain width ratio, 1000 grain weight, yield/plant exhibited high heritability with high genetic advance, while number of grains/panicle exhibited low heritability with low genetic advance while time of heading, time of maturity exhibited high genetic advance. Remaining characters exhibited high heritability with moderate genetic advance. Amongst all the yield attributes, number of grains/plant was found to possess maximum genetic variation apparently controlled by additive genes. Thus, this trait deserves top most priority in selection. These results indicated the involvement of increased additive gene action and therefore, selection to increase the frequency of additive gene will be effective to a certain extent.

High heritability with low genetic advance was found for time of heading. Low heritability with low genetic advance was observed for number of grains/panicle. This indicated that these characters might be under the control of non-additive (dominance and epistasis) gene action, offering limited scope for improvement these traits through simple selection.

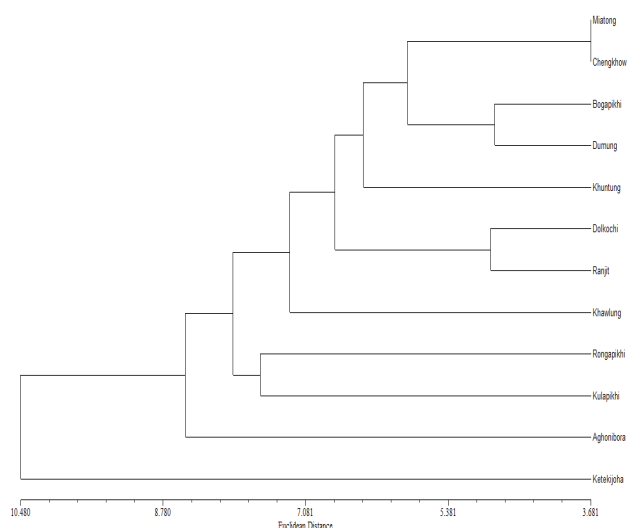


Fig. 1. Dendrogram based on all morphological characters

Correlation coefficient at genotypic and phenotypic level

The correlation coefficient both at genotypic and phenotypic level were computed between all possible pairs of morphological characters presented in Table 5.

Grain yield/plant had positive relation with number of grains/plant, grain length and 1000 grain weight at genotypic level. Number of grains/plant positively correlated with grain length/grain width ratio, decorticated grain length/decorticated grain width ratio but negatively correlated with length leaf blade, plant height, panicle length, stem length, grain width, decorticated grain width at genotypic level. The 1000 grain weight showed positive correlation with length of leaf blade, width of leaf blade, stem thickness, number of grains/panicle, grain width and decorticated grain width at genotypic level. Grain length showed positive correlation with width of the leaf blade, number of grains/panicle, stem thickness and decorticated grain length.

Analysis of genetic diversity through cluster analysis

Euclidean distance analysis based on these traits among 12 varieties in all combinations revealed that highest distance was found between variety Keteki Joha and Khawlung indicating that they are highly diverse in nature. They can be distinguished based on a large number of characters viz. phenol, grain aroma, panicle secondary branching, presence/ absence of awn, lemma palea colour, panicle exertion, plant height, leaf characters etc. Lowest Euclidean distance was found between variety Chengchow and Miatong, indicating genetic proximity among two varieties. However they can be distinguished based on the characters viz. attitude of panicle secondary branching, panicle exertion, colour tip of lemma. The dendrogram (Fig.1) revealed a separate identity of Aghoni Bora followed by Keteki Joha. The variety Keteki Joha possess grain aroma and showed negative result in phenol test might be a reason for such differentiation of this variety from the others. Rest of the varieties could be grouped in to three sub clusters.

This experiment revealed significant genetic variation and diversity among the genotypes of Singpho community. The genotype may be used for breeding HYVs as they may offer new gene/alleles for yield and adaptation. So a systematic effort for their characterization and DNA fingerprinting will go in a long way for their IPR protection and conservation.

Table 5. Estimates of correlation coefficient of morphological characters

Character	Length of the leaf blade	Width of the leaf blade	Plant height	Panicle Length	Stem length	Stem thickness	Panicle no./plant	Time of heading	No. of grain/panicle	No. of grain/plant	Grain length	Grain width	Grain length/Grain width	Decoricated grain length	Decoricated grain width	Decoricated grain length / decoricated grain width	1000 grain weight	Yield/ plant
Length of the leaf blade	1	0.489	0.878**	0.636*	0.866**	0.341	-0.417	-0.377	0.351	-0.813**	0.030	0.506	-0.449	-0.184	0.660*	-0.684*	0.625*	-0.155
Width of the leaf blade	0.468	1	0.441	0.247	0.441	0.802**	-0.464	-0.319	0.824**	-0.289	0.608*	0.702*	-0.378	0.368	0.597*	-0.354	0.680*	0.422
Panicle height	0.866**	0.413	1	0.601*	0.997**	0.286	-0.167	-0.548	0.579*	-0.623*	-0.032	0.484	-0.434	-0.056	0.440	-0.410	0.527	-0.093
Panicle length	0.606*	0.215	0.587*	1	0.542	0.034	-0.432	-0.264	0.466	-0.588*	-0.011	0.316	-0.276	0.235	0.227	-0.173	0.347	-0.243
Stem length	0.854**	0.414	0.997**	0.525	1	0.298	-0.136	-0.553	0.567	-0.602*	-0.032	0.481	-0.431	-0.080	0.442	-0.416	0.522	-0.076
Stem thickness	0.326	0.740**	0.280	0.043	0.290	1	-0.487	-0.129	0.526	-0.014	0.639*	0.563	-0.215	0.297	0.600*	-0.339	0.700*	0.511
Panicle no./ plant	-0.419	-0.462	-0.159	-0.385	-0.132	-0.456	1	0.104	-0.270	0.389	-0.261	-0.371	0.270	-0.287	-0.563	0.451	-0.466	-0.193
Time of heading	-0.370	-0.298	-0.545	-0.264	-0.548	-0.130	0.098	1	-0.497	0.370	0.175	-0.509	0.564	0.238	-0.224	0.334	-0.143	0.140
No. of grain/panicle	0.197	0.520	0.384	0.298	0.376	0.320	-0.143	-0.310	1	-0.136	0.658*	0.576*	-0.202	0.758**	0.286	0.093	0.584*	0.400
No. of grain/plant	-0.798**	-0.270	-0.615*	-0.572	-0.594*	-0.007	0.369	0.372	-0.022	1	0.351	-0.629*	0.754**	0.339	-0.715**	0.821**	-0.458	0.696*
Grain length	0.036	0.583*	-0.030	-0.011	-0.030	0.626*	-0.263	0.171	0.408	0.340	1	0.092	0.407	0.659*	0.121	0.203	0.484	0.819**
Grain width	0.496	0.670*	0.476	0.302	0.472	0.534	-0.359	-0.502	0.445	-0.609*	0.088	1	-0.868**	0.072	0.832**	-0.676*	0.728**	0.088
Grain length/Grain width	-0.431	-0.351	-0.428	-0.264	-0.426	-0.194	0.255	0.555	-0.187	0.732**	0.407	-0.864**	1	0.274	-0.715**	0.744**	-0.403	0.336
Decoricated grain length	-0.175	0.359	-0.055	0.225	-0.078	0.287	-0.291	0.233	0.505	0.333	0.662*	0.074	0.268	1	-0.094	0.505	0.331	0.509
Decoricated grain width	0.638*	0.577*	0.428	0.216	0.430	0.578*	-0.548	-0.221	0.224	-0.683*	0.132	0.813**	-0.684*	-0.072	1	-0.891**	0.816**	0.105
Decoricated grain length / Decoricated grain width	-0.668*	-0.347	-0.404	-0.168	-0.409	-0.332	0.436	0.331	0.041	0.800**	0.194	-0.667*	0.723**	0.491	-0.888**	1	-0.536	0.238
1000 grain weight	0.615*	0.646*	0.525	0.340	0.521	0.691*	-0.450*	-0.142	0.386	-0.451	0.479	0.716**	-0.396	0.328	0.799**	-0.532	1	0.627*
Yield/plant	-0.158	0.398	-0.093	-0.240	-0.076	0.524	-0.189	0.147	0.332	0.678*	0.795**	0.085	0.326	0.500	0.107	0.230	0.613*	1

* = Significant at 5% level of significance; ** = Significant at 1% level of significance; Upper matrix= Genotypic correlation coefficients; Lower matrix= Phenotypic correlation coefficient.

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Yield and Quality Assessment of Ginger (*Zingiber officinale* Rosc.) Genotypes

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(Received: 19 July 2010; Revised: 17 July 2012; Accepted: 18 July 2012)

Ginger (*Zingiber officinale* Rosc.) is an important spice crop used either in the form of fresh rhizome or dried ground ginger. It is principally used as an ingredient in various spice blends in food processing and beverage industries. In north eastern region of India, ginger is an important cash crop, which support the livelihood and improve the economic level of tribal community. In the present study, 33 genotypes including some local genotypes of ginger was undertaken to identify the desirable type and proper stage of harvesting for commercial production. The changes in yield, dry matter, fiber, starch, protein and essential oil were determined at four stages of maturity *i.e.* five, six, seven and eight months after sowing these ginger genotypes. The increase in yield was non significant after seven months of sowing. With the advent of maturity, study revealed that dry matter, fibre, and starch content of rhizome increases while protein and oil content decreases. The genotypes Jugijan, Suprabha and Varada can be harvested at early stages (6 months after sowing) while Nadia and Mahima may be harvested at full maturity for high yield and better quality *i.e.* low fiber and high volatile oil recovery. It is concluded that ginger crop could be harvested after seven months of sowing due to increase in yield and quality parameter which was non significant after seven months.

Key Words: Genotypes, Quality, Yield, *Zingiber officinale*

Introduction

Ginger (*Zingiber officinale* Rosc.) is an important spice crop used either in the form of fresh rhizome or dried ground ginger. It is principally used as an ingredient in various spice blends in the food processing and beverage industries. Ginger is commercially available in various forms such as green ginger, dry ginger, ginger powder, ginger oil, ginger oleoresin and preserved ginger (Kizhakkayil and Sasikumar, 2009). The refreshing aroma and the pungent taste makes ginger an essential ingredient of most world cuisine and of the food processing industry. In western countries, ginger is used in gingerbread, biscuits, cakes, puddings, soups, pickles, beer and wine (Sanwal *et al.*, 2010). In Saudi Arabia, it is predominantly used for flavouring coffee (Pruthi, 1993). Although ginger is grown in Jamaica, Sierra Leone, Nigeria, South China, Japan, Taiwan and Australia, the Indian ginger is considered as one of the best in the world (Philip, 1989). Among all spices, ginger is the main cash crop supporting the livelihood and

improving the economic level of many ginger growers of north eastern region (Yadav *et al.*, 2004). The North Eastern Hill (NEH) region of India is accounting 49% of India's ginger area and 72% of production (Rahman *et al.*, 2009).

The varieties presently grown are not much suitable for dry ginger production and there is no nearby market for green ginger in bulk quantities. Thus to make the crop remunerative, it has been essential to convert at least a part of the harvest in low volume high cost produce, like dry ginger. A good quality ginger is one which contains less fiber and high protein and fat. Though, the amount of fiber, protein, fat etc. varies from variety to variety but the stage of harvesting also affect the quality characters in ginger (Ratnambal *et al.*, 1987; Vernin and Parkanyi, 2005). Therefore, the present investigation was undertaken to identify the desirable types and proper stage of harvesting for commercial production of ginger for different end uses *i.e.* dehydrated ginger, oil, oleoresin, etc.

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Materials and Methods

Field experiments were conducted for two consecutive seasons during 2006-2008 (April-December) at the ICAR Research Complex for the NEH Region, Umiam, Meghalaya, India. The experimental site was located at 26° N latitude and 92° E longitude, with an elevation of 950 m above mean sea level. The soil was a sandy loam in texture, acidic (pH 5.4), having an organic carbon content of 1.9 %, with 286.97, 11.24 and 206.76 kg/ha of available N, P and K, respectively.

The experimental design was a randomized block with 33 genotypes having three replications. A rhizome size weighing 40-50g having at least two active buds were planted at a spacing of 30 × 25 cm on raised beds with a plot size of 5.1 × 3.0 m² during first week of April in each growing season. The rhizomes were harvested 5, 6, 7, and 8 months after sowing, where periodical development of rhizomes, dry matter, fiber, starch, protein and volatile oil were determined. The fresh samples were peeled off, dried in a hot air oven at 60°C until a constant mass was reached and then ground for chemical analysis. The dry matter content of rhizome was determined according to the procedure in the AOAC (1965). Crude fiber was determined with a Fibertec 2021 Fiber CapTM system (Foss Tecator AB, Hoganas, Sweden) as per AOAC (1965). Volatile oil content on dry weight basis were determined as per AOAC (1997), while the crude protein was estimated by multiplying the nitrogen content of rhizome by a factor of 6.25 (based on the assumption that nitrogen constitutes 16% of a protein). The starch was estimated with anthrone reagent method (Malik and Singh, 1980). Data were subjected to ANOVA (Gomez and Gomez, 1984), and if year is found non significant, the data were pooled and appropriate means were separated with Least Significant Difference analysis.

Results and Discussion

Rhizome Yield

From the pooled analysis of 2 years data on rhizome yield, it was found that rhizome yield of any genotype was not stabilized in all the four stages of harvesting (Table 1). The genotype, Mahima had highest yield at 150 days of harvesting followed by 294 Vars, Jugijan and Moran; while Jugijan, Suprbha and Varada did well both at 150 and 180 days of harvesting. At full maturity stage (240 days) the highest yield was recorded in Nadia followed by Varada and Mahima though the difference

was non significant. The variety Jugijan and Suprabha performed better than other genotypes at early stage of harvesting *i.e.* 150-180 days while harvesting at full maturity, Nadia, Varada and Mahima were better option than other genotypes for yield. The average value of 33 genotypes for different traits at different stages of harvesting presented in Table 3. It shows that the most significant increase in rhizome yield was between 150 to 180 days. A relative percentage increase of 60.15, 34.14 and 19.67 in the yield took place between 5-6, 6-7 and 7-8 months, respectively, after sowing.

Dry Matter

At the first sampling, dry matter was higher in Jugijan than the other genotypes, while the genotypes Karakal and Var 35 had higher dry matter content at remaining stages of harvesting (Table 1) *i.e.* 180, 210, 240 days. It is observed that dry matter content increased with maturity (Table 3). However, the dry matter build up in the green rhizome was found higher between 5-6 months than by 6-7 and 7-8 months.

Fiber Content

On an average, the crude fiber content at 150 days was 2.9% and increased to 6.41% at full maturity (Table 3). Though the increase in fiber content was noticed up to the last stage of harvesting, the maximum rise in the fiber content observed between 150 to 180 days of harvesting (Fig 1). The genotypes namely, China, Tura Local, Mahima, Kachai Ginger and Nadia had low amount of fiber content than the other genotypes. Fully matured ginger had crude fiber about 2.25 times higher than first harvesting. Jogi *et al.* (1972) also reported the similar kind of trend for crude fiber.

Starch Content

With the advent of maturity, the starch content followed increasing trend (Table 2, Fig 1). In the most genotypes there were little increase in starch content between 150-180 days, but there was considerable increase between 180-210 days and 210-240 days and it was almost double at full maturity than first harvesting. The genotypes 14 Vars, Karakal and Suprabha had high amount of starch content.

Protein Content

A non significant change in protein content was recorded between 5-6 months. In contrast the yield, dry matter, fiber and starch content, the protein content decreased

Table 1. Yield, dry matter and fibre content of ginger germplasm at different harvesting stages

Genotypes	Yield (q/ha)				Dry matter (%)				Crude fiber (%)			
	150 days	180 days	210 days	240 days	150 days	180 days	210 days	240 days	150 days	180 days	210 days	240 days
45 Vars	62.16	112.80	173.26	202.26	11.17	15.93	20.42	23.86	3.20	3.69	4.91	6.71
64 Vars	75.29	125.43	180.16	191.35	12.05	15.48	18.97	21.35	3.09	4.21	5.93	6.57
40 Vars	70.74	112.32	167.76	182.26	11.99	16.15	19.64	22.45	3.16	4.44	5.78	6.59
Khonsa	81.78	126.24	150.89	190.97	11.86	15.78	18.29	23.86	2.90	4.02	4.98	6.15
Jugjjan	91.75	148.45	193.16	210.29	14.13	17.12	20.15	23.12	2.94	4.82	5.32	6.74
Suprabha	86.66	143.26	192.20	215.47	10.67	13.42	17.82	21.93	2.79	3.63	4.78	5.77
142 Vars	62.65	117.59	167.26	193.26	12.48	18.76	21.14	23.67	2.89	3.83	5.12	5.89
Karakal	79.26	116.65	167.30	198.70	11.12	17.88	22.82	25.43	3.04	4.58	5.42	6.50
Manipuri o l	48.66	101.34	164.47	171.26	10.35	15.15	18.32	21.18	2.57	4.26	5.87	6.77
China	68.65	109.25	152.60	168.25	11.95	13.66	18.74	21.15	1.98	3.02	4.60	5.16
Burdwan	74.26	119.33	163.28	183.70	10.66	14.15	17.78	19.57	3.34	5.27	6.88	8.03
Ernad	81.25	122.76	158.95	196.36	10.95	16.34	18.50	22.78	2.95	3.87	5.88	6.59
294 Vars	92.26	136.60	180.60	217.61	10.73	14.55	18.18	23.98	3.18	4.10	5.28	6.75
35 Vars	80.64	130.63	163.29	188.74	10.13	17.82	21.40	25.62	3.45	5.01	6.07	7.21
Basar	78.65	136.30	187.29	209.40	11.41	16.74	21.36	22.54	3.19	4.36	5.78	7.02
Rejatha	77.78	110.82	182.44	213.95	12.64	16.09	17.48	20.89	2.67	3.43	4.74	5.88
Deomali	60.65	112.74	175.51	190.39	10.76	13.98	18.12	22.81	3.32	4.26	5.64	6.54
116 Vars	76.34	116.75	154.09	199.91	10.60	14.36	17.26	21.65	3.46	5.19	6.28	7.66
179 Vars	84.65	127.61	171.33	201.75	11.29	15.62	18.66	22.80	2.76	3.90	4.98	6.56
Mahima	93.24	131.78	191.88	223.43	12.54	14.43	18.97	20.70	2.45	3.54	4.32	5.66
Pune	63.70	116.84	166.96	183.26	10.92	13.37	17.64	19.76	2.87	4.06	4.99	6.24
Varada	83.23	137.64	189.26	224.60	11.84	14.65	18.40	21.38	2.99	3.26	4.87	5.93
Tura Local	65.26	137.04	160.27	178.26	12.15	15.45	18.24	21.90	2.25	3.80	4.13	5.50
Thingpui	69.06	109.84	154.66	193.41	12.51	17.91	20.25	22.47	2.01	3.13	4.65	5.74
Moran	91.50	122.72	165.75	198.15	11.36	15.40	20.48	24.02	2.12	3.79	4.70	6.25
27 Vars	83.66	127.95	175.39	202.61	11.42	15.78	18.47	21.93	3.15	4.47	5.87	6.88
Khasi Local	54.66	98.65	122.65	147.65	9.88	13.12	18.05	20.12	3.25	4.75	5.59	7.02
204 Vars	79.15	128.62	175.42	199.95	9.26	13.49	17.40	20.24	3.30	4.96	5.82	6.16
Thinglaidon	73.85	131.33	168.28	184.25	11.18	16.25	19.04	22.38	2.66	3.46	5.00	5.86
14 Vars	62.94	99.26	162.44	178.20	11.02	15.26	18.74	22.49	2.75	4.26	5.43	6.64
Kachai Ginger	80.80	124.46	173.26	200.98	12.50	16.24	19.52	24.87	3.10	4.22	5.09	5.72
Nagaland ocal	76.88	110.42	163.26	191.80	9.98	14.14	16.89	19.80	2.95	4.19	5.02	6.93
Nadia	102.64	123.88	176.20	232.80	10.48	15.55	19.14	22.25	3.00	3.94	5.16	5.88
CD at 5%	1.62	2.95	2.91	4.55	0.24	0.34	0.33	0.43	0.02	0.99	0.51	0.28
CV%	15.70	10.12	8.46	8.94	8.77	9.34	7.24	7.12	13.51	13.92	11.30	9.77

Table 2. Percentage starch, protein and essential oil in ginger germplasm at different harvesting stage

Genotypes	Starch (%)				Protein (%)				Essential oil (%)			
	150 days	180 days	210 days	240 days	150 days	180 days	210 days	240 days	150 days	180 days	210 days	240 days
45 Vars	20.66	22.15	33.45	44.54	14.90	14.72	9.54	7.24	2.30	2.10	2.00	1.50
64 Vars	22.44	24.36	31.32	40.37	12.50	12.74	8.60	7.12	2.85	2.30	1.90	1.80
40 Vars	18.60	20.50	30.69	39.45	12.24	13.42	9.12	8.10	2.50	2.30	1.80	1.45
Khonsa	23.75	23.90	34.16	44.24	15.00	13.63	8.41	6.23	3.10	2.70	2.55	1.80
Jugijan	25.05	25.98	32.16	42.34	13.18	13.74	7.72	7.26	2.85	2.40	1.75	1.35
Suprabha	27.48	29.30	36.42	47.12	14.25	13.78	8.14	6.12	3.00	2.35	1.90	1.80
142 Vars	20.12	24.35	31.26	40.78	12.42	12.56	6.24	5.77	3.05	2.65	2.15	1.90
Karakal	19.25	23.35	37.60	48.20	12.00	12.85	9.75	8.90	3.00	2.20	1.80	1.35
Manipuri o l	21.26	25.16	32.42	41.70	13.62	12.56	8.25	5.75	2.75	2.60	2.10	1.45
China	20.30	24.63	35.08	43.68	14.25	13.50	7.45	7.25	2.85	2.20	1.90	1.85
Burdwan	25.28	26.15	33.14	42.74	12.60	12.80	8.00	6.10	2.60	2.45	1.85	1.60
Ernad	26.20	31.10	33.77	45.16	13.00	11.80	7.50	7.60	3.15	2.90	2.15	1.70
294 Vars	19.45	21.18	32.47	44.60	15.20	14.36	9.58	6.40	2.55	2.40	2.10	1.60
35 Vars	26.30	27.62	33.70	46.80	12.24	11.45	7.94	5.54	3.55	2.80	2.20	1.70
Basar	23.64	24.95	31.42	43.19	13.20	13.46	6.45	7.02	3.10	2.95	2.15	1.30
Rejatha	22.25	24.76	30.41	42.42	15.32	13.46	8.64	6.20	3.90	3.30	2.85	2.15
Deomali	21.70	24.50	33.52	43.44	13.33	13.20	7.46	6.20	3.55	3.05	2.40	1.90
116 Vars	26.15	238.32	34.42	40.18	14.55	12.76	7.42	5.12	2.80	2.10	1.70	1.60
179 Vars	25.50	26.13	37.12	46.09	12.50	13.26	8.66	6.44	3.05	2.90	1.85	1.65
Mahima	19.98	21.26	29.18	41.12	16.20	14.80	9.22	7.24	3.00	2.60	1.95	1.70
Pune	22.40	26.29	33.83	41.47	15.25	14.20	10.12	7.15	3.55	2.45	1.80	1.45
Varada	22.18	25.30	31.93	38.88	14.60	13.40	8.60	8.75	3.40	2.75	1.90	1.75
Tura Local	23.60	28.19	34.76	44.55	16.24	14.56	9.15	7.20	2.90	2.75	2.10	1.55
Thingpui	24.33	26.12	32.60	43.80	14.00	12.80	7.56	5.45	3.20	2.80	2.40	1.80
Moran	24.96	25.45	33.60	43.12	14.60	12.50	8.50	8.45	2.95	2.80	2.10	1.75
27 Vars	22.41	23.30	31.57	39.80	13.60	14.30	9.65	7.20	3.55	2.40	1.70	1.25
Khasi Local	26.66	29.40	37.35	47.81	14.20	12.80	7.40	5.50	2.75	1.90	1.45	1.10
204 Vars	21.33	24.70	30.42	41.74	12.45	12.80	9.10	7.65	3.10	2.45	1.80	1.25
Thinglaidon	22.45	25.05	33.30	44.67	16.20	14.50	9.50	8.80	2.70	2.70	2.05	1.45
14 Vars	27.20	29.45	38.07	48.52	13.10	14.25	8.50	7.90	3.20	3.05	2.20	1.60
Kachai inger	25.32	26.45	32.40	41.64	12.70	13.45	8.65	8.40	3.45	2.60	1.90	1.70
Nagaland cal	24.12	29.44	35.38	43.03	15.60	14.20	9.40	8.65	3.70	2.50	2.30	1.85
Nadia	20.05	24.66	35.10	44.76	13.25	13.50	8.85	8.20	2.40	2.15	1.50	1.45
CD at 5%	0.53	0.47	0.43	0.47	0.42	0.28	0.20	0.24	0.16	0.16	0.16	0.12
CV%	10.98	116.33	6.64	5.89	9.20	6.13	11.16	15.59	12.67	12.52	14.40	14.27

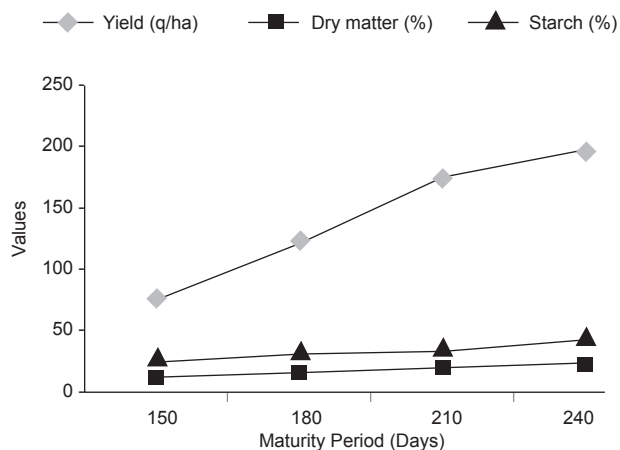


Fig. 1. Changes in yield, dry matter and starch with crop maturity

with maturity (Table 3). Between 6-7 months a significant decrease in almost all the varieties was recorded and it was continue upto full maturity but at lesser extent (Table 3). A relative percentage of decrease, 3.6, 58 and 20% in the protein content took place between 5-6, 6-7 and 7-8 months after sowing. At the first sampling, the protein content was higher in Tura local and Mahima, while at full maturity it was found higher in Karakal, Thinglaidon and Varada (Table 2).

Essential Oil

With the advent of maturity, the essential oil also decreased and it was recorded highest (3.04%) at 150 days. At full maturity it was almost half of the first sampling (Fig 2). Accumulation of starch and *in vitro* loss of volatiles decrease the essential oil content during ontogenesis of rhizomes (AOAC, 1965). The presence of essential oil in the outer skin established by histochemical

Table 3. Effect of different stages of harvesting on rhizome yield and quality

Maturity period (days)	Yield (q/ha)	Dry matter (%)	Crude fibre (%)	Starch (%)	Protein (%)	Volatile oil (%)
150	76.20	11.33	2.90	23.10	13.89	3.04
180	122.04	15.46	4.11	31.92	13.40	2.56
210	173.71	18.98	5.30	33.46	8.46	2.01
240	195.92	22.27	6.41	43.39	7.06	1.61
Mean	141.97	17.01	4.68	32.97	10.70	2.31
CD at 5%	24.90	2.01	0.44	1.94	0.42	0.16
CV%	37.80	27.62	32.34	25.22	32.25	27.15

examination of ginger peel confirms decreasing levels of essential oil during rhizome development (Mangalakumari *et al.*, 1984). The genotype Rejatha had highest amount of volatile oil at all stages of harvesting followed by Nagaland Local and Deomali.

Correlation between yield and quality characters with maturity

With the advent of maturity, yield, dry matter, fiber, and starch content increased, and the correlation between them was also statistically significant (Table 4). The level of protein content and volatile oil decreased significantly as maturity progressed. Yield was negatively correlated with protein and volatile oil content. These results were in close agreement with the findings of Ratnambal *et al.* (1987). Dry matter recovery was also negatively correlated with protein and volatile oil during rhizome development. A positive correlation of starch and fiber with dry matter further confirmed accumulation of these constituents during maturation. Protein and volatile oil showed negative correlation with all the characters under study; however, these two characters were positively and significantly correlated with each other. The starch build up during maturation evidently reduces essential oil levels.

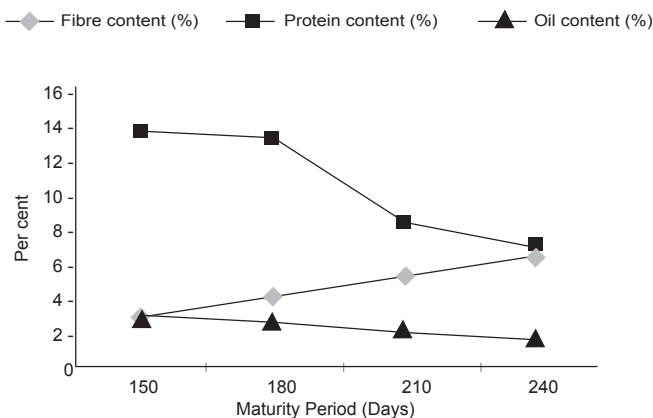


Fig. 2. Changes in quality characters with crop maturity

The results indicated that the genotypes Jugijan, Suprabha and Varada could be harvested at early stages (5-6 months) because at this stage they had higher dry matter and low fibre content besides higher yield. The genotypes Nadia and Mahima are suitable for harvesting at full maturity. The genotype Rejatha had higher amount of oil content at all stages of maturity. From the study it may be concluded that the ginger crop could be harvested after seven months of sowing because after that the increase in yield was non-significant and other quality parameters like fiber, oil, etc. were also in acceptable limit.

Table 4. Correlation matrix for ginger yield and quality parameters with crop maturity

Parameters	Maturity	Yield (q/ha)	Dry matter (%)	Fibre (%)	Starch (%)	Protein (%)	Volatile oil (%)
Maturity	1.000	0.989**	0.824**	0.790**	0.881**	-0.842**	-0.880**
Yield (q/ha)		1.000	0.925**	0.984**	0.910**	-0.902**	-0.910**
Dry matter (%)			1.000	0.812**	0.875**	-0.742**	-0.720**
Fibre (%)				1.000	0.973**	-0.652*	-0.990**
Starch (%)					1.000	-0.896**	-0.651*
Protein (%)						1.000	0.764**
Volatile oil (%)							1.000

** Significant at 1% and * 5%

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Chromatographic Profiles of Fruits and Flowers of Russian Olive (*Elaeagnus angustifolia* L.) Morpho-variants from Ladakh, India

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(Received: 02 April 2012; Revised: 05 July 2012; Accepted: 23 July 2012)

Russian olive (*Elaeagnus angustifolia*) is a multipurpose tree with fruits and flowers being used by locals since ages for its medicinal value. This species is commonly known as 'Sersing' and represented by five different morpho-variants in the Ladakh region. The present study was carried out to find out phytochemical differences among these five morpho-variants of Russian olive with the help of chromatographic studies. The chemical profiles of fruit and flower extracts obtained using TLC indicate diversity among the variants. Similarly, gas chromatograms of fruit volatiles presented clear evidence of qualitative as well as quantitative differences among the variants. In fruits, presence of stigmaterol was also reported. This study was the first attempt to obtain intra-species diversity through chemical profiling using chromatographic techniques which can be used as fingerprints for identification of these variants.

Key Words: Chemical diversity, Chromatograph, Russian olive, Secondary metabolites, Stigmaterol

Introduction

Ladakh (32°15'-36° N and 75°15'-80°15' E) located in the Western Trans-Himalayas, is a high altitude desert steppe lying between altitudes 2650-7672 m (Humbert-Droz and Dawa, 2004). Extremely low temperatures (25°C below freezing point), meager precipitation (<250 mm annual), diurnal pattern of temperature fluctuations and abridged growing season with insignificant precipitation are the characteristic climatic features.

Russian olive (*Elaeagnus angustifolia* L.), a small Eurasian tree, is distributed from Spain in the west to China in the east through western and central Asia (Hooker, 1890). In India, the species grow in Ladakh region of north-western Himalayas and is represented by five different fruit morphotypes (Anup Raj *et al.*, 2010). Locally, this species is known as 'Sersing' and the variants as *bee*, *chapacha*, *balti*, *marpo* and *ringmo*. Though, Russian olive grows throughout Ladakh it thrives well in relatively warmer climate of district Kargil within an altitudinal range of 2650-2900 m above mean sea level. The villages where the species grows naturally are Shillikchey, Hardass, Poyen, Mingi, Goma Kargil, Chikten and some parts of the Kargil city. Different parts of the plants are being used in the Amchi system of medicines in Ladakh.

Morphological variations among different varieties of Russian olive have been reported from different regions throughout its distribution range (Musegjan, 1958; Goncharova and Glushenkova, 1990; Lancaster, 1993; Huang and Jiang, 2005). But no chemical data is available which can supplement the morphological data. Thus, in this study chromatographic profiles of fruits and flowers of the five Russian olive variants were analyzed to find out variety-specific differences in chemical composition among them.

Materials and Methods

Fruits and flowers of five different morpho-variants of Russian olive (*Elaeagnus angustifolia* L.) were collected from Kargil district during December 2010 and June 2011, respectively, and were analysed at Molecular and Structural Biology (MSB) Laboratory, Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow for chromatographic studies during July-August, 2011.

Phytochemical Extraction from Plant Tissue Matrix

Pulp from fruits of each variant of Russian olive (*viz.*, *bee*, *balti*, *ringmo*, *marpo* and *chapacha*) was separated from seed. A known weight (2 g) of fruit pulp and flowers of each variant was ground using mortar-pestle and kept overnight in 50 % aqueous methanol (20 ml). After this

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initial extraction, the aqueous methanol extracts were sequentially extracted in equal volumes of chloroform and ethyl acetate, respectively. Each extraction was done thrice for getting maximum yield. Chloroform and ethyl acetate fractions were dried, re-dissolved in HPLC grade methanol and stored at 4°C for TLC analysis.

For HPLC analysis, phytochemicals from fruit pulp were first extracted using 50 percent aqueous methanol. Then the methanol extract was defatted using equal volumes of n-hexane followed by liquid-liquid partitioning with chloroform. The chloroform extract was dried and re-dissolved in HPLC grade methanol and kept at 4°C for TLC and HPLC analysis to find out the presence of stigmasterol in the fruit pulp. Each extraction was done thrice. A pure stigmasterol standard was also prepared in HPLC grade methanol and subjected to TLC and HPLC for comparison.

Thin Layer Chromatography

After spotting the chloroform fraction of fruit and flower extract on pre-coated silica gel plates of 10 X 20 cm (60 F₂₅₄; MERCK Inc.), five different solvent systems were tested for separation of compounds. Two solvent systems (toluene: ethyl acetate: formic acid; 10:8:2 and ethyl acetate: methanol: water; 100:16.5:13.5) were found suitable for the development of chromatograms. Ultra violet light, iodine vapours and anisaldehyde reagent spray were used for visualization. The chromatograms thus developed were recorded digitally and analysed using Digital Imaging System (Multi Doc-It Imaging System for TLC). Similarly ethyl acetate fractions were also chromatographed and analysed.

Head Space Gas Chromatography (HS-GC) Analysis

A Perkin Elmer gas chromatograph (Clarus 500) equipped with capillary column (50 m x 0.32 mm, Perkin Elmer Inc.) and attached with Turbomatrix 16 headspace sampler was used for HS-GC analysis of fruits and flowers of Russian olive.

Sample: Two g fruits of each variant were filled into a 20 ml vial.

GC conditions: A FID detector was used for the percentage determination of volatile components. Oven temperature was programmed as follows: 40°C for 5 min, ramping to 150°C at 5°C/min, hold at 150°C for 5 min and again ramping from 150°C to 210°C at 7.5°C/min. Injector temperature: 270°C; carrier gas: N₂ with

a flow rate of 1 mL/min; detector temperature: 250°C; split ratio: 1:20; and sample size: 1 µl.

HS conditions: Oven temperature – 120°C; needle temperature – 100°C; transfer line temperature – 100°C; sample thermostating – 15 min; pressurising time – 5 min.

High Performance Liquid Chromatography Analysis

HPLC (Waters 600) equipped with autosampler (Waters 717 plus) and Photodiode Array (PDA) detector (Waters 2996) was used for HPLC analysis. The column used was Reverse Phase C₁₈ column. The mobile phase consisted of two solvents: methanol (A) and water (B), each containing 0.05% acetic acid. The solvent gradient in volumetric ratios of solvents A and B was as follows: from 0 to 30 min, 40 to 60% A; from 30 to 45 min, 60 to 75% A; from 45 to 54 min, 75 to 95% A; from 54 to 55 min, 95 to 100% A at a flow rate of 0.60 ml/min; from 55 to 60 min at 100% A at a flow rate of 1.00 ml/min; from 60 to 64 min, 100 to 40% A and flow rate from 1.00 ml/min to 0.60 ml/min; and finally from 64 to 65 min at 40% A and flow rate 0.60 ml/min. This mobile phase was filtered through a 0.40 µm membrane filter (Millipore), while samples were through Acrodisc Syringe Filter (0.2 µm Supor Membrane Filter), prior to use. Injection volume of 10 µl was used for all the observations. The chromatographic peak of the stigmasterol was confirmed by comparing its retention time and UV spectra with those of the reference standard of stigmasterol. The detector was scanned from 210 to 400 nm.

Results

Results of TLC analysis are presented in Tables 1 and 2 and Figures 1 and 2. A perusal of these data and figures alludes to the qualitative differences present in phytochemical composition among the fruits and flowers of the mopho-variants of Russian olive. For example, in the chloroform extract of fruits, band number 5 ($R_f=0.62$) and 6 ($R_f=0.74$) were present only in *chapacha* while band 3 ($R_f=0.13$) was present only in *bee* and *ringmo* varieties (Table 1). Likewise, bands 6, 7, 10, 11 and 12 present in TLC profile of ethyl extract of fruits were able to discriminate these varieties from one another (Fig.1). Among the 13 bands found in the chloroform extract of flowers, only 1 ($R_f=0.02$), 8 ($R_f=0.41$) and 13 ($R_f=0.95$) bands were common in all the varieties (Table 2). Similarly, qualitative as well as quantitative

Table 1. R_f values of TLC bands representing different compounds separated and visualized in the chloroform and ethyl acetate extract of fruit samples

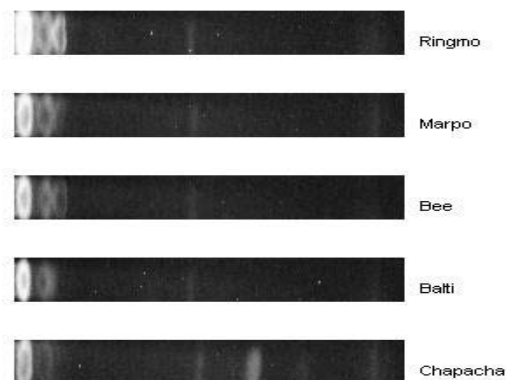
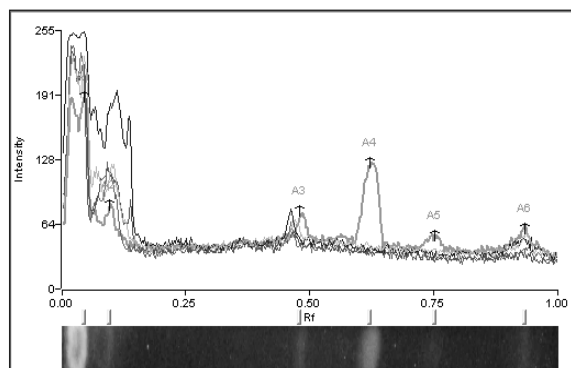
Band	R_f Values				
	Bee	Balti	Ringmo	Marpo	Chapacha
Chloroform extract					
1	0.04	0.04	0.04	0.04	0.04
2	0.09	0.09	0.09	0.10	0.10
3	0.13	—	0.13	—	—
4	0.47	0.46	0.46	0.46	0.47
5	—	—	—	—	0.62
6	—	—	—	—	0.74
7	0.94	0.94	0.94	0.94	0.94
Ethyl acetate extract					
1	0.06	0.05	0.05	0.09	0.06
2	0.1	0.11	0.1	0.12	0.11
3	0.16	0.18	0.17	0.17	0.17
4	0.23	0.23	0.23	0.24	0.24
5	0.26	0.26	0.26	0.27	0.27
6	—	0.33	—	—	0.33
7	—	—	—	—	0.57
8	0.63	0.63	0.63	0.63	0.63
9	0.75	0.75	0.75	0.75	0.75
10	0.89	0.88	0.89	—	—
11	—	0.93	0.92	0.92	0.93
12	0.95	0.95	0.95	0.96	—

“—” indicates absence

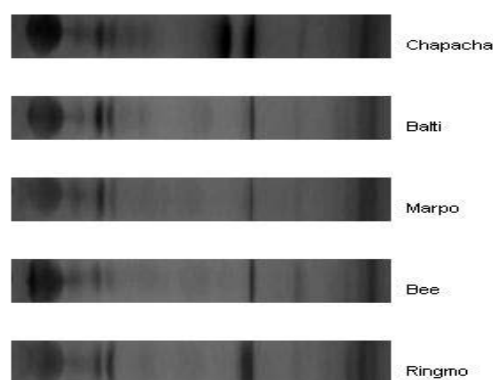
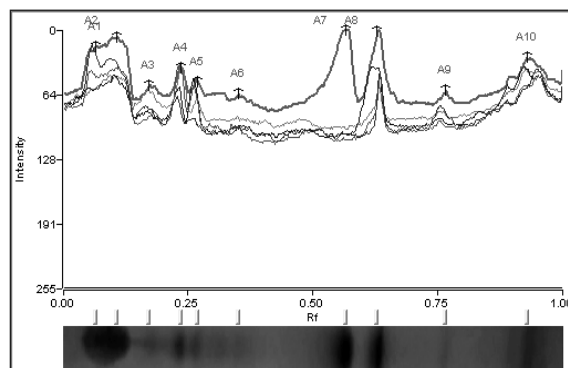
Table 2. R_f values of TLC bands representing different compounds separated and visualized in the chloroform and ethyl acetate extracts of flowers

Band	R_f Values				
	Bee	Balti	Ringmo	Marpo	Chapacha
Chloroform extract					
1	0.02	0.02	0.02	0.02	0.02
2	0.15	0.15	—	0.15	0.15
3	—	0.16	—	—	—
4	—	—	—	0.2	—
5	—	—	0.23	—	—
6	—	—	0.27	—	—
7	—	—	0.34	—	—
8	0.41	0.41	0.41	0.41	0.41
9	0.45	0.45	—	0.45	—
10	0.54	0.54	—	0.54	0.54
11	0.63	0.63	—	0.63	0.63
12	0.87	0.87	0.87	—	0.87
13	0.95	0.95	0.95	0.95	0.95
Ethyl acetate extract					
1	0.04	—	0.04	0.04	0.04
2	0.10	0.10	—	0.10	0.10
3	0.18	0.18	0.18	0.18	0.18
4	0.45	—	0.45	0.45	0.45

“—” indicates absence.



a) Chloroform extract



b) Ethyl acetate extract

Fig. 1. Thin Layer Chromatogram of a) chloroform and b) ethyl acetate extracts of fruit samples of each variant of Russian olive

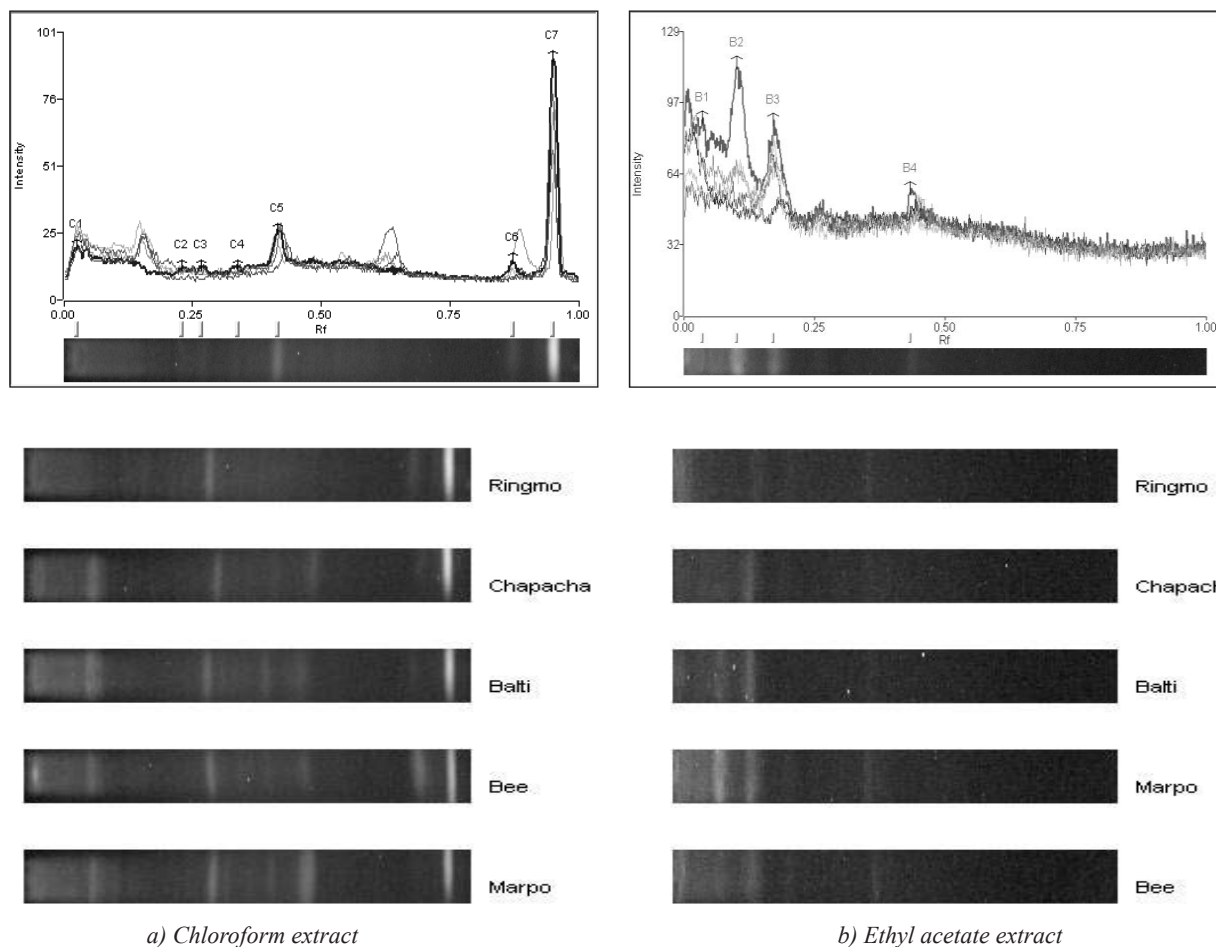


Fig. 2. Thin Layer Chromatogram of a) chloroform and b) ethyl acetate extracts of flowers of each variant of Russian olive

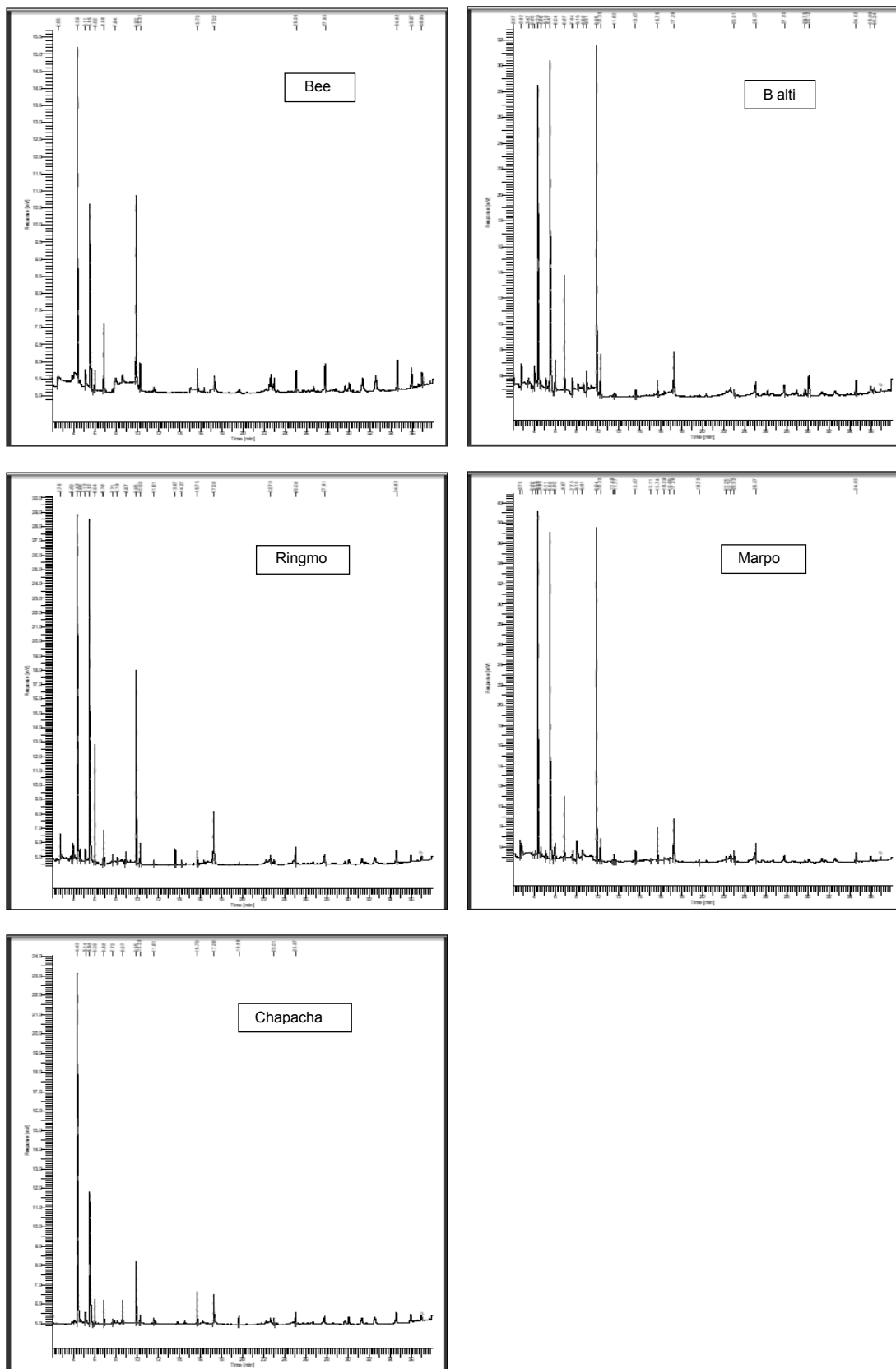
differences (relative composition) among the varieties with respect to the volatiles present in fruits of Russian olive were quite evident as indicated by HS-GC analysis (Table 3; Fig. 3). Table 3 depicts the proportion of major fruit volatiles present in Russian olive varieties. These 10 volatiles constituted about 85 % or more of the total volatiles in all these varieties. The compound 1 (RT=2.7 minute) was present only in two variants namely, *ringmo* and *marpo* while the 2nd compound (RT=4.04 minute) was found only in *balti*. Though rest of the volatile compounds were present in each variant, their relative composition was quite different.

The thin layer chromatogram of chloroform extract developed in the solvent system of CHCl₃ (70 mL), toluene (24 mL), MeOH (8 mL) and ethyl acetate (4 mL), and anisaldehyde spray (p-anisaldehyde 250 µL, water 40 mL, acetone 10 mL and perchloric acid 5 mL) indicated presence of stigmasterol in only one

variant (*bee*) of Russian olive. This result was further confirmed by HPLC analysis using stigmasterol standard (Fig. 4).

Discussion

Many studies in other species, have proved that chemical profiles of secondary plant products based on chromatographic data are valuable in taxonomic studies. Heidi *et al.* (1997), showed marked intraspecific variation in many of their volatiles in two of the species of genus *Narcissus* using headspace collection and GC-MS analysis of flower volatiles. Similarly, in a chemotaxonomic study of genus *Crataegus* using paper chromatography, Arjmandi *et al.* (2009) showed that the genus can be classified into one section, five series, and 13 taxa at species and infra-species level. The result of flavonoid data were well correlated with other taxonomic data. In a study on phenolics, stability in chemical profile of individual trees suggests that quality is tightly controlled



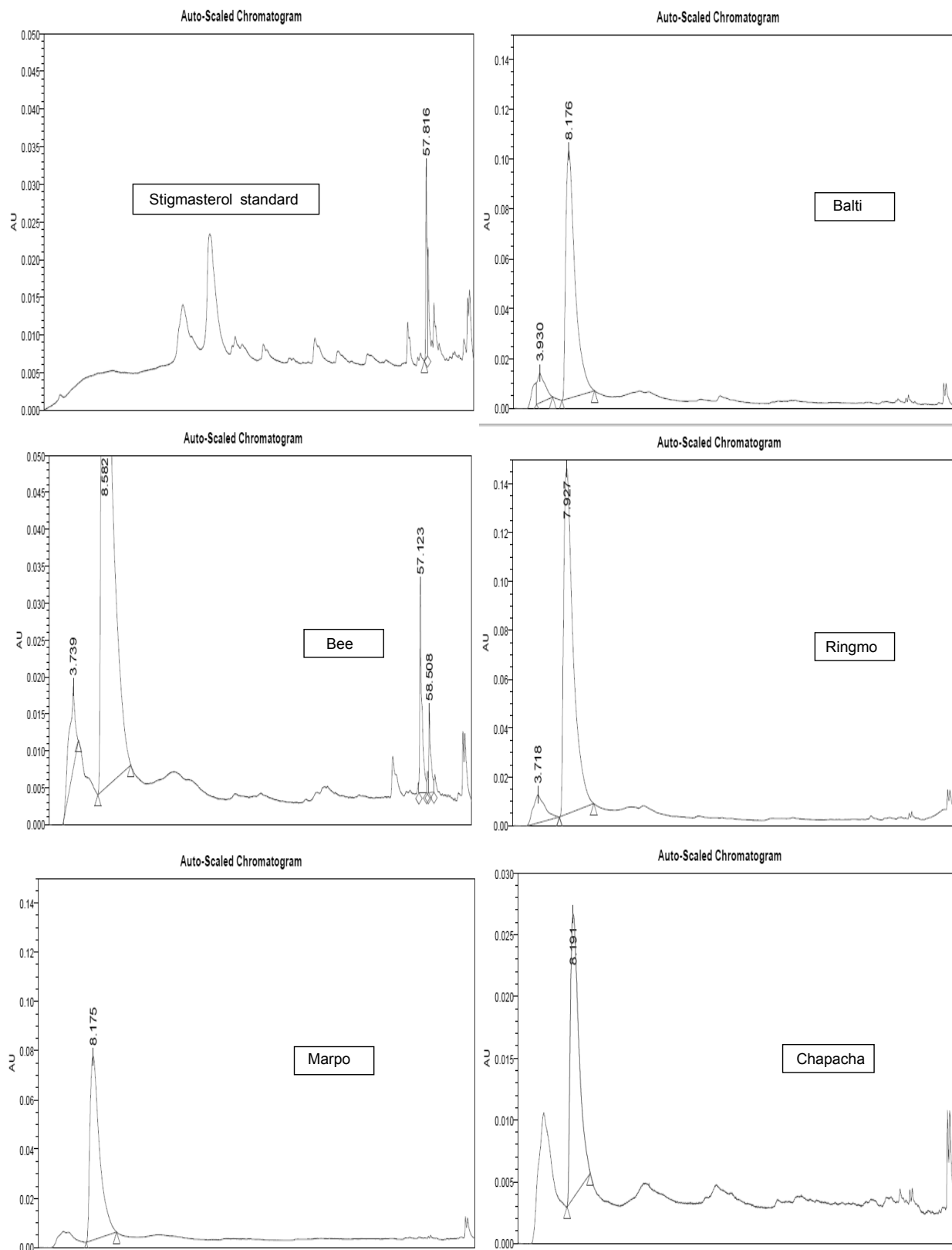


Fig. 4: HPLC plots of stigmasterol standard and fruit extracts of Russian olive variants

Classificatory Analysis in Little Millet Germplasm Collections of Odisha

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(Received: 24 September 2011; Revised: 31 December 2011; Accepted: 07 January 2012)

Twenty two genotypes of little millet (*Panicum sumatrense* Roth.) were evaluated under 12 environments. Data on 14 metric traits including grain yield were analysed to classify the entries into different groups following four methods of multivariate analysis. The genotypes were grouped into different clusters following D² analysis, canonical analysis, metroglyph analysis and numerical classificatory analysis. Clustering pattern in different methods indicated that the test genotypes were grouped into three clusters following D² analysis as well as canonical analysis, while they were divided into five groups in metroglyph analysis. Following the UPGMA method of numerical taxonomic approach, the genotypes were grouped into four, five and eight clusters at 75%, 80% and 85% phenon levels, respectively. The study of clusters formed by different methods indicated that the metroglyph analysis was easy and simple, and useful method of initial grouping for large number of collections. But the numerical taxonomic approach for classification of the biological populations is more potent in comparison to other methods to distinctly discriminate the genotypes for their use in recombination breeding.

Key Words: Canonical, D² static, Little millet, Metroglyph and numerical classificatory analysis, Multivariate analysis, *Panicum sumatrense*

Introduction

Genetic diversity in germplasm lines is generally considered as an important criterion in deciding appropriate plant breeding methods for crop improvement. Precise information on the nature and magnitude of genetic divergence in the population helps the plant breeder in choosing the diverse parents for purposeful hybridization (Arunachalam, 1981; Samsuddin, 1985). The importance of cluster analysis to determine the extent of variability was reported earlier (Mahalanobis, 1936). D² statistics has been utilized extensively for estimating genetic divergence in a number of crop plants with diverse breeding systems (Murty and Arunachalam, 1966; Bhatt, 1970). Although D² statistics is a quantitative measure of genetic divergence, the clustering pattern of the genotypes is arbitrary. The classification using generalized distance is workable when the number of entries is not very large. While classifying large number of germplasm collections in rice, Vairavan *et al.* (1973) used canonical analysis for initial grouping. But simple two-dimensional representation of multidimensional disposition of varieties cannot be as exact as the Tocher's method of grouping which scans the full multidimensional space, even when the two canonical vectors account for high proportion of variation (Arunachalam, 1981).

On the other hand, metroglyph analysis has been used in many crop plants as a method for initial grouping (Anderson, 1957). In the numerical classificatory analysis, the general similarity coefficient of Gower (1971) has been used for clustering of populations at appropriate phenon level (Sneath and Sokal, 1973). An attempt has been made in the present study to classify 17 little millet germplasm collections from Odisha along with five check varieties. The classification of germplasm into different clusters following these methods was compared for determination of genetic closeness or divergence among the germplasm. The efficient method(s) would be preferred by plant breeders for an effective classificatory analysis of various crops.

Materials and Methods

The investigation was carried out at the Central Research Station, Orissa University of Agriculture & Technology (OUAT), Bhubaneswar, during the period from *kharif* 2006 to *kharif* 2007 under 12 different environmental conditions generated through different dates of sowing. The test genotypes consisting of 17 local germplasm collected from nine different districts of Odisha were evaluated along with 2 varieties of OUAT, Bhubaneswar and three varieties of Tamil Nadu Agricultural University

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(TNAU), Coimbatore as checks. The genotypes were sown in a Randomized Complete Block Design (RCBD) with three replications and observations were recorded for grain yield and 13 component characters. D² analysis and clustering by Tocher's method were done following Rao (1952). Canonical analysis was carried out according to Anderson (1957). For grouping in metroglyph analysis, a method was devised to delineate the performance of the genotypes into three classes in respect of yield and ten other component characters. The grand mean (M) and standard deviation (SD) were calculated for each character. The performance of the entries in respect of the eleven characters was ranked as high with mean values more than (M + 0.7SD), low with mean values less than (M – 0.7SD) and medium with mean values of (M ± 0.7SD). Accordingly, the genotypes were grouped into three classes i.e. low, medium and high for each of the eleven characters and numerically scored on three point scale as 1, 2 and 3 respectively. In the numerical classificatory analysis, the general similarity coefficient (S_G) of Gower (1971) was used as a measure of resemblance between different operational taxonomic units or OTUs (entries included in the investigation). The S_G values were calculated following Sneath and Sokal (1973). Basing on the matrix of the S_G values, phenogram (dendrogram) was constructed using UPGMA (un-weighted pair-group method using arithmetic average) technique in one of the SAHN (sequential, agglomerative, hierarchic, non-overlapping) clustering methods. Finally, the clusters were identified at appropriate phenon levels.

Results and Discussion

Pooled analysis of variance over environments showed highly significant differences among the test genotypes in respect of all 14 characters (Table 1). The significant differences due to environments and differential response of the genotypes to changing environments as revealed from the significance of interaction components warranted grouping of the genotypes to identify the genetically diverse ones to ensure success in recombination breeding. The bias in clustering of genotypes in different environments, presumably due to differential response of different characters, could be eliminated by pooled analysis.

In the multivariate analysis, 14 characters contributed differently to the total D² for each pair of varieties. The major contributors to genetic diversity were 1000-grain

Table 1. Analysis of variance for 14 characters of 22 genotypes of little millet pooled over 12 environments

Character	Mean square				
	Reps/Env. (24)@	Genotype (21)	Environ- ment (11)	G X E (231)	Pooled error (504)
Grain yield (GY)	3.0	98.19**	2731.49**	20.51**	2.20
Days to heading (DH)	2.6	128.80**	989.28**	12.08**	0.82
Plant height (PH)	2.8	660.65**	3828.32**	45.47**	4.43
Flag leaf length (FLL)	0.5	29.03**	270.68**	6.51**	0.66
Flag leaf area (FLA)	0.2	19.72**	170.48**	3.52**	0.24
Panicle length (PL)	0.3	62.78**	391.09**	6.75**	0.70
Panicle exsertion (PE)	0.1	8.76**	847.30**	3.11**	0.26
Panicle number (PN)	3.5	410.53**	6835.36**	141.95**	7.48
Panicle weight (PW)	0.002	0.05**	0.92**	0.01**	0.001
Panicle yield (PY)	3.8	153.01**	3765.77**	33.49**	2.92
Straw yield (SY)	1.4	301.29**	9817.65**	90.28**	4.11
Biological yield (BY)	5.5	757.60**	18834.86**	156.46**	7.56
Harvest index (HI)	8.5	97.18**	4478.94**	36.20**	5.05
1000-grain weight (GW)	0.01	0.44**	2.09**	0.02**	0.0004

@Figures in parentheses indicate the degrees of freedom

weight (33 %) and days to heading (17%), accounting for 50% of the total divergence followed by plant height (15%). Contribution of days to flowering and 1000-grain weight to total divergence has also been reported in rice, common millet and little millet (Mahapatra *et al.*, 1995, Reddy *et al.*, 1996; Arunachalam *et al.*, 2005). Following the Tocher's method, the twenty-two entries were grouped into three clusters and the clustering was in broad agreement with the groupings obtained by using the first two canonical vectors. Cluster I comprised of 20 genotypes which included four released varieties namely Kolab and Sabar (released from OUAT, Bhubaneswar) and PRC3 and CO 2 (released from TNAU, Coimbatore). Cluster II consisted of KCM 309, one local germplasm of Kalahandi district of Odisha, while cluster III contained check variety TNAU 98 (released

from TNAU, Coimbatore). The most divergent clusters were cluster II and III followed by clusters I and III having average inter-cluster distance (D^2 value) of 67.7 and 36.5, respectively. Hence, hybridization between genotypes in diversified clusters is likely to yield better recombinants in segregating population.

In the metroglyph analysis, computation of scoring index of the genotypes in respect of the characters revealed that the genotype TNAU 98 had the highest score, while KCM 594 and RCM 4 had the lowest score (Table 2). Basing on the scoring index, the genotypes were grouped into five clusters:

- Cluster I: KCM 84, KCM 103, KCM 121, KCM 153, KCM 309, KCM 404, KCM 405, RCM 7, RCM 10, RCM 16, RCM 20, RCM 22, Kolab, PRC 3
 Cluster II: KCM 42, KCM 102D, Sabar, CO 2
 Cluster III: KCM 594, RCM 4
 Cluster IV: RCM 17
 Cluster V: TNAU 98

In this classification, the single multivariety cluster of D^2 analysis was observed to form three multivariety clusters indicating the subtle differences among the genotypes in the group. Hence, crosses between such genotypes in a cluster (cluster I of D^2 analysis) will provide scope for obtaining transgressive segregants in recombination breeding programme.

In the numerical taxonomic approach, all the 14 characters were used to calculate similarity coefficients (S_G) and the dendrogram prepared on the basis of similarity coefficients showed the different clusters at various phenon levels (Table 3). The genotypes could be broadly classified into four clusters both at 70 % and 75 % phenon level, viz. cluster I comprising 18 genotypes, cluster II consisting of one, cluster III with two genotypes and cluster IV having one genotype. While increasing the phenon level to 80 % and 85 %, the multivariate cluster I was further dissociated into two and five sub-clusters, respectively. The 18 genotypes in cluster I were grouped into two sub-clusters, i.e. IA and IB comprising of fourteen and four genotypes, respectively at 80 per cent phenon level. When the phenon level was increased up to 85 per cent, the sub-clusters IA and IB were further sub-divided into three and two genotypic constellations, respectively. Thus sub-cluster IA was further divided into IA_1 , IA_2 and IA_3 with 11, 2 and 1 genotypes, respectively. Similarly, sub-cluster IB was dissociated into IB_1 and IB_2 , each with two genotypes. Through the numerical taxonomic approach, it was possible to discern the subtle genotypic differences between the test entries grouped into different clusters and/or subclusters at different phenon levels. This subtle

Table 2. Numerical score of mean performance of 22 genotypes of little millet for 11 characters pooled over 12 environments

Genotype	**GY	PH	FLA	PL	PE	PN	PW	BY	HI	DH	GW	Total Score
KCM 42	3	2	2	2	2	2	3	2	3	2	2	25
KCM 84	3	2	2	2	2	3	2	2	2	2	2	24
KCM102D	3	2	2	2	2	2	3	3	3	3	2	27
KCM 103	2	1	2	2	2	3	1	1	2	2	2	20
KCM 121	2	2	2	2	2	3	2	2	2	2	2	23
KCM 153	2	2	2	2	2	2	2	2	2	2	2	22
KCM 309	2	3	2	2	1	1	3	2	1	3	1	21
KCM 404	2	2	1	2	2	2	2	2	2	2	2	21
KCM 405	2	2	2	2	1	2	2	2	2	2	2	21
KCM 594	1	1	1	1	2	1	1	1	1	1	2	13
RCM 4	1	1	1	1	2	1	1	1	1	1	2	13
RCM 7	2	2	2	1	3	2	3	2	3	2	2	24
RCM 10	1	2	2	2	3	2	1	1	2	2	2	20
RCM 16	2	2	2	2	3	2	2	2	2	2	2	23
RCM 17	1	2	2	1	2	1	2	2	2	2	1	18
RCM 20	2	2	2	2	2	2	2	2	2	2	2	22
RCM 22	2	2	2	1	3	1	3	2	3	2	2	23
Kolab	2	2	2	2	1	3	1	2	1	2	2	20
Sabar	2	2	3	2	2	3	2	3	2	2	2	25
PRC 3	1	2	2	2	2	2	1	2	1	2	2	19
CO 2	3	2	2	2	2	3	2	3	2	2	2	25
TNAU 98	3	3	3	3	3	2	3	3	2	3	3	31
Mean												21.82
SD												04.05
0.7SD												02.84

**N:B: Abbreviations for characters as in Table 1.

Table 3. Composition of clusters /sub-clusters identified from the dendrogram at different phenon level

Number of clusters/sub clusters at different phenon level			Genotypes
75%	80%	85%	
I (18)*	IA (14)	IA ₁	KCM 84, KCM 103, KCM 12, KCM 153, KCM 404, KCM 405, RCM 10, RCM 16, RCM 20, Kolab, PRC 3
		IA ₂	RCM 7, RCM 22
		IA ₃	RCM 17
	IB (4)	IB ₁	KCM 42, KCM 102D
		IB ₂	Sabar , CO 2
II (1)	II (1)		KCM 309
III (2)	III (2)		KCM 594, RCM 4
IV (1)	IV (1)		TNAU 98

* Figures in parentheses indicate number of genotypes in the respective clusters

genetic differences among the test entries gives scope for selection of desirable types in recombination breeding programme.

A comparison of different clustering patterns showed that the genotypes were grouped into three clusters in D² analysis, five in metroglyph analysis, and four, five and eight clusters in UPGMA method of numerical taxonomic approach at 75 %, 80 per cent and 85 % phenon levels, respectively. It is therefore evident that the metroglyph analysis seems to be easy and simple, and can be used for initial grouping when the number of collections is large. But the numerical taxonomic approach for classification of the biological populations into different groups is more potent to distinctly discriminate the genotypes for their use in recombination breeding.

Acknowledgement

The germplasm collection received from the NATP on Plant Biodiversity operating in the Department of Plant Breeding & Genetics, OUAT, Bhubaneswar, is highly acknowledged.

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Table 3. Composition of major fruit volatiles in Russian olive variants

S. No.	Retention time (minute)	Relative proportion of each volatiles (% of total volatiles)				
		Bee	Balti	Ringmo	Marpo	Chapacha
1	2.70	–	–	1.57	1.40	–
2	4.04	–	2.18	–	–	–
3	4.39	30.06	20.01	27.88	23.64	47.31
4	5.52	23.30	24.18	27.64	25.13	23.57
5	6.03	1.55	2.37	7.96	0.90	2.49
6	6.87	6.26	7.25	2.33	4.31	2.89
7	9.94	18.66	23.09	15.33	24.51	8.04
8	10.33	2.45	2.87	1.64	1.72	0.89
9	15.74	1.78	0.94	1.00	2.46	4.15
10	17.28	0.28	3.27	4.64	3.69	4.44
11	others	15.6	13.84	10.01	12.24	6.22

“–” indicates absence.

by genotype, which provides a recognition tool for chemotaxonomy (Laitinen *et al.*, 2000).

In the present study also, the chromatographic data were found to be of taxonomic importance. These data indicated that the five fruit morphotypes of Russian olive were distinct from each other in the phytochemical compositions of their fruits and flowers. This is the first report producing chromatographic profile of fruit and flower extracts and fruit volatiles of Russian olive in which variant-specific chemical pattern was observed. Results of TLC and HPLC indicated the presence of stigmaterol only in the fruits of *bee* variant. Presence of stigmaterol in Russian olive fruit has not been reported previously, though other sterol, β -sitosterol has been reported in this species in earlier studies (Goncharova and Glushenkova, 1990; Goncharova *et al.*, 1993).

These results thus confirm diversity based upon phytochemical profiling present among the variants of the species found in Ladakh, corroborating with existing ethnobotanical information and morphometric data. These profiles can be used as fingerprints for the identification of these varieties or to distinguish this species from other species.

Acknowledgements

We express a deep sense of gratitude to Dr RS Sangwan, HOD, MSB Laboratory, CIMAP for extending an unfettered access to the laboratory facilities for this study. The first author is indebted to SKUAST-K, for granting him sabbatical for this study. He is also grateful to the Indian Academy of sciences, Bangalore for providing financial assistance under Summer Research Fellowship Programme, 2011.

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Assessment of Genetic Diversity Using Quantitative and Qualitative Traits in Hazelnut

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(Received: 01 June, 2012; Revised: 08 August 2012; Accepted: 09 August 2012)

The study conducted on to assess the genetic diversity on hazelnut in Kashmir valley, the results indicate genetic diversity with regard to morphological, yield, yield attributing and quality attributes. Maximum nut weights were recorded in SKAU-H-0035 whereas, kernel per cent registered maximum in SKAU-H-0003 and early nut maturity was recorded in SKAU-H-0041. Highest kernel weight (0.69g/kernel) were found in SKAU-H-0041 whereas lowest (0.43 g/kernel) in SKAU-H-0034 genotype. Highest yield were found in SKAU-H-0014. Crude fat content was recorded highest in SKAU-H-0020, whereas, highest crude protein content was noted in SKAU-H-0012.

Key Words: *Corylus colurna*, Flowering, Kernel, Maturity, Nut, Variability

Introduction

The Himalayan hazelnut botanically known as *Corylus colurna* L. considered as *C. jacquemontii* Decne (Kasapligil, 1963) (family Corylaceae) is typically a temperate zone nut crop (Westwood, 1993). It is locally known as “Virin” in Kashmir (Wanchoo, 2000). Hazelnuts are deciduous trees or shrubs scattered over the temperate region of Northern Hemisphere, extending from Japan, China, Turkey, India and Europe to North America Spain (Sharma, 1991). *Corylus colurna*, occurs in mixed temperate forest from Hindukush Mountain in Northern Afganistan through Pakistan and Indian Himalayan region to western Nepal. *C. ferox* Wall., the Himalayan hazel occurs at high elevations (1700-3500m) in the eastern part of the Himalayan in India, Nepal, and NW Yunnan province of China.

In USA hazelnut is so popular that it has been declared as Oregon States state nut. The nuts are small in sized and hard shelled. The flesh (kernel) of the hazelnut is highly nutritious and contains about 12.6% proteins, 62.4% fats. Himalayan species *Corylus colurna* which is naturally available in Kashmir could not be exploited due to poor yielding behaviour of trees and having hard nuts considering the aforementioned fact an exploration programme was carried out to exploit the genetic variability of the natural habitats of Jammu and Kashmir.

Materials and Methods

An extensive exploration programme for identification, selection and evaluation of hazelnut was carried out at Dachigam Wildlife Sanctuary during 2006 to 2008 which is situated at an elevation of 16,00-4,250 m between 34°-10'N and 74°-50' to 75°-10'E altitudinal range. During course of study 41 trees were indentified and earmarked and named with prefix SKAU-Hazelnut (SKAU-H) with serial of genotypes to record data on foliage on various vegetative, nut and kernel characters. Leaf shape was recorded by measuring the leaf length and breadth with scale and ratio was worked out (Mir, 2002), staminate catkins per cluster and their appearance period, pistillate colour was recorded, quantitative traits like tree height, tree spread were recorded by measuring tape, tree volume was calculated using the formula, $\text{Volume} = \frac{4}{3}\pi ab^2$ or $\frac{4}{3}\pi a^2b$ and trunk cross sectional area was calculated by $(\text{Diameter})^2 / 4\pi$ as suggested by Westwood (1983). Data on all the features pertaining to descriptive characteristics was recorded as per the “Descriptor of Hazelnut Bioversity” FAO (2008) standard format.

Results and Discussion

Genetic Variability in Hazelnut Genotypes with Regard to Quantitative and Qualitative Traits.

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The data on growth and yield characteristics of identified hazelnut genotypes are presented in Table 1. Tree height varied from 6.50 to 22.46 m, the genotype SKAU-H-0014 was found to be tallest (22.46 m), whereas, SKAU-H-0041 was smallest (6.50 m). Tree spread was found to be in the range of 3.20 to 10.40 m, the maximum spread was recorded in SKAU-H-0012 (10.40 m) whereas; the lower tree spread was recorded in SKAU-H-0041 (3.20 m). The maximum volume was recorded in SKAU-H-0014 (122.89 m³) whereas, the minimum volume was noted in SKAU-H-0041 (34.83 m³). Maximum Trunk Cross Sectional Area (T.C.S.A.) was registered in SKAU-H-0014 and SKAU-H-0023 (0.38 m²) respectively, whereas, the minimum (0.06 m²) in SKAU-H-0038 (Table 1).

Remarkable variations in morphological characters were noted in identified hazelnut genotypes. Leaf length was found maximum (15.53 cm) in SKAU-H-0037, and lowest (13.53 cm) was in SKAU-H-0041 genotypes. Leaf width and petiole length was found highest in SKAU-H-0031 (11.34 cm) and SKAU-H-0037 (4.35 cm) and minimum was in SKAU-H-0023 (9.26 cm) and SKAU-H-0003 (3.41 cm) respectively. Maximum leaf area was found in SKAU-H-0020 (131.77 cm²) and minimum in SKAU-H-0008 (112.33 cm²). The leaf shape factor was ranged between 1.30 to 1.57, leaf shape varied from round to ovate to elongated, nine genotypes viz., SKAU-H-0004, SKAU-H-0012, SKAU-H-0016, SKAU-H-0017, SKAU-H-0020, SKAU-H-0029, SKAU-H-0031, SKAU-H-0032, and SKAU-H-0034 were found with round shape, whereas two genotypes SKAU-H-0023 and SKAU-H-0027 were having elongated leaf shape and rest of the genotypes produce ovate shaped leaves (Table 1).

Maximum (5.53) number of catkins per cluster were noted in SKAU-H-0012 and minimum in SKAU-H-0029, rest genotypes were in between. Maximum length of catkins (11.66 cm) was recorded in SKAU-H-0040, shortest (7.66 cm) in SKAU-H-0019. Catkins appear earliest in SKAU-H-0040 and SKAU-H-0041 and late in SKAU-H-0001, SKAU-H-0002, SKAU-H-0003, SKAU-H-0004, SKAU-H-0005, SKAU-H-0022, SKAU-H-0023, SKAU-H-0024 and SKAU-H-0025. Maximum pistillate flowers per cluster (7.53) were noted in SKAU-H-0008; while as minimum (4.20) were found in SKAU-H-0024. Very early stigmatic styles were appeared in SKAU-H-0040 and SKAU-H-0041 and very late in SKAU-H-0006, SKAU-H-0007, SKAU-H-0019,

SKAU-H-0020 and SKAU-H-0021 (Table 2).

SKAU-H-0019, (3.54), was found with maximum nuts/cluster followed by SKAU-H-0034, and SKAU-H-0035 with 3.53 each whereas minimum (2.13) was in SKAU-H-0041. Large nut size (16.50mm) and small (14.84 mm) was recorded in SKAU-H-0041 and SKAU-H-0001 respectively.

Nut roundness index registered maximum in SKAU-H-0026 (0.95mm) and minimum in SKAU-H-0041 (0.67mm). Out of 41 genotypes, only one SKAU-H-0041 produce oblong-elongated shaped nuts, five genotypes viz., SKAU-H-0004, SKAU-H-0010, SKAU-H-0014, SKAU-H-0020 and SKAU-H-0023 produce roundish-ovate shaped nuts and rest of the genotypes produce flatish shaped nuts.

Maximum nut weight was noted (1.83 g/nut) in SKAU-H-0035, while as minimum (1.28 g) in SKAU-H-0004. Very thick shell (2.25 mm) was noted in SKAU-H-0037 and thin shelled (1.04 mm) nut was SKAU-H-0041 (Table 3). Highest kernel weight (0.69 g) noted in SKAU-H-0041 whereas least Kernel weight (0.43 g) was in SKAU-H-0034. Maximum kernel percentage (41.70) was found in SKAU-H-0003 and minimum (25.23 %) was in SKAU-H-0037. Further Thompson (1977) found very high heritability for this traits. Genotype SKAU-H-0020 registered maximum crude fat content (54.96 %) whereas, minimum crude fat content was recorded 44.65% in SKAU-H-0040, highest (18.22 %) crude protein content were found in SKAU-H-0012, whereas, lowest in SKAU-H-0026 (11.07%) (Table 3). Sharma and Sharma (2004) registered remarkable variation in different nut and kernel characters in seedling population of hazelnut grown in Pangri, Solong, Sungri and Nichor area of Himachal Pradesh. Sharma and Kumar (2001) recorded sectional variation in hazelnut from Himachal Pradesh. The maturity in Hazelnuts starts from 16th August and completed up to 19th September. Early maturity was observed in SKAU-H-0041 which starts from 16th of August and completed up to 1st week of September, however, late maturity was observed in three genotypes, namely SKAU-H-009, SKAU-H-0025 and SKAU-H-0028 which starts from 5th September and completed up to 19th September.

The harvesting period of mature nuts in identified genotypes were recorded between 5th to 26th September within the range of 22 days. The mature nuts were first harvested from SKAU-H-0041 on 5th September whereas,

Table 1. Growth and yield characteristics of hazelnut genotypes

Genotype	Leaf length (cm)	Leaf width (cm)	Leaf area (cm ²)	Leaf shape factor*	Petiole Length (cm)	Tree height (m)	Tree spread (m)	Tree volume (m ³)	Trunk cross-sectional area (m ²)	Maturity period	Harvesting date	Nut yield (kg/tree)
SKAU-H-0001	15.20	10.50	120.01	1.46 b	4.25	11.00	5.40	167.86	0.11	28 Aug.-10 Sep.	15 Sep.	2.5
SKAU-H-0002	15.50	11.06	128.26	1.40 b	3.81	15.50	6.80	375.08	0.26	25 Aug.-9 Sep.	14 Sep.	3.5
SKAU-H-0003	15.11	11.00	125.72	1.38 b	3.41	13.63	7.12	361.33	0.14	1 Sep.-15 Sep.	21 Sep.	3.8
SKAU-H-0004	14.50	11.06	116.23	1.30 a	3.85	9.09	5.15	125.54	0.13	23 Aug.-6 Sep.	12 Sep.	3.5
SKAU-H-0005	14.66	10.51	119.77	1.40 b	3.48	19.69	9.39	906.16	0.36	25 Aug.-10 Sep.	16 Sep.	3.5
SKAU-H-0006	14.48	10.16	117.97	1.42 b	3.98	12.50	6.36	264.60	0.10	26 Aug.-10 Sep.	15 Sep.	2.6
SKAU-H-0007	15.23	11.10	127.19	1.37 b	3.93	14.30	5.90	260.50	0.18	29 Aug.-13 Sep.	19 Sep.	2.7
SKAU-H-0008	13.71	9.83	112.33	1.39 b	4.06	13.50	7.60	408.07	0.14	22 Aug.-3 Sep.	9 Sep.	2.5
SKAU-H-0009	14.45	10.40	121.40	1.38 b	4.18	19.25	9.50	908.72	0.33	5 Sep.-19 Sep.	26 Sep.	3.2
SKAU-H-0010	14.71	10.33	118.38	1.42 b	3.60	12.50	7.13	331.62	0.13	25 Aug.-7 Sep.	16 Sep.	2.0
SKAU-H-0011	14.98	10.89	121.03	1.36 b	3.51	18.23	8.74	728.36	0.22	30 Aug.-15 Sep.	23 Sep.	3.5
SKAU-H-0012	14.33	10.83	116.43	1.32 a	3.98	21.16	10.4	1197.73	0.36	24 Aug.-6 Sep.	14 Sep.	4.0
SKAU-H-0013	14.11	10.36	115.28	1.36 b	3.73	20.39	10.3	1131.50	0.31	24 Aug.-6 Sep.	15 Sep.	3.9
SKAU-H-0014	14.00	10.08	114.31	1.38 b	4.13	22.46	10.2	1222.89	0.38	28 Aug.-10 Sep.	19 Sep.	4.2
SKAU-H-0015	14.36	9.76	112.93	1.48 b	3.95	15.31	6.83	369.99	0.22	26 Aug.-10 Sep.	18 Sep.	2.9
SKAU-H-0016	14.76	11.32	123.47	1.30 a	3.88	9.45	5.61	154.92	0.08	29 Aug.-13 Sep.	21 Sep.	2.5
SKAU-H-0017	14.40	10.76	115.95	1.33 a	4.03	17.51	8.50	661.68	0.31	25 Aug.-8 Sep.	15 Sep.	3.8
SKAU-H-0018	14.15	10.38	115.37	1.36 b	3.66	16.39	7.23	446.85	0.24	23 Aug.-6 Sep.	13 Sep.	2.5
SKAU-H-0019	14.20	10.29	118.52	1.37 b	3.63	13.25	7.51	389.75	0.14	23 Aug.-6 Sep.	13 Sep.	3.5
SKAU-H-0020	14.65	10.76	131.77	1.35 a	3.93	18.75	8.03	630.80	0.36	24 Aug.-6 Sep.	14 Sep.	3.6
SKAU-H-0021	15.33	10.43	119.32	1.49 b	3.66	11.30	5.91	205.85	0.11	23 Aug.-6 Sep.	14 Sep.	2.3
SKAU-H-0022	14.60	10.48	121.33	1.39 b	4.23	13.36	7.15	356.43	0.14	29 Aug.-13 Sep.	20 Sep.	2.6
SKAU-H-0023	14.51	9.26	120.54	1.57 c	4.03	19.82	9.41	916.51	0.38	30 Aug.-15 Sep.	23 Sep.	3.0
SKAU-H-0024	15.31	11.00	128.66	1.38 b	3.51	15.53	6.82	377.77	0.31	31 Aug.-16 Sep.	21 Sep.	3.6
SKAU-H-0025	14.20	10.33	118.30	1.37 b	3.83	9.50	5.53	151.48	0.10	5 Sep.-19 Sep.	24 Sep.	3.5
SKAU-H-0026	14.51	10.40	117.07	1.40 b	3.86	14.50	7.30	404.38	0.23	3 Sep.-16 Sep.	21 Sep.	2.3
SKAU-H-0027	14.31	9.58	113.08	1.51 c	4.01	12.36	5.82	219.10	0.14	4 Sep.-16 Sep.	23 Sep.	2.2
SKAU-H-0028	14.75	10.06	124.75	1.47 b	4.18	18.50	8.36	676.64	0.30	5 Sep.-19 Sep.	25 Sep.	3.4
SKAU-H-0029	14.65	10.86	131.60	1.34 a	3.60	15.73	7.60	475.17	0.22	30 Aug.-15 Sep.	23 Sep.	3.6
SKAU-H-0030	14.15	10.41	114.43	1.36 b	3.96	13.75	7.30	383.18	0.14	30 Aug.-15 Sep.	21 Sep.	3.1
SKAU-H-0031	15.30	11.34	114.27	1.34 a	4.06	19.50	7.90	636.89	0.35	28 Aug.-10 Sep.	18 Sep.	3.3
SKAU-H-0032	14.36	10.90	125.80	1.31 a	3.85	14.50	7.25	109.87	0.19	2 Sep.-15 Sep.	21 Sep.	2.9
SKAU-H-0033	14.25	9.86	123.17	1.46 b	3.60	12.50	7.50	367.96	0.11	24 Aug.-6 Sep.	15 Sep.	2.8
SKAU-H-0034	14.73	10.93	121.53	1.35 a	3.88	8.69	4.50	91.98	0.08	28 Aug.-10 Sep.	17 Sep.	2.3
SKAU-H-0035	14.53	10.51	115.52	1.39 b	3.71	17.50	8.32	633.96	0.32	26 Aug.-10 Sep.	18 Sep.	2.9
SKAU-H-0036	15.23	11.01	129.65	1.38 b	3.73	13.64	7.14	363.9	0.16	24 Aug.-6 Sep.	15 Sep.	3.5
SKAU-H-0037	15.53	10.76	120.00	1.40 b	4.35	13.50	6.39	287.57	0.13	27 Aug.-10 Sep.	16 Sep.	2.5
SKAU-H-0038	14.03	9.98	118.55	1.40 b	3.98	7.38	4.21	68.12	0.06	30 Aug.-15 Sep.	20 Sep.	2.3
SKAU-H-0039	14.60	10.63	118.18	1.36 b	3.50	9.53	5.68	160.73	0.13	30 Aug.-15 Sep.	21 Sep.	3.5
SKAU-H-0040	15.15	10.33	119.57	1.47 b	3.98	10.81	6.50	238.74	0.14	20 Aug.-3 Sep.	10 Sep.	3.4
SKAU-H-0041	13.53	9.81	121.17	1.37 b	4.18	6.50	3.20	34.83	0.07	16 Aug.-1 Sep.	5 Sep.	0.5
L.S.D (0.05)	1.66	1.57	20.43	0.21	0.80	-	-	-	-	-	-	-
± S.E. _{diff.}	0.83	0.79	10.27	0.10	0.40	-	-	-	-	-	-	-

*Leaf Shape: a = round, b = ovate and c = elongated

Table 2. Staminate and pistillate inflorescence characteristics of hazelnut genotypes

Genotype	Staminate catkins / cluster(no.)	Catkin length (cm)	Appearance period of staminate catkins	Pistillate flowers/ cluster(no.)	Appearance period of stigmatic styles
SKAU-H-0001	4.00	8.33	Late-July	4.90	Mid-March
SKAU-H-0002	4.33	8.93	Late-July	5.70	Mid-March
SKAU-H-0003	4.53	9.00	Late-July	6.50	Mid-March
SKAU-H-0004	4.60	8.33	Late-July	5.53	Mid-March
SKAU-H-0005	4.00	8.73	Late-July	5.00	Mid-March
SKAU-H-0006	5.06	9.26	Mid-July	5.73	Late-March
SKAU-H-0007	3.66	9.76	Mid-July	4.86	Late-March
SKAU-H-0008	4.06	8.56	Late-June	7.53	Mid-February
SKAU-H-0009	3.66	8.13	Late-June	6.03	Mid-February
SKAU-H-0010	3.86	9.86	Late-June	6.20	Mid-February
SKAU-H-0011	4.00	9.70	Late-June	5.13	Mid-February
SKAU-H-0012	5.53	8.16	Late-June	6.46	Mid-February
SKAU-H-0013	4.86	10.10	Late-June	5.93	Mid-February
SKAU-H-0014	4.20	8.83	Early-July	6.86	Late-February
SKAU-H-0015	3.46	10.50	Early-July	6.70	Late-February
SKAU-H-0016	3.80	8.70	Early-July	5.66	Late-February
SKAU-H-0017	3.53	10.43	Early-July	5.23	Late-February
SKAU-H-0018	4.33	7.90	Early-July	5.00	Late-February
SKAU-H-0019	3.13	7.66	Mid-July	5.23	Late-March
SKAU-H-0020	4.33	10.10	Mid-July	5.73	Late-March
SKAU-H-0021	5.40	8.03	Mid-July	6.20	Late-March
SKAU-H-0022	3.46	9.40	Late-July	6.36	Mid-March
SKAU-H-0023	4.86	8.66	Late-July	5.90	Mid-March
SKAU-H-0024	4.26	8.33	Late-July	4.20	Mid-March
SKAU-H-0025	4.53	9.16	Late-July	5.90	Mid-March
SKAU-H-0026	5.26	10.06	Mid-July	5.53	Early March
SKAU-H-0027	4.46	9.00	Mid-July	4.46	Early March
SKAU-H-0028	4.46	9.66	Mid-July	6.03	Early March
SKAU-H-0029	3.00	8.40	Mid-July	5.56	Early March
SKAU-H-0030	4.86	8.56	Mid-July	5.13	Early March
SKAU-H-0031	4.40	8.60	Early-July	5.90	Mid-March
SKAU-H-0032	4.26	10.40	Early-July	5.80	Mid-March
SKAU-H-0033	4.00	9.43	Early-July	5.10	Mid-March
SKAU-H-0034	3.93	9.06	Early-July	6.23	Mid-March
SKAU-H-0035	5.33	8.06	Early-July	5.53	Mid-March
SKAU-H-0036	5.06	8.33	Late-June	5.66	Late-February
SKAU-H-0037	4.40	8.83	Late-June	5.80	Late-February
SKAU-H-0038	4.20	8.50	Late-June	6.60	Late-February
SKAU-H-0039	5.00	8.00	Late-June	5.20	Late-February
SKAU-H-0040	4.60	11.66	Mid-June	6.00	Early- February
SKAU-H-0041	3.20	8.00	Mid-June	5.10	Early- February
L.S.D (0.05)	2.85	2.85	–	2.76	–
± S.E. diff.	1.44	1.43	–	1.40	–

Table 3. Nut and kernal characteristics of hazelnut/genotypes

Genotype	Nuts/ cluster (no.)	Nut roundness index (mm)	Nut size index (mm)	Nut Shape factor*	Nut weight (g)	Shell thickness (mm)	Kernel weight (g)	Kernel percentage (%)	Special Characters	
									Crude Fat contents (%)	Crude Protein contents (%)
SKAU-H-0001	3.39	0.89	14.84	0.93b	1.32	1.65	0.48	36.35	49.22	14.37
SKAU-H-0002	3.44	0.87	15.04	0.96b	1.38	1.69	0.50	36.49	54.01	17.93
SKAU-H-0003	3.43	0.86	14.88	0.96b	1.33	1.71	0.55	41.70	53.20	13.78
SKAU-H-0004	3.39	0.87	15.24	0.97b	1.28	1.71	0.50	39.44	47.76	17.03
SKAU-H-0005	3.43	0.89	15.15	0.94b	1.50	1.58	0.45	30.24	48.84	16.19
SKAU-H-0006	3.45	0.91	15.00	0.91b	1.37	1.63	0.47	34.79	47.04	15.78
SKAU-H-0007	3.49	0.85	14.86	0.90a	1.43	1.67	0.47	32.90	47.40	14.85
SKAU-H-0008	3.52	0.89	15.40	0.95b	1.52	1.74	0.46	30.60	51.63	15.73
SKAU-H-0009	3.49	0.88	15.76	0.96b	1.55	1.62	0.53	34.03	48.69	16.23
SKAU-H-0010	3.43	0.89	15.36	0.97b	1.48	1.64	0.55	37.70	49.44	16.34
SKAU-H-0011	3.49	0.88	14.96	0.96b	1.47	1.58	0.46	31.91	49.97	17.55
SKAU-H-0012	3.46	0.92	15.06	0.91b	1.67	1.77	0.54	32.18	48.37	18.22
SKAU-H-0013	3.51	0.88	15.37	0.95b	1.52	1.71	0.50	33.65	48.79	13.39
SKAU-H-0014	3.42	0.88	15.33	0.97b	1.45	1.92	0.48	33.62	49.33	15.67
SKAU-H-0015	3.45	0.89	15.12	0.96b	1.48	1.78	0.44	29.81	48.99	16.82
SKAU-H-0016	3.45	0.89	15.27	0.93b	1.71	2.01	0.53	31.09	53.67	13.13
SKAU-H-0017	3.49	0.92	15.12	0.91b	1.61	1.78	0.51	31.78	48.30	15.14
SKAU-H-0018	3.48	0.91	15.40	0.92b	1.50	1.75	0.54	36.82	49.62	12.85
SKAU-H-0019	3.54	0.89	15.32	0.96b	1.44	1.65	0.44	30.62	48.54	14.99
SKAU-H-0020	3.45	0.87	15.27	0.97b	1.43	1.71	0.52	36.43	54.96	17.55
SKAU-H-0021	3.47	0.88	15.26	0.94b	1.68	1.97	0.45	27.13	48.35	16.99
SKAU-H-0022	3.45	0.91	15.68	0.90a	1.64	2.18	0.52	32.47	49.22	14.60
SKAU-H-0023	3.48	0.87	15.48	0.98b	1.77	1.94	0.51	29.40	50.34	13.85
SKAU-H-0024	3.41	0.89	15.40	0.96b	1.65	2.05	0.47	29.31	45.20	16.05
SKAU-H-0025	3.45	0.89	15.39	0.94b	1.67	1.81	0.48	29.65	52.02	11.61
SKAU-H-0026	3.47	0.95	15.65	0.88a	1.81	1.95	0.50	27.98	49.62	11.07
SKAU-H-0027	3.45	0.92	15.38	0.92b	1.59	2.17	0.44	27.93	50.86	14.28
SKAU-H-0028	3.51	0.90	15.30	0.92b	1.69	2.13	0.54	32.51	47.74	13.72
SKAU-H-0029	3.50	0.92	15.33	0.90a	1.67	2.09	0.46	28.25	52.16	14.10
SKAU-H-0030	3.46	0.90	15.31	0.94b	1.55	1.96	0.45	29.85	48.61	15.16
SKAU-H-0031	3.47	0.90	15.56	0.93b	1.49	2.12	0.53	37.04	50.30	15.25
SKAU-H-0032	3.51	0.92	15.63	0.91b	1.44	2.09	0.45	32.95	48.75	14.76
SKAU-H-0033	3.41	0.87	15.41	0.96b	1.63	2.10	0.46	28.52	51.48	13.44
SKAU-H-0034	3.53	0.90	15.20	0.93b	1.57	1.89	0.43	27.29	48.96	14.37
SKAU-H-0035	3.53	0.90	15.55	0.92b	1.83	1.99	0.53	29.76	50.29	14.35
SKAU-H-0036	3.43	0.89	15.07	0.94b	1.49	2.08	0.46	31.84	51.68	13.74
SKAU-H-0037	3.46	0.91	15.26	0.92b	1.79	2.25	0.45	25.23	48.11	15.90
SKAU-H-0038	3.41	0.90	15.47	0.92b	1.59	1.91	0.46	30.92	46.89	15.00
SKAU-H-0039	3.40	0.92	15.38	0.92b	1.70	1.96	0.45	26.42	50.55	14.85
SKAU-H-0040	3.43	0.94	15.63	0.89a	1.80	2.06	0.48	26.83	44.65	16.49
SKAU-H-0041	2.13	0.67	16.50	1.35c	1.71	1.04	0.69	40.34	45.01	11.94
L.S.D (0.05)	0.15	0.08	0.75	0.09	0.26	0.38	0.10	9.07	9.20	6.16
± S.E. diff.	0.10	0.04	0.38	0.05	0.13	0.19	0.05	4.60	4.63	3.10

*Nut shape: a = flatish, b = roundis ovate, c = oblong elongated

SKAU-H-0009 was harvested very late (26th September). The maximum yield was noted in SKAU-H-0014 (4.2 kg) and the minimum yield of 0.5 kg in SKAU-H-0041. Variation in yield might be due to factors governing pollination and genetic make up of individual genotypes,

Rana (2004) reports that hazelnut starts commercial bearing late and average yield registered 2.0 to 2.5 kg per tree.

The nut weight is highly heritable character, therefore larger nut size can be used in selection of better types

for commercial as well as for further improvement programme. The major emphasis in this investigation was given to identify the best genotypes, which are superior in yield, yield attributing, nut and kernel quality characters. The extent of genetic variability in studied genotypes indicates the scope of exercising exploration programme in Kashmir valley for proper exploitation of available population for identification of better types.

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SHORT COMMUNICATION

Genetic Variability in Bell Pepper (*Capsicum annum* L.) Under High Altitude Temperate Environment

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(Received: 25 October 2011; Revised: 30 January 2012; Accepted: 30 March 2012)

For genetic restructuring of bell pepper aimed for increasing the productivity, the genetic variability, heritability and genetic advance was assessed. The present research study conducted at Central Institute of Temperate Horticulture during summer season 2009 and 2010 involving thirty four genotypes of bell pepper for nine quantitative characters. The results revealed that PCV was greater than corresponding GCV for all the traits. High GCV and heritability accompanied by moderate to high genetic gain was observed for number of fruits and fruit weight which could be improved by selection in early generations. Fruit length and fruit diameter exhibited high heritability coupled with moderate GCV and low genetic gain which needs selection over several successive generations following hybridization for their edification. Pimento, SH-SP-52-1, SH-SP-610-1, SH-SP-610, CITH-SP-2, SH-SP-603 and SH-SP-52 were found potential and can be exploited for their potential in the temperate region.

Key Words: *Capsicum annum*, Genetic advance, Genetic variability, Heritability

Sweet pepper [*Capsicum annum* (L)] is a potential high value vegetable and one of the most remunerative off-season crop of mid and high hilly regions of India in particular Jammu & Kashmir. At present, productivity of bell pepper in Jammu & Kashmir is very low due to non-availability of quality seeds of high yielding varieties suitable to temperate regions. A few old varieties are still being recommended for commercial cultivation, which indicate that very limited improvement work has been carried out because of narrow genetic base of the crop (Singh *et al.*, 1993). There is a need for genetic restructuring of the bell pepper germplasm for increasing the productivity considering the preference of the consumers for typical bell shaped fruits with moderate size. The genetic improvement of any crop depends on magnitude of genetic variability and the extent of heritability of economically important characters. Therefore, a field investigation was carried out with an objective to study the genetic variability, heritability and genetic advance in bell pepper genotypes.

The present investigation was carried out at experimental farm of the Central Institute of Temperate Horticulture, Srinagar, Jammu & Kashmir during 2009 and 2010. Thirty four genetically diverse genotypes of bell pepper collected from various parts of the country. Row-to-row and plant-to plant spacing was maintained at 60 and 45 cm, respectively. All the recommended

cultural practices were followed to raise the normal crop. Data were recorded on nine important quantitative traits viz., plant height (cm), plant spread (cm), no. of primary branches, , fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g), fruit yield per plant (kg), and pericarp thickness (mm). The experiment was conducted under randomized block design replicated three times and average data of two years were analyzed as per the method suggested by Gomez and Gomez (1983). Genotypic and phenotypic coefficient of variation (Burton and Devane, 1953), heritability in broad sense, and genetic advance were computed according to Johnson *et al.* (1955).

Analysis of variance revealed that mean square estimates were significant for all the characters indicating sufficient diversity among the genotypes. The mean performance of the accessions (Table 1) revealed a wide range of variability for all the traits. The variation was the highest for average fruit weight followed by number of fruits per plant, plant height, plant spread, fruit length, peel, number of primary branches/plant and lowest in fruit yield. Maximum plant height recorded in Pimento genotype and minimum in SH-SP-1. The maximum plant spread measured in BSS-398 and minimum CITH-SP-4 genotype. More number of primary branches/plant was recorded in the genotype SH-SP-610-1, whereas highest number of fruits/plant was borne by variety SH-SP-610;

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Table 1. Mean performance of bell pepper genotypes in relation to different quantitative traits

Genotype	Plant height (cm)	Plant spread (cm)	Primary branches	No. of fruits	Fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit peel thickness (mm)	Yield (kg/plant)
SH-SP-5	44.33	42.66	4.67	20.00	108.00	6.66	6.96	0.38	1.38
SH-SP-52	54.00	39.33	5.33	32.66	51.50	4.43	5.36	0.34	1.76
SH-SP-3-1	58.33	43.66	4.33	34.00	38.46	6.70	4.46	0.32	1.31
SH-SP-706	53.00	35.66	5.67	32.66	52.50	5.53	5.66	0.45	1.20
BSS-398	60.00	54.33	4.67	20.66	100.23	9.90	6.40	0.44	1.97
SH-SP-32	49.66	38.33	5.00	28.33	48.10	5.30	5.16	0.37	1.34
SH-SP-4	40.33	44.00	4.33	22.00	58.40	4.20	6.23	0.44	1.28
SH-SP-624	62.00	41.66	4.33	30.66	66.90	6.40	5.90	0.36	2.05
SH-SP-32-1	49.66	34.66	3.66	13.66	95.53	8.00	5.90	0.42	1.32
SH-SP-603	46.33	38.33	4.00	25.00	95.90	6.13	7.23	0.49	2.37
SH-SP-1	34.66	32.66	3.66	22.33	105.90	9.40	5.43	0.42	2.36
Sh-SP-32-2	49.66	36.66	5.00	27.33	39.46	5.00	4.83	0.30	1.07
Sh-sp-624	62.00	41.33	4.33	30.67	41.90	6.06	5.33	0.43	1.28
SH-SP-4-1	44.66	35.66	4.66	23.67	38.66	3.60	5.43	0.72	0.90
SH-SP-610	57.66	39.33	4.33	35.00	39.50	5.06	4.93	0.43	1.36
Sh-SP-461	56.00	42.33	3.67	28.67	67.30	11.73	3.40	0.48	1.88
SH-SP-321	48.66	34.33	3.68	13.67	63.23	7.20	4.73	0.49	0.86
Green Bell	55.00	41.66	3.66	36.66	34.30	6.20	4.46	0.43	1.25
CITH-SP-2	48.00	46.00	3.66	8.00	134.66	6.60	6.86	0.74	1.07
SH-SP-603-1	44.00	34.33	4.66	23.67	69.33	4.86	5.63	0.32	1.63
Pimento -1	60.66	29.33	5.00	21.33	76.86	12.00	5.06	0.61	1.62
SH-SP-610	51.66	41.33	5.00	47.66	57.86	7.53	4.76	0.41	2.76
CITH-SP-1	40.33	31.33	5.00	18.00	84.26	6.93	6.03	0.39	1.48
Nishat-1	37.66	44.33	5.00	9.66	89.56	7.73	6.66	0.74	0.876
Pimento	70.66	35.66	5.33	33.66	90.23	13.80	4.90	0.49	3.16
SH-SP-52-1	54.00	40.66	5.33	37.66	82.63	5.33	6.40	0.43	3.13
SH-SP-610-1	43.66	33.66	7.33	24.33	54.16	5.63	5.63	0.43	1.32
Bhowali Local	63.66	46.33	6.66	22.00	71.80	7.06	5.63	0.48	1.58
Venidale	36.66	30.33	4.66	11.33	69.43	7.20	5.40	0.48	0.78
CITH-SP-3	48.00	39.00	5.33	23.33	66.60	6.50	5.53	0.41	1.55
SH-SP-2 -1	44.00	40.33	5.33	11.33	85.63	6.46	5.90	0.42	0.97
SH-SP-706-1	47.33	39.33	7.33	32.33	63.40	9.96	4.36	0.62	2.05
SH-SP-5-3	43.00	30.00	5.00	19.66	88.23	13.83	4.03	0.32	1.73
Orobelle	44.00	36.33	5.33	16.67	70.40	6.36	6.36	0.41	1.16
CD at 5%	6.34	5.35	1.23	5.90	23.03	1.39	0.789	0.06	0.81
CV%	7.74	8.46	15.60	14.65	24.80	11.80	8.78	10.73	54.90

however CITH-SP-1 recorded the highest fruit weight. On the other hand maximum fruit length recorded in Pimento and minimum in SH-SP-4-1. Fruit diameter was highest in SH-SP-603 followed by SH-SP-5 whereas, fruit pericarp thickness was found maximum in CITH-SP-1 and Nishat -1 followed by SH-SP-4 -1. The highest fruit yield per plant was recorded in pimento, followed by SH-SP-52-1 (3.13 kg), SH-SP-610 and least in Venidale. Among the genotypes tested. Pimento, SH-SP-52-1, SH-SP-610-1,

SH-SP-610, CITH-SP-1,, SH-SP-603 and SH-SP-52 appeared to possess greater potentiality for exploitation to circumvent fruit numbers, fruit weight, fruit length, diameter, yield and its components in bell pepper.

The genetic parameters estimated Table 2. showed that high PCV and GCV were observed for fruit yield/plant whereas they were moderate for number of fruit per plant, average fruit weight, fruit length, fruit pericarp thickness and number of primary branches/plant

Table 2. Estimates of variance and other genetic parameters in bell pepper

Character	Range	Mean $\pm$ SE (m)	PCV (%)	GCV (%)	Heritability (broad sense) as %	Genetic advance %	Genetic advance % of mean
Plant height (cm)	34.66-70.66	50.09 $\pm$ 2.24	18.12	16.38	81.72	15.28	30.38
Plant spread (cm)	29.33-54.33	38.67 $\pm$ 1.89	15.50	12.98	70.15	8.66	22.39
Primary branches	3.66-7.33	4.85 $\pm$ 0.43	22.99	16.89	53.94	1.23	25.36
No. of fruits	8.00-47.66	24.65 $\pm$ 2.08	38.70	35.82	85.6	16.82	68.31
Fruit weight (g)	34.3-134.66	70.61 $\pm$ 8.13	38.52	29.48	58.55	32.55	46.09
Fruit length (mm)	3.6-13.83	7.21 $\pm$ 0.49	36.96	34.74	89.65	4.88	67.68
Fruit diameter (cm)	3.4-7.23	5.49 $\pm$ 0.27	17.26	14.86	74.14	1.45	26.41
Fruit peel thickness (mm)	0.30-0.74	0.45 $\pm$ 0.02	26.30	24.01	83.35	20.31	45.14
Yield (kg/plant)	0.78-3.16	1.58 $\pm$ 0.28	64.79	30.38	22.00	0.49	31.01

which suggested greater phenotypic as well as genotypic variability among the accessions and responsiveness of these traits for making further improvement by selection. These results further confirmed by (Vani *et al.*, 2007; Ukkund *et al.*, 2007). A high degree of disparity between PCV and GCV was observed for fruit yield per and average fruit weight depicting their susceptibility to environmental fluctuation. Heritability in broad sense ranged from 22% fruit yield to 89.65% for fruit length. Such moderate to high values of heritability for all the characters illustrated that they were least influenced by environmental modification and their substantial improvement can be made using standard selection procedures.

High estimates of genetic advance percentage of mean were noticed for number of fruits per plant and fruit length which explained that they could be improved to a large extent. High estimates of heritability coupled with low genetic gain were observed for fruit length, number of fruits, plant height and fruit diameter which may be attributed to the non-additive gene effects and these traits can be improved through hybridization and use of hybrid vigour (Panse and Sukhatme, 1956). Fruit yield and number of primary branches showed low heritability

associated with low genetic advance indicating the role of non additive genes for these traits suggesting thereby that their improvement could be achieved through heterosis breeding.

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SHORT COMMUNICATION

Genotype x Environment Interactions for Forage Productivity in Oats (*Avena sativa* L.)

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(Received: 19 December 2011; Revised: 01 August 2012; Accepted: 8 August 2012)

Stability parameters in 33 oat genotypes were studied to obtain information on the magnitude and nature of G x E interactions and stability for forage yield. These genotypes evaluated under three environments i.e. E₁ (2006-07), E₂ (2007-08) and E₃ (2008-09), depicted significant interaction with the environments for both green fodder and dry matter yields. OS 7, a high yielding genotype and responsive to favourable environment, was found to be the most unstable one for both the characters. The high yielding genotypes which were stable over environments and responsive to favourable conditions included JHO-851, OS-297 and OS 293. The genotypes OS 311, OS 315, JHO 2000-6 and JHO 2000-2 were high yielding, responsive to poor environment and least deviating from regression while UPO 271 was found to be high yielding, responsive to average environment and stable one.

Key Words: Forage productivity, Oats, *Avena sativa*, G x E interaction

Oats (*Avena sativa* L.) is an important cereal forage crop in the temperate, sub temperate and tropical climates of the world. It provides high tonnage of nutritious green fodder in a short period of 100-120 days. It is generally widely adapted in northern and north western regions of India where it is extensively grown in winter season under limited irrigation facilities. Genotype x Environment interactions constitutes a serious problem in recommending a variety for a specific region because crop outcome is a product of the genotype and the environment in which crop has been grown (Zaheri and Bahraminejad, 2012). Environment for commercial cultivation cannot be changed but genotype can be modified to suit the available soil and climate related environmental conditions. Ideal variety is always one, which possesses general adaptation with higher yield potential. A variety is considered to be more adaptive or stable if it has high mean but low degree of fluctuations in yielding ability when grow over diverse environments (Arshad *et al.*, 2003). As such, screening of genotypes under varying environmental conditions is an essential part of the breeding programmes. Stability across many locations and years could increase both repeatability and heritability of important traits (Akcura, *et al.*, 2005; and Wekai *et al.*, 2010).

The present study was, therefore, aimed at investigating the stability parameters in 33 genotypes to obtain information on the magnitude and nature of G x E interactions and stability for forage yield in oats in order to identify high yielding and stable genotypes.

The field experimental was conducted at Regional Agricultural Research Station, Rajouri of Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu (J&K), during the *rabi* seasons of 2006-07, 2007-08 and 2008-09 under normal fertility conditions. Thirty three genotypes of forage oats, including two national checks (NC) viz. JHO 851 and Kent; and one zonal check (ZC) viz. Sabzar (Table 1) differing in forage productivity, comprised the experimental material for the present study. These genotypes were evaluated under three environments i.e. E₁ (2006-07), E₂ (2007-08) and E₃ (2008-09). Each of the environments was considered as an independent environment. The genotypes were sown in the first week of November each year i.e. November 7th, 2006, November 5th, 2007 and November 3rd, 2008 for E₁, E₂ and E₃, respectively. Sowings were done in randomized complete-block design (RCBD) with three replicates in plots each having four rows of 4 m length with inter-row spacing of 30 cm. Each genotype was harvested in two

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cuts, first cut at 50 per cent blooming stage which falls at 90-95 days after sowing and second cut at 60-65 days after first cut. Recommended doses of N (80 Kg/ha) and P (40 Kg/ha) were applied. N was applied in two split doses (first dose of 40 Kg/ha at the time of seeding and the second dose of 40 Kg/ha N after first cut). One pre-sown irrigation and two irrigations during crop growth cycle (first at tillering stage and second after first cut) were ensured. Data on green fodder yield were obtained from each plot of size 4.80 m². One Kg green fodder sample of each genotype was oven dried and from this dry matter yield was calculated in Kg/plot. The analysis for green fodder and dry matter yield was done after converting the data into quintals/ha. The data were subjected to stability analysis using established model suggested by Eberhart and Russel (1966).

The joint regression analysis (Table 1) revealed that significant variability among environments varying from year to year as well as among genotypes for both the characters. Appraisal of data further revealed that genotypes interacted significantly with the environments for both green fodder and dry matter yields. Non-significant environment (linear) variance for green fodder yield suggested that variation among environments is not linear for this trait. However, this variation was found to be linear for dry matter yield, revealing thereby that the prediction of the trait across environments was possible (Muhammad, *et al.*, 1993). However, variance due to G x E (linear) was highly significant implying thereby the differential yield performance of genotypes under different environments but with considerably varying reaction norms i.e. the linear sensitivity of different genotypes was variable. Therefore, prediction for most of the genotypes appears to be possible for green fodder and dry matter yield. Thus most of the variation was due to linear differences between linear slopes of regression for the characters studied. Such observations have been made earlier by Link *et al.*, 1994, Malhotra *et al.*, 1995; Hussain *et al.*, 2002). Besides,

the non-significant pooled deviation for both the traits suggests that the performance of different genotypes did not fluctuate significantly from their respective linear path of response to environments.

Mean green fodder yield (q/ha), regression (b) and deviation from regression (Sd²) for 33 genotypes in three environments are given in Table 2. The over all mean performance of 33 genotypes varied from 271.48 q/ha (UPO 265) to 382.32 q/ha (OS311) for green fodder yield and from 53.23 q/ha (JHO 99-1) to 73.67 q/ha (OS 7) for dry matter yield. Data in Table 2 further revealed that most of the genotypes out yielded the check (Kent). However, six genotypes out yielded the better check (JHO 851) both for green fodder and dry matter yield. Among these, OS 311, OS 7, OS 315, UPO 271 and JHO 2000-6 gave significantly higher green fodder and dry matter yields over both the checks. Genotypes JHO 851, OS 314, OS 297, OL 1193, OS 313, UPO 212, JHO 99-2, OS 7, Black Nip, OL 1235, UPO 265, HJ 8 and OS 293 had regression coefficient more than unity for both green fodder and dry matter. Therefore, these genotypes may be expected to perform well under good environmental conditions. Genotypes UPO 271, JH 8, JHO 99-5, JHO 2000-4 and HFO 114 possessed 'b' values close to unity and were thus average responsive to changes in environments and could perform well under average environmental conditions. Genotypes JHO 99-1, OS 295, OL 9, OS 6, Sabzar, Kent, and FG 22 had 'b' values less than unity and could be expected to give better yield under poor environments. Among the genotypes studied for comparative performance of green fodder and dry matter, OS 7 was high yielding, but the most unstable genotype for both the characters. Remaining all the genotypes were stable for both green fodder and dry matter yield, as they had non-significant values for deviation from regression. In the present study, the term stability as advocated by Jatasra and Paroda (1979) has been used. Observations with respect to identification of high yielding and stable strains of oats over environments have been made earlier (Gupta and Singh, 1997, Wani *et al.*, 2002, Nehvi *et al.*, 2007, Sun *et al.*, 2009; Wekai *et al.*, 2010).

Taking all the three parameters into consideration it could be noted that genotypes JHO 851, OS 297 and OS 293 were high yielding, responsive to favourable environments and stable ones. The genotypes OS 311, OS 315, JHO 2000-6 and JHO 2000-2 were high yielding, responsive to poor environment and stable over environments. Out of the high yielding genotypes, UPO 271 was found to

Table 1. Joint regression analysis of green and dry matter yield in oats

Source	d.f.	Mean Squares	
		Green fodder yield	Dry matter yield
Genotypes (G)	32	2478.37**++	110.46**++
Environ. (E)+(GXE)	66	2696.82**++	93.98**++
Environ. (Linear)	1	1.12	035.55**++
G X E (Linear)	32	4485.18**++	60.68**++
Pooled deviation	33	1044.33	37.13
Pooled error	192	827.99	31.89

** Against pooled error at 1% level

++ Against pooled deviation at 1% level

Table 2. Stability parameters for green and dry matter yield in oats

Genotype	Green Fodder Yield			Dry Matter Yield		
	Mean	b	S ² d ²	Mean	b	S ² d ²
JHO 99-1	287.46	-0.57	-285.77	53.23	-0.59	-16.62
UPO 271	366.96	1.05	-619.56	69.23	1.05	6.07
OS 295	350.39	0.34	3443.46**	60.48	0.37	91.55
JH 8	320.62	1.06	-151.43	58.29	0.99	-5.01
OS 315	373.88	0.78	778.32	71.92	0.82	-23.97
OL 9	322.98	-0.48	299.67*	56.69	-0.17	-3.62
JHO851(NC)	364.11	2.68**	-796.14	67.43	2.61	-31.86
OS 314	313.47	1.39	-818.59	59.14	1.37	-29.81
OS 297	379.69	1.38	940.81	64.35	1.25	-14.04
S 3021	326.15	0.82	0.86	62.72	0.80	-2.78
OL 1193	286.17	1.11	-810.42	55.81	1.17	-27.65
OS 296	334.16	0.98	1140.06	59.86	0.86	-30.42
OS 313	345.14	1.88	-678.31	63.24	1.80	-24.94
W 11	328.04	0.37	927.12	61.89	0.39	28.90
UPO212(NC)	341.02	1.23	411.55	66.87	1.29	10.95
JHO 99-2	333.24	2.02	-692.94	59.24	2.27	14.19
OS 7	373.81	2.91	5989.95**	73.67	2.88	242.79**
OS 303	340.40	0.10	-475.14	63.89	0.12	-13.40
OS 311	382.32	0.30	-352.19	67.71	0.66	-24.94
JHO 2000-2	355.00	0.92	-615.90	65.74	0.88	-21.84
OS 6	320.90	-0.17	132.84	57.32	-0.18	83.69
Sabzar (ZC)	315.46	-0.07	778.07	55.35	-0.10	16.94
Black nip	296.22	2.27	-746.82	54.20	2.03	-29.12
JHO 2000-6	367.35	0.90	743.99	72.04	0.95	24.97
OL 1235	332.40	1.58	152.11	57.31	1.45	-1.35
UPO 265	271.48	1.40	208.58	49.36	1.31	9.29
HJ 8	349.86	1.77	-699.08	68.74	1.83	-27.30
JHO 99-5	295.04	1.01	-620.09	56.74	1.00	-21.12
Kent (NC)	315.81	0.12	-434.03	57.42	0.12	-19.06
JHO 2000-4	298.50	1.00	-744.93	53.30	0.94	-26.00
HFO 114	330.06	1.05	1142.26	55.94	0.90	30.76
OS 293	351.57	1.70	83.88	60.61	1.55	-8.80
FG 22	331.16	0.09	-792.41	64.02	0.17	-30.31
Overall Mean	333.36			61.32		

* Significant at 5 per cent level

** Significant at 1 per cent level

be high yielding under average environment and stable one.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXVth meeting held on June 01, 2012 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 19 germplasm lines out of 99 proposals considered. The information on registered germplasm is published with

the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. DDK 1037 (IC0590877; INGR12001), a Wheat (*Triticum dicoccum*) Germplasm with a Resistance to Loose Smut and Flag Smut Disease

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Emmer wheat (*Triticum dicoccum* (Schrank.) Schubl.), commonly known as *dicoccum* wheat is cultivated in parts of Karnataka, Maharashtra, Tamil Nadu and Gujarat. It possesses high protein and dietary fibre content and therefore, is considered as more nutritious compared to bread and durum wheat. Among the major diseases, rusts (stem & leaf), loose smut and flag smut cause yield losses in *dicoccum* wheat. The genotype DDK 1037 is developed from the cross HW-1092/DDK-1006//SHIVANI KHAPLI//DDK-1001 following the pedigree method at UAS, Dharwad. During evaluation stages, it showed high level of resistance to loose smut and flag smut diseases. It also showed resistance to stem and leaf rusts during evaluation (Anonymous, 2009; 2010; 2011).

Morpho-agronomic characteristics: The genotype DDK 1037 was evaluated along with the check varieties DDK-1009 and MACS-2971 across the *dicoccum* growing zones of India over two years from 2008-09 to 2009-10. Based on yield potential, it was on par with MACS-2971 and showed about 6% yield advantage

over another check DDK-1009. It also showed distinct features in terms of profuse tillering, dwarf growth habit and green foliage.

Associated characters and cultivated practices: Genotype DDK 1037 also showed resistance to stem and leaf rusts, foot rot and moderately resistant to *Heterodera avenae* (Anonymous, 2009; 2010; 2011).

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Table 1. Yield and disease data of DDK 1037 and checks under coordinated multi-location evaluation

Genotypes	Mean yield (q/ha)	Loose smut				Flag smut			
		2009-10		2010-11		2008-09		2009-10	
		HS	AS	HS	AS	HS	AS	HS	AS
DDK 1037	37.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DDK 1009 ©	35.0	24.6	9.0	15.6	4.7	-	-	-	-
MACS 2971 ©	37.4	0.0	0.0	0.0	0.0	-	-	-	-

Mean yield of 3 years (2008-09 to 2010-11); HS- Highest Score, AS – Average score

*Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

2. Pusa 1602-06-24-5-45 (IC0593847; INGR12002), an Elite Paddy (*Oryza sativa*) Restorer Line with Basmati Quality and Blast Resistance Gene *Piz5*

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Pusa1602-06-24-5-45 is an elite Basmati quality restorer line with blast resistance gene *Piz5* conferring resistance against blast disease caused by *Magnaporthe oryzae*. It has been developed through a breeding strategy involving marker aided foreground selection for the gene *Piz5*, coupled with phenotypic selection for agronomic, grain and cooking quality traits, for recovery of recurrent parent genome. C101A51, an isogenic line in the background of *indica* rice variety CO-39 was used as donor for *Piz5* gene and PRR78, an elite Basmati quality restorer was the recurrent parent. Foreground selection for the gene *Piz5* was performed using linked SSR marker AP5930 (Fjellstrom *et al.*, 2006). Since the recurrent parent PRR78 is a restorer line, a microsatellite marker RM6100 linked with fertility restorer (*Rf1*) gene in PRR78 (Prakash, 2003) was employed for selection of *Rf1* gene. Background selection was performed using 62 STMS markers polymorphic between C101A51 and PRR78. The extent of recurrent parent genome in the improved line Pusa1602-06-24-5-45 is 86.66 % and it complete resistance to all the four virulent races under artificial inoculation as well as in hot spot locations in comparison to control PRR78 (Table 1). The agronomic, grain and cooking quality traits of the improved line Pusa1602-06-24-5-45 and its recurrent parent PRR78 are presented in Table 2. The performance of the improved hybrid Pusa RH10-02-3 developed crossing Pusa1602-06-24-5-45 was on par with Pusa RH10 along with high level of resistance to blast disease both under artificial inoculation as well as UBN in hotspot locations (Singh *et al.*, 2012).

For 0-5 Scale under artificial inoculation: Score 0-2 Resistant, 3 as Moderately Resistance and 4-5 as Susceptible.

For 0-9 Scale in UBN at hotspot location: Score 0-3 Resistant, 4-5 as Moderately Resistant, 6 as Moderately Susceptible and 7-9 as Susceptible.

Table 1. Reaction of the improved line Pusa1602-06-24-5-45 and the parental lines, PRR78 and C101A51, to rice blast isolates under artificial inoculation and in Uniform Blast Nursery at two hotspot locations

Name of isolate/ hotspot location	Pusa1602-06-24-5-45	PRR78	C101A51
Disease Reaction under artificial inoculation (0-5 Scale)			
Mo-ni-007	2	5	0
Mo-ni-012	2	4	0
Mo-ni-018	0	4	1
Mo-ni-019	0	5	0
Disease Reaction in UBN trials (0-9 Scale)			
ARS, Mugad	1	7	2
VPKAS, Almora	4	7	3

Table 2. Agronomic traits and % recurrent parent genome (RPG) recovery in Pusa1602-06-24-5-45 in comparison of the recurrent parent PRR78

Characters	PRR78	Pusa1602-06-24-5-45
Days to 50 % flowering	88.0	90.0
Plant height (cm)	114.8	126.8
Number of tillers	10.2	12.0
Panicle length (cm)	24.8	27.2
Number of filled grains/ panicle	189.0	214.0
Spikelet fertility (%)	91.34	89.26
Test weight (g)	27.55	29.07
Yield (q/ha)	58.25	66.53
% Superiority over PRR78	-	14.23
Recurrent Parent Genome recovery (%)	-	86.66
Kernel length before cooking (mm)	7.98	8.87
Kernel breadth before cooking (mm)	1.68	1.87
Kernel length after cooking (mm)	14.13	13.67
Kernel breadth after cooking (mm)	2.07	2.27
Kernel elongation ratio	1.77	1.53
Alkali spreading value	7	7
Aroma	2	2

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3. Pusa 1603-06-11-4-19 (IC0593848; INGR12003), an Elite Paddy (*Oryza sativa*) Restorer Line with Basmati Quality and Blast Resistance Gene *Pi54*

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Pusa1603-06-11-4-19 is an elite Basmati quality restorer line with blast resistance gene *Pi54* conferring resistance against blast disease caused by *Magnaporthae oryzae*. It has been developed through a breeding strategy involved marker aided foreground selection for the gene *Pi54* and background selection coupled with phenotypic selection for agronomic, grain and cooking quality traits, for recovery of recurrent parent genome. Tetep, an *indica* rice variety was used as donor for *Pi54* gene and PRR78; an elite basmati quality restorer was the recurrent parent. Foreground selection for the gene *Pi54* was performed using a marker RM206 linked to *Pi54* (Sharma *et al.*, 2005). Since the recurrent parent PRR78 is a restorer line, a microsatellite marker RM6100 linked with fertility restorer (*Rf1*) gene in PRR78 (Prakash, 2003) was employed for selection of *Rf1* gene. Background selection was performed using 62 STMS markers polymorphic between Tetep and PRR78. The extent of recurrent parent genome in the improved line Pusa1603-06-11-4-19 is 87.66 % and it complete resistance to all the four virulent races under artificial inoculation as well as in hot spot locations in comparison to recipient parent, PRR78 and donor parent Tetep (Table 1). The improved line Pusa1603-06-11-4-19 is superior to recurrent parent PRR78 for yield by 13.06%. The agronomic, grain and cooking quality traits of the improved line Pusa1603-06-11-4-19 and its recurrent parent PRR 78 are presented in Table 2. The performance of the improved hybrid Pusa RH10-03-4 developed crossing Pusa1603-06-11-4-19 was superior to PusaRH10 (23.23 g/ plant compared to 21.33 g/ plant in PusaRH10) along with maximum level of resistance to blast disease both under artificial

Table 1. Reaction of the improved line Pusa1603-06-11-4-19 and the parental lines, PRR78 and Tetep, to rice blast isolates under artificial inoculation and in Uniform Blast Nursery at two hotspot locations.

Name of isolate/ hotspot location	Pusa1603-06-11-4-19	PRR78	Tetep
Disease Reaction under artificial inoculation (0-5 Scale)			
Mo-ni-007	2	5	0
Mo-ni-012	2	4	0
Mo-ni-018	0	4	0
Mo-ni-019	0	5	0
Disease Reaction in UBN trials (0-9 Scale)			
ARS, Mugad	2	7	1
VPKAS, Almora	3	7	3

Table 2. Agronomic traits and percent recurrent parent genome (RPG) recovery in Pusa1603-06-11-4-19 in comparison of the recurrent parent PRR78

Characters	PRR78	Pusa1603-06-11-4-19
Days to 50 % flowering	88	88
Plant height (cm)	114.8	119.60
Number of tillers	10.2	11.60
Panicle length (cm)	24.8	28.20
Number of filled grains/ panicle	189	201
Spikelet fertility (%)	91.34	91.34
Test weight (g)	27.55	29.44
Yield (q/ha)	58.25	65.85
% Superiority over PRR78	-	13.06
Recurrent Parent Genome recovery (%)	-	87.66
Kernel length before cooking (mm)	7.98	8.07
Kernel breadth before cooking (mm)	1.68	1.67
Kernel length after cooking (mm)	14.13	12.67
Kernel breadth after cooking (mm)	2.07	2.47
Kernel elongation ratio	1.77	1.57
Alkali spreading value	7	7
Aroma	2	2

References

- Fjellstrom R, AM McClung and AR Shank (2006) SSR markers closely linked to the Pi-z locus are useful for selection of blast resistance in a broad array of rice germplasm. *Mol. Breed.* **17**: 149-157.
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3. Pusa 1603-06-11-4-19 (IC0593848; INGR12003), an Elite Paddy (*Oryza sativa*) Restorer Line with Basmati Quality and Blast Resistance Gene *Pi54*

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Pusa1603-06-11-4-19 is an elite Basmati quality restorer line with blast resistance gene *Pi54* conferring resistance against blast disease caused by *Magnaporthea oryzae*. It has been developed through a breeding strategy involved marker aided foreground selection for the gene *Pi54* and background selection coupled with phenotypic selection for agronomic, grain and cooking quality traits, for recovery of recurrent parent genome. Tetep, an *indica* rice variety was used as donor for *Pi54* gene and PRR78; an elite basmati quality restorer was the recurrent parent. Foreground selection for the gene *Pi54* was performed using a marker RM206 linked to *Pi54* (Sharma *et al.*, 2005). Since the recurrent parent PRR78 is a restorer line, a microsatellite marker RM6100 linked with fertility restorer (*Rf1*) gene in PRR78 (Prakash, 2003) was employed for selection of *Rf1* gene. Background selection was performed using 62 STMS markers polymorphic between Tetep and PRR78. The extent of recurrent parent genome in the improved line Pusa1603-06-11-4-19 is 87.66 % and it complete resistance to all the four virulent races under artificial inoculation as well as in hot spot locations in comparison to recipient parent, PRR78 and donor parent Tetep (Table 1). The improved line Pusa1603-06-11-4-19 is superior to recurrent parent PRR78 for yield by 13.06%. The agronomic, grain and cooking quality traits of the improved line Pusa1603-06-11-4-19 and its recurrent parent PRR 78 are presented in Table 2. The performance of the improved hybrid Pusa RH10-03-4 developed crossing Pusa1603-06-11-4-19 was superior to PusaRH10 (23.23 g/ plant compared to 21.33 g/ plant in PusaRH10) along with maximum level of resistance to blast disease both under artificial

Table 1. Reaction of the improved line Pusa1603-06-11-4-19 and the parental lines, PRR78 and Tetep, to rice blast isolates under artificial inoculation and in Uniform Blast Nursery at two hotspot locations.

Name of isolate/ hotspot location	Pusa1603-06-11-4-19	PRR78	Tetep
Disease Reaction under artificial inoculation (0-5 Scale)			
Mo-ni-007	2	5	0
Mo-ni-012	2	4	0
Mo-ni-018	0	4	0
Mo-ni-019	0	5	0
Disease Reaction in UBN trials (0-9 Scale)			
ARS, Mugad	2	7	1
VPKAS, Almora	3	7	3

Table 2. Agronomic traits and percent recurrent parent genome (RPG) recovery in Pusa1603-06-11-4-19 in comparison of the recurrent parent PRR78

Characters	PRR78	Pusa1603-06-11-4-19
Days to 50 % flowering	88	88
Plant height (cm)	114.8	119.60
Number of tillers	10.2	11.60
Panicle length (cm)	24.8	28.20
Number of filled grains/ panicle	189	201
Spikelet fertility (%)	91.34	91.34
Test weight (g)	27.55	29.44
Yield (q/ha)	58.25	65.85
% Superiority over PRR78	-	13.06
Recurrent Parent Genome recovery (%)	-	87.66
Kernel length before cooking (mm)	7.98	8.07
Kernel breadth before cooking (mm)	1.68	1.67
Kernel length after cooking (mm)	14.13	12.67
Kernel breadth after cooking (mm)	2.07	2.47
Kernel elongation ratio	1.77	1.57
Alkali spreading value	7	7
Aroma	2	2

inoculation as well as UBN in hotspot locations (Singh *et al.*, 2012).

For 0-5 Scale under artificial inoculation: Score 0-2 Resistant, 3 as Moderately Resistance and 4-5 as Susceptible.

For 0-9 Scale in UBN at hotspot location: Score 0-3 Resistant, 4-5 as Moderately Resistant, 6 as Moderately Susceptible and 7-9 as Susceptible.

References

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4. Pusa 1509-03-1-7-2 (IC0593942; INGR12004), an Elite, Semi-Dwarf, Basmati Type, Early Maturing Paddy (*Oryza sativa*) Germplasm with Superior Grain and Cooking Quality

Ashok Kumar Singh¹, s Gopala Krishnan¹, M Nagarajan², KK Vinod², PK Bhowmick¹, SS Atwal³, Rakesh Seth³, NK Chopra³, VP Singh¹, KV Prabhu¹, Devinder Singh¹, Sudesh Kumar¹ and G Raveendran²

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Pusa1509-03-1-7-2 was developed from the cross Pusa 1301/ Pusa Basmati 1121 through pedigree method of breeding. It is an elite high quality Basmati rice variety which recorded an average yield advantage of 34.2 % over Taraori Basmati in the National Basmati Trials of the All India Coordinated Rice Improvement Programme over two years. Pusa1509-03-1-7-2 has semi-dwarf stature with non-lodging and non-shattering habit and early maturity and thus overcomes the major weakness of most widely grown Basmati rice variety Pusa Basmati 1121. The agro-morphological description of the genotype Pusa1509-03-1-7-2 is provided in Table 1. Quality wise it has aromatic extra long slender grains (8.41mm) with very occasional grain chalkiness, very good kernel length after cooking (19.1 mm), desirable ASV (7.0) and intermediate amylose content (21.24%). In the panel test conducted at DRR, Hyderabad during *Kharif* 2010 and 2011 in the AICRIP, Pusa1509-03-1-7-2 (IET 21259) has been ranked the best among the Basmati varieties and other cultures tested for two consecutive years for its cooked

Table 1. Agro morphological description of the genotype Pusa 1509-03-1-7-2 (IET21959)

Characteristics	Description
Plant height (cm)	100
Plant type	Semi-dwarf
No. of tillers /plant	10-12
No. of panicles/ m ²	303
Days to 50 % flowering	94
Panicle type	Long panicle
Panicle exertion	Complete
Awning	Occasionally present
Apiculi colour	Straw colour
1000-Grain weight (g)	27.03
Kernel length (mm)	8.41
Kernel breadth (mm)	1.86
L/B ratio	4.52
Elongation ratio	2.25
Kernel appearance	Extra long slender and translucent
Hulling recovery (%)	78.8
Milling recovery (%)	68.9
Head rice recovery (%)	47.3
Alkali value	7.0
Amylose content (%)	21.24

inoculation as well as UBN in hotspot locations (Singh *et al.*, 2012).

For 0-5 Scale under artificial inoculation: Score 0-2 Resistant, 3 as Moderately Resistance and 4-5 as Susceptible.

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rice appearance, cohesiveness, tenderness, taste, aroma, elongation and over all acceptability by the panelist at DRR, Hyderabad (Directorate of Rice Research, 2010; 2011). Pusa1509-03-1-7-2 shows moderate resistance to leaf blast and brown spot diseases. Owing to its early maturity, cultivation of Pusa Basmati 1509 can help saving 4 irrigations compared to Pusa Basmati 1121 while economizing the cost of agri-inputs and permitting higher cropping intensity resulting in better economic

gains to the farmers.

References

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5. IPU 99-167m (IC 0594172- INGR 12005), a Unique Urdbean (*Vigna mungo*) Mutant with Protruded Stigma a Case for Functional Male Sterility

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Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh

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Black gram is a highly self-pollinated crop with cleistogamous diadelphous flowers. While studying the range of morphological variability in black gram germplasm, a spontaneous mutant was isolated from a genotype IPU 99-167 (Kumar *et al.*, 2003; 2009). This mutant resulted the heterostyly condition due to protruded stigma and crumpled petals, leading to functional male sterility. This condition favours the outcrossing which may be helpful not only in artificial hybridization but also for population improvement and F_1 hybrids development in self-pollinated crops. This mutant had potential for use in hybridization program to obtain hybrid seeds without emasculation and thus could have been conveniently used as female parent in hybridization program.

Mutant plants although indistinguishable from normal plants until the onset of flowering have dark green foliage, large number of flowers and a few small pods with one or two seeds as against normal cleistogamous flowers, green foliage and normal pods with 5-7 seeds. The mutant was phenotypically distinct from normal plants in various aspects (Table 1). It attained more height (79.55±9.12 cm) with increased number of nodes (17.00±1.34) and reduced number of primary branches (3.22±0.26) as compared to 45.60±1.90 cm height, 14.40±0.93 nodes and 4.00±0.32 primary branches in normal plants. Peduncle length increased significantly in mutant plants whereas pods per plant, pod length, pods per cluster and seeds per pod decreased drastically. Pods per plant were comparatively very less in number with

Table 1. Morphological and floral characteristics of normal and mutant plants of IPU 99-167 in black gram

Character	Mean ± SE	
	IPU 99-167 (Normal)	IPU 99-167m (Mutant)
Plant height (cm)	45.60±1.90	79.55±9.12
Number of primary branches	4.00±0.32	3.22±0.26
Number of nodes	14.40±0.93	17.00±1.34
Leaf length (cm)	7.84±0.45	9.16±0.77
Leaf width (cm)	3.82±0.54	3.97±0.49
Peduncle length (cm)	5.56±0.68	9.20±0.82
Pods/plant	65.00±9.12	4.10±0.28
Pod length (cm)	4.24±0.12	2.91±0.12
Pods/cluster	2.60±0.26	1.10±0.08
Seeds/pod	6.00±1.23	1.23±0.09
Calyx	9.2±1.18	7.5±0.46
Keel petals	10.1±0.62	8.2±0.63
Standard petal	11.2±0.58	8.1±0.63
Pistil length	11.4±1.50	18.3±0.54
Stamen length	10.5±0.77	6.2±0.52

retarded pods and there was no seed set in earlier studies as well (Seenaiah *et al.*, 1990). Flower size was reduced with small inward folded petals. Calyx, keel and standard petals in mutant flowers were smaller in size than those in normal flowers, resulting in a structural anomaly of the corolla. The mutant had protruded stigma due to long pistil (18.30±0.54 mm) as compared to 11.4±1.50 mm in normal flowers. Stamens were shorter with thin filament in mutant than in normal flowers.

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The mutant classified as functional male sterile invariably exhibited the other plant characteristics described above, indicating that the mutant gene had pleiotropic effect on many traits. The inheritance of this trait was also worked out suggesting single gene control of the trait (Kumar *et al.*, 2011). Flower mutants imparting functional male sterility have been reported in many agriculturally important crops like tomato, egg plant, *Brassica* species, soybean, cowpea, green gram and groundnut

References

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6. SPS 5 (IC 0594173; INGR 12006), an Urdbean (*Vigna mungo*) Germplasm with Unique Feature of Sympodial Bearing

Sanjeev Gupta, Shiv Kumar and Debjoti Sen Gupta

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Urdbean is grown in different seasons/ cropping systems and, therefore, no single plant type can perform satisfactorily in all the environments. In urdbean, three plant types (erect, semi spreading and spreading) are present. Normal pod bearing is common feature where pods are coming in clusters on each internode having long peduncles and arranged on main and sub branches on the stem. Occurrence of sympodial pod bearing like soybean in urdbean is not a common phenomenon. However, main stem bearing and sympodial bearing have been found in other plant species like cotton, soybean and chilli. Introduction of sympodial branching habit into existing cultivars may lead to increased pod numbers and enhanced harvest index without reduction in biological yield. Rao and Samy (1999) studied the inheritance of different plant types in urdbean and indicated that new

plant types had potential for developing genotypes with high biological yield coupled with high level of harvest index of refashioning and compacting the plant type

Evaluation of 300 accessions at Indian Institute of pulses Research resulted in identification of a unique line SPS 5 with sympodial pod bearing habit. This plant type is similar to soybean type which had longer main stem, shorter internodes and short bearing branches leading to better pod setting and pod number per plant. The new plant type has potential to produce higher yield under increased plant density.

References

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7. DRMR WFM 1 (IC 0593926; INGR 12007), an Indian Mustard (*Brassica juncea*) Germplasm with White Petal Colour

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Bright yellow petal colour is the characteristics of family Brassicaceae, however, the white petal flowers in mustard (*Brassica juncea* L.) are also observed. White/yellow petal colour, being distinct in phenotype, may be a useful morphological marker for many studies in breeding programme. In the present investigation, white and yellow petal flowers were observed in F₃ generation of a cross B 33 X Sanjuncta Asech, both bear yellow flower. These plants were selfed and in the subsequent generations (F₄ – F₇), near isogenic lines (NIL) with white and yellow petal flower colour were developed. Crosses between yellow and white flower plants were attempted during 2005-06 and subsequently (during 2005-06 to 2007-08), F₁, F₂, BC₁ (F₁ X yellow petal) and BC₂ (F₁ X white flower) generations were developed. These generations (P₁, P₂, F₁, F₂, BC₁, and BC₂) were grown during 2008-09 and observations on petal colour were recorded. Inheritance studies revealed that flower colour in *Brassica juncea* is governed by dominant digenic epistasis, yellow colour being dominant over white.

Observations were recorded on days to flower initiation, plant height (cm), main shoot length (cm), primary branches, seeds per siliqua and 1000 seed weight (g) on 5 plants from DRMR WFM 1, Sanjuncta Asech and B 33 each. The mean values presented in Table 1 indicated that DRMR WFM 1 is an early maturing line with short plant height and medium size seeds with white flower colour. This line will be useful as a morphological marker for genetic studies as well as in breeding programme.

Table 1. Characterization of DRMR White Flower Mustard 1 (DRMR FM1):

Trait	DRMR WFM 1	Sanjuncta Asech	B33
Days to flower initiation	43	47	48
Primary branches	4.8	4.5	5.2
Plant height (cm)	140	145	202
Main shoot length (cm)	70	50	85
Seeds/siliqua	14.2	15.6	12.7
1000 seed weight (g)	4.2	3.8	4.1
Days to maturity	125	128	135
Petal colour	white	yellow	yellow

8. Bast fibre shy (*bfs*) Mutant (IC0593936; INGR12008), a Jute (*Corchorus olitorius*) Mutant with Defective Bast Fibre Development

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A unique secondary phloic mutant of dark jute (*Corchorus olitorius* L.) has been developed at the Central Research Institute for Jute and Allied Fibres (CRIJAF), Barrackpore (Kolkata). It has been registered as a bast fibre-shy (*bfs*) mutant because it is defective in bast fibre development, but develops normal secondary phloic fibre (SPF) bundles and produces lignin-rich fibres upon biological retting (Kundu *et al.*, 2012). This mutant was developed from its wild type *C. olitorius* cv. JRO 632, a leading dark (tossa) jute cultivar in India and neighboring countries, by induced physical mutagenesis (thermal neutron) of dry seeds.

Morpho-agronomic characteristics

The *bfs* is a dwarf mutant, with a significantly shorter plant type than its wild type JRO 632 (Fig. 1). However, its most diagnostic phenotype is dissected ribbon leaves, which are distinguished by minute trifid leaves that, on maturity, are discontinuous in the margins and dissected into irregularly shaped ribbons supported by the major veins. In addition, the *bfs* is distinguished by stunted growth, pre-mature flowering, early maturity and distinct changes in root architecture and system. Chief morpho-agronomic characteristics of this mutant are presented in Table 1.

7. DRMR WFM 1 (IC 0593926; INGR 12007), an Indian Mustard (*Brassica juncea*) Germplasm with White Petal Colour

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A unique secondary phloic mutant of dark jute (*Corchorus olitorius* L.) has been developed at the Central Research Institute for Jute and Allied Fibres (CRIJAF), Barrackpore (Kolkata). It has been registered as a bast fibre-shy (*bfs*) mutant because it is defective in bast fibre development, but develops normal secondary phloic fibre (SPF) bundles and produces lignin-rich fibres upon biological retting (Kundu *et al.*, 2012). This mutant was developed from its wild type *C. olitorius* cv. JRO 632, a leading dark (tossa) jute cultivar in India and neighboring countries, by induced physical mutagenesis (thermal neutron) of dry seeds.

Morpho-agronomic characteristics

The *bfs* is a dwarf mutant, with a significantly shorter plant type than its wild type JRO 632 (Fig. 1). However, its most diagnostic phenotype is dissected ribbon leaves, which are distinguished by minute trifid leaves that, on maturity, are discontinuous in the margins and dissected into irregularly shaped ribbons supported by the major veins. In addition, the *bfs* is distinguished by stunted growth, pre-mature flowering, early maturity and distinct changes in root architecture and system. Chief morpho-agronomic characteristics of this mutant are presented in Table 1.

Table 1. Important morpho-agronomic characteristics of the *bfs* mutant

Plant part	Description
Whole plant	Type, annual herb; height, short; branching habit, medium; harvest maturity, early
Stem	Color, green; diameter, shorter; internode length, short; Basal stem root primordial modified as spine like outgrowth, present; shape, cylindrical; surface, glabrous
Leaf	Angel, erect; apex, aristate; arrangement, cauline; base, cuneate; filiform appendages, long; lamina color, green; lamina surface, glabrous; margin, palmatipartite; petiole color, green; petiole hair, present; shape, dissected ribbon; stipule color, green; venation, arcuate; vein color, green
Flower	Anther color, pale yellow; calyx pigmentation, green; color distinctness of pedicel articulation, green; corolla color, pale yellow; floral bud color, green; floral stalk color, green; pedicel articulation position, middle; time to 50% flowering, early; type, complete
Capsule	Dehiscence, present; pigmentation, green; shape, cylindrical; seeds per capsule, less; seed color, still grey; seed size, medium; valves per capsule, five; 100 seed weight, less
Root	Root architecture, spreading type
Fibre	Fibre content, very less; fineness, fine; tensile strength, average and weak

Associated characters

The *bfs* mutant has ten- and seven-fold lesser bast fibre and wood yield, respectively than its wild type. Fibre contains about 9% lignin. In contrast to *dlpf* mutant of *C. capsularis* (Sengupta and Palit, 2004), this mutant is normal in SPF lignification, but concurrently defective in wood development. Since it represents a loss-of-function mutation of the vascular cambium, it is a valuable resource for genomics-assisted dissection of bast fibre differentiation and signal transduction pathways controlling its biogenesis *in planta*.

References

Kundu A, D Sarkar, NA Mandal, MK Sinha and BS Mahapatra (2012) A secondary phloic (bast) fibre-shy (*bfs*) mutant of dark jute (*Corchorus olitorius* L.) develops lignified fibre cells but is defective in cambial activity. *Plant Growth Regul.* **67**: 45-55.

Sengupta G and P Palit (2004) Characterization of a lignified secondary phloem fibre-deficient mutant of jute (*Corchorus capsularis*). *Ann. Bot.* **93**: 211-220.

9. IL-11-239 (IC0593646; INGR12009), a Berseem (*Trifolium alexandrinum*) Germplasm with Black (dark tan) Seed Against Normal Yellow Seed

DR Malaviya, Aradhan Yadava, AK Roy, P Kaushal and Mridul Chakraborti
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Berseem is one of the most important winter season fodder crop grown in 2 m ha area in India. Berseem seeds are invariably yellow in colour. Because of narrow genetic base of the crop, interspecific hybridization using embryo rescue technique was attempted for transfer of traits like disease resistance, quality, yield etc. Several interspecific hybrids of *Trifolium alexandrinum* (berseem clover) with different related wild species have been developed at IGfRI and transferred to field conditions (First world report). One such hybrid of *T. alexandrinum*

x T. apertum (both parents are yellow seeded) expressed black seed colour (dark tan) in some of the segregating F₂ progenies. However, the heritability of the character was low (20-30%) and displayed varied degree of expressivity. Repeated cycles of artificial selection coupled with selfing in insect proof net house were carried out in these progenies. Except black seed colour emphasis was given to select the plants showing the morphological features closer to *T. alexandrinum*. Heritability of the character (black seed coat) displayed progressive improvement

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with advancement of generation. After six generation of selfing, the character showed stability with varying degree of expressivity, suggesting multigenic control of the trait. The seeds are expected to contain higher tannin concentration in its seed coat, which may confer better resistance to pathogens in the early stages of seedling development. Interestingly, both the parents were yellow seeded and there is no report available for accessions showing black seed colour in either of the species. This is possibly arising due to genomic interaction of *T. apertum* and *T. alexandrinum*. Further studies on this trait may lay a greater insight into the nature of inheritance and utility in berseem breeding programme. Further to

mention that black (dark tan) seeded Berseem has never been reported. This being the first report of stabilization of such seed colour.

References

- Anonymous (2003-04) *Annual Report 2003-04 IGRI, Jhansi* p 26.
- Malaviya DR, AK Roy, P Kaushal, A Yadav and M Chakraborti (2011) Black seed coat colour: *de-novo* expression of novel trait in interspecific hybrid derivative of *Trifolium alexandrinum* x *Trifolium apertum*. Abstract volume. National Symposium on "Forage resource and livestock for livelihood, environment and nutritional security". Sept. 10-11, 2011, Range Management Society of India. IGRI, Jhansi India, p 38.

10. IL-11-238 (IC0593647; INGR12010), a Berseem (*Trifolium alexandrinum*) Germplasm with Tetraploid Plant and Pentafoliate Leaves

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A plausible approach for increasing yield of Berseem could be through increasing photosynthetic area i.e. leaf area. Presence of multifoliate leaves is supposed to substantially increase the photosynthetic area of the plants. The proportion of leaves in Berseem is associated with number of leaves per plant, with number and size of leaflets on the leaf. Cultivars of Berseem clover possess trifoliate leaves however, occasional occurrence of multifoliate plants is observed sporadically in natural population.

Hence, efforts of a decade resulted in plants types near 100% penetrance and 90% expressivity of pentafoliate. The genetics of the trait is still not clear. Hence, in order to understand the genetics of the trait and to see the effect of ploidy dosage effect induced tetraploid of the line viz. Penta 1 (previously registered with NBPGR, INGR 09045) was developed through colchicine treatment (seedlings immersed in 0.1 and 0.2% colchicine solution for 24 and 48 hrs). A distinct characteristic feature observed in C₀ generation of the induced pentafoliate tetraploid plants was the presence of serrate margin and prominent rachis in the leaves and

bold seeds. Leaves were thick, succulent, and hairy with apical notch and presence of pigmentation on the outer margin.

The study revealed that the autotetraploids had better expression of pentafoliate trait in induced tetraploid plants than in diploid plants. The morphological characters were well maintained in next generations also. The ploidy in different generations was confirmed through Flow Cytometric leaf scan analysis using Partec PAII ploidy analyzer. The seed lot being submitted is stabilized Tetraploid Pentafoliate in C5 generation.

Further to mention that such a high degree of penetrance and expressivity of pentafoliate trait in a tetraploid has never been reported either in Egyptian clover or in any *Trifolium* species. This being the first report of induction and stabilization of polyploidy in Egyptian clover with pentafoliate leaves.

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- Anonymous (2010) *Annual Report 2009-10 IGRI, Jhansi*, p 11.

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11. 190-P3 (IC0593648; INGR12011), a Self-incompatible, Tetraploid Berseem (*Trifolium alexandrinum*) Germplasm

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Berseem plant possess typical palmate trifoliate leaves and is found in diploid ($2n=16$) in nature. Efforts of this group of scientists for about decade resulted development of induced tetraploids and study on its mode of pollination. Berseem in its diploid form is also reported to be self incompatible in Egyptian conditions. Indian reports are in favour of self compatible. However, our findings reveal that there lines with different mode of pollination (Roy *et al.*, 2005).

The tetraploid variety Pusa Giant developed by IARI has depolyploidized and in a fresh attempt IGFRI developed few tetraploids of berseem through colchicines treatment. The study revealed that the autotetraploids had bigger leaves with serrate margin and hairiness. Out

of some 4x lines evaluated for its mode of pollination, the present line was found to be most vigorous and self incompatible. The proposed line 1-90 P3 showed high seed set under controlled bees visit. In this population, hand tripping had no effect on seed set as the fertilization required pollen transfer from a neighboring plant with different 'S' alleles.

Further, to mention that self incompatibility in Berseem in tetraploid background has never been reported.

References

Roy AK, DR Malaviya and P Kaushal (2005) Pollination behaviour in different breeding populations in Egyptian clover. *Plant Breed.* **124**: 171-175.

12. EC329299 (INGR12012), Berseem (*Trifolium alexandrinum*) Germplasm as a Self-compatible & Self Pollinating Diploid

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T. alexandrinum commonly known as Berseem or Egyptian clover is an important winter annual fodder legume cultivated in Egypt, Mediterranean basin and Indian subcontinent. For an effective genetic improvement programme, it is imperative to have an adequate knowledge of the breeding system. Its mode of pollination is reported to be cross pollinated in Egyptian conditions. Identification of self-compatible populations and development of inbreds is likely to expose the hidden variability among populations of Berseem. The breeding method entails the development of inbreds and the production of hybrid seed. Hence, the present study was undertaken to estimate the extent of self-

compatibility among different populations of Berseem (Egyptian clover) based on seed set per inflorescence under different treatments. Our findings revealed that these lines with different mode of pollination (Roy *et al* 2005). The proposed line Saidi (EC 329299) belonged to Self compatible and self pollinating group. This ecotype shows considerable seed set under the caged condition indicating that pollinators do not play significant role.

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13. DSG-6 (IC0588956; INGR12013), a Sponge gourd (*Luffa cylindrica*) Germplasm with Highly resistant to *Tomato Leaf Curl New Delhi Virus*

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Sponge gourd is a popular low cost vegetable grown throughout India. Recently *Tomato Leaf Curl New Delhi Virus* (ToLCNDV: genus *Begomovirus*, family Geminiviridae), the causal virus of tomato leaf curl has been reported to be associated with sponge gourd and causing a yield loss upto 100 % in north Indian plains during *kharif* season under epidemic condition (Sohrab *et al.*, 2003). The diseased plant is characterized by yellow spots appearing on newly emerging leaves, followed by a mosaic appearance and upward curling of the upper leaves. In cases of severe attack, the leaves of the plant are small and distorted and misshapen fruits are produced. The virus is transmitted through sap as well as whitefly (*Bemisia tabaci* Hemiptera-Aleyrodidae). The genotype DSG-6 was developed at Indian Agricultural Research Institute, New Delhi by selection from local material collected from village Bulandi, Hoogly district of West Bengal. It was screened under natural epidemic condition and found to be completely resistant to *Tomato leaf curl New Delhi virus*, during rainy season which is conducive for white fly multiplication and the spread of disease. The result was also confirmed through challenge inoculation

with purified strain of the virus under insect proof green house (Islam *et al.*, 2010, 2011).

Morpho-agronomic characteristics

Leaves of the genotype DSG-6 are dark green, reniform, six lobed, nearly glabrous, non-hairy, smooth with long petioles. Trailing or climbing vines with stem and tendrils. Stem is angular monoecious with annual vines, inflorescence is clustered, racemose, flowers unisexual, male flower large in number in cluster, yellow and showy with long peduncle. Female flowers are borne solitary on short and round peduncle and are yellow in colour. Fruits are elongated elliptical (20-25cm), straight, attractive dark green with thick skin and superficial stripe, average fruit weight 110 g, flesh tender, suitable for spring-summer and *Kharif* seasons. It is ready for first harvesting in 40-45 days after sowing in *Kharif* season and 50-55 days after sowing in spring summer season. DSG-6 is highly resistant to *Tomato leaf curl New Delhi virus* during rainy season which is conducive for white fly multiplication and the spread of the said disease (Tables 1, 2).

Table1. Screening of DSG-6 under natural epidemic condition during *kharif* season 2008-2010

Genotype	2008		2009		2010	
	Yield (t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category
DSG-6	14.38	0.00 (I)	14.8	3.21 (HR)	13.75	4.33 (HR)
CHSG-1	1.95	100.00 (HS)	2.36	98.48 (HS)	2.15	97.50 (HS)
CHSG-2	2.01	99.33 (HS)	2.25	96.86 (HS)	2.34	95.25 (HS)
PSG-9	1.84	99.33 (HS)	1.99	95.10 (HS)	2.03	97.55 (HS)
KG-3/134 (IC 284787)	1.92	98.00 (HS)	1.85	99.05 (HS)	2.07	95.88 (HS)

I: Immune; HS: Highly susceptible; HR: Highly Resistant

Table 2. Screening of DSG-6 for resistance to Tomato leaf curl New Delhi virus through challenge inoculation (*Bemisia tabaci*) under greenhouse condition during 2008

Genotype	Source	Vulnerability Index	Category
DSG-6	IARI, New Delhi	3.33	Highly Resistant
CHSG-1	HARP, Ranchi	100.00	Highly susceptible
CHSG-2	HARP, Ranchi	100.00	Highly susceptible
PSG-9	PAU, Ludhiana	99.33	Highly susceptible
KG-3/134 (IC 284787)	NBPGR, New Delhi	98.67	Highly susceptible

References

Islam S, AD Munshi, B Mandal, Ravinder Kumar and T K Behera (2010) Genetics of resistance in *Luffa cylindrica* Roem. against *Tomato leaf curl New Delhi virus*. *Euphytica* **174**: 83-89.

Islam S, AD Munshi, M Verma, L Arya, B Mandal, TK Behera, R Kumar and SK Lal (2011) Screening of *Luffa cylindrica* Roem. for resistance against *Tomato Leaf Curl New Delhi Virus*, inheritance of resistance, and identification of SRAP markers linked to the single dominant resistance gene. *J. Hort. Sci. Biotech.* **86**: 661-667.

Sohrab SS, B Mandal, RP Pant, A Varma (2003) First report of association of *Tomato leaf curl New Delhi virus* with yellow mosaic disease of *Luffa cylindrica* in India. *Plant Dis.* **87**: 1148.

14. PreGy-1 (IC0591254; INGR12014), a Bitter Gourd (*Momordica charantia*) Germplasm with Predominately Gynoecious Habit

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Bitter gourd is a typical monoecious cucurbit and being a member of Cucurbitaceae it also exhibits various sex forms. In recent past gynoecious sex form has been reported (Behera *et al.*, 2006) in Indian germplasm which is governed by a single recessive gene 'gy-1' (Behera *et al.*, 2009). Regardless of genetic control, both studies suggest that such gynoecious lines hold promise for the development of gynoecious F₁ hybrids as it avoids manual emasculation and pollination by the by increases the yield and earliness of the hybrid. But, maintenance of gynoecious lines is very difficult and those can be maintained through sib-mating and in-vitro methods. These methods are very cumbersome and time taking. However, the use of predominately gynoecious lines derived from segregating population of gynoecious and monoecious hybrids has significant role in bitter gourd crop improvement.

One improved and commercial monoecious cultivar Pusa Do Mausami was used as male parent to develop cross on gynoecious line, DBGy-201. This gynoecious line was previously developed from one distinct germplasm population, and has been maintained through tissue culture followed by selfing after modifying into hermaphrodite sex form. One F₁ (DBGy-201 x Pusa

Do Mausami) plant was selfed using a staminate flower from the same plant to obtain fruits containing F₂ seeds. The successive segregating progenies were also developed by selfing in same fashion. The plants were observed for the presence of pistillate and staminate flowers throughout the growing season. Moreover, in the subsequent generations particularly in F₆ population one line (PDMGy) was extracted having very high percentage of pistillate (female) flowers and high yield potential which was named as PreGy-1.

Morpho-agronomic characteristics of PreGy-1

Vine is medium long 2.3 m with inter nodal length of 4.7-5.9 cm. Leaves dark green, reniform, six lobed, non-hairy, smooth with long petioles. Trailing or climbing vines with stem and tendrils. Stem angular monoecious with annual vines, flowers unisexual, yellow and showy with long peduncle in male flower. This line has high female: male ratio of 5:1 to 7:1 against 1:9 in Pusa Do

Table 1. Performance of PreGy-1 during Spring-Summer season of 2009-10 and 2010-11

Genotype	Yield (q/ha)	
	2009-2010	2010-2011
PreGy-1 (IC-0591254)	272.50	256.00
Pusa Do Mausami (check)	157.0	150.00

Table 2. Screening of DSG-6 for resistance to Tomato leaf curl New Delhi virus through challenge inoculation (*Bemisia tabaci*) under greenhouse condition during 2008

Genotype	Source	Vulnerability Index	Category
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CHSG-2	HARP, Ranchi	100.00	Highly susceptible
PSG-9	PAU, Ludhiana	99.33	Highly susceptible
KG-3/134 (IC 284787)	NBPGR, New Delhi	98.67	Highly susceptible

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14. PreGy-1 (IC0591254; INGR12014), a Bitter Gourd (*Momordica charantia*) Germplasm with Predominately Gynoecious Habit

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Bitter gourd is a typical monoecious cucurbit and being a member of Cucurbitaceae it also exhibits various sex forms. In recent past gynoecious sex form has been reported (Behera *et al.*, 2006) in Indian germplasm which is governed by a single recessive gene 'gy-1' (Behera *et al.*, 2009). Regardless of genetic control, both studies suggest that such gynoecious lines hold promise for the development of gynoecious F₁ hybrids as it avoids manual emasculation and pollination by the by increases the yield and earliness of the hybrid. But, maintenance of gynoecious lines is very difficult and those can be maintained through sib-mating and in-vitro methods. These methods are very cumbersome and time taking. However, the use of predominately gynoecious lines derived from segregating population of gynoecious and monoecious hybrids has significant role in bitter gourd crop improvement.

One improved and commercial monoecious cultivar Pusa Do Mausami was used as male parent to develop cross on gynoecious line, DBGy-201. This gynoecious line was previously developed from one distinct germplasm population, and has been maintained through tissue culture followed by selfing after modifying into hermaphrodite sex form. One F₁ (DBGy-201 x Pusa

Do Mausami) plant was selfed using a staminate flower from the same plant to obtain fruits containing F₂ seeds. The successive segregating progenies were also developed by selfing in same fashion. The plants were observed for the presence of pistillate and staminate flowers throughout the growing season. Moreover, in the subsequent generations particularly in F₆ population one line (PDMGy) was extracted having very high percentage of pistillate (female) flowers and high yield potential which was named as PreGy-1.

Morpho-agronomic characteristics of PreGy-1

Vine is medium long 2.3 m with inter nodal length of 4.7-5.9 cm. Leaves dark green, reniform, six lobed, non-hairy, smooth with long petioles. Trailing or climbing vines with stem and tendrils. Stem angular monoecious with annual vines, flowers unisexual, yellow and showy with long peduncle in male flower. This line has high female: male ratio of 5:1 to 7:1 against 1:9 in Pusa Do

Table 1. Performance of PreGy-1 during Spring-Summer season of 2009-10 and 2010-11

Genotype	Yield (q/ha)	
	2009-2010	2010-2011
PreGy-1 (IC-0591254)	272.50	256.00
Pusa Do Mausami (check)	157.0	150.00

Mausami (check). The fruits reach edible stage in about 45 days from sowing; fruits dark green, long (16-18cm), medium thick (3.2-4.2 cm dia), with 7-8 continuous ridges, fruit weight 85-90g.

References

Behera TK, SS Dey. and PS Sirohi (2006) DBGy-201 and DBGy-202: Two gynoeious lines in bitter gourd (*Momordica*

charantia L.) isolated from indigenous source. *Indian J. Genet.* **66**: 61-62.

Behera TK, SS Dey, AD Munshi, Ambika B Gaikwad, Anand Pal and Iqbal Singh (2009).Sex inheritance and development of gynoeious hybrids in bitter gourd (*Momordica charantia* L.). *Sci. Horti.* **120**: 130-133.

15. CARI Brinjal-1 (IC0585684; INGR12015), a Brinjal (*Solanum melongna*) Germplasm with a Bacterial wilt Resistant

Krishna Kumar, PK Singh, Ajanta Birah, Shrawan Singh, Naresh Kumar, AK Singh, DR Singh and RK Gautam

Central Agricultural Research Institute, Port Blair-744101, Andaman and Nicobar Islands
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Brinjal (*Solanum melongen* L.) is one of the most important vegetable crops of Andaman and Nicobar Islands wherein, the production of healthy crop is challenged by the Bacterial wilt caused by *Ralstonia solanacearum*. Bacterial wilt is one of the most important diseases of solanaceous crops in most parts of the country, including Andaman and Nicobar Islands. The disease is devastating in hot and humid climate and can cause up to 100% losses. Unfortunately, the majority of resistant material from mainland does not survive Island wilt conditions. CARI Brinjal 1 is the germplasm developed by repeated selection and purification cycles from the local collection at Central Agricultural Research Institute (CARI), Port Blair.

Morpho-agronomic characteristics

The plant is medium tall, semi spreading type with profuse branching habit, smooth stem and leaves are light greenish in colour. Fruits are oblong in shape, light green in colour, medium compact fruit and pendent fruit position with low seediness. Seeds are medium in shape and size and light yellow in colour. The developed germplasm, CARI Brinjal-1 not only survives under wilt pathogen sick condition but also gives better yield compared to other varieties tested under Island conditions.

Associated characters and cultivated practices

The germplasm has performed consistently well across the years and locations under wilt conditions where other varieties could not survive.

Table 1. Yield performance of CARI Brinjal 1 (CARI B-1) during 2008-09 and 2009-10 at CARI Farm

Varieties/genotypes	2008-09	2009-10	Average yield (t/ha)
CARI Brinjal-1	28.3	34.0	31.1
Manjira Gota	8.6	6.6	7.6
Pusa Purple Long	24.5	28.1	26.3
Arka Keshav	15.3	19.8	17.6
Arka Nidhi	11.7	12.0	11.9
C.D. (p=0.05)	3.3	2.9	
C.V. (%)	9.7	7.6	

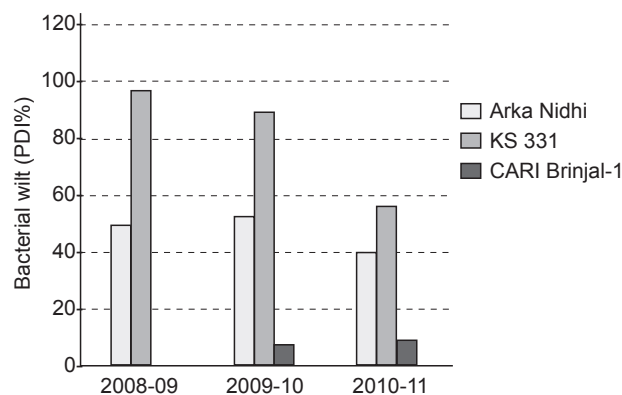


Fig. 1. Bacterial wilt incidence in CARI Brinjal-1 along with checks during 2008-11 at CARI, Port Blair, India

The detailed study and results associated with the germplasm have been published in annual report of the Institute, presented in international and national conferences as given below.

Mausami (check). The fruits reach edible stage in about 45 days from sowing; fruits dark green, long (16-18cm), medium thick (3.2-4.2 cm dia), with 7-8 continuous ridges, fruit weight 85-90g.

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Krishna Kumar, PK Singh, Ajanta Birah, Shrawan Singh, Naresh Kumar, AK Singh, DR Singh and RK Gautam

Central Agricultural Research Institute, Port Blair-744101, Andaman and Nicobar Islands
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C.V. (%)	9.7	7.6	

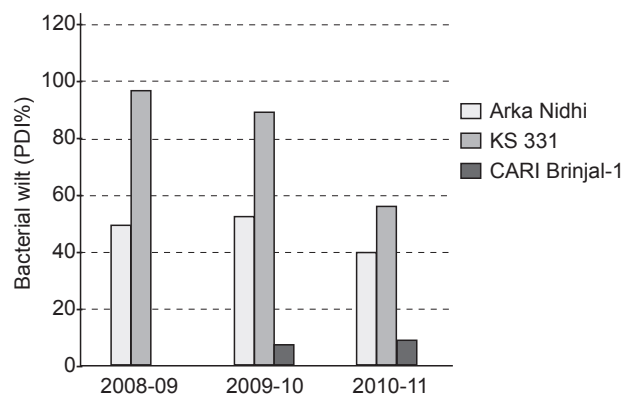


Fig. 1. Bacterial wilt incidence in CARI Brinjal-1 along with checks during 2008-11 at CARI, Port Blair, India

The detailed study and results associated with the germplasm have been published in annual report of the Institute, presented in international and national conferences as given below.

References

- Anonymous (2010) Annual Report 2009-10. Central Agricultural Research Institute, Port Blair.
- Singh Shrawan, DR Singh, VB Pandey, LB Singh, A Birah, Krishna Kumar and RC Srivastava (2011) Initial screening of indigenous vegetable crops of Andaman Islands for biotic stresses. In “9th National Symposium on Crop Health Management for Sustainable Agri-horticultural Cropping

System” held at Central Agricultural Research Institute, Port Blair from 17-19, Feb 2011, pp. 167.

- Kumar Krishna, Naresh Kumar, PK Singh, Ajanta Birah, AK Singh, DR Singh and RK Gautam (2012) CARI Brinjal 1: An ideal intercrop in the plantation based cropping system in Islands. Abst. National Seminar on Technologies for Improving Productivity of Spices and Plantation Crops, February, 27-28, 2012, Port Blair, p102.

16. SBIEC 11001 (IC0594462; INGR12016), a Sugarcane (*Erianthus X Saccharum* sp Hybrid) Germplasm with High Biomass Potential

P Govindaraj and US Natarajan

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(E-mail: sugaris@vsnl.com)

SBIEC 11001 was developed from cross between IK 76-92 (*Erianthus arundinaceus*) and 98 N1 1405 (interspecific hybrid involving *Saccharum officinarum* and *Saccharum spontaneum*) for introgressing high biomass yield and high fibre content from the former parent. The clone was selected through hybridization and clonal selection method at Sugarcane Breeding Institute, Coimbatore. The germplasm had high biomass potential and recorded harvestable biomass yield of 279.01 t/ha/year which is 92.10% higher compared to a high yielding sugarcane clone ISH 100 with 145.24 t/ha. Dry matter production of this germplasm was 101.23 t/ha and ISH 100 generated 33.90 t/ha which is 198.61 % higher. Fibre % cane of SBIEC 11001 (26.38) was also more compared to ISH 100(16.44) with an increase of 45.92%. The clone is a fast growing, high tillering, amenable for multiple ratooning, medium thick cane without split. Bud is medium size and triangular shaped. Leaf sheath is green with smooth hairs and dewlap is absent. Even under suboptimal management conditions the clones can produce good biomass yield.

Development of energy cane is a viable option for the sugar factories for continuous supply of economically

Table 1. Performance of SBIEC 11001 for energy cane traits

Clone	Harvestable biomass t/ha	Fibre % cane	Juice Brix %	Dry matter %	Dry matter yield t/ha
SBIEC 11001	279.01	26.38	9.75	36.28	101.23
SBIEC 11002	247.53	22.58	15.92	34.38	85.10
SBIEC 11003	222.53	23.94	15.04	35.97	80.04
SBIEC 11004	193.83	30.21	7.80	39.18	75.94
IA 1167	208.95	22.56	16.88	35.53	74.25
SBIEC 11005	181.79	25.55	16.60	39.88	72.50
SBIEC 11006	197.22	25.77	11.00	35.24	69.50
IA 3135	160.49	23.48	17.51	37.88	60.80
SBIEC 11007	191.05	25.91	8.09	29.38	56.13
ISH 100	145.24	16.44	18.21	23.34	33.90

viable feed stock to cogeneration units for the generation of electricity even during the off season. At present there is no energy cane variety to cater the needs of this green power industry and this clone can be cultivated to cater the off-season requirement of feedstock.

Reference

- Govindaraj P (2011) *Annual Report*. Sugarcane Breeding Institute 2010-11, p 28.

References

- Anonymous (2010) Annual Report 2009-10. Central Agricultural Research Institute, Port Blair.
- Singh Shrawan, DR Singh, VB Pandey, LB Singh, A Birah, Krishna Kumar and RC Srivastava (2011) Initial screening of indigenous vegetable crops of Andaman Islands for biotic stresses. In “9th National Symposium on Crop Health Management for Sustainable Agri-horticultural Cropping

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- Kumar Krishna, Naresh Kumar, PK Singh, Ajanta Birah, AK Singh, DR Singh and RK Gautam (2012) CARI Brinjal 1: An ideal intercrop in the plantation based cropping system in Islands. Abst. National Seminar on Technologies for Improving Productivity of Spices and Plantation Crops, February, 27-28, 2012, Port Blair, p102.

16. SBIEC 11001 (IC0594462; INGR12016), a Sugarcane (*Erianthus X Saccharum* sp Hybrid) Germplasm with High Biomass Potential

P Govindaraj and US Natarajan

Sugarcane Breeding Institute, Coimbatore-641007, Tamil Nadu

(E-mail: sugaris@vsnl.com)

SBIEC 11001 was developed from cross between IK 76-92 (*Erianthus arundinaceus*) and 98 N1 1405 (interspecific hybrid involving *Saccharum officinarum* and *Saccharum spontaneum*) for introgressing high biomass yield and high fibre content from the former parent. The clone was selected through hybridization and clonal selection method at Sugarcane Breeding Institute, Coimbatore. The germplasm had high biomass potential and recorded harvestable biomass yield of 279.01 t/ha/year which is 92.10% higher compared to a high yielding sugarcane clone ISH 100 with 145.24 t/ha. Dry matter production of this germplasm was 101.23 t/ha and ISH 100 generated 33.90 t/ha which is 198.61 % higher. Fibre % cane of SBIEC 11001 (26.38) was also more compared to ISH 100(16.44) with an increase of 45.92%. The clone is a fast growing, high tillering, amenable for multiple ratooning, medium thick cane without split. Bud is medium size and triangular shaped. Leaf sheath is green with smooth hairs and dewlap is absent. Even under suboptimal management conditions the clones can produce good biomass yield.

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Table 1. Performance of SBIEC 11001 for energy cane traits

Clone	Harvestable biomass t/ha	Fibre % cane	Juice Brix %	Dry matter %	Dry matter yield t/ha
SBIEC 11001	279.01	26.38	9.75	36.28	101.23
SBIEC 11002	247.53	22.58	15.92	34.38	85.10
SBIEC 11003	222.53	23.94	15.04	35.97	80.04
SBIEC 11004	193.83	30.21	7.80	39.18	75.94
IA 1167	208.95	22.56	16.88	35.53	74.25
SBIEC 11005	181.79	25.55	16.60	39.88	72.50
SBIEC 11006	197.22	25.77	11.00	35.24	69.50
IA 3135	160.49	23.48	17.51	37.88	60.80
SBIEC 11007	191.05	25.91	8.09	29.38	56.13
ISH 100	145.24	16.44	18.21	23.34	33.90

viable feed stock to cogeneration units for the generation of electricity even during the off season. At present there is no energy cane variety to cater the needs of this green power industry and this clone can be cultivated to cater the off-season requirement of feedstock.

Reference

- Govindaraj P (2011) *Annual Report*. Sugarcane Breeding Institute 2010-11, p 28.

17. SBIEC 11002 (IC0594463; INGR12017), a Sugarcane (*Saccharum* sp) Germplasm with a Dual Purpose Energy Cane

P Govindaraj and A Suganya

Sugarcane Breeding Institute, Coimbatore-641007, Tamil Nadu

(E-mail: sugaris@vsnl.com)

SBIEC 11002 was selected from cross involving Co 1148 (sugarcane commercial hybrid) and SES 404 (*Saccharum spontaneum*) for combining juice brix, high biomass yield and high fibre content by following hybridization and clonal selection method at Sugarcane Breeding Institute (ICAR), Coimbatore. The clone recorded high harvestable biomass yield (247.53 t/ha/year) with 70.43% increase over the high yielding sugarcane clone ISH 100 (145.24 t/ha). Dry matter production of this clone (85.23 t/ha) was 151.03% higher than ISH 100 (33.90 t/ha). Fibre % cane of this clone (22.58) was also 37.35% more than ISH 100 (16.44). In addition, it has 15.92 % of juice brix which can be used for direct fermentation to produce alcohol. It is a fast growing, heavy tillering, medium thick and erect cane without any splits. Bud is medium size and ovate shaped. Leaf sheath is greenish yellow without spines.

Cogeneration and distillation plants in the sugar factory complex face shortage of feed stock from the sugar factories during off season. Development of energy cane offers great scope for continuous supply of feed stock even during the off season. Dual purpose varieties

can simultaneously supply feedstock to cogeneration and distillation units through baggase and sugarcane juice respectively. At present there is no energy cane variety to cater the needs of these industries. SBIEC 11002 is a dual purpose energy cane which combines the high fibre content and juice brix which can be profitably exploited for this purpose.

Table: Performance of SBIEC 11002 for energy cane traits

Clone	Harvestable biomass t/ha	Fibre % cane	Juice Brix %	Dry matter %	Dry matter yield t/ha
SBIEC 11002	247.53	22.58	15.92	34.38	85.23
IA 1167	208.95	22.56	16.88	35.53	74.25
SBIEC 11005	181.79	25.55	16.60	39.88	72.50
SBIEC 11006	197.22	25.77	11.00	35.24	69.50
IA 3135	160.49	23.48	17.51	37.88	60.80
SBIEC 11007	191.05	25.91	8.09	29.38	56.13
ISH 100	145.24	16.44	18.21	23.34	33.90

Reference:

Govindaraj P (2011) Annual Report, Sugarcane Breeding Institute 2010-11, p 28.

18. Co 0230 (IC0594465; INGR12018), Sugarcane (*Saccharum* sp) Germplasm with High Ratooning Ability for Subtropical Zone

P Govindaraj and N Vijayan Nair

Sugarcane Breeding Institute, Coimbatore-641007, Tamil Nadu

(E-mail: sugaris@vsnl.com)

Co 0230 is a clone with excellent ratooning potential. It is early maturing, high yielding, water logging tolerant and red rot resistant clone selected from the cross CoLk 8102 x Co 775 through hybridization and clonal selection. This clone was identified from Sugarcane Breeding Institute, Research Centre, Motipur and evaluated in Zonal Varietal Trials 2004–05 to 2007–08 under AICRP(Sugarcane). Co 0230 recorded high cane yield of 68.30 t/ha compared to the best standard CoSe 95422 (63.12 t/ha). This accounted for 8.21% improvement. In ratoon crop the proposed

clone recorded 68.46 t/ha which is 16.35% improvement over CoSe 95422. The clone was rated as R at Pusa and MR at Motipur and Seorahi by plug method of testing for red rot. Under nodal method of testing the clone was rated as resistant in all the three locations tested. Under water logging condition it recorded 51.34% higher yield than the check BO 99. It has dark purple canes with heavy wax coating, non lodging, medium sized round buds, good tillering with semi droopy canopy, tolerant to water logging and very good ratooner.

17. SBIEC 11002 (IC0594463; INGR12017), a Sugarcane (*Saccharum* sp) Germplasm with a Dual Purpose Energy Cane

P Govindaraj and A Suganya

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can simultaneously supply feedstock to cogeneration and distillation units through baggase and sugarcane juice respectively. At present there is no energy cane variety to cater the needs of these industries. SBIEC 11002 is a dual purpose energy cane which combines the high fibre content and juice brix which can be profitably exploited for this purpose.

Table: Performance of SBIEC 11002 for energy cane traits

Clone	Harvestable biomass t/ha	Fibre % cane	Juice Brix %	Dry matter %	Dry matter yield t/ha
SBIEC 11002	247.53	22.58	15.92	34.38	85.23
IA 1167	208.95	22.56	16.88	35.53	74.25
SBIEC 11005	181.79	25.55	16.60	39.88	72.50
SBIEC 11006	197.22	25.77	11.00	35.24	69.50
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Ratoon yield is very poor in north central zone and the clone can serve as a parent for improving ratoon performance. Water logging tolerance and red rot resistance are the additional traits which can be also simultaneously transferred from this clone in the varietal development programme.

19. DWRL-1 (IC0590878; INGR12019), Wheat (*Triticum aestivum*) Germplasm with Lodging resistance Carrying Dwarfing Genes, High Protein and Resistance to Rust (Lr19)

BS Tyagi¹, Sindhu Sareen¹, Gyanendra Singh¹, SC Bhardwaj² and Indu Sharma¹

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Wheat crop in Indo-Gangetic plains *i.e.* high fertility & productive areas is facing the problem of lodging due to erratic weather at milk/dough stage. A dwarf genotypes viz. DWRL-1 was developed in the background of NIAW 34 by incorporating brown rust resistance gene Lr 19 and selected from the population of cross NIAW 34 / Lr 19 (RL 6010)// CMH 81A-575. This genotype is in homozygous condition and is having faster early growth and showed good tillering capacity thus giving higher harvest index. In addition, this line also possesses higher protein content than the best check PBW 343. This is a triple gene dwarf with average height of around 54 cms. It also matures in early thus escaping the late heat of North West Plains Zone and can be used as the donors for dwarfing trait and brown rust resistance in improving tall genotypes.

Characteristic/morpho-agronomic description	Remark/Observation
Brown rust	Resistant under field (natural) and artificial conditions.
Yellow rust	Resistant under field (natural) and artificial conditions.
Black rust resistance	Resistant to predominant pathotypes.

Reference

All Indian Co-ordinated research programme (Sugarcane). Principal Investigator's Report of Crop Improvement, 2007-08, pp 331-332.

Triple gene dwarf lines with lodging resistance

Genotype	Pedigree	Height (cm)	Spike length (cm)	Tillers/ meter	Protein (%)	Yield (q/ha)
DWRL-1	NIAW 34/Lr 19 (RL 6010) // CMH81A-575	54	11	160	13	56
PBW 343		93	11	150	11.5	50

Dwarfing genes in DWRL-1

DWRL-1 was studied to detect the dwarfing genes with known molecular markers for height reducing genes. Using perfect markers, three most important major height reducing genes, *Rht-B1b*, *Rht-D1b* and *Rht8* were evaluated. A PCR reaction was carried out and we could detect allele of ~ 237 bp of *Rht-B1b* while *Rht-D1b* shows ~254 bp size bands. For detection of *Rht8* gene microsatellite marker *Xgwm26* was used which showed 192 bp dominant allele. This locus is closely linked to the *Rht8* (0.6 cM distally). The presence of this allele as hat redactor of height in genome has been reported by many researchers.

Ratoon yield is very poor in north central zone and the clone can serve as a parent for improving ratoon performance. Water logging tolerance and red rot resistance are the additional traits which can be also simultaneously transferred from this clone in the varietal development programme.

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BS Tyagi¹, Sindhu Sareen¹, Gyanendra Singh¹, SC Bhardwaj² and Indu Sharma¹

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Black rust resistance	Resistant to predominant pathotypes.

Reference

All Indian Co-ordinated research programme (Sugarcane). Principal Investigator's Report of Crop Improvement, 2007-08, pp 331-332.

Triple gene dwarf lines with lodging resistance

Genotype	Pedigree	Height (cm)	Spike length (cm)	Tillers/ meter	Protein (%)	Yield (q/ha)
DWRL-1	NIAW 34/Lr 19 (RL 6010) // CMH81A-575	54	11	160	13	56
PBW 343		93	11	150	11.5	50

Dwarfing genes in DWRL-1

DWRL-1 was studied to detect the dwarfing genes with known molecular markers for height reducing genes. Using perfect markers, three most important major height reducing genes, *Rht-B1b*, *Rht-D1b* and *Rht8* were evaluated. A PCR reaction was carried out and we could detect allele of ~ 237 bp of *Rht-B1b* while *Rht-D1b* shows ~254 bp size bands. For detection of *Rht8* gene microsatellite marker *Xgwm26* was used which showed 192 bp dominant allele. This locus is closely linked to the *Rht8* (0.6 cM distally). The presence of this allele as hat redactor of height in genome has been reported by many researchers.