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Acknowledgements

The current issue of the Cruciferae Newsletter (vol. 30) is published online from the Brassica website (<http://www.brassica.info/info/publications/cruciferae-newsletter.php>). The present issue contains 27 contributions. Members of the editing board would like to acknowledge the authors for the quality of their contributions. For future issues, we would be grateful if all the authors could read and follow carefully the author recommendations before submitting their manuscript, in order to facilitate the editing process. In particular, it is necessary to mention one of the listed topics that is the most relevant to the presented work (see the list at the end of the present issue).

Finally, we would like to thank all the members of the Brassica team of INRA-Agrocampus Ouest-Univ. Rennes1 for their constant support.

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In this issue

Acknowledgements **2**

Table of contents **3**

Author contributions **5**

AGRONOMY AND VARIETY TRIALS

- Marta Francisco, Pablo Velasco, Margarita Lema, María Elena Cartea
Performance of *B. rapa* varieties as turnip greens and turnip tops. Effect of environment and genotype...6
- M.K.Khushu, A.K.Tiku, Mahender Singh
Photosynthetically active radiation (PAR) distribution in mustard canopy.....9
- F.A. Sheikh, S. Najeeb, A. G. Rather, M. A. Ahanger, N. A. Teeli
Impact of front line demonstrations in increasing the productivity of brown sarson (*Brassica rapa* L.) under temperate agroclimatic conditions of Kashmir Valley11
- F. A. Sheikh, A. G. Rather, S. Najeeb, M. A. Ahanger, N. A. Teeli
Performance of linseed (*Linum usitatissimum*) under temperate climatic conditions of Kashmir Valley...13

DISEASE RESISTANCE

- M. Lema, P. Soengas, P. Velasco, R. Abilleira, M.E. Cartea
Resistance to black rot in a Spanish Brassica collection15
- Sunil C. Cherukuri, Prikshit Plaha, Rjan Sharma
Evaluation of some cultivated Brassicas and their related alien species for disease resistance18
- H.K. Singh, R.B. Singh, K. Kumar, O.P. Verma
Sources of resistance of *Brassica* genotypes against powdery mildew under late sown condition.....23

BREEDING STRATEGIES

- Z.A. Dar, Shafiq A. Wani., Gulzaffar, Ahmad. I., F. A. Sheikh., A. Ishfaq., Razvi, M., M. Habib
GxE interaction for seed yield and oil content in brown sarson (*Brassica rapa* L.) under temperate conditions.....25
- Mahesh Kumar, P. Kalia, S. R. Sharma, P. Saha
Genetic variability for curd traits in heat tolerant cauliflower.....28
- A. K. Misra
Variability for agromorphological traits in germplasm of yellow sarson (*Brassica rapa* L. var. yellow sarson).....33
- M.L. Meena, Ram, Rubee Lata, S.R. Sharma
Inter-relationship and path analysis for quality traits in cabbage (*Brassica oleracea* var. *capitata* L.).....37
- S. S. Dey*, S.R. Sharma, Chander Parkash and R. Bhatia
Green hypocotyl in cauliflower (*Brassica oleracea* var. *botrytis* L.): Inheritance and use in hybrid breeding.....42
- F.A. Sheikh, A. G. Rather, S. Najeeb, M. A. Ahanger, N. A. Teeli
Development of yellow seeded *Brassica rapa* L. through intervarietal hybridization.....45
- S.M. Razvi, S.K. Gupta, S. Najeeb, M. N. Khan, Z. A. Dar, Gul Zafar, M. A. Bhat
Analysis of generation means for yield and its component traits in rapeseed (*B. napus* L.).....47

DEVELOPMENTAL AND REPRODUCTIVE BIOLOGY

- K.H. Singh, R.K. Mahawar, J.S. Chauhan, Arvind Kumar
Extent of natural outcrossing in Indian mustard (*Brassica juncea* L. Czern & Coss).....55
- Debabrata Mitra, Chandreshwar Prasad
Allelopathic influence of Malabar nut (*Adhatoda vasica* Nees.) I on turnip (*Brassica rapa* L.): II. Fertilization value.....58

M. L. Chhabra, Dhiraj Singh, N. K. Thakral Phytohormones induced promotion in seed germination of Indian mustard (<i>Brassica juncea</i> L. Czern & Coss.) under water stress conditions.....	62
M.K.A. Durrani, Chandreshwar Prasad Allelopathic influence of basil extracts on <i>Brassica rapa</i> L.: IV. Plant height, branches/plant and silique/plant.....	65
R. Bhatia, S. S. Dey, Chander Parkash Diversification of CMS system in snowball cauliflower through introgression of <i>Trachystoma ballii</i> sterile cytoplasm.....	68
SEED QUALITY	
<hr/>	
Sunita Singh, R. P. Singh, H. K. Singh, K. Kumar Nutritional quality evaluation of new varieties/strains of Indian mustard (<i>Brassica juncea</i> L. Czern & Coss).....	72
Sunita Singh, R. P. Singh, H. K. Singh, K. Kumar Fatty acid composition of Indian mustard (<i>Brassica juncea</i> L. Czern & Coss).....	75
METABOLIC STUDIES	
<hr/>	
Pablo Velasco, Marta Francisco, Margarita Lema, María Elena Cartea Secondary metabolites in different species of Brassica vegetables grown in greenhouse.....	78
Iftikhar Ali, Hafiz Munir Ahmad, Syed Anwar Shah Consideration for metabolomic studies regarding glucosinolates in brassica oilseeds.....	81
GENETIC RESOURCES	
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Chander Parkash, R.D. Meena Assessment of genetic variability and correlation analysis in sprouting broccoli	84
Hafiz Munir Ahmad, Syed Anwar Shah, Iftikhar Ali Development of low erucic acid mustard (<i>Brassica juncea</i> L.) mutants.....	87
Chander Parkash, S.S. Dey, M.R. Dhiman, Reeta Bhatia, R.D. Meena Evaluation of SI and CMS systems based F1 hybrids of cabbage under temperate conditions of India....	89
GENETIC TRANSFORMATION AND BIOTECHNOLOGIES	
<hr/>	
Gohar Taj, Anil Kumar, K.C.Bansal, G.K.Garg Introgression of osmotin gene leads to enhanced drought tolerance in <i>Brassica juncea</i>	92

Author contributions

Section 1: Agronomy and variety trials (p 6-14)

Section 2: Disease resistance (p15-24)

Section 3: Breeding strategies (p 25-54)

Section 4: Developmental and reproductive biology (p55-71)

Section 5: Seed quality (p72-77)

Section 6: Metabolic studies (p78-83)

Section 7: Genetic resources (p84-91)

Section 8: Genetic transformation and Biotechnologies (p92-94)

Performance of *B. rapa* varieties as turnip greens and turnip tops. Effect of environment and genotype

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Introduction

Brassica rapa is an important species of the genus *Brassica* widely cultivated in the world as a vegetable and for edible and industrial oil. In Galicia (Northwestern Spain) and in the coldest regions of Portugal *Brassica rapa* subsp. *rapa* L. includes three different crops: turnips, turnip greens and turnip tops. Turnips are the thickened roots, turnip greens are the young leaves harvested in the vegetative period, while turnip tops are the floral shoots and surrounding leaves. They have been under cultivation for a large period since they were among the first vegetables to be introduced into the Western Iberian Peninsula (Gómez-Campo, 1999).

A collection of *B. rapa* subsp. *rapa* from northwestern Spain is currently kept at 'Misión Biológica de Galicia' (CSIC, Spain). This collection was preliminary evaluated based on agronomical and morphological traits by Padilla et al. (2005). One hundred and twenty *B. rapa* varieties of this collection were evaluated finding that in many cases, the same landrace is sown for more than one purpose. However, the potential yield of these varieties and the stability of performance have yet not been explored. Based on this previous classification twelve varieties were selected with the aim of determining the most promising varieties for turnip greens and/or turnip tops fresh production to be included in future breeding programs.

Materials and Methods

Twelve local varieties of *B. rapa* were evaluated at three locations in Northwester Spain over two years. Varieties were transplanted in a randomized complete block design with three replications. Several agronomic and morphological data were recorded. The Sites Regression method (SREG) (Crossa and Cornelius, 1997) was used to study the fresh production of these varieties and the stability of the genotypes. Each environment was defined as the combination of a year and a location resulting in seven different environments under study. Since this method does not allow missing data, 11 varieties were evaluated for turnip greens assessment and seven varieties for turnip tops at five locations. For this method, principal components (PC) analysis was made on residuals of an additive model with locations as the only main effects. A two-dimensional biplot called GGE biplot (G plus GE interaction) of the two first PCs was plotted (Yan et al., 2000). Genotypes and locations were displayed in the same plot. These analyses were made by a SAS (SAS, 2007) program.

Results and Discussion

The analysis of variance for SREG showed that turnip greens fresh matter and turnip tops fresh production were significantly affected by E, which explained 44% and 40% of the total variation, respectively; while GGE accounted for 46% and 58% of total sum of squares. Genotype main effects (G) accounted for the 69% and 64% of the GGE variation of turnip greens fresh matter and turnip tops fresh production, respectively. Therefore, the variation due to G was larger than due to the GE interaction, but GE interaction was significant, meaning that differences among genotypes vary across environments.

The PC1 and PC2 together, which make up a GGE biplot, explained 89% and 90% of the total GGE variation of turnip greens and turnip tops fresh production, respectively. If the primary effects of sites from the SREG model are all of the same sign as it was in the present study, presents a noncrossover GE interaction (Fig. 1a and 1b) (Yan et al., 2000; Crossa et al., 2002). The two dimensional biplot for leaf fresh matter (Fig 1a) showed that MBG-BRS0550 and MBG-BRS0082 were the best genotypes in almost all studied environments, although MBG-BRS0472 and MBG-BRS0184 also showed good performance at these environments. On the other hand, the varieties MBG-BRS0451 and MBG-BRS0163 had the highest fresh production at Oroso 2008. The low genotypic PC2 score found for MBG-BRS0472 represents proportionate response of the genotype across environments, which means a stable genotype. The two dimensional biplot for turnip tops fresh production (Fig. 1b) showed that MBG-BRS0472 and MBG-BRS0143 had the highest performance as turnip tops at all locations over years. The variety MBG-BRS0163 was the most stable genotype, but presented low values in all

environments. The varieties MBG-BRS0173, MBG-BRS0197 and MBG-BRS0401 had bad performance as turnip greens and tops. Salcedo 2008 appeared as the most productive and stable environment for both crops.

Conclusion

Varieties evaluated in this work displayed enough variability to differentiate among appropriate and stable varieties for turnip greens and/or turnip tops fresh production. The varieties MBG-BRS0550, MBG-BRS0082, MBG-BRS0184 and MBG-BRS0472 had good agronomical performance as turnip greens, besides this last variety was the most stable across locations and years. The suitable varieties for turnip tops production were MBG-BRS0472 and MBG-BRS0143. Salcedo was the most stable and productive location for both crops. For future crop breeding programs should be take GE interaction into consideration, which affect turnip greens and tops fresh production. Furthermore, the identification of the best variety at a specific growing environment would be useful to breeders and producers.

Acknowledgements

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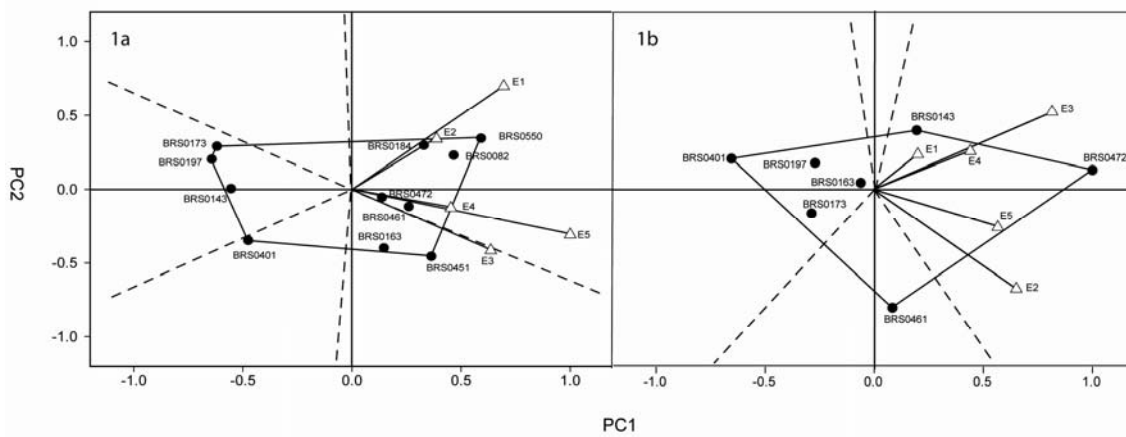


Figure 1. The G + GE interaction (GGE) biplot based on the fresh production of 11 *B. rapa* varieties for turnip greens (Fig. 1a) and five varieties for turnip tops (Fig. 1b) at five environments. Environments are E1 (Oroso 2007), E2 (Guitiriz 2007), E3 (Oroso 2008), E4 (Guitiriz 2008), E5 (Salcedo 2008). The polygon shown with tiny dots made with the genotypes which are on vertex. The intermediate sized dotted lines are the perpendicular lines to each side of the polygon; it shows which genotype(s) were grouped together as the most promising in a specific environment(s).

Photosynthetically active radiation (PAR) distribution in mustard canopy

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Introduction

The sun is the primary source of energy supplying 99.9 percent of energy for various physical, biological, biochemical etc. processes taking on the earth. Absorbed radiation defines the yield of a crop in particular region. The radiation interception has an important role in plant growth and dry matter production. The amount of dry matter production largely depends on the incident solar radiation. The efficiency of conversion depends on the balance between photosynthesis and respiration and is most conveniently expressed as the amount of dry matter produced per unit PAR interception. The radiation interception is strongly related to dry matter production. Several workers viz: Subramanian and Ratnam (1969), Bishnoi and Ram Niwas (1992), and Khushu & Mahender Singh (2008) studied the solar radiation over field crops. In view of its importance of an experiment was carried out to study the radiation characteristics in mustard crop under sub tropical areas of Jammu.

Materials and Methods

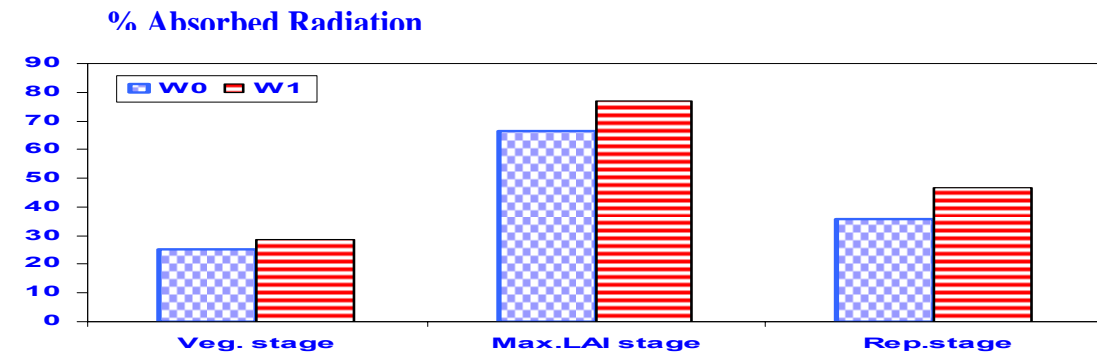
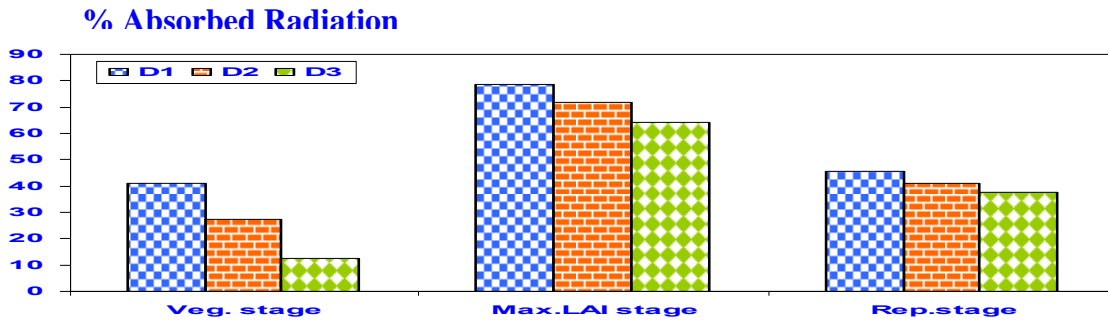
Field experiment was conducted during *rabi* season 2006-07 at research farm of Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu (32° 40' N, 74° 58' E and 332 m.a.s.l) having sandy loam soil with medium water holding capacity and poor in nitrogen, phosphorous and potash. The treatments included three dates of sowing: 10th October (D₁), 25st October (D₂) and 5th November (D₃) and two mustard varieties Pusa bahar (V₁) and Varuna (V₂) under rainfed and irrigated conditions, respectively with four replications. Periodically Photosynthetically Active Radiation (PAR) data were recorded in mustard crop under different treatments with the help of quantum sensors (Model LI-191SA) attached to data logger Licor-1400.

Results and Discussion

The solar energy components were recorded at different phenophases in both mustard cultivars (Varuna and Pusa bahar) sown under rainfed as well as irrigated conditions. The utilized solar energy recorded at three phenophases among different treatments *i.e.*, dates of sowing, rainfed and irrigated conditions in Varuna and Pusa bahar are presented in Fig.1 (a), (b) and (c), respectively. The utilized solar energy was found more in early sown crop as compared to normal and late sowing in all the phenophases except at reproductive stage, where the utilized energy was same in early and normal sowings in D₁ and D₂. The utilized energy was found more at maximum LAI stage in all the dates of sowing, whereas less at early vegetative period due to leaf area differences of these stages. In case of rainfed and irrigated conditions, the percentage of absorbed energy was found more in irrigated condition in all the stages. In case of cultivars, Varuna variety has absorbed more radiation as compared to Pusa bahar at vegetative, maximum LAI as well reproductive stage. The results also revealed that the utilized energy increased with the advancement of the crop and found maximum at flowering stage and thereafter it decreases in both Varuna and Pusa bahar under both cultivars of mustard crop in both irrigated and rainfed conditions.

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% Absorbed Radiation

at three phenophases in mustard crop under different treatments a) Dates of sowing, b) Irrigated and rainfed conditions and c) varieties.

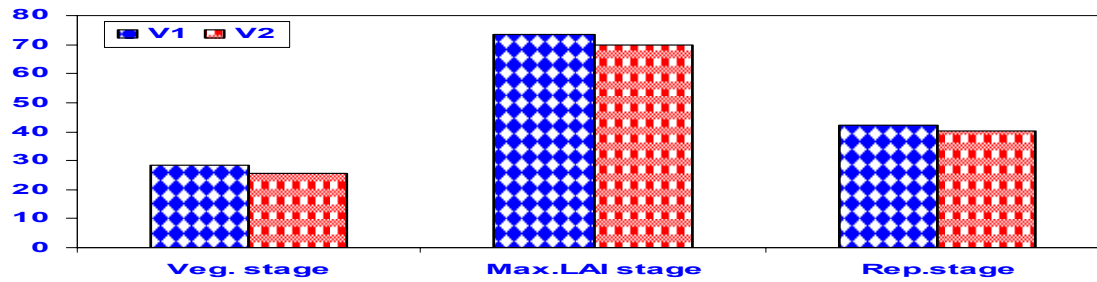


Fig 1. Percentage of absorbed radiation

D₁: 10th October
 D₂: 25th October
 D₃: 5th November

W₀ : Rainfed
 W₁ : Irrigated

V₁ : Pusa bahar
 V₂: Varuna

Impact of front line demonstrations in increasing the productivity of brown sarson (*Brassica rapa* L.) under temperate agroclimatic conditions of Kashmir Valley

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The State of J&K, despite significant advancement in oilseed production technology, particularly in rapeseed-mustard is lying much behind in achieving a break through in oilseed production. The state occupies little more than 64 thousand hectares under oilseed crop with annual production of 53.5 thousand qtls with an average productivity of 8.45 q/ha (Table 1). Brown sarson (*Brassica rapa* L.) is major oilseed crop of Kashmir valley which is grown in *rabi* season and covers an area of more than 47 thousand hectares. This is the only crop of the rapeseed-mustard group which fits well in the oilseed – paddy rotation prevailing in the valley of Kashmir and is the dominant *rabi* crop of the Kashmir valley. The present productivity level of brown sarson in the valley is not quite high mainly due to the fact that the improved production technologies (Table 2) developed by the university as well as the potential of elite varieties of Brown sarson has not been yet fully demonstrated among the farming community of this region .

This centre conducted the FLDs on Brown sarson during 2004-05 to 2008-09 demonstrating the potential of the released variety (Gulchin) of Brown sarson and its improved package of practice to the farmers (Table 3). The average yield superiority of 19.5 % was realized from the improved variety and improved package of practice in comparison to Local variety / local package of practice practiced by the farmers.

Table 1. Area, production and productivity of oilseed in J&K State during 2004-05 to 2007-08

Year	Area (000 ha)	Production (000 q)	Average yield (q/ha)
2004-05	64.49	407	6.31
2005-06	63.01	366	5.8
2006-07	64.30	413	6.42
2007-08	63.27	535	8.45

Source: Digest of Statistics 2007-08, Directorate of Economics & Statistics, Govt. of J&K

Table 2. Improved agro-production techniques developed

Sowing time	Last week of September to mid of October
Spacing (cm)	10 cm plant to plant and 30 cm row to row
Seed rate (kg ha ⁻¹)	Line sowing 7.5kg/ ha
Fertilizer responsiveness	60:30:20:20 NPK&S (kg / ha)
Harvesting	2 nd to 3 rd week of May
Weed management	Application of Pendimethalin @ 1 kg ha ⁻¹ provides effective control against weeds.

Table 3. Results of Front line Demonstrations conducted during 2004-05 to 2008-09

Year	Eco-system	Technology demonstrated	Area (ha)	Yield (q/ha)		Yield advantage (%)
				Improved variety / improved package of practice	Local variety / local package of practice	
2004-05	Rainfed	Variety (Gulchin) / package of practice	6	9.80	8.7	12.6
2005-06	-do-	-do-	12	10.30	9.0	14.4
2006-07	-do-	-do-	10	10.7	8.8	21.5
2007-08	-do-	-do-	8	10.5	8.5	23.5
2008-09	-do-	-do-	8	11.5 q	9.2	25.0
Average over years			8.80	10.56	8.84	19.50

Performance of linseed (*Linum usitatissimum*) under temperate climatic conditions of Kashmir Valley

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Linseed is an important oilseed crop grown for both seed and fiber as well. It is basically an industrial oilseed crop. Globally it is grown in an area of 3.07 m ha with a production of 2.57 mt. India is the 2nd largest (21.21%) linseed growing country in the world after Canada and production wise it ranks 4th (8.2%) in the world after Canada (40.51%), China (18.68%) and USA (10.89%). At present linseed is cultivated on about 4.36 lakh ha. with the production of 1.67 lakh tons in the country grown as a Rabi crop (Srivastava, 2008).The crop is predominantly grown under rainfed as well as input starved conditions due to which the national average productivity (385 kg/ha) is very low as compared to the world average (852 kg/ha).The major impediments for the lower national average productivity are that the crop is grown under sub marginal , un irrigated , input starved and poor crop management conditions. Linseed has 37-42% oil, 20-24% proteins and 15-30% sugars. Linseed oil is a drying oil mostly used in the paint and varnish industry. The special utility of linseed is due to its high levels (50 %) of linolenic acid, 18 carbon fatty acid with three double bonds. The oil is highly unstable because of its highly unsaturated fatty acid content and hence is not easily suited as a cooking medium (Nagaraj, 2008)

In an effort to popularize linseed and to identify promising and high yielding material for agro-climatic conditions of the valley of Kashmir, which has great potential area for its cultivation in orchard areas, Karewas and under rain fed areas, research trials were conducted during Rabi 2008 & 2009 under All India Coordinated Programme. The results revealed that highest seed yield of 7.1 q/ha were recorded for LCK-7034 followed by NDL-2005-34 and L-001 which had a seed yield of 6.1 and 6.0 q/ha respectively. LCK-7034 showed yield superiority of 38 .0% over national check T-397 (5.1 q/ ha).The crop matured well before the transplanting of the paddy crop and thus fitted well in the cropping pattern prevailing in the valley of Kashmir. The high yielding varieties identified could be popularized through Front Line Demonstrations in this region so that linseed could be introduced as 2nd Rabi oilseed crop after rapeseed mustard.

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Table 1. Performance of linseed under Kashmir Valley conditions

Entry	Days to 50% flowering	Days to maturity	No. of primary branches/plant	No. of secondary branches/plant	Plant height (cm)	Number of capsules /plant	Seeds/ capsule	1000-Seed weight (g)	Seed yield/ ha (q)
PCL-1-106	55.7	103.3	5.9	8.5	58.0	54.0	6.2	8.8	5.94
LCK-7034	52.7	102.0	6.0	6.9	48.5	52.8	8.5	8.6	7.05
NL-260	50.0	105.3	3.9	6.3	43.8	42.4	7.3	8.9	4.08
PKDL-74	53.7	109.7	5.4	7.5	52.7	44.7	8.2	9.0	5.50
NDL-2005-34	51.3	103.3	4.4	6.6	42.7	48.3	8.5	9.2	6.08
LMS-P-3	50.3	104.3	4.5	6.3	41.3	40.1	7.2	8.1	4.11
BAU-06-8	55.0	106.3	4.6	7.4	52.0	37.7	6.7	8.6	3.47
SLS-71	50.7	101.3	3.6	5.0	35.7	30.7	5.7	8.0	2.77
KL-219	57.3	105.3	4.4	5.7	46.9	41.5	8.7	9.2	5.11
Padmini (AC)	49.0	101.7	3.4	6.1	44.8	40.8	7.3	8.9	5.19
RLC-117	54.7	102.3	4.5	7.1	52.1	44.5	6.1	9.3	5.00
Sheela (ZC)	55.3	100.7	4.8	6.3	52.7	43.1	6.4	9.3	3.88
T-397 (NC)	49.7	102.0	3.8	6.7	43.3	44.3	6.4	9.2	5.11
L-001	49.7	101.0	4.6	8.0	52.8	53.5	8.9	9.3	6.00
\bar{X}	52.50	103.48	4.56	6.73	47.66	44.30	7.30	8.89	4.95
SE	0.47	1.15	0.14	0.65	1.40	1.93	0.28	0.08	0.48
CD(P=0.05)	1.16	2.85	0.36	1.62	3.50	4.80	0.69	0.21	1.20
CV (%)	7.54	5.92	7.48	16.78	10.10	7.53	6.54	4.63	16.88

DISEASE RESISTANCE

Resistance to black rot in a Spanish Brassica collection

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Introduction

Xanthomonas campestris pv. *campestris* (Xcc), causal agent of black rot, is widely distributed around the world in Brassica crops causing severe yield losses. The seedborne bacteria can survive in crop debris or crucifer weeds, introducing in the plant through hydathodes and wounds. While in warm and humid regions Xcc can cause plant dead, in coastal temperate areas it produces necrotic lesions on leaf margin, which decrease the value of the product on fresh market. In northwestern Spain, black rot has been recently identified in several Brassica crops (Lema et al. 2008). In this region, the production is mainly by small growers who do not use healthy plant material and disease-free seeds and, consequently, the pathogen can rapidly widespread. No studies involving either the pathogen or screens for resistance in this area have been conducted. For disease control the use of resistant cultivars is highly recommended but for most Brassica crops, especially in local crops, resistant cultivars are not offered and sources of resistance are very limited or even unknown. In the last years, the search for new sources of resistance has been race-specific since the existence of six races of the pathogen was described by Vicente et al. (2001). In addition to monogenic race-specific, a quantitative race-nonspecific resistance has been described (Soengas et al. 2007, Taylor et al. 2002). Recently, Fargier and Manceau (2007) added three new races (7 to 9), being races 1 and 4 are the most virulent and widespread, accounting for most black rot cases around the world. Sources of resistance to Xcc in Brassica genomes have been examined by different researchers but the use of resistant cultivars has only had limited success and available sources with useful levels of resistance are scarce. Moreover, most of these works focused in cabbage due to its economical value, while the search for resistance in other Brassica crops has been more restricted. Therefore, the objective of this work was to identify new sources of resistance to races 1 and 4 of Xcc in several Brassica crops.

Materials and Methods

Five hundred and twenty six accessions from Germplasm Bank in the Misión Biológica de Galicia-CSIC (Spain) belonging to three *Brassica* species were screened for black rot resistance together with several resistant and susceptible controls establish by Vicente et al. (2001). These accessions comprises 76 of *B. napus* (including *napus*, *napobrassica*, *oleifera* and *pabularia* groups), 256 of *B. oleracea* (including *acephala*, *capitata* and *costata* groups) and 194 of *B. rapa* subsp. *rapa*. Bacterial isolates of race 1 type strain HRI3811 and race 4 type strain HRI1279A provided by Warwick-HRI-Wellesbourne, UK were used. Bacterial cultures were grown in bacterial screening media 523 at 30 °C during 48 h prior to inoculation and were diluted in sterile tap water until suspension reached a density of 5×10^8 cfu mL⁻¹. Fourteen to sixteen four weeks old plants per accession were artificially inoculated in greenhouse conditions following the methodology described by Lema-Marquez et al. (2007). The disease severity caused by each Xcc race was quantitatively rated using a 1 (resistant) to 9 (susceptible) scale. Analyses of variance were performed for disease score and were combined across races by using the GLM procedure of SAS (2002). Accessions and races were considered as fixed effects whereas replications (plants within accessions) were considered as a random factor. Comparisons of means were performed for each trait by using Fisher's protected Least Significant Difference (LSD) at the 0.05 level of probability. The sums of squares for accessions were orthogonally divided into groups in *B. napus* and *B. oleracea* species.

Results and Discussion

Brassica napus

Race 1 was more virulent on the tested materials than race 4. No race-specific resistance was found to race 1. Most cultivars were susceptible except Russian kale, from the *pabularia* group, which showed some resistant plants and some other accessions with some partially resistant plants. High levels of race-specific resistance to

race 4 were found, particularly in the *pabularia* group, although great variability within accessions was identified. Three improved cultivars (Ragged Jack kale, Friese Gele, Valle del Oro) and four landraces (Russian kale, MBG-BRS0037, MBG-BRS0041, MBG-BRS0131) showed plants with some degree of resistance to both races (Table 1), then possible race-nonspecific resistance can be involved. These accessions could be directly used in breeding programs, either to improve the cultivar per se or like donors of race-specific resistance to other Brassica cultivars. Different selection criteria applied on *B. napus* crops according to their use could lead to an indirect selection for Xcc resistance.

Brassica oleracea

The accessions performed statistically distinct against two races, being race 1 slightly more virulent on tested materials than race 4. Most accessions were susceptible to both races, except cabbage cultivars 'Balón' and 'Quintal de Alsacia' showing some plants with different level of resistance to races 1 and 4, indicating that race-nonspecific resistance can be involved. Kale landraces MBG-BRS0286 and MBG-BRS0070 showed an intermediate mean disease score for races 1 and 4, respectively (Table 1). These accessions can be crossed to cabbage cultivars and may provide new combinations of resistance genes with protection against black rot in cabbage production areas.

Brassica rapa

Partial resistance was found in several landraces to race 1 and resistance and partial resistance in several landraces to race 4. Three landraces were identified as potential race-nonspecific resistant (Table 1). Sources of resistance were identified in different crops of the subspecies (turnips, turnip greens and turnip tops) and they can be grown directly after selection for resistance or they can be used to introgress resistance in other germplasm or commercial varieties.

Conclusions

Race 1 was much more virulent on tested materials than race 4. Most of the *B. rapa* (72%) and *B. napus* (55%) accessions showed resistance to race 4 although a great variability within accessions was found, probably due to a mixture of genotypes. Noteworthy were data recorded in *B. oleracea* accessions where existing sources of resistance are limited. According these results local materials can be used in breeding programs taking in account that they are heterogeneous due to mixture of genotypes and intercrossing among varieties probably associated with poor isolation.

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Table 1. Percentage of resistant plants and mean disease score for Xcc races 1 and 4 for the most promising accessions from Germplasm Bank in the Misión Biológica de Galicia included in this study

Species	Group	Accession	Resistant plants		Mean disease score	
			Race 1	Race 4	Race 1	Race 4
			-----(%)-----		----- (1-9)-----	
<i>Brassica napus</i>	<i>pabularia</i>	MBG-BRS0041	0	100	8.6	1.8
	<i>pabularia</i>	Russian kale	25	50	5.3	3.5
	<i>oleifera</i>	Valle del Oro	0	47	8.6	3.9
	<i>napobrassica</i>	Friese Gele	0	33	7.1	5.3
	<i>pabularia</i>	MBG-BRS0037	0	33	8.1	5.9
	<i>pabularia</i>	MBG-BRS0131	0	33	7.8	5.9
	<i>napus</i>	Ragged Jack kale	0	12	7.9	7.2
<i>Brassica oleracea</i>	<i>acephala</i>	MBG-BRS0070	0	63	9.0	4.5
	<i>capitata</i>	Balon	7	8	6.8	7.1
	<i>capitata</i>	Quintal de Alsacia	22	0	6.7	7.9
	<i>acephala</i>	MBG-BRS0286	0	0	6.5	9.0
<i>Brassica rapa</i>		MBG-BRS0259	0	100	8.3	1.3
		MBG-BRS0417	0	53	6.9	3.9
		MBG-BRS0262	0	42	7.7	4.2
		MBG-BRS0215	20	17	6.2	5.3
		MBG-BRS0479	0	66	6.7	6.6

DISEASE RESISTANCE

Evaluation of some cultivated Brassicas and their related alien species for disease resistance

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Introduction

The genus *Brassica* is one of the core genera in the subtribe *Brassicinae* and includes a number of oilseed crops. These crops have wide adaptation and are grown under varied agroclimatic regions. The oilseed *Brassica* commonly known as rapeseed-mustard are the second largest oilseed crop next to groundnut in terms of area and production in India (Misra *et al.*, 2010). Indian mustard (*Brassica juncea*) occupies nearly 90% of the total cultivated area amongst other six cultivated species of *Brassica* group (Kumar & Misra 2007). *Alternaria* blight, caused by *Alternaria brassicae* (Berk.) Sacc. and *A. brassicicola* (Schew.) Wiltshire, is one of the most destructive disease of *Brassica* species around the world. Estimates of yield quantity and quality losses due to this disease vary between 10 to 70 per cent in the species of oilseed Brassicas (Kolte, 1985). White rust caused by the fungus *Albugo candida* (Pers. ex. Lev.) Kuntze is another important disease of many members of the genus *Brassica* (Saharan and Verma, 1992). Yield losses due to this disease range between 20 to 60 per cent (Petrie and Vanterpool, 1994).

These diseases can be effectively and economically managed through host plant resistance. Though resistant sources against white rust are available in cultivated *Brassica* species, no such resistance source is available for *Alternaria* blight. Nevertheless, it becomes inevitable to identify resistance sources in wild species and recourse made to wide hybridization for its transfer to the cultivated ones.

Materials and Methods

The material for the investigation comprised 25 genotypes of cultivated Brassicas and 9 of related wild species (Table 1) procured from different Departments/Research Stations of the CSK HPKV, Palampur or collected from different areas of Himachal Pradesh, India. The genotypes were screened for *Alternaria* blight by artificially inoculating the detached leaves with *Alternaria brassicae*. *A. brassicae* and *A. brassicicola* were isolated from naturally infected leaves obtained from the Oilseeds Research Station, Kangra. Since *A. brassicicola* is of minor importance, causing ~ 5 per cent infection, *A. brassicae* was used for screening the material under study. Cultures were grown in dark at room temperature on a modified medium comprising 20 per cent tomato juice, calcium carbonate (75 mg/l), rose bengal (40 mg/l) and agar (2%). Conidia were washed off the tubes with distilled water, filtered through cheesecloth and resuspended in distilled water to a concentration of approximately 1×10^5 /ml for inoculation. Four leaves of each genotype were screened twice. Plants could not be screened at the same time, however, in each experiment; known susceptible variety 'Varuna' of *B. juncea* was included.

Detached leaves were placed on a filter paper and moistened with 50 ppm kinetin in a petri dish to prevent yellowing. A few droplets of *A. brassicae* conidial suspension were placed on each leaf and incubated for 4-5 days at room temperature under continuous white fluorescent light. The severity of disease was assessed visually and scored following the 1-3 scale of Conn *et al.* (1990) (Table 2).

For white rust inoculation, *Albugo candida* zoospores from naturally infected *Brassica* leaves, obtained from the Oilseed Research Station, Kangra were used. To prepare inoculum, zoospores from rust pustules on fresh leaves were suspended in ice-cold distilled water in conical flasks, filtered through a double-sieve and stirred gently with a glass rod to disperse zoospores. These flasks were incubated in refrigerator for 3-4 hours, and the suspension adjusted to approximately 1.5×10^5 zoospores/ml. Plants were inoculated in the evening by spraying the zoospore suspension to run-off. Inoculated plants were incubated for 3 days under a moist polythene bag in a moist chamber to maintain high humidity. Although, a high relative humidity was maintained under the polythene, plants were sprayed with distilled water 3-4 times a day for leaf wetness.

Three days after inoculation, plants were kept in the screen house for disease development and disease severity was recorded on 14th day after inoculation. A disease severity scale (0-4) was used following Verma *et al.* (1999) for assessing white rust infection on leaves (Table 3; Fig 1). Severity ratings reflected both number and size of pustules as well as the degree of sporulation.

Results and Discussion

All the accessions of cultivated species, *viz.*, *B. campestris*, *B. oleracea*, *B. nigra*, *B. juncea*, *B. napus* and *B. carinata* were susceptible to *A. brassicae* (Table 4). It appears that no true source of resistance is available currently in the cultivated genotypes against *Alternaria* blight.

Among the wild accessions, WBK 1 (*Sisymbrium* spp.), *Camelina sativa*, *Capsella bursa-pastoris* and *Raphanus raphanistrum* were free from the disease (Fig. 2), whereas *Sinapis alba* and WBL 1 (*Sisymbrium* spp.) showed mixed response on the detached leaves. *Alternaria* blight resistance has been reported in *Camelina sativa*, *Capsella bursa-pastoris* (Tewari and Conn, 1993) and *Alliaria petiolata* (Westman and Dickson, 1998). However, in the present study, *A. petiolata* was found susceptible to *A. brassicae*. The resistance found in the above wild crucifers could be transferred in cultivated Brassicas.

All the genotypes of *B. juncea*, and cultivars DK 1 and Bhawani of *B. campestris* var. *toria* were susceptible to white rust, whereas, genotypes of *B. oleracea*, *B. nigra*, *B. napus* and *B. carinata* were resistant to white rust (Table 4, Fig. 3). The identified resistant cultivars can be incorporated in the breeding programmes of oilseed Brassicas. All the wild genotypes were highly resistant to the white rust (Fig. 3), except *Sinapis alba*, which gave resistant reaction. *Capsella bursa-pastoris* has been reported to be resistant to Indian isolates of *A. candida* (Verma *et al.*, 1999).

There is great diversity in the local cultivars of *Brassica* species in Himachal Pradesh and, at the same time, wild species of *Cruciferae* thrive well in different agroclimatic regions. These wild species could be valuable resources in crop improvement, as they might possess important traits including resistance to biotic and abiotic stresses, and quality attributes. In this contest, some of the wild species, like *Sinapis alba*, *Camelina sativa*, *Cardamine impatiens*, *Sisymbrium* spp., *Alliaria petiolata*, *Capsella bursa-pastoris* and *Raphanus raphanistrum* could be the potential ones. However, these species have remained mostly unutilized for the improvement of cultivated oleiferous Brassicas for developing cultivars with improved disease resistance and quality attributes. Resistance identified in the wild accessions to both the diseases and especially to *Alternaria* blight could be valuable source for the introgression of resistance in the cultivated species through wide hybridization.

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Table 1 List of material used and source

Species; chromosome number; genome	Variety/ Genotype	Source
Cultivated species		
<i>Brassica campestris</i> L. var. <i>toria</i> ; 2n=20; AA	DK 1, Bhawani	Oilseed Research Station, Kangra
<i>B. campestris</i> L. var. <i>brown sarson</i> ; 2n=20; AA	BSH 1, KBS 3	Oilseed Research Station, Kangra
	Manikaran Local	Local collection from Manikaran
<i>B. campestris</i> L. var. <i>chinensis</i> ; 2n=20; AA	Palampur Green	Department of Vegetable Science
<i>B. oleracea</i> L. var. <i>capitata</i> ; 2n=18; CC	KGAT III, Pusa Drum Head	Department of Vegetable Science
<i>B. oleracea</i> L. var. <i>botrytis</i> ; 2n=18; CC	Pusa Snowball K 1, Palam Upahar	Department of Vegetable Science
<i>B. nigra</i> (L.) Koch; 2n=16; BB	Ohri	Local collection from Palampur
<i>B. juncea</i> (L.) Czern. & Coss.; 2n=36; AABB	RL 1539, Varuna, Kranti, Pusabold, RCC 4,	Oilseed Research Station, Kangra
<i>B. juncea</i> L. ssp. <i>rugosa</i> ; 2n=36; AABB	Pahari Rai	Local collection from Palampur
<i>B. napus</i> L.; 2n=38; AACC	Hyola 401, GSL 9103, HPN 1, Neelam, GSL 1	Oilseed Research Station, Kangra
<i>B. carinata</i> A. Braun; 2n=34; BBCC	HPC 1, PCC 5	Oilseed Research Station, Kangra
	Ethiopian Local	Department of Plant Breeding & Genetics
Wild Species		
<i>Sisymbrium</i> spp.; 2n=14, 16	WBK 1, WBK 2, WBL 1	Local collection from Sangla Local collection from Kukumseri
<i>Camelina sativa</i> (L.) Crantz; 2n=28, 40, 42	CS 1	Department of Biochemistry
<i>Cardamine impatiens</i> L.; 2n=16	CI 1 1	Local collection from Palampur
<i>Sinapis alba</i> L. Syn. <i>Brassica hirta</i> L.; 2n=24	SA 1	Department of Biochemistry
<i>Alliaria petiolata</i> ; 2n=36	AP 1	Local collection from Palampur
<i>Capsella bursa-pastoris</i> (L.) Medik; 2n=32	CB 1	Local collection from Palampur
<i>Raphanus raphanistrum</i> L.; 2n=18	RR 1	Local collection from Palampur

Table 2. Scale/Description of the symptom for *Alternaria* blight

Response of healthy leaves	Score	Inference
Necrosis and chlorosis	3	Highly Susceptible
Localized necrotic flecks	2	Susceptible
No symptoms; fungal growth inhibited	1	Resistant

Table 3. Scale/Description of the symptom for white rust

Score	Response	Inference
0	Healthy	Highly resistant
1	Trace	Resistant
2	Light	Moderately resistant
3	Moderate	Susceptible
4	Severe	Highly susceptible



Figure 1. Disease severity scale for assessing white rust infection on leaf
 0 = Highly resistant, 1= Moderately resistant, 2 and 3= Susceptible, 4= Highly susceptible

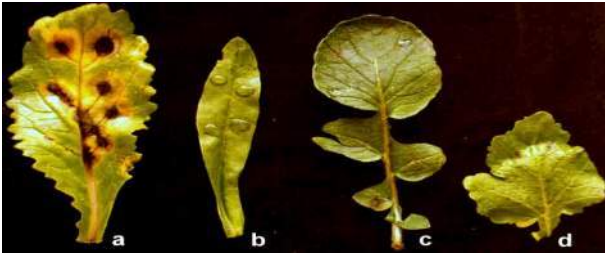


Figure 2. Reaction of cultivated Brassicas and related wild species to *Alternaria* blight
 a = *B. juncea* ssp. *rugosa* Pahari Rai (Susceptible), b = *Camelina sativa* (Resistant), c = *Raphanus raphanistrum* (Resistant), d = *Sinapis alba* (Resistant)

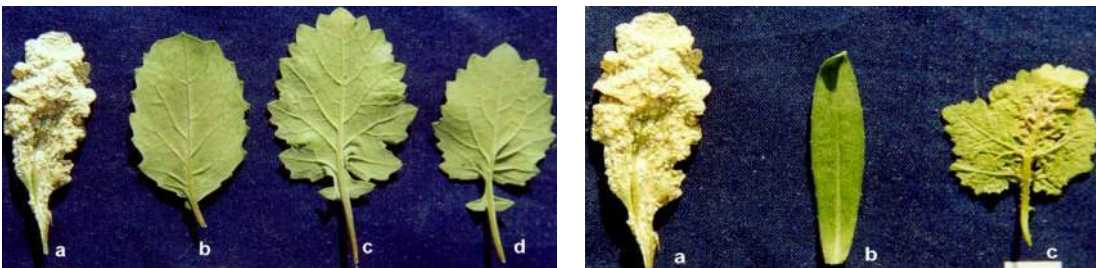


Figure 3. Reaction of cultivates Brassicas and related wild species to white rust
 Left: a = *B. juncea* cv. *Varuna* (Susceptible), b = *B. napus* cv. *GSL 9103* (Resistant), c = *B. napus* cv. *GSL 1* (Resistant), d = *B. napus* cv. *Hyola 401* (Resistant).
 Right: *B. juncea* cv. *Varuna* (Susceptible), b = *Camelina sativa* (Resistant), c = *Sinapis alba* (Resistant).

Table 4. Reaction of cultivated Brassicas and related wild species to *Alternaria brassicae* and white rust (*Albugo candida*).

Species/ Genotype	<i>Alternaria</i> blight			White rust	
	Disease score	Yellow halo	Remarks	Disease score	Remarks
Cultivated					
<i>B. campestris</i>					
DK 1	3	++	Susceptible	3	Susceptible
Bhawani	3	++	Susceptible	3	Susceptible
BSH 1	3	++	Susceptible	0	Highly resistant
KBS 3	3	++	Susceptible	0	Highly resistant
Manikaran Local	3	++	Susceptible	0	Highly resistant
Palampur Green	3	++	Susceptible	0	Highly resistant
<i>B. oleracea</i>					
KGAT III	3	++	Susceptible	0	Highly resistant
Pusa Drum Head	3	++	Susceptible	0	Highly resistant
Pusa Snowball K 1	3	++	Susceptible	0	Highly resistant
Palam Upahar	3	++	Susceptible	0	Highly resistant
<i>B. nigra</i>					
Ohri	3	++	Susceptible	0	Highly resistant
<i>B. juncea</i>					
RL 1539	3	++	Susceptible	4	Highly susceptible
Varuna	3	++	Susceptible	4	Highly susceptible
Kranti	3	++	Susceptible	4	Highly susceptible
Pusabold	3	++	Susceptible	4	Highly susceptible
RCC 4	3	++	Susceptible	4	Highly susceptible
Pahari Rai	3	++	Susceptible	0	Highly resistant
<i>B. napus</i>					
Hyola 401	3	++	Susceptible	0	Highly resistant
GSL 9103	3	++	Susceptible	0	Highly resistant
HPN 1	3	++	Susceptible	0	Highly resistant
Neelam	3	++	Susceptible	0	Highly resistant
GSL 1	3	++	Susceptible	0	Highly resistant
<i>B. carinata</i>					
HPC 1	3	+	Susceptible	0	Highly resistant
PCC 5	3	+	Susceptible	0	Highly resistant
Ethiopian Local	3	++	Susceptible	0	Highly resistant
Wild					
<i>Sisymbrium</i> spp.					
WBK 1	1	-	Resistant	0	Highly resistant
WBK 2	3	++	Susceptible	0	Highly resistant
WBL 1	2,3	+, ++	Susceptible	0	Highly resistant
<i>Camelina sativa</i>	1	-	Resistant	0	Highly resistant
<i>Cardamine impatiens</i>	3	+	Susceptible	0	Highly resistant
<i>Sinapis alba</i>	1,2	-, +	Susceptible	1	Resistant
<i>Alliaria petiolata</i>	3	+	Susceptible	0	Highly resistant
<i>Capsella bursa-pastoris</i>	1	-	Resistant	0	Highly resistant
<i>Raphanus raphanistrum</i>	1	-	Resistant	0	Highly resistant

DISEASE RESISTANCE

Sources of resistance of *Brassica* genotypes against powdery mildew under late sown condition

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Rapeseed mustard is the major oilseeds crop of Uttar Pradesh. *Alternaria brassicae* (Berk.) Sacc., *A. brassicicola* (Schew.) Wiltshire and *Albugo candida* (Pers. ex. Lev.) Kuntze, are important pathogens reducing the yield substantially, but in harveste paddy fields the rapeseed-mustard suffers from powdery mildew disease caused by *Erysiphe cruciferarum* Opiz. Ex Junnel (Vasudeva 1958 and Bhandar *et al.* 1963), a minor disease earlier, this, has become major one and cause heavy yield losses up to 42.4% (Singh and Singh, 2003 and Singh and Singh, 2004). The resistance breeding is one of the most economical methods for the management of the diseases. Although various fungicides are recommended for the control of powdery mildew (Rathore and Rathore, 1995 and Singh and Singh, 2003) but they have adverse effect on environment. Two hundred genotypes of rapeseed-mustard were evaluated for their response to powdery mildew during 2005-06 and 2006-07 crop seasons under late sown condition at the Research Farm of Genetics and Plant Breeding of this University. The trial was conducted in the third week of December in single row of 3m length having 30 x 10cm spacing in augmented design. Susceptible check Varuna was sown after every five test genotypes and flanked the trial all around with paired rows to serve as infector. Disease severity was recorded on three leaves one each from top, middle and bottom from ten randomly selected plants from each genotype, after one month appearance of disease following 0-5 scale as mentioned below.

S.No.	Scale	Description	Reaction
1	0	apparent symptoms absent	Disease Free
2	1	1-10% leaf area mildewed	Resistant (R)
3	2	11-25% leaf area mildewed	Moderately resistant (MR)
4	3	26-50% leaf area mildewed	Moderately susceptible (MS)
5	4	51-75% leaf area mildewed	Susceptible (S)
6	5	Over 75% leaf area mildewed	Highly susceptible (HS)

Out of 200 genotypes (Table 1) screened, 20 genotypes, namely, EC-414309, PBC-9221, NPC-14, BAUSM-92-1-1, PBC-2004-1, EC-339000, EC-338997, GSL-1, HNS-004, ONK-1, NRCDR-515, PBC-2002-2, NPC-15, OCN-3, EC-399299, NUDB-26-11, CAN-133, NPN-1, RGN-55, NRCDR-837 showed consistently resistant reaction in both the years, while nine genotypes *viz.*, EC-399296, EC-399301, EC-399313, PHR-2, CAN-130, RAURD-101, RH-9301, SKM-9328, IJWHJ-001 were moderately resistant. Besides these, thirty genotypes exhibited moderately susceptible, 71 susceptible and 70 highly susceptible reactions. Sangwan and Mehta (2001) also reported few genotypes of *Brassica carinata* and *B. napus* resistant to powdery mildew. Singh and Singh (2003) reported eight genotypes resistant and 20 genotypes moderately resistant out of 230 genotypes screened.

Management of powdery mildew disease through the host resistance is an eco- friendly and cost-effective approach. The genotypes identified as resistant in this study have sown consistent resistant reaction over the years under high disease pressure. These genotypes may be used as source of resistance for developing the resistant variety of agronomic value.

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Table 1. Reaction of Brassica genotypes against Powdery mildew under late sown condition

Scale	Entries
0	Nil
1	PBC-9221, NPC-14, BAUSM-92-1-1, PBC-2004-1, EC-339000, EC-338997, GSL-1, HNS-004, ONK-1, EC-414309, NRCDR-515, PBC-2002, NPC-15, ONC-3, EC-399299, NUDB-26-11, CAN-133, NPN-1, RGN-55, NRCR-837
2	EC-399296, EC-399301, EC-399313, PHR-2, RAURD-101, RH-9301, SKM-9328, IJWHJ-001, CAN-130
3	ELM-079, PAB-2020, EC-414320, YET-17, LES-1-27, ID-6, JGM-01-04, JGM-01-05, RAURD-7910, EC-399302, PRN-598, JYM-10, PBN-2002, PBN-2001, NDR-03-5, NDR-03-6, ORT-5-2, NDT-03-2, NDT-03-3, PYS-2001-1, PT-2002-25, PTC-99-11, EC-414291, EC-414293, NDYS-017, NDYS-117, NDYS-2, NDYS-128, PYS-2002-2, PYS-2005
4	KLM-945, TERI-LGM-06, PQR-2001-3, NRCDR-514, PAB-2001, PAB-2002, RH-0345, RN-573, EC-414322, EC-399312, YRN-6, LET-10, PBR-210, TK-04-01, TL-96-7, RH-9904, JMM-18, RH-0213, DMH-1, ELM-079, NPJ-99, SKM-301, KLM-145, LET, JMMWR-941-1-2, JYM-10, YRN-6, BIO-190-96, PBR-283, YSB-9, RK-2001, RGN-39, LET-14, RK-2002, DLM-81, RAUDYS-9702, EC-414299, BIO-322-93, HUJM-2001, PBR-253, JMW-946-3-13, RGN-94, RTM-2002, HYPR-97, RM-101, RGN-101, NRCDR-2, JTC-55, PBG-1986, RGN-142, BIO-13-01, PR-2003-30, PR-2002-8, PR-2003-27, PR-2001-64, PQR-2004-2, NPJ-100, NPJ-102, RK-02-3, PR-2001-42, BIO-169-96, RN-573, HUJM-101, CS-330-2-KP-2, CS-611-1-3-6, RM-11, PRO-2101, NDR-9902, PBR-275, GSL-1, EC-414295, NDYS-133-1
5	ALM-933, BIO-Q-108-2000, LET-3, LET-18, PQR-9701-46, PQR-2001, VARUNA, EC-414306, EC-414317, EC-414310, EC-414324, BIO-190-96, PBR-300, RK-05-1, NDR-9902, RK-02-5, JGM-901, PBR-91, RGN-34, RGN-55, RGN-56, JMM-04-5, JMM-04-2, KRANTI, NDM-871, EC-414295, RAURD-02-01, EJ-15, BIO-13-01, RM-105, RGN-124, JS-19, RK-04-2, CS-234-2, PR-2003-27, NDYS-2018, NDYS-132, NRCDR-05, NRC-323-1, RGN-73, LES-1-27, SKM-149, SAL-9, NRCDR-2, LET-14, PBC-9221, RK-9903, BIO-Q-442-99, JPJ-93, CS-611-1-3-5, CS-101-4-P2, SKM-109, SKM-139, SKM-125, SKM-9928, RH-2004, RH-0007, PBR-558, PR-2002-20, PQR-2004-1, ROHINI, RGN-73, RK-02-4, SKM-9927, NDT-03-3, TMA, NDT-03-1, EC-414301, YSB-9, VARDAN

GxE interaction for seed yield and oil content in brown sarson (*Brassica rapa* L.) under temperate conditions

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Abstract

Ten genotypes of brown sarson were evaluated over three locations for analysis of stability parameters with respect to seed yield per plant and oil content. Significant differences were observed for seed yield per plant and oil content among genotypes. G x E interaction (Linear) was significant suggesting that performance of genotypes across environments could be predicted with greater precision. NGB-3, NGB-6 & NGB-9 exhibited stability for both seed yield and oil content.

Keywords

Seed yield, oil content, genotypes, stability, brown sarson

Introduction

Brown sarson (*Brassica rapa* L.) is one of the most important oleiferous Brassicas cultivated in the North Western regions of India (Singh *et al*, 2007). It is either grown as a pure crop or as a mixture with other major rabi crops in mostly rainfed areas of the country. In Kashmir valley and high altitude regions of Jammu divisions brown sarson is the only edible oilseed crop being cultivated during rabi season. The crop is popular among the farmers as its cultivation fits well in the rice-oilseed rotation. The crop is cultivated under harsh wintery conditions. Till now not much work has been carried out on genetic improvement of brown sarson. Hence, it is imperative to develop high yielding varieties with high oil content in this crop. Besides, yield potential the variety should also possess stability in its performance over a range of environments.

Materials and Methods

Ten diverse genotypes of brown sarson namely NGB-1, NGB-2, NGB-3, NGB-4, NGB-5, NGB-6, NGB-7, NGB-8, NGB-9 and NGB-10 maintained in the germplasm repository of the Division of Plant Breeding and Genetics were utilized for the study. The genotypes were grown at three locations viz., Experimental Farm, Division of Plant Breeding and Genetics (L1), Regional Rice and Research Station (RR & RS) Khudwani (L2) and Faculty of Agriculture and Regional Research Station Wadura (L3). In each location all the genotypes were evaluated in a complete randomized block design with three replications in two rows of 3 meter length. The row- to -row and plant-to-plant distances maintained were 30 cm and 10 cm, respectively. Recommended package of practices were followed to raise a good crop. Seed yield per plant was recorded on ten randomly selected plants at each location. Oil content was estimated using NMR. Statistical analysis was carried out as per Eberhart and Russell (1966) model.

Results and Discussion

Joint regression analysis indicated that varieties and environments differed significantly for seed yield per plant and oil content (Table 1). Significant genotype x environment interaction for seed yield per plant and oil content indicated differential expression of genotypes for these traits over environments. Significant G x E interaction for seed yield and other traits was found by Kakani (1989), Meena (1997) and Jakhar and Yadav (2010). Environmental variances were significant for seed yield per plant. Variance due to environment + (Variety x environment) component was significant for seed yield per plant. Partitioning of this variability indicated divergent linear response to the environmental changes. Similar results have been found by various workers (Gupta and Pratab, 2007; Krishnand and Bhajan, 1997 and Singh & Gupta, 2003).

According to Eberhart and Russell (1966) a variety is considered to be stable over different environments if it shows high mean performance with unit regression coefficient ($b_i = 1$) and minimum deviation from the regression line (s^2_{di}). The critical perusal of Table 2 revealed that for all the genotypes both linear effect ($b_i = 1$) as well as deviation from the regression line (s^2_{di}) were non-significant for seed yield per plant and oil

content except NGB-2, NGB-4 & NGB-5. Bradshaw (1965) suggested that maximum fitness can be obtained by adjustment in the plastic component traits. In a population homeostatically buffered, expression of component traits may shift in compensating manner in the changing environment in order to perform well in the final trait, otherwise high unpredictable G x E interaction would result.

From the above study NGB-3, NGB-6 & NGB-9 were satisfying the criterion of stability for both seed yield per plant and oil content, hence these genotypes should be recommended for cultivation in Kashmir.

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Table 1. Joint regression analysis for seed yield and oil content tested over three locations.

Source of variation	d.f	Mean sum of squares	
		Seed yield per plant	Oil content
Varieties (var)	9	0.48**	38.60**
Environments (Env.)	2	3.46**	0.78*
Var. x Env.	18	0.30*	0.80*
Env. + (Var. x Env.)	20	0.22**	0.30
Env. Linear	1	6.91**	0.65
Var. x Env. (Linear)	9	0.12	0.20
Pooled deviation	10	0.09	0.41
Pooled error	60	0.14	0.38

** significant at $P < 0.001$; *Significant at $P < 0.005$

Table 2. Mean values and stability parameters (bi and s2di) of brown sarson genotypes for seed yield and oil content.

Genotype	Seed yield per plant			Oil content		
	X	Bi	S2di	X	Bi	S2di
NGB-1	8.37	- 0.28	-0.01	40.50	-2.77	0.12
NBG-2	7.70	0.92	-0.01	42.10	3.41	1.64**
NBG-3	8.05	1.30.560	0.07	41.60	0.99	1.10
NBG-4	7.72	1.73	0.18	42.20	2.89	0.91*
NBG-5	7.90	0.96	0.13	41.90	1.24	1.20**
NBG-6	8.20	0.85	-0.06	40.70	0.92	0.15
NBG-7	6.33	1.05	-0.04	42.90	2.56	0.11
NBG-8	8.17	0.88	0.11	41.00	1.10	-0.33
NBG-9	7.39	1.13	-0.07	42.60	3.20	0.45
NBG-10	6.18		-0.03	42.80	2.25	-0.17
Population mean	6.47	0.70		40.51		
S.E m + -	0.10			0.18	4.18	

Significant at $P < 0.005$, x = genotype mean, bi = regression value, s2di = deviation from linearity

Genetic variability for curd traits in heat tolerant cauliflower

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Abstract

An investigation was carried out to study the genetic variability for curd traits in heat tolerant cauliflower (*Brassica oleracea* var. *botrytis* L.) at the research farm of the Division of Vegetable Science, IARI, New Delhi. The study was carried out in randomized block design with three replications and observations were recorded for 11 different parameters from 32 genotypes. Analysis of variance revealed that the mean sum of squares due to genotype were highly significant for all the characters studied indicating sufficient genetic variation in these genotypes. The genotypes DC-98-4, DC-98-10 and DC-124 were found superior to other genotypes with respect to curd characteristics. The overall values of PCV were higher than those of GCV. High heritability along with high genetic advance as percent of mean was recorded for curd compactness and net curd weight.

Key words:

Genetic Variability, heritability, and heat tolerant cauliflower.

Introduction

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the most important vegetable belonging to the family Brassicaceae. With the evolution of Indian cauliflower, it is now being grown during summer and rainy season also. There is a need to increase overall production to meet the inflating demand. This can be achieved by adopting the high yielding F₁ hybrids. To evolve new varieties, the role of genetic variability, its transmissibility into the progeny and the nature of inheritance are of paramount importance in selecting the best genotype for immediate improvement in yield. Thus, the nature and magnitude of variability present in the gene pool for different characters determine the success of genetic improvement in any character particularly curd characteristics. The pattern of inheritance of quantitative characters is highly complex and can be understood through the study of genetic parameters such as variability, heritability and genetic advance.

Materials and Methods

The present study comprising 32 cauliflower genotypes was carried out at the research farm of the Division of Vegetable, IARI, New Delhi, during the year 2005-06. The seedlings were transplanted in each plot having 5.76 m² area at 50cm between and 45 cm within the row distance in a Randomized Block Design with three replications. Observations were taken from five randomly selected plants from each plot for eleven quantitative traits viz; stem length, plant height, number of leaves per plant, gross plant weight, leaf size, curd depth, curd diameter, curd compactness, harvest index, dry matter and net curd weight. All the data were averaged and subjected to analysis of variance (Panse and Sukhatme, 1984). The genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) were calculated as per Burton (1952). Heritability (broad sense) and genetic advance as per cent of mean were computed by following the methods of Allard (1960) and Johnson *et al.* (1955), respectively.

Results and Discussion

The presence of variability is necessary for the success of breeding programme. Analysis of variance was significant for all the characters studied showing difference among the genotypes. This indicates sufficient genetic variability to be exploited in a breeding programme and was reflected in the broad range observed for each trait (Table1). The stem length ranged from 4.52 to 15.13 cm with grand mean of 9.22 ± 0.433 cm. The plant height had an overall mean and range of 53.04 ± 1.06 and 46.23 to 65.40, respectively. Number of leaves per plant ranged from 16.31 to 27.41 with a grand mean of 22.05 ± 0.540 . The overall mean gross plant weight was 1.000 ± 0.077 kg with a range of 0.710 to 1.400 kg. The genotypes had leaf size ranging from 413.32 to 754.77 cm² and averaging 568.44 ± 11.417 cm². The curd depth ranged from 4.97 to 7.70 with a grand mean of 6.21 ± 0.22 cm. In the plants curd diameter ranged from 7.94 to 13.10 cm with a grand mean of 10.77 ± 0.125 cm. The genotype DC-98-4 recorded the most compact curd ranging from 30.40 to 110.11. The grand means for the genotypes were 54.91 ± 3.395 . The net curd weight ranged from 0.210 to 0.410 kg with a grand mean of 0.320 ± 0.014 kg. The genotypes had mean harvest index of 33.10 ± 2.031 per cent with a range of 18.19 to

48.43 per cent. The dry matter content ranged from 9.20 to 18.06 per cent with a mean of 13.24 ± 0.54 per cent. The mean sum of squares due to genotypes was highly significant for all the characters studied indicating sufficient genetic variation in these genotypes for these characters. The result indicated sufficient genetic variation among the genotypes assessed, which suggested that selection will be successful for the observed traits using the present material. Also, different genotypes with extreme values for a particular character can be used as a source for that character. Significant differences among genotypes for different traits have been reported by Radhakrishna and Korla (1994); Sharma *et al.*, (2000) and Batra and Singh (2000).

Mean performance of the genotypes for different characters along with character wise overall mean are given in Table 2. The genotype DC-22 had the longest stem whereas the stem length of DC-113 was shortest. Among the genotypes, DC-98-4 was the shortest and DC-22 the tallest. The genotype DC-10 had the highest number of leaves per plant. Gross plant weight was highest in the variety Pusa Deepali. Line DC-85 recorded the smallest leaf size, whereas it was highest in the line 23000. The greatest curd depth was recorded for Pant Gobhi. Line DC-5 recorded the smallest curd diameter whereas it was highest in variety Pant Gobhi. DC-112 recorded the highest net curd weight. Line DC-7 had the highest, whereas PK-3 had the lowest harvest index. Lowest dry matter was obtained in the line DC-122 and the highest in the line DC-41-5. Based on *per se* performance, the lines DC-98-4, DC-124 and DC-98-10 were identified for morphological and curd characteristics. Thus, it can be inferred that selection has to exercise for specific traits in individual genotypes. The phenotypic and genotypic coefficients of variation (PCV), heritability and genetic advance as percent of mean were worked out to various morphological characters (Table 3). GCV ranged from 10.98 to 48.60 per cent and PCV from 11.26 to 48.66 per cent. The result showed higher PCV than GCV, which indicated environmental interference in the manifestation of these characters. These findings are in agreement with those of Jamwal *et al.* (1992).

Plant height had the lowest estimate for PCV and GCV. The low estimate of GCV indicated that the genotypes possessed comparatively low genetic variation for these characters. Under such situation, the breeder may go for creation of new variability either by hybridization or by mutation and subsequently selection can be practiced. In the present investigation, characters like stem length, plant height, number of leaves per plant, curd diameter and net curd weight had high estimates of heritability. It suggested that the highly heritable nature of variability in these characters respond to selection more effectively. The estimates of heritability were moderate to high for other characters like curd depth. High heritability can be attributed to the greater role of additive gene and additive x additive gene action, which can be exploited by following simple selection. Similar reports have also been put forward by Rastogi *et al.* (1995), Singh *et al.* (1995) and Reddy and Varalakshmi (1995).

High heritability coupled with high genetic advance were noted for curd compactness, net curd weight suggesting thereby that these traits could be considered as reliable indices for selection and higher responses of this trait could be expected from selection. High heritability coupled with moderate genetic advance was expressed by traits like gross plant weight, stem length, harvest index and dry matter. It indicated equal contribution of additive and non-additive gene action for these traits. Therefore, the heritable variability in the breeding materials for curd compactness and net curd weight content could be exploited for improvement through selection.

Conclusion

The result indicated the presence of adequate genetic variability within the germplasm evaluated for the improvement of quantitative traits. The highest direct effects on yield can be exerted by net curd weight and stem length. Plant height and number of leaves per plants were governed by non-additive gene action and heterosis breeding should be resorted to for the improvement of these characters. To improve the yield parameter, selection should be made for the positively associated characters viz., net curd weight and harvest index. This may lead to development of high yielding genotypes in the early maturity groups of cauliflower.

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Table 1. Range and mean values for different characters of 32 genotypes of heat tolerant cauliflower

Component	Stem length (cm)	Plant height (cm)	Number of leaves per plant	Gross plant weight (kg)	Leaf size (L×B) cm ²	Curd depth (cm)	Curd diameter (cm)	Curd compactness	Harvest index (%)	Dry matter (%)	Net curd weight (kg)
Range	4.52-15.13	46.23-62.40	16.31-27.41	0.710-1.400	413.32-754.77	4.97-7.70	7.94-13.10	30.40-110.11	18.19-48.43	8.44-18.06	0.210-0.410
MSS	25.42	69.88	32.54	0.10	28732.13	1.27	6.34	862.25	162.99	24.74	0.01
Mean	9.22	53.04	22.05	1.000	568.44	6.21	10.77	54.91	33.10	13.24	0.320
SEm±	0.433	1.06	0.540	0.077	11.417	0.216	0.125	3.395	2.031	0.539	0.014
CD (P=0.05)	0.866	2.12	1.08	0.15	22.83	0.432	0.25	6.79	4.06	1.078	0.028

Table 3. Estimates of parameters of variability for quantitative characters in 32 heat tolerant cauliflower genotypes

S. No	Character	Heritability (broad sense)	GCV	PCV	GA as % mean
1	Stem length (cm)	0.973	22.57	22.87	45.92
2	Plant height (cm)	0.974	16.23	16.45	32.99
3	Number of leaves per plant	0.903	17.39	18.30	34.06
4	Gross plant weight (kg)	0.926	25.73	26.75	51.05
5	Leaf size (L×B) cm ²	0.998	48.60	48.66	100.02
6	Curd depth (cm)	0.937	13.56	14.01	27.11
7	Curd diameter (cm)	0.951	10.98	11.26	22.08
8	Curd compactness	0.895	38.12	40.28	74.31
9	Harvest index (%)	0.773	21.94	24.96	39.83
10	Dry matter (%)	0.841	12.55	13.69	23.75
11	Net curd weight (kg)	0.938	34.82	35.95	69.64

Table 2. Mean performance of 32 heat tolerant cauliflower genotypes for different quantitative characters

Genotype		Stem length (cm)	Plant height (cm)	Number of leaves per plant	Gross plant weight (kg)	Leaf size (L×B) cm ²	Curd depth (cm)	Curd dia (cm)	Curd compactness	Harvest index (%)	Dry matter (%)	Net curd weight (kg)
1	DC-1	12.74	61.11	23.87	0.980	520.8E	6.08	10.17	50.8	29.63	13.87	0.290
2	DC-4	12.80	58.08	26.22	1.080	620.0E	6.21	10.98	45.6	27.03	17.02	0.290
3	DC-5	11.39	56.61	23.66	0.780	560.3E	6.30	7.94	88.8	41.16	15.23	0.320
4	DC-6	10.73	57.35	27.26	0.710	632.5E	5.82	9.43	69.2	43.36	14.30	0.310
5	DC-7	11.22	57.13	27.30	0.830	431.9E	5.96	11.65	59.1	48.43	15.27	0.400
6	DC-8	10.84	52.18	23.51	0.940	513.7E	5.19	10.05	69.5	32.67	14.70	0.310
7	DC-9	8.32	49.86	16.31	0.740	436.7E	5.69	11.58	53.0	46.01	15.34	0.340
8	DC-10	12.24	57.91	27.41	0.840	373.5E	5.89	12.84	48.4	47.25	16.98	0.400
9	DC-22	15.13	62.40	20.85	0.830	544.9E	6.14	12.10	40.1	36.69	16.90	0.300
10	DC-33-8	12.63	58.20	22.74	1.050	737.1E	6.77	12.17	46.3	37.56	14.56	0.390
11	DC-84	12.30	52.98	22.24	1.100	580.5E	6.92	12.53	44.4	37.15	16.81	0.410
12	cc-12	12.68	51.33	24.02	0.860	594.2E	5.16	11.10	55.2	34.69	14.80	0.300
13	cc-14	12.31	51.52	23.38	0.920	657.4E	5.81	10.20	71.3	39.90	15.92	0.370
14	cc-15	7.94	49.71	23.25	0.930	585.94	5.76	9.12	76.9	34.20	14.56	0.320
15	DC-83	9.15	55.81	20.64	1.110	697.11	6.01	11.10	48.5	27.85	11.53	0.310
16	DC-18	10.26	47.63	26.17	0.930	607.7E	5.81	8.86	77.4	32.79	9.61	0.310
17	23000	11.38	48.85	23.36	1.140	754.77	5.93	10.12	60.1	27.40	9.98	0.310
18	DC-98-4	6.13	46.23	16.63	0.950	520.94	4.97	9.11	110.11	40.22	12.92	0.380
19	DC-41-5	6.68	47.55	16.97	0.770	545.5E	5.80	8.20	61.8	27.66	18.06	0.210
20	DC-85	9.74	54.70	17.99	0.990	413.3E	6.19	11.09	46.6	30.33	17.78	0.300
21	DC-98-10	8.74	56.88	19.32	1.270	457.8E	7.29	12.74	37.8	30.30	11.93	0.380
22	DC-112	5.68	58.63	19.31	1.090	592.6E	7.15	11.81	47.7	37.24	11.26	0.410
23	DC-113	4.52	45.28	21.35	0.900	441.3E	6.00	12.16	42.8	35.67	11.49	0.320
24	DC-122	5.39	46.61	22.04	1.100	690.8E	7.07	12.99	30.4	27.89	9.20	0.310
25	DC-124	6.78	48.62	26.26	1.030	514.1E	6.96	10.00	46.1	27.18	9.27	0.280
26	aa(395)	7.41	49.82	23.61	1.360	615.4E	7.10	11.10	39.1	22.75	11.62	0.300
27	PK-3	6.36	48.69	21.25	1.210	536.2E	6.20	9.53	44.8	18.19	9.63	0.220
28	754	9.67	58.09	23.21	0.780	510.0E	5.50	9.03	55.6	27.39	11.30	0.210
29	VV-5-6-2	4.74	47.33	17.41	0.980	592.9E	6.41	9.72	45.1	24.07	12.66	0.240
30	Pusa Deepali	7.39	49.25	20.65	1.400	696.9E	6.26	10.22	62.0	24.90	10.92	0.350
31	Pant Gobhi	6.89	54.04	20.76	1.220	506.87	7.70	13.10	30.4	30.29	9.74	0.370
32	First Crop Ageti	5.13	56.86	16.54	1.310	705.77	6.72	12.01	51.1	31.33	8.44	0.410
SEm±		0.433	1.06	0.540	0.077	11.417	0.216	0.125	3.39	2.031	0.539	0.014
CD (P=0.05)		0.866	2.12	1.08	0.15	22.8E	0.432	0.25	6.7	4.06	1.078	0.028

BREEDING STRATEGIES

Variability for agromorphological traits in germplasm of yellow sarson (*Brassica rapa* L. var. yellow sarson)

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Introduction

Rapeseed-mustard is an important group of crop plants with great economic value world wide. Oilseeds *Brassica* are the second most important source of edible oil after groundnut in the India. The *Brassica rapa* var *yellow sarson* commonly know as yellow sarson is one of the most important member of *Brassicaceae* family grown in India. This is grown since ancient time due to the presence of comparatively higher percentage of oil in the seed, shorter crop duration and attractive seed coat colour. North-eastern India is considered as primary centre of origin, however genetic diversity found in eastern Uttar Pradesh and West Bengal. The improvement for yield and other traits not only depends upon the amount of variability present in the germplasm but also its proper evaluation and further utilization in the breeding programmes. Germplasm provides the valuable reservoir of variability on which selection can be made for evolving superior genotypes or it may be utilized as parent / donor in hybridization programmes. Hence, there is an ardent need for proper evaluation and characterization of germplasm resources. Evaluation and characterization of germplasm is necessary to search useful donors in rapeseed-mustard (Chatterjee 1992, Kumar *et al.*, 2004 and Kumar and Misra, 2007). The present study was under taken to find out variability parameters for 16 agro-morphological traits in respect of yellow sarson germplasm augmented from different eco-geographical sources within the country.

Materials and Methods

Fifty five accessions of yellow sarson were evaluated and characterized during rabi (post rainy) season of 07-08 in an augmented complete block design with three checks (NDYS 2, RS 1 and YST 151) at the Directorate of Rapeseed–Mustard Research, Bharatpur (Rajasthan), India. Each genotype was sown in paired rows of 3m length with 30 x 10 cm spacing. Recommended standard agronomic package of practices and plants protection measures were adopted. Randomly tagged ten plants were selected at appropriate growth stages to record observations on morphological traits namely, initiation of flowering, 50% flowering, maturity, plant height, primary and secondary branches per plant, main shoot length, siliquae on main shoot, siliqua length, siliqua beak length and seeds per siliqua. Post harvest observations include seed yield per plant, 1000-seed weight, harvest index and quality traits (oil and protein content). The mean values for each character were considered for computation, except for days to flower initiation, 50 % flowering and days to maturity (which was recorded on whole plot basis). One thousand seeds were counted by electronic seed counter (Contador, Germany) and weighed by electronic balance. Oil and protein content were analyzed by Near Infrared Reflectance Spectroscopy (Dickey- John, Instalab 600). Replication wise data for each character were subjected for statistical analysis. Range, mean, coefficient of variation were computed using standard statistical methods by Gomez and Gomez (1984) and correlation coefficient were calculated according to the procedure of Singh and Chaudhary (1977).

Results and Discussion

The material under study had sufficient genetic variability for most of the traits as indicated by the coefficient of variation (Table 1). The difference among germplasm was highly significant for most of the characters under study. Among the 16 traits studied, the maximum variability was observed for secondary branches per plant (CV 116.5 %) followed by seed yield per plant (CV 73.5 %). However, the least variability was observed for days to maturity (CV 1.5 %) followed by oil content (CV 4.8 %). Similar trends of genetic variations have also been reported in some of the earlier reports on oilseed *Brassica* (Yadav *et al.*, 1997, Kumar *et al.*, 2001, Misra *et al.*, 2004, 2005 and Patel and Patel 2005).

Promising donors identified on the basis of superiority over checks for various economic traits (Table 2), which can be utilized for future breeding programmes. Accession MYSL 201 appeared to be a good source for seed yield per plant, oil content and seeds per siliqua. Accession PYS 9802 was observed for useful donor having oil content, harvest index and showing early maturity. Accession RAUDYS 9702 had early 50% flowering,

maturity and also having high siliquae on main shoot.

To enhance the productivity of this crop under different production systems or to facilitate selection, correlation among the traits was worked out. Knowledge of relationship between yield and its components is essential as this may help in constructing suitable selection criteria for yield. Seed yield per plant had positive and significant correlation with primary and secondary branches per plant, siliquae on main shoot, siliqua length, harvest index, main shoot length, plant height, oil content and 1000-seed weight (Table 3). Whereas, seed yield per plant showed negative correlation with 50% flowering, initiation of flowering and protein content. This is conformant of some of the earlier reports on yellow sarson (Kumar *et al.*, 2001, Katiyar *et al.*, 2004, Patel and Patel 2005 and Misra *et al.*, 2006). Other yield contributed traits also showed positive and significant correlation namely 1000-seed weight with plant height, primary branches and secondary branches per plant, main shoot length, siliquae on main shoot and siliqua length; siliquae on main shoot with primary branches and secondary branches per plant, main shoot length and plant height; oil content with primary branches per plant, siliquae on main shoot and harvest index; siliqua length with plant height, primary branches per plant and main shoot length. Hence, suitable adjustment should be made at the time of selection for these characters. Similar trend of correlation were also observed in Indian mustard (Yadav *et al.*, 1997 and Misra *et al.*, 2006, 2007) and yellow sarson (Misra *et al.* 2006).

Considering variability and correlation together the present accessions proved to be an important gene pool of useful traits and many accessions can be utilized for breeding programmes to develop suitable varieties for different agro climatic conditions and also to improve yield and quality.

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Table 1. Range, mean and coefficient of variation (cv) for different agro-morphological traits in yellow sarson germplasm

Character	Range	Mean \pm SEm	CV (%)	Checks		
				YST 151	NDYS 2	RS 1
Initiation of flowering	56.0-92.0	76.2 \pm 1.2	11.3	54.0	68.0	63.0
50% flowering	65.0 - 97.0	89.1 \pm 1.1	8.9	83.0	80.0	77.5
Primary branches	3.0 - 11.2	6.2 \pm 0.2	27.4	6.6	9.6	8.8
Secondary branches	2.5 - 12.0	2.5 \pm 0.4	116.5	2.7	1.6	6.3
Seeds per siliqua	11.4 - 37.9	22.3 \pm 0.8	25.3	15.6	36.3	13.1
Siliquae on main shoot	29.2 – 78.6	44.2 \pm 1.4	23.8	41.0	67.2	69.5
Days to maturity	132.0 - 140.0	136.4 \pm 0.3	1.5	134.0	137.0	137.0
Plant height (cm)	53.2 - 151.4	100.0 \pm 3.4	25.4	110.4	132.2	110.5
Main shoot length (cm)	25.6 – 63.8	45.2 \pm 1.3	21.7	46.6	54.6	51.6
Siliqua length (cm)	3.5 – 5.2	4.2 \pm 0.1	11.1	4.2	4.6	4.4
Siliqua beak length (cm)	1.1 - 2.6	1.7 \pm 0.1	22.3	1.4	2.3	1.8
Seed weight (g)	2.3 - 5.1	3.4 \pm 0.1	19.0	3.0	3.4	2.7
Seed yield per plant (g)	1.1 – 23.4	6.4 \pm 0.6	73.5	8.5	23.4	11.0
Harvest index (%)	14.3 - 35.8	23.9 \pm 0.7	20.4	19.9	27.4	29.1
Protein content (%)	19.4 - 24.3	22.1 \pm 0.2	5.1	20.5	21.5	21.2
Oil content (%)	36.5 - 45.8	41.0 \pm 0.3	4.8	39.5	43.6	42.5

Table 2. Promising accessions of yellow sarson

Character	Name of accessions
Initiation of Flower	< 54.0 : NDYS 9504, SSK 9203, YSCN 14, RAUDYS 9702
50% Flowering	< 77.5:SSK 9203, YSCN 14, DYS 7
Maturity duration	< 134.0: RAUDYS 9702, PYS 9802, NIC 7172, IC147993
Plant height	< 110.4: IC 199735, IC 199738, IC 147993
Primary branches per plant	> 9.6: YSC 35, MYSL 209
Main shoot length	>54.6: YSC 5, IC 386314, YSC 35, YSPG 842
Siliquae on main shoot	> 69.5:RAUDYS 9702, YSCN 14
Siliqua length	> 4.6: NDYS 9, YSC 92, YSC 12, IB 1464
Seeds per siliqua	> 36.3:SSK 6, IC 199739, MYSL 201
Seed weight	>3.4: MYSL 209, SSK 9203, YSC 17, NDYS 9
Harvest index	> 29.1: PYS 9801, PYS 9802, SSK 9203, IC 147913
Seed yield per plant	> 23.4:YSC 5, YSC 35, MYSL 201
Protein content	> 21.5:IC 199743, NIC 1172, NDYS 9504, YSC 90
Oil content	> 43.6: MYSL 201, PYS 9801, PYS 9802, IC 199741

Table 3. Correlation between seed yield and its components traits in yellow sarson germplasm

Traits	#IF	FF	DM	PH	PB	SB	MSL	SMS	HI	SS	SL	SBL	SW	PC	OC
FF	0.764**														
DM	-0.025	-0.031													
PH	-0.218*	-0.292**	0.337**												
PB	-0.348**	-0.387**	0.125	0.694**											
SB	-0.421**	-0.496**	0.110	0.635**	0.624**										
MSL	-0.272*	-0.410**	0.332**	0.849**	0.588**	0.634**									
SMS	-0.536**	-0.612**	0.034	0.577**	0.654**	0.558**	0.705**								
HI	-0.309**	-0.376**	-0.132	-0.029	0.150	0.030	0.061	0.305**							
SS	0.067	0.226*	0.193	-0.003	0.155	-0.224*	-0.170	-0.141	-0.078						
SL	0.088	0.074	0.172	0.580**	0.405**	0.172	0.435**	0.201	-0.070	0.155					
SBL	0.113	0.086	0.471**	0.090	0.148	-0.157	0.020	-0.021	-0.057	0.415**	0.283**				
SW	-0.344**	-0.465**	0.050	0.485**	0.418**	0.579**	0.467**	0.315**	0.105	-0.172	0.268*	-0.047			
PC	0.342**	0.404**	0.187	-0.002	-0.210	-0.070	-0.065	-0.220*	-0.369**	-0.110	-0.043	-0.079	-0.086		
OC	-0.367**	-0.532**	-0.191	0.014	0.232*	0.094	0.067	0.272*	0.473**	0.132	-0.016	0.068	0.174	-0.833**	
SYP	-0.386**	-0.475**	0.183	0.552**	0.745**	0.532**	0.594**	0.601**	0.312**	0.153	0.286**	0.091	0.418**	-0.386**	0.525**

*, ** Significant at 5 and 1% respectively

#IF: Initiation of flowering, FF: 50% flowering, PB: Primary branches per plant, SB: Secondary branches per plant, MSL: Main shoot length, PH: Plant height, SMS: Siliquae on main shoot, DM: Maturity duration, SBL: Siliqua beak length, SL: Siliqua length, SYP: Seed yield per plant, SS: Seeds per siliqua, HI: Harvest index, SW: 1000-Seed weight, PC: Protein content and OC: Oil content

BREEDING STRATEGIES

Inter-relationship and path analysis for quality traits in cabbage (*Brassica oleracea* var. *capitata* L.)

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Abstract

An experiment was conducted during the winter seasons of 2006-08 at Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University Lucknow to investigate the genetic variability, inter-relationship and path analysis for quality traits in 30 diverse cabbage genotypes of tropical and subtropical origin. A wide range of variation was observed for all most all traits. C-10 recorded the maximum amount of sulphur (75.30mg), carotenoids (95.84 μ), ascorbic acid (39.95mg/100g), iron (0.82mg), potassium (296.65mg), zinc (0.31mg), calcium (57.90mg) and dry matter (9.67mg). 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. Phenotypic coefficient of variation and genotypic coefficient of variation were highest for ascorbic acid and lowest for potassium and calcium. The genotypic correlation coefficient higher than the corresponding phenotypic correlation coefficient for all the parameters. Thus, these traits may be effectively be used as a selection criterion for screening potential genotypes in a breeding programme.

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 (Singh *et al.* 2009). 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. 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.* 2010). 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 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 of tropical and subtropical origin belonging to white, red and savoy types viz 'C-1', 'C-2', 'C-3', 'C-4', 'C-5', 'C-6', 'C-7', 'C-8', 'C-9', 'C-10', 'C-11', 'C-12', 'C-13', 'C-14', 'C-15', 'C-16', 'C-17', 'Golden Acre', 'Pusa Mukta', 'Early Drum Head', 'Red Cabbage-20', 'Pusa Synthetic', 'Pusa Ageti', '1923', 'MR-1', 'KK-3', 'KK-2', 'Pride of India', 'Prem Nath', and 'Red Rock Mammoth's. Each genotype was planted in a plot having 3.0 × 2.7 m area in 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 2006-2008. Geographically, Babasaheb Bhimrao Ambedkar University, Vidya Vihar, Rae Bareilly Road, Lucknow, is situated at 80.52 °E longitude and 26.56 ° N latitude at an altitude of 111 m above mean sea level. The climate of Lucknow is sub-tropical with minimum and maximum temperatures and humidity ranging between 5.5°C and 42°C and 80%, respectively with an annual rainfall around 750 mm. The ascorbic acid and total carotenoid 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 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. Correlation and path coefficient analysis were calculated as per formulae suggested by Al-jibouri *et al.* (1958), and Dewey and Lu (1959), respectively.

Results and Discussion

The analyses of variance for eight quality traits revealed that mean square were highly significant for all. The extent of variability with respect to various characters in different diverse genotypes of cabbage 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 (Table 1). 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). Therefore, to give an idea about the magnitude of variability present in a population. 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 Singh *et al.* (2009). The genotypic coefficient of variation provides help to measures 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 (1951) 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. 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.

The phenotypic as well as genotypic correlations between different pairs of traits are presented in Table 2 showed higher estimates of correlation coefficient than the corresponding phenotypic. This indicated little role of environment in the expression of genetic relationship on the phenotypes. The dry matter significant and positive correlation coefficients with all quality traits (sulphur, ascorbic acid, carotenoids, iron, potassium, calcium and zinc). Ghebramlak *et al.* (2004) also reported a positive correlation coefficient with all the quality characters. The significant positive associations suggest that selection should be oriented towards higher content of total carotenoids, ascorbic acid, sulphur, calcium, iron, potassium and zinc and thus, ultimately resulting in higher dry matter content. The highly significant and positive association among the various quality traits indicated immense scope for the nutritional quality improvement in cabbage.

Correlation coefficients indicate only the general association between any two traits without tracing any possible causes of such association. In such association the path coefficient analysis at genotypic level (Table 3) is done to partition the correlation co-efficient into direct and indirect effect of different quality parameters. Positive direct effect on the dry matter was the highest for sulphur (0.608) followed by iron (0.452). total carotenoids (-0.434) potassium (-0.024) and calcium (0.055) exhibited a negative direct effect on dry matter content but these negative direct effect was neutralized due high positive indirect effect through sulphur content (0.194, 0.219 and 0.362) respectively on dry matter which are quite close to its correlation coefficient (0.675) and indicated that a direct selection through these traits would be very effective. Hence, sulphur is proved to be the most effective selection index while carrying out genetic improvement in cabbage. In quality characters, the residual effect at genotypic level was less compared to the residual effect at phenotypic level.

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Table 1. 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
Carotenoids (μ g/100g)	27.05	95.84	49.37 \pm 0.63	25.52	25.42	99.30	25.76	52.18
Sulphur (mg/100g)	22.15	75.30	41.91 \pm 0.46	26.30	26.23	99.50	22.59	53.90
Iron (mg/100g)	0.23	0.82	0.48 \pm 0.03	26.86	24.29	81.80	0.22	45.83
Potassium (mg/100g)	196.25	296.65	234.35 \pm 1.39	8.39	8.33	98.50	39.89	17.02
Zinc (mg/100g)	0.13	0.31	0.20 \pm 0.01	18.08	14.07	60.50	0.05	25.00
Calcium (mg/100g)	41.25	57.90	46.38 \pm 0.56	7.54	7.25	92.30	6.65	14.34
Dry matter (mg/100g)	6.80	11.58	9.67 \pm 0.30	12.80	11.64	82.80	2.11	21.82

Table 2. Estimates of genotypic (G) and phenotypic (P) correlation coefficients for the biochemical (quality) traits in cabbage genotypes.

S. No	Traits		X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈
1	X ₁	G	1.000	0.602**	0.372**	0.496**	0.343*	0.519**	0.298*	0.494**
		P	1.000	0.598**	0.369**	0.448**	0.341*	0.417**	0.276*	0.468**
2	X ₂	G		1.000	0.319*	0.857**	0.600**	0.419**	0.544**	0.675**
		P		1.000	0.317*	0.771**	0.594**	0.327*	0.496**	0.644**
3	X ₃	G			1.000	0.182	0.360**	0.696**	0.285*	0.595**
		P			1.000	0.169	0.356**	0.536**	0.259*	0.570**
4	X ₄	G				1.000	0.479**	0.371**	0.320*	0.696**
		P				1.000	0.431**	0.254*	0.272*	0.601**
5	X ₅	G					1.000	0.297*	0.251	0.403**
		P					1.000	0.236	0.235	0.383**
6	X ₆	G						1.000	0.422**	0.559**
		P						1.000	0.282*	0.413**
7	X ₇	G							1.000	0.358**
		P							1.000	0.313*
8	X ₈	G								1.000
		P								

*Significant at = 0.05, ** significant at p = 0.01

X₁ = Ascorbic acid (mg/100g), X₂ = Total carotenoids s(μ g/100g), X₃ = Sulphur (mg/100g), X₄ = Iron (mg/100g)

X₅ = Potassium (mg/100g),

X₆ = Zinc (mg/100g), X₇ = Calcium (mg/100g), X₈ = Dry matter (mg/100g)

Table 3. Estimates of direct (diagonal) and indirect (off diagonal) for quality traits at genotypic level in cabbage genotypes.

Characters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	Correlation with dry matter
X ₁	-							
X ₁	0.282	-0.262	0.226	0.224	-0.008	0.084	-0.027	0.519**
X ₂	-0.170	-0.434	0.194	0.388	-0.014	0.053	-0.037	0.420**
X ₃	-0.105	-0.139	0.608	0.082	-0.009	0.080	-0.033	0.694**
X ₄	-0.140	-0.372	0.111	0.452	-0.011	0.090	-0.039	0.371**
X ₅	-0.097	-0.261	0.219	0.217	-0.024	0.071	-0.022	0.297*
X ₆	-0.084	-0.236	0.173	0.145	-0.006	0.282	-0.020	0.422**
X ₇	-0.139	-0.293	0.362	0.315	-0.010	0.101	-0.055	0.559**

Residual effect = 0.364, *Significant at p = 0.05, ** significant at p = 0.01

X₁ = Ascorbic acid (mg/100g), X₂ = Total carotenoids (µg/100g), X₃ = Sulphur (mg/100g), X₄ = Iron (mg/100g)

X₅ = Potassium (mg/100g), X₆ = Zinc (mg/100g), X₇ = Calcium (mg/100g)

Green hypocotyl in cauliflower (*Brassica oleracea* var. *botrytis* L.): Inheritance and use in hybrid breeding

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Abstract

Morphological markers are useful in identifying associated traits in advance. In snowball cauliflower, the hypocotyls color is generally purple. Development of SI line with green hypocotyls would be useful in differentiating sibs from the hybrid seedlings in the nursery stage. We have developed one SI line, Kt-32gh with green hypocotyls. In studying the heritability, it was found that single recessive gene controls the green pigmentation in hypocotyls. However, modifier genes play significant role in determining extent of purple pigmentation. This line may be used as parent in the development of SI based F₁ hybrids in snowball cauliflower.

Introduction

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is a major vegetable crop cultivated through out the world. Presently, most of the cultivated area under cauliflower is occupied by F₁ hybrids. Two important pollination control mechanisms viz. self-incompatibility (SI) and cytoplasmic male sterility (CMS) are used for hybrid seed production of cole crops. However, SI is the most widely used system (Wanatabe and Hinata, 1999). The best studied mechanisms of SI act by inhibiting the germination of pollen on stigmas, or the elongation of the pollen tube in the styles. These mechanisms are based on protein-protein interactions, each mechanism being controlled by a single locus termed 'S', which has many different alleles in the species population. The SI system is very weak to strong in various vegetable Brassicas. However, the strength is determined by the nature of particular S locus. Molecular analysis of the S-locus region shows that this locus is a complex locus spanning many kilobases and containing several physically linked transcriptional units that co-segregate perfectly with SI phenotype (Boyes et al., 1997, Casselman et al., 2000).

Among the cole crops, SI system is weak in snowball cauliflower. Moreover, SI system is not stable under high temperature conditions and resulted into 'sibs' in the production of F₁ hybrid seeds. It is not possible to differentiate the sib seeds from F₁ hybrids. Thus, it resulted into low uniformity in F₁ population in the field, which is highly undesirable. But it is possible to identify sibs in the seedling stage itself if any morphological marker is available at this stage. Thus, only F₁ hybrids would be transplanted in the field after elimination of sibs in the nursery itself. It would also be useful in determining the stability of SI system in the parents used for the production of F₁ hybrid seeds. The hypocotyl color in cauliflower is generally purple because of anthocyanin accumulation. Hypocotyl color can be determined through visual observation after 4-7 days of seed germination. Green hypocotyl may be resulted through blockage in anthocyanin synthesis pathway and

most probably due to gene mutation. The present study involved determination of inheritance pattern of green hypocotyl and its incorporation in SI genotypes of cauliflower. So, the developed genotypes would be useful as a parent in the production of F₁ hybrid seeds.

Materials and Methods

Development of SI lines of Kt-32gh: Cauliflower line with green hypocotyls Kt-32gh was taken for the study. It was selfed for three generations to determine any segregation for this trait. After two generations of selfing few plants were identified with strong self-incompatibility and green hypocotyl. They were maintained through bud pollination. The level of self incompatibility was determined through estimation of fertility index (Watts, 1965). For selfing the plants were covered individually with muslin cloth selfing bag. Few plants were also kept in the open with out any cover to record seed set under natural condition.

Inheritance of green hypocotyl: The genotype, Kt-32gh with green hypocotyl was crossed with cauliflower inbred, PHJ with dark purple hypocotyl to produce F₁ hybrids. Reciprocal crosses were also made to determine any cytoplasmic inheritance of hypocotyl color. Both the inbreds were selfed through bud pollination for maintenance. In the next season, 50 F₁ plants of reciprocals were studied. Hypocotyls color was recorded in the seedling stage (7 days of seed germination). One F₁ plant (Kt-32gh × PHJ) was selfed by collecting pollen from the same plant through bud pollination to develop F₂ population. The same plant was pollinated by collecting pollen from Kt-32gh to develop test cross populations. The F₂ and testcross populations were studied for hypocotyl colour in the next season to determine inheritance pattern of green hypocotyl in cauliflower.

Results and Discussion

Seeds of parental lines, Kt-32gh and PHJ, the F₁, the F₂ and testcross populations were sown in the pots in open condition. All the F₁ seedlings had purple hypocotyl. There was no difference in hypocotyl color in the reciprocal crosses. However, segregation for hypocotyl color was recorded in the F₂ and test-cross populations (Table 1). The F₂ progenies, derived from selfing of two F₁ plants had 238 and 266 plants, respectively. These two F₂ progenies segregated in a ratio of 169 purple: 69 green and 189 purple: 77 green hypocotyls, respectively. The test-cross progenies derived from two plants had 134 and 121 plants, respectively. The test cross progenies segregated in 74 purple: 60 green and 66 purple: 55 green hypocotyls, respectively. The F₂ progeny was pooled, and the segregation ratio showed a good fit to a 3 purple: 1 green colored hypocotyls. The expected ratio of the testcross would be 1 purple: 1 green, and the results of the chi-square analysis indicated a good fit to a 1:1 ratio.

The F₂ and test cross data revealed that in the line Kt-32gh line of snowball cauliflower the green colored hypocotyls is under the control of a single recessive gene. The intensity of purple pigmentation varied in the F₂ and test cross progenies. This indicated though the green color hypocotyl is controlled by a major recessive gene, the developments of purple pigmentation in the hypocotyls were influenced by modifier genes. This study was in agreement with the gene list of brassicas (Wills, 1977). Pigmentation genes can be used as markers to facilitate the recognition of plants, homozygous for S alleles. Such plants are necessary in kale breeding for the production of 100 per cent hybrid seed (Thompson and Taylor, 1965).

The fertility index in the line Kt-32gh was 2.2 indicating few lines with green hypocotyls with homozygous 'S' locus were identified. Thus, this line can be used in the development of F₁ hybrids utilizing SI system. Any sibs occurred in the line during the production of F₁ hybrids can be detected in the nursery stage if the other parents of the hybrid have purple hypocotyls. Thus, green hypocotyl in the line Kt-32gh can be used as morphological marker for determining purity in F₁ seeds developed through SI system. The line can be used as both male and female parent when both the parental lines are self incompatible and can be used as female parent when the pollen parent is self-compatible.

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- Table 1. Chi square (χ^2) analysis for goodness of fit of F₂ (3:1) and test cross (1:1) population ratio for inheritance of green colored hypocotyl

Table 1. Chi square (χ^2) analysis for goodness of fit of F₂ (3:1) and test cross (1:1) population ratio for inheritance of green colored hypocotyl

Generation	Observed ratio (Purple:Green)	Expected ratio (Purple:Green)	χ^2	P Value
F ₂ (Plant#1)	169:69	3:1	2.06	0.1-0.2
F ₂ (Plant#2)	189:77	3:1	2.20	0.1-0.2
F ₂ (Pooled)	358:146	3:1	4.22	0.02-0.05
Test cross (Plant#1)	74:60	1:1	1.46	0.2-0.3
Test cross (Plant#2)	66:55	1:1	1.00	0.3-0.5
Test cross (Pooled)	140:115	1:1	2.44	0.1-0.2

Development of yellow seeded *Brassica rapa* L. through intervarietal hybridization

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Abstract

An experiment was conducted during the winter seasons of 2006-08 at Department of Applied Plant Science. The brown sarson (*Brassica rapa* L. ssp. brown sarson) has low oil content due to thick seed coat. Intervarietal hybridization was successfully attempted to develop yellow seeded brown sarson with oil content 43.4% as compared to 39.95 % in the check, thus recording a significant increase of 8.6% increase in the oil content over the standard check.

Keywords

Brown sarson, Intervarietal hybridization, oil content

Introduction

Annually about 64 thousand hacteres are planted to oilseed crop in Jammu and Kashmir (India) with a total oilseed production of 53.5 thousand quintals and productivity level of 8.45 q/ha (Table 1). Brown sarson (*Brassica rapa* L. ssp. brown sarson) is a major oilseed crop of Kashmir valley which is grown in *rabi* season and covers an area of more than 47 thousand ha. (Anonymous, 2008) .This is the only crop of the rapeseed-mustard group which fits well in the prevalent Rice –Oilseed rotation. The existing varieties of brown sarson have low oil content due to thick seed coat. As yellow seeded forms in *Brassica* spp. have higher seed oil and protein and lower fibre contents than black seeded ones. Hence attempt was made to develop brown sarson with yellow seed coat to increase the oil content in the existing elite lines of brown sarson.

Materials and Methods

Intervarietal hybridization using varieties viz., BS3 (brown sarson) and Kosec-18 (yellow sarson) was attempted. The selection up to F₅ generation resulted in the development of six stabilized yellow seeded brown sarson populations, morphologically similar to brown sarson except for seed coat colour. These lines have been selected for evaluation against standard check, KS101 for yield and oil content during *rabi* 2008-09.

Results and Discussion

In the present study, genes for yellow seed coat were successfully transferred from A genome of yellow sarson to A genome of brown sarson resulting in the development of five stable yellow seeded brown sarson populations. The results revealed the significant differences among the yellow seeded lines for yield and oil

content against the check (Table 2). Maximum seed yield of 11.0 q/ha was recorded for YBS-2 which was 12.35% more than the standard check (9.79 q/ha). The oil content was 43.4% in YBS-2 as compared to 39.95 % in Gulchin, thus recording a significant increase of 8.6% increase in the oil content over the standard check (Gulchin). These yellow seeded lines also had morphological and maturity traits almost akin to brown sarson. Yellow seeded *Brassica napus* (AACC) was developed through interspecific crosses between *B. napus* with yellow seeded *B. juncea* (AABB) and *B. carinata* (BCC) in order to introgress genes for yellow seed colour from A genome of *B. juncea* and C genome of *B. carinata* into A and C genomes of *B. napus*, respectively (Rashid et al. 1994). Yellow sarson was also successfully used in the introgression of yellow seed colour to black seeded *B. napus* (Rahman 2001).

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Table 1. Area, production and productivity of oilseed in J&K State during 2004-05 to 2007-08

Year	Area (000 ha)	Production (000 q)	Average yield (q/ha)
2004-05	64.49	407	6.31
2005-06	63.01	366	5.8
2006-07	64.30	413	6.42
2007-08	63.27	535	8.45

Table 2. Seed yield (q/ha) of yellow seeded brown sarson populations

Entry	Mean seed yield (q/ha)	Oil content (%)	1000 seed weight
YBS-1	7.90	43.7	4.0
YBS-2	11.00	43.4	3.8
YBS-3	7.56	42.2	3.5
YBS-4	8.86	41.9	3.4
YBS-5	7.75	41.5	3.7
Gulchin (Check)	9.79	39.95	2.5
MEAN	8.81		
SE	0.40		
CD (P<0.05)	0.80		
CV (%)	5.45		

Analysis of generation means for yield and its components traits in rapeseed (*B. napus* L.)

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Abstract

Generation mean analysis involving six generations of each of the three crosses done from four genetically diverse parents, was used to elucidate the inheritance of seed yield and its components in rapeseed. Both, additive and non-additive gene action was involved in the inheritance of most of the traits, however, the relative contributions of dominance gene effects was higher than the additive gene effects in almost all the three crosses for most of the traits. Duplicate type of gene action was involved in the expression of the traits except for days to bloom, no. of silique per plant, seed yield per plant and harvest index (%) in cross BCN-14 X DGS-1, for 1000-seed weight and no. of silique per plant in BCN-14 X GSC-3A and for 1000-seed weight in cross NUDB-09 X DGS-1. The potence ratio of more than unity and significant estimate of heterosis was observed for majority of traits in the material. These observations imply the importance of biparental mating pattern or reciprocal recurrent selection so as to take care of both components of variation for improvement of the crop.

Keywords

Brassica napus; generation mean; scaling tests; six parameter model.

Introduction

B. napus commonly grown in Europe and receiving greater attention in Northern India because of its high productivity and resistance to insects and pests. The improvement potential may be limited because of limited genetic variability in this crop. *B. napus* will provide a new oiliferous crop and may replace traditionally grown oilseed crops in Jammu and Kashmir which are commonly *B. juncea* and *B. campestris* var brown sarson. In this investigation diverse genetic materials collected from different sites were put into hybridisation program for developing superior F1 hybrids and building genotypes to be used in breeding program. Knowledge about the nature of gene effects and components of genetic variance helps in evolving effective breeding strategies for improving the available germplasm. The present investigation have been carried out to estimate the types of gene effects and their magnitudes for seed traits and some other characters for their further utilization in breeding programmes.

Materials and Methods

The present study was conducted in the Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu. The experimental material consisted of three crosses viz., BCN-14 x DGS-1, BCN-14 x GSC-3A and NUDB-09 x DGS-1 involving four parents namely BCN-14, DGS-1, GSC-3A and NUDB-09 chosen primarily on the basis of their genetic diversity for different agronomic and yield traits. Due to self pollinating nature of the crop either because of its amphidiploidy or other sort of genetic phenomena, inbreeding coefficient approaches unity ($F=1$). The F1 crosses made during rabi 2004-2005 at the experimental farm of the Division of Plant Breeding and Genetics, Chatha were advanced to the F2 generations as well as BC1 and BC2 in order to constitute a complete set of six basic generations, viz., P1, P2, F1, F2, BC1, BC2. The F1 generation was generated by hand emasculation of randomly selected plants from two parental strains (P1 & P2) grown in cages. In the next generation F1 plants grown under controlled conditions and F2 seed was developed. Subsequently F1 plants were backcrossed in the same generation to both of the parents to generate BC1 and BC2.

These six basic generations were sown for evaluation in a randomized complete block design with three replications during *rabi* 2005-2006 at main campus Chatha. In each replication, parents, F1s and backcrosses were grown in single row, while F2 were in three rows. Ten competitive, representative plants were selected in each generation except in F2 in which 25 plants were selected. The row to row and plant to plant distances were 45 cm and 15 cm, respectively. Recommended agronomic practices were utilized on the crop. The data was recorded on the nine traits; number of days to bloom (on plot basis), number of primary branches, number of secondary branches, pod length (cm), number of seeds/silique, 1000 seed weight (g), number of silique/plant, seed yield/plant (g) and harvest index (%). The gene effects were estimated from the six generations of a cross according to the procedure outlined by Mather and Jinks (1982). The three parameters model was fitted (m, d and h) and then tested for non-allelic interaction by individual scaling tests of Mather (1949) and by Joint scaling test of Cavalli (1952).

Results and Discussion

Analysis of variance indicated highly significant differences ($P<0.01$) for all traits. Among different generations within the cross, mean sum of squares were again significant for all of the three crosses for all the characters under present investigation (Table 1).

The basic set of six generations means for the three crosses were employed to estimate various genetic effects for seed yield and other important characters. Mather's A, B and C scaling tests as well as joint scaling tests showed that simple additive-dominance model was inadequate in all the three crosses for all the characters (Table 2) except A scale for harvest index and seed yield per plant in case of cross BCN-14 x DGS-1 and C scale for number of seeds/silique for cross combination NUDB-09 x DGS-1. Thus the significance of scaling test and joint scaling tests indicated the failure of the simple additive dominance model in all three crosses for majority of the characters under study indicating that the genetic variance cannot be ascribed wholly to the additive and dominance gene effects. The significance of the scaling tests also revealed the failure of non-epistatic model in all three crosses for nearly all characters. This failure of simple additive dominance model can be attributed to the presence of epistasis and thus the assumption of no epistasis was biologically unrealistic for the polygenic traits such as seed yield.

Due to failure of non-epistatic model, six parameters viz., m, (d), (h), (i) (j) and (l) were estimated from the six basic generations i.e., P1, P2, F1, F2, BC1 and BC2 (Table 3). The additive gene effects were significant for all characters in all of the three crosses except for number of secondary branches in crosses BCN-14 x DGS-1 and BCN-14 x GSC-3A, days to bloom and pod length in cross BCN-14 x DGS-1, and number of primary branches in cross NUDB-09 x DGS-1. These results confirm the earlier results of Singh and Srivastava (1999) who reported the preponderance of additive gene effects for primary branches, silique length, seeds/silique and seed yield per plant in Indian mustard (*B. juncea*). Malik et al. (1995) recorded the preponderance of

additive gene effects for number of primary and secondary branches and number of silique on the main shoot in *B. napus*. Pathak *et al.* (2002) reported the role of additive gene action for days to 50% flowering, seeds/silique, branches and plant height. The dominance effects (h) were significant in all three crosses for all the characters. Lakshmi Kant and Gulati (2001) observed dominance gene effects for days to maturity, seed yield per plant and oil content in Indian mustard. Chatterjee and Bhattacharya (1986) recorded dominance gene effects for early flowering and maturity in rapeseed (*B. napus* L.). Some other research has indicated the importance of both additive and dominance gene effects in the inheritance of some agronomic traits in *Brassica napus* (Indu Varsha *et al.*, 1991; Thakur and Sagwal, 1997), which is in close agreement with the present findings. It was also observed that the relative contribution of dominance gene effects was higher than the additive gene effects in all three crosses for most characters.

Based on the 6-parameter model, the three epistatic components were found to be significant for almost all the characters in three the crosses. However, the type and magnitude of the three epistatic effects varied from cross to cross. For example additive x additive component (i) was non-significant for cross combinations BCN-14 x DGS-1 and NUDB-09 DGS-1 for pod length and number of seeds/silique. Similarly additive x dominance components (j) was non-significant for pod length and 1000 seed weight in cross BCN-14 x DGS-1. The dominance (h) and dominance x dominance (i) gene effects were of opposite sign in many characters in the three crosses, thus revealing the duplicate type of epistasis (D) except for days to bloom, number of silique/plant, seed yield per plant and harvest index in cross BCN14 x DGS-1 and 1000 seed weight, number of silique per plant and harvest index in cross BCN-14 x DGS-1 thus revealing the importance of all the three types of interactions in two of the three crosses while, in cross NUDB-09 x DGS-1, additive x dominance (j) and dominance x dominance (l) effects were equally important and the additive x additive (i) effects were less important for this cross. Indu Varsha *et al.* (1999) demonstrated non allelic interaction for seed yield and plant height in *B. napus*. Similarly, the evidence of epistasis was found in Indian mustard by Singh and Srivastava (1999) for silique/main receme, 1000 seed weight, secondary branches/plant, seed/silique and seed yield per plant and by Thakral *et al.*, (2000) for length of main shoot and 1000 seed weight. Duplicate type of epistasis has also been reported by Rishipal *et al.* (1993) for many seed traits and by Indu Varsha *et al.* (1999) in the inheritance of seed yield.

The Table 3 also revealed the potence ratio of more than unity for all the characters in the crosses BCN-14 x GSC-3A and NUDB-09 x DGS-1 except for number of secondary branches in former and number of primary branches in latter. However, in cross BCN-14 x DGS-1 the potence ratio of less than one was observed for number of primary and secondary branches, pod length and number of silique per plant. The estimates of potence ratio are reliable only when the genes of like effects are completely associated in parental lines and when all (h) components have the same sign (unidirectional dominance) at all the loci. The potence ratio may be overestimated when (d) component is underestimated due to the dispersion of genes in the parents.

A significant and positive estimate of heterosis was observed for all three crosses for seed yield per plant which was also associated with high inbreeding depression in the F2 generation for the trait. Significant heterosis was also observed for number of primary and secondary branches and harvest index in all the three crosses. Significant heterosis was also observed for the number of silique/plant except for the cross NUDB-09 x DGS-1. Inbreeding depression was found significant for number of secondary branches and harvest index for all the three crosses. For the remaining characters inbreeding depression was either negligible or significant in one or the other cross.

The results further elucidated that high heterotic effects in the F1 generations for the various characters were not always associated with high inbreeding depression in the F2 generations. This suggests the importance of non-allelic interaction in the manifestation of the heterosis in crosses.

The information to define a proper breeding methodology depends on nature and magnitude of gene effects. The present study of generation mean analysis revealed that both additive as well as non-additive genetic effects are important in the inheritance of most of the seed character. However, non-additive gene effects have

been found to be more important than additive effects for almost all the characters in the present experimental material. *B. napus* a self pollinated crop. The genetic variability resulting from dominance, additive or both types of gene actions can be effectively utilized by hybridization, selection programmes or by selection programmes that such programmes exploit both additive and dominance components, such as reciprocal recurrent selection.

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Table 1. Analysis of variance for maturity, morphological, yield and yield attributing traits among different generations within crosses in *B. napus*.

Cross		Mean sum of squares								
		No. of days to bloom	No. of primary branches	No. of secondary branches	Pod length (cm)	No. of seeds/silique	1000 seed weight (g)	No of silique per plant	Seed yield per plant (g)	Harvest index (%)
BCN-14 x	Rep	0.383	0.000	0.145	0.001	0.001	0.00004	121.211	0.026	0.077
DGS-1	Gen	618.33**	10.38**	50.222**	0.966**	14.075**	0.0194**	151477.95**	6.210**	22.978**
	Error	0.322	0.091	0.041	0.00027	0.001	0.00005	12106	0.012	0.001
BCN-14 x	Rep	0.256	0.03	0.018	0.000	0.000	0.0002	0.437	0.121	0.187
GSC-3A	Gen	55.065**	21.949**	26.833**	1.283**	9.907**	0.278**	256031.80**	7.162**	18.083**
	Error	0.552	0.049	0.064	0.00054	0.002	0.0007	0.538	0.02	0.026
NUDB-09 x	Rep	0.200	0.121	0.061	0.001	20.457	0.00004	222.289	0.019	0.013
DGS-1	Gen	273.458**	2.789**	47.416**	1.077**	32.563**	0.17**	68306.003**	33.372**	154.18**
	Error	0.914	0.050	0.169	0.00038	20.528	0.0001	222.557	0.01	0.015

Table 2. Estimates of genetic components based on generation means (Three parameters model weight) and different scaling test for maturity, morphological, yield and yield attributing traits in *B. napus*

Types of gene effect and scaling test	No. of days to bloom	No. of primary branches	No. of secondary branches	Pod length (cm)	No. of seeds/silique	1000 seed weight (g)	No of siliquae per plant	Seed yield per plant (g)	Harvest index (%)
BCN-14 x DGS-1									
M	65.301 ± 0.02	11.00 ± 0.02	18.07 ± 0.01	6.01 ± 0.002	19.15 ± 0.003	5.37 ± 0.0001	783.26 ± 0.04	27.034 ± 0.01	14.61 ± 0.01
D	2.59 ± 0.02**	-1.36 ± 0.002**	-3.12 ± 0.01**	-0.48 ± 0.002**	-2.82 ± 0.003**	0.05 ± 0.001**	160.38 ± 0.04**	-0.42 ± 0.001**	2.65 ± 0.01**
H	12.7 ± 0.03**	-1.56 ± 0.04**	-3.4 ± 0.03**	0.17 ± 0.004**	1.84 ± 0.005**	0.18 ± 0.01**	-238.26 ± 0.05**	3.63 ± 0.014**	1.82 ± 0.02**
Scaling test									
A	-62.77 ± 0.111**	-6.80 ± 0.07**	-5.06 ± 0.09**	-0.46 ± 0.006**	-4.11 ± 0.01**	-0.14 ± 0.002**	-589.5 ± 0.16**	0.003 ± 0.045	5.88 ± 0.03**
B	19.37 ± 0.013**	2.651 ± 0.10**	-9.25 ± 0.11**	-2.00 ± 0.007**	-9.01 ± 0.007**	-0.15 ± 0.002**	835.47 ± 0.29**	-1.98 ± 0.021**	-6.76 ± 0.03**

C	-17.53 ± 0.48**	-6.83 ± 0.14**	14.64 ± 0.12**	1.36 ± 0.013**	-9.38 ± 0.01**	-0.07 ± 0.003**	324.13 ± 10.22**	-2.36 ± 0.064**	-9.27 ± 0.06**
Joint scaling test	346527.80**	10604.78**	51442.24**	198214.1**	2039184.00**	8722.02**	21775750.00**	10686.40**	141774.00**
BCN-14 x GSC-3A									
M	78.31 ± 0.02	13.09 ± 0.01	12.72 ± 0.02	5.90 ± 0.001	12.82 ± 0.002	5.32 ± 0.001	410.61 ± 0.06	24.42 ± 0.016	14.33 ± 0.01
D	-3.18 ± 0.03**	0.87 ± 0.01**	0.50 ± 0.01**	-0.45 ± 0.001**	0.03 ± 0.002**	-0.02 ± 0.001**	408.62 ± 0.06**	-2.30 ± 0.016**	-0.30 ± 0.01**
H	-4.22 ± 0.004**	-5.00 ± 0.02**	-2.34 ± 0.04**	1.50 ± 0.001**	5.12 ± 0.002**	0.64 ± 0.001**	-3.37 ± 0.10**	8.005 ± 0.026**	-2.37 ± 0.03**
Scaling test									
A	18.79 ± 0.11**	-5.95 ± 0.04**	-12.6 ± 0.06**	0.36 ± 0.01**	0.30 ± 0.003**	-0.85 ± 0.002**	-8.4722 ± 0.18**	-20.057 ± 0.089**	-10.53 ± 0.08**
B	3.86 ± 0.11**	10.27 ± 0.05**	-11.67 ± 0.06**	-0.18 ± 0.008**	-2.06 ± 0.008**	-0.76 ± 0.003**	-484.50 ± 0.25**	-4.347 ± 0.38**	-4.52 ± 0.09**
C	28.89 ± 0.61**	-3.43 ± 0.17**	-15.1 ± 0.16**	-0.12 ± 0.01**	-6.61 ± 0.008**	-1.40 ± 0.004**	-861.18 ± 0.35**	-28.803 ± 0.11*	-17.02 ± 0.14**
Joint scaling test	5148.60**	83106.88**	46347.14**	16330.36**	885795.30**	23784.60**	23376720.00**	91311.33**	2037.67**
NUDB-09 x DGS-1									
M	74.69 ± 0.01	9.06 ± 0.02	12.555 ± 0.01	6.36 ± 0.002	22.23 ± 0.01	5.22 ± 0.001	56775 ± 0.02	27.94 ± 0.003	20.09 ± 0.01
D	-9.55 ± 0.01**	0.24 ± 0.02**	2.93 ± 0.01**	-0.41 ± 0.002**	-1.38 ± 0.001**	-0.01 ± 0.001	7.84 ± 0.01**	1.41 ± 0.003**	5.97 ± 0.01**
H	1.93 ± 0.03**	-1.60 ± 0.03**	-2.78 ± 0.01**	0.84 ± 0.004**	-0.65 ± 0.003	0.56 ± 0.001**	-366.2 ± 0.03**	516 ± 0.012**	-7.99 ± 0.11**
Scaling test									
A	-6.32 ± 0.11**	-1.22 ± 0.08**	-5.41 ± 0.06**	-1.41 ± 0.009**	4.54 ± 0.168**	0.57 ± 0.004**	296.39 ± 0.13**	-8.75 ± 0.064**	-6.74 ± 0.05**
B	-21.13 ± 0.06**	-3.16 ± 0.12**	7.97 ± 0.11**	-1.60 ± 0.009**	-3.84 ± 0.004**	-0.93 ± 0.0034**	-6.36 ± 0.07**	-4.11 ± 0.026**	-20.59 ± 0.01**
C	24.45 ± 0.25**	-7.11 ± 0.11**	6.01 ± 0.11**	-2.86 ± 0.01**	-2.66 ± 1.68	-1.49 ± 0.004**	781.24 ± 13.87**	-9.39 ± 0.102**	-45.76 ± 0.06**
Joint scaling test	1470.340**	3738.32**	13924.14**	867.45.98**	2328552.00**	27718.34**	5123690.00**	34829.31**	2248463**

*, **, significant at 5 and 1% level respectively

Table 3. Estimates of genetic components based on generation means (six parameters model) potence ratio heterosis and inbreeding depression for maturity, morphological, yield and yield attributing traits in B. napus

Parameters	No. of days to bloom	No. of primary branches	No. of secondary branches	Pod length (cm)	No. of seeds/silique	1000 seed weight (g)	No of silique per plant	Seed yield per plant (g)	Harvest index (%)
Cross BCN-14 x DGS-1									
M	39.24 ± 0.50	10.17 ± 0.14	46.67 ± 0.01	9.93 ± 0.00	23.63 ± 0.01	5.62 ± 0.003	856.34 ± 10.22	26.73 ± 0.06	12.79 ± 0.07
D	6.07 ± 0.00	1.33 ± 0.03**	-2.95 ± 0.00	-0.62 ± 0.00	-1.89 ± 0.007**	0.04 ± 0.001**	222.39 ± 0.04**	-0.43 ± 0.01**	-0.51 ± 0.01**
H	27.12 ± 1.07**	-1.10 ± 0.36**	-78.23 ± 0.05**	-9.66 ± 0.02**	-16.52 ± 0.03**	-0.54 ± 0.009**	-129.13 ± 20.46**	2.60 ± 0.14**	6.38 ± 0.15**
I	28.12 ± 0.50**	2.68 ± 0.14**	-28.96 ± 0.15**	-3.8 ± 0.00	-3.24 ± 0.01**	-0.22 ± 0.03**	-78.51 ± 10.22**	0.38 ± 0.05**	4.39 ± 0.05**
J	82.15 ± 0.17**	-9.45 ± 0.11**	4.18 ± 0.01**	1.54 ± 0.00	4.90 ± 0.01**	0.003 ± 0.003	-1425.32 ± 0.033**	1.99 ± 0.048**	16.64 ± 0.05**
L	15.27 ± 0.58 **	1.46 ± 0.24**	43.28 ± 0.27**	6.30 ± 0.01**	16.36 ± 0.02**	0.51 ± 0.006**	-167.10 ± 10.24	1.60 ± 0.08**	0.49 ± 0.10**
Type of epistasis	C	D	D	D	D	D	C	C	C
Potence ratio	4.46	0.82	-	-	8.74	13.0	0.58	6.04	12.50 **
Heterosis over better parent	0.111 ± 0.04**	-0.25 ± 0.06**	0.19 ± 0.05**	-0.02 ± 0.00	0.05 ± 0.00	0.02 ± 0.00	-0.44 ± 0.06**	0.160 ± 0.01**	0.20 ± 0.02**
Inbreeding depression	0.300 ± 0.12	0.05 ± 0.04	0.56 ± 0.05**	-0.1 ± 0.0000	0.17 ± 0.000	0.02 ± 0.00	-0.33 ± 2.55	0.081 ± 0.01**	0.19 ± 0.02**
Cross BCN-14 x GSC-3A									
M	83.34 ± 0.62	4.01 ± 0.17	23.68 ± 0.14	5.61 ± 0.01	15.26 ± 0.00	5.65 ± 0.005	1117.47 ± 0.32	22.33 ± 0.13	12.79 ± 0.12
D	-3.39 ± 0.03**	2.27 ± 0.01**	0.13 ± 0.23	-0.46 ± 0.001**	-1.64 ± 0.003**	0.01 ± 0.001	353.73 ± 0.11*	-0.172 ± 0.01**	0.05 ± 0.01**
H	5.40 ± 1.27**	16.68 ± 0.36**	-39.41 ± 0.32**	2.32 ± 0.04**	11.81 ± 0.03**	-1.30 ± 0.013**	-2376.9 ± 0.8**	-6.145 ± 0.32**	-7.40 ± 0.32 **
I	-6.23 ± 0.62	7.76 ± 0.17**	-9.05 ± 0.14**	0.30 ± 0.01**	4.85 ± 0.008**	-0.21 ± 0.005	-47.0.54 ± 0.13**	4.40 ± 0.12**	1.96 ± 0.12**
J	14.93 ± 0.14**	-16.22 ± 0.05**	-1.02 ± 0.008**	0.55 ± 0.01**	2.36 ± 0.008**	-0.09 ± 0.004**	-362.71 ± 0.03**	-15.71 ± 0.09**	-6.00 ± 0.09**
L	-16.4 ± 0.66**	-12.08 ± 0.20**	-33.42 ± 0.70**	-0.48 ± 0.03**	-3.09 ± 0.014**	1.83 ± 0.008	1802.27 ± 0.52**	20.00 ± 0.20**	13.081 ± 0.23**
Type of epi	D	D	D	D	D	C	C	D	D
Potence ratio	1.592	7.34	-	5.04	7.20	5.83	13.0	6.71	
Heterosis own matter parent	-0.018 ± 0.15	-0.38 ± 0.03**	0.19 ± 0.005**	1.69 ± 0.00	0.10 ± 0.00	0.101 ± 0.03**	0.13 ± 0.00	-0.45 ± 0.10**	
Inbreeding depression	-0.132 ± 0.15	-0.08 ± 0.05	0.30 ± 0.05**	0.10 ± 0.00	0.14 ± 0.00	0.14 ± 0.075**	0.11 ± 0.00	0.30 ± 0.08**	
Cross NUDB-09 x DGS-1									
M	129.50 ± 0.27	7.42 ± 0.15	18.46 ± 0.03	6.81 ± 0.014	16.10 ± 0.84	5.34 ± 0.003	1053.12 ± 1387	31.4 ± 0.11	
D	-12.62 ± 0.02**	-0.01 ± 0.02	5.46 ± 0.03**	-0.41 ± 0.002**	-4.51 ± 0.84**	0.09 ± 0.01**	-11.21 ± 0.04**	1.43 ± 0.004**	
H	-128.62 ± 0.6**	-1.35 ± 0.43**	-9.545 ± 0.68**	-2.12 ± 0.031**	11.72 ± 2.52**	1.05 ± 0.03**	-1039 ± 27.74**	-7.40 ± 0.30**	

I	$-51.90 \pm 0.27^{**}$	$2.22 \pm 0.15^{**}$	$-3.46 \pm 0.31^{**}$	$-0.15 \pm 0.014^{**}$	3.36 ± 0.00	$0.64 \pm 0.02^{**}$	$-491.22 \pm 13.87^{**}$	$1.96 \pm 0.12^{**}$	
J	$1480 \pm 0.12^{**}$	$1.43 \pm 0.13^{**}$	$-13.38 \pm 0.13^{**}$	$0.19 \pm 0.012^{**}$	$8.39 \pm 1.68^{**}$	$-0.07 \pm 0.006^{**}$	$302.75 \pm 0.14^{**}$	$-6.00 \pm 0.09^{**}$	
L	$79.36 \pm 0.34^{**}$	$2.67 \pm 0.28^{**}$	$0.90 \pm 0.37^{**}$	$3.17 \pm 0.025^{**}$	$-4.05 \pm 1.68^{**}$	$0.09 \pm 0.02^{**}$	$201.19 \pm 13.87^{**}$	13.08 ± 0.23	
Type of epistasis	D	D	D	D	D	C	D	D	
Potence ratio	10.19	-	1.74	5.10	2.59	11.6	94.47	148.00	
Heterosis over better parent	0.234 ± 0.30	$-0.09 \pm 0.004^*$	$-0.52 \pm 0.06^{**}$	0.10 ± 0.00	0.00 ± 0.00	0.07 ± 0.00	-0.65 ± 0.070	$0.24 \pm 0.06^{**}$	
Inbreeding depression	-0.059 ± 0.06	$0.15 \pm 0.04^{**}$	$-0.41 \pm 0.07^{**}$	0.16 ± 0.00	0.11 ± 0.000	0.10 ± 0.00	-1.93 ± 3.46	$0.33 \pm 0.06^{**}$	

*, ** significant at 5 and 1% level respectively

Extent of natural outcrossing in Indian mustard (*Brassica juncea* L. Czern & Coss)

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Abstract

Extent of outcrossing was studied in Indian mustard (*B. juncea*) using two morphological markers; glossiness of stem and leaves and petal colour. The extent of outcrossing was found higher when studied using glossiness marker than that estimated using the petal colour. The range of outcrossing on individual plant basis was high; hence the population improvement strategy may be followed.

Keywords

Outcrossing, glossiness, petal colour, Indian mustard

Introduction

The breeding methods for the improvement of a crop are determined on the basis of its mating system. Indian mustard, a predominant oilseed crop of Indian subcontinent is considered as a self pollinated crop; hence pureline and pedigree methods of selection have widely been employed in the varietal development of this crop. Studies on extent of out crossing has recently gained importance in this crop to study the rate of gene flow from genetically modified (GM) to non genetically modified crops (Funk, 2006) and the seed production studies of hybrids where high rate of outcrossing is desired. The main objective of this study was to determine the extent of outcrossing in Indian mustard from near neighbourhood.

Materials and Methods

Plants with two distinct classes of phenotypic markers; glossy and non-glossy type appearance of plants (marker 1) and yellow and white petal colour (marker 2) were used in this investigation to ascertain the extent of natural outcrossing. Glossiness appears due to spontaneous mutation. It is characterized by bright green and shining leaves and stem. This trait is visible from vegetative stage. White petal flowers in mustard are often observed. Plants with recessive phenotypes; non glossy (marker 1), white petal (marker 2) were planted in between the plants with dominant phenotypes of respective markers (glossy, yellow petal) in different isolated plots of 5 m length to ensure that plants with recessive phenotypes non-glossy, white petals were surrounded from all sides by respective dominant phenotype (glossy, yellow petal) plants in vicinity for two years during 2006-07 and 2007-08. Open pollinated seeds from plants with non-glossy, white flower plants were harvested on single plant basis from each plot and their progenies were grown during 2008-09. The glossy/non-glossy in progenies of first plot and yellow/white petal plants in second plot were counted to assess the outcrossing rate.

The frequency of outcrossing was estimated in percent on the basis of number of glossy type plants in marker 1 and white petal plants in marker 2 considering the non-glossy and white petal (recessive genotypes) as the result of selfing and glossy and yellow petal as the result of outcrossing.

Results and Discussion

Extent of outcrossing estimated by using the glossiness marker is presented in table 1. A total of 896 plants from the progenies of 20 plants were observed of which 248 were glossy type and 648 were non-glossy. The average outcrossing extent was 27.7 % with a range of 12.5 to 46.2 % on the basis of single plant progeny. In the second year a total of 937 plants were observed of which 273 were glossy and remaining 664 plants were non-glossy. The average outcrossing extent estimated to be 29.1 % with a range of 7.1 to 47.1 %. In petal colour, the seeds harvested from white petal plants were grown in plant to progeny rows and yellow petal plants were counted. As presented in table 2, out of 5583 plants, 1128 had yellow petals in the year 2006-07. The average outcrossing extent was 20 % with a range on single plant basis from 11.4 to 42.9 %. In the year 2007-08, 999 plants had yellow petals out of 4199 plants thus the average outcrossing extent was 24 % with a range of 14.3 to 58.1 % on single plant basis.

In Brassica pollen movement occurs by wind as well as by insects. Wind transferred pollen has been detected upto 1.5 km from the source plant (Timmons et al. 1995). In low temperature and high humidity conditions, pollen may survive 4 or 5 days but in warm and low humidity conditions survival time may drop to 1 or 2 days (Myers, 2006). The earlier reports about the extent of outcrossing vary from 7.6 to 18.1 % (Labana and Banga 1984), 14 % (Howard et al. 1915), 11.94 to 24.0 % (Chauhan et al. 1987), 16.6 % (Ram Bhajan et al. 1991), 6.5 to 9.8 % (Abraham, 1994). Various markers flower colour (Abraham, 1994), seed coat colour (Chauhan et al. 1986; 1987) and erucic acid have been used for estimating the outcrossing extent. The use of flower colour has colour discrimination effects by pollinators and the use of erucic acid requires extensive laboratory analyses. Purple leaf colour is also undesirable due to its complex genetics. The rate of outcrossing in *B. juncea* varied from 20 to 29.1 %. The ranges of outcrossing on individual plant basis were high ranging from 7.1 to 47.1 % (based on glossiness marker) and 11.4 to 58.1 % (based on petal colour marker). Considering such high rate of outcrossing, the non additive component may be harnessed through heterosis breeding or through population improvement. The maintenance breeding shall need stringent steps to ensure the purity of genotypes. This study, further warrents the research on the aspects of biological and environmental factors, which influence the rate of outcrossing and also on pollen dispersal particularly in GM varieties/hybrids to prevent the pollen dispersal from GM to non GM crops.

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Table 1. Percent outcrossing on the basis of frequency of glossy/non glossy plants in Indian mustard.

Row no.	Number of plants						Percent outcrossing	
	I year			II year			I year	II year
	Glossy type	Non- glossy type	Total	Glossy type	Non- glossy type	Total		
1	14	36	50	18	26	44	28.0	40.9
2	9	24	33	6	36	42	27.3	14.3
3	12	84	96	17	33	50	12.5	34.0
4	8	17	25	2	25	27	32.0	7.4
5	12	29	41	33	42	75	29.3	44.0
6	17	26	43	20	32	52	39.5	38.5
7	6	42	48	5	41	46	12.5	10.9
8	17	20	37	14	23	37	45.9	37.8
9	18	21	39	12	26	38	46.2	31.6
10	15	21	36	8	29	37	41.7	21.6
11	6	20	26	21	32	53	23.1	39.6
12	9	33	42	8	9	17	21.4	47.1
13	15	86	101	23	33	56	14.9	41.1
14	11	26	37	15	27	42	29.7	35.7
15	6	18	24	23	32	55	25.0	41.8
16	15	18	33	3	39	42	45.5	7.1
17	9	35	44	11	36	47	20.5	23.4
18	17	23	40	6	20	26	42.5	23.1
19	14	30	44	8	42	50	31.8	16.0
20	18	39	57	20	81	101	31.6	19.8
	248	648	896	273	664	937	27.7	29.1

Table 2. Percent outcrossing on the basis of frequency of yellow and white petal plants in Indian mustard

Row no.	Number of plants						Percent outcrossing	
	I year			II year			I year	II year
	yellow petal	white petal	Total	yellow	white	Total		
1	90	161	251	45	255	300	35.9	15.0
2	68	173	241	54	270	324	28.2	16.7
3	110	309	419	35	166	201	26.3	17.4
4	133	177	310	56	177	233	42.9	24.0
5	17	132	149	36	102	138	11.4	26.1
6	33	247	280	55	330	385	11.8	14.3
7	32	158	190	68	49	117	16.8	58.1
8	42	166	208	60	108	168	20.2	35.7
9	46	251	297	61	67	128	15.5	47.8
10	83	399	482	48	144	192	17.2	25.0
11	18	136	154	56	187	243	11.7	23.1
12	55	200	255	59	79	138	21.6	42.9
13	57	229	286	64	73	137	19.9	46.7
14	58	190	248	41	213	254	23.4	16.1
15	41	275	316	56	205	261	13.0	21.4
16	35	203	238	35	161	196	14.7	17.9
17	42	217	259	37	146	183	16.2	20.2
18	45	230	275	43	160	203	16.4	21.2
19	60	302	362	48	148	196	16.6	24.5
20	63	300	363	42	160	202	17.4	20.8
	1128	4455	5583	999	3200	4199	20	24

Allelopathic influence of Malabar nut (*Adhatoda vasica* Nees.) I on turnip (*Brassica rapa* L.): II. Fertilization value

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Abstract

Aqueous leaf and flower extracts of *Adhatoda vasica* Nees. had stimulatory effect on number of ovules/pistil of turnip (*Brassica rapa* L.) in M₁ generation, but its higher doses are deleterious. Contrary to this, there was inhibitory effect of both the extracts on number of seeds/siliqua and Fertilization value, Greater inhibitory or stimulating effect of the leaf extract was noted at all the used concentrations in comparison to the flower extract.

Keywords

Allelopathy, *Adhatoda*, turnip, fertilization value, dose

Introduction

Allelopathy refers to the beneficial and harmful effects of one plant on another plant(s) growing in vicinity, both crop and weed species, by the release of chemicals from plant parts through leaching, root exudation, volatilization, residue decomposition and other processes in both natural and agricultural systems (1, 8, 14, 16). Biochemical interactions occur when the allelochemicals (secondary plant metabolites) produced by one plant escapes into the environment and influence the survival, growth and development of another plant growing nearby (5, 9, 10, 11, 17). Malabar nut (*Adhatoda vasica* Nees) of family Acanthaceae, is a small evergreen, perennial shrub growing throughout the Indian peninsula up to an altitude of 1300 m on wastelands in a variety of habitats and types of soil. The plant parts have been used extensively in Ayurvedic medicine for over 2000 years primarily for respiratory disorders. Leaf juice is given in chronic bronchitis, asthma, dysentery and diarrhea. A paste of the leaves is applied to the abdomen to treat urinary disorders. It has been used by European herbal practitioners as an antispasmodic, expectorant and febrifuge. Besides it is used in treating diseases like abscesses, anthrax, tuberculosis, jaundice, scabies, pneumonia and urticaria. Extensive researches have been done on agricultural crops for getting superior varieties for obtaining more yield, disease resistance and quality improvement, but virtually no works have been done to investigate the allelopathic potential of the drug yielding or medicinally important plants on survival, growth and development of our valuable crops. Number of ovules present in the ovary is regarded as an important component of fertility since they develop into seeds after successful fertilization. Keeping this in view, present work has been carried out to know the allelopathic impact of the medicinally important plant, *Adhatoda vasica*, on the fertilization value of turnip (*Brassica rapa* L.). With the help of this, it is possible to evaluate the number of ovules capable of forming

seeds.

Materials and Methods

'Purple Top White' cultivar of turnip constituted the material for present investigation. To make the leaf and flower extracts, a field grown malabar nut plant was selected and 250 g mature leaves and flowers were detached from this separately. The leaves and flower samples were dried separately at 60° C. Then they were grinded to pass through 1 mm screen and stored at room temperature. Sterilized distilled water was used to make the leaf and flower extracts separately in 40: 1 (V/W) water: sample ratio. After this, it was kept in refrigerator for 18 hours. Now the suspension was centrifuged at 900g for 15 minutes and then vacuum filtered through 0.4 µm polycarbonate filter to obtain the mother solution, and from this the solutions of different concentrations (20, 40, 60, 80 and 100 %) were made by adding required amount of distilled water. 300 turnip seeds were treated in each concentration for a period of 24 hours. For control, the seeds were soaked in distilled water only. Then the treated seeds were thoroughly washed in double distilled water and sown immediately in different pots of equal size having homogenous soil, along with Control to raise M₁ plants. M₂ populations were grown from the seeds collected from M₁ through selfing. 100 pistils, 10 from each plant, in each case were pressed between two microscope slides after putting a drop of 2% KI solution to count the number of ovules present in the pistil to compute mean number of ovules/pistil (MNO). A hundred of siliques, 10 from each plant, were dissected with the help of a pair of needles to compute mean number of seeds/siliqua (MNS). The ratio of MNS to MNO x 100 gave the percentage of fertilization value (FV). The treatments were replicated four times in Complete Randomized Design. The data were analyzed statistically using Critical Difference (C D) at 5% level of significance. All the results are presented in Table 1.

Results and Discussion

The aqueous leaf and flower extracts of *Adhatoda vasica* demonstrated stimulatory effects on number of ovules/pistil of turnip, particularly at the lower and moderate doses. A progressive increase in this trait occurred from 20% to 60% concentrations, followed by a gradual decrease from 80% to 100% in M₁ generation. A further increase took place in M₂ at all the doses. Maximum stimulation was seen at 60% concentration and the minimum at 20%. Contrary to this, there was inhibitory effect of both kinds of treatment on seeds/siliqua and fertilization value of turnip. A gradual decrease in both the traits was noted from lower to higher used concentrations in M₁ generation. Some recovery took place at all concentrations in M₂ under both kinds of treatment, but not to the extent of control. Remarkably lesser stimulatory or inhibitory effect of the flower extract was noted on both the traits at all the used concentrations.

Moderate higher doses of the leaf extract of periwinkle (*Catharanthus roseus* Don.) exhibited deleterious effect on FV of turnip (12). Carrot weed (*Parthenium hysterophorus* L.) leaf and flower extracts had retarding effect on FV of turnip (13). The lower doses of the leaf extract of neem (*Azadirachta indica* A. Juss.) and azadirachtin - based biopesticide had inducing effect on FV of *Brassica rapa* L., but their higher doses were harmful (11). The crude neem oil treatment exhibited inducing effect on FV of turnip (6).

Seed set is a character of paramount importance in view of yield production and crop improvement. It is the ultimate product of interactions among a number of quantitative traits which are known to be controlled by different sets of polygenes. Molisch (8) coined the term 'allelopathy' which refers to all stimulatory and inhibitory biochemical interactions between the plants including microbes. The allelopathic plants control the environment in which they live. Allelopathy is one of the triggers for succession of vegetation in a natural ecosystem. The medicinal plants have strong allelopathic potential (2, 3, 4, 7, 10, 11). Vasicine is the major alkaloid present in all parts of the plant body of *Adhatoda vasica*. The leaves also contain vasicinone, 7-methoxyvasicinone, vasicinol, adhatodine, adhatonine, adhavaicinone, anisotine, 3-hydroxyanisotine, desmethoxyaniflorine, vasicoline, and vasicolinone 6-9 and essential oil. The flowers contain β-sitosterol-D-glucoside, kaempferol, glycoside, kaempferol and quercetin. Under present investigation

biochemical interactions occurred when the allelochemicals present in the leaf and flower extracts of malabar nut came in contact with the embryo of seed during treatment which ultimately influenced the growth and development of the turnip plants raised from the treated seeds. At present it is difficult to ascertain out of the various constituents present in the leaf and flower extracts which one, or a group of these, is causal factor for inhibition or stimulation of the concerned traits of turnip. Obviously, it requires further biochemical investigations. *Adhatoda vasica* is a medicinal plant and it is invariably believed that the medicines of plant origin are safe and can be consumed without any special care, but it is not so. Sometimes they have serious side effects (15). *Adhatoda* – based medicines and extracts too, may be toxic. Hence their use in large amount, particularly at higher concentrations, may prove hazardous. The term 'allelopathy' is relatively new, but the concept is quite old. It is expected that in near future the knowledge of allelopathy will play a vital role in crop production, agro forestry and horticulture in developed as well as developing countries. Besides it has potentiality to emerge as one of the strategic sciences to reduce the environmental pollution. The rich plant diversity in India offers a significant opportunity for future research in this field.

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Table 1. Effect of Malabar nut extracts on fertilization value of turnip.

Dose (%)	Number of ovules/pistil (MNO)				Number of seeds/siliqua (MNS)				Fertilization Value (FV%)			
	Leaf extract		Flower extract		Leaf extract		Flower extract		Leaf extract		Flower extract	
	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)
Control	16.1	16.3	16.2	16.3	14.6	14.8	14.7	14.7	90.7	90.8	90.7	90.2
20	17.2 (+ 6.8)	17.9 (+9.8)	17.2 (+6.2)	18.7 (+14.7)	12.6 (-13.7)	13.4 (-9.6)	13.6 (-7.5)	14.2 (-3.4)	73.3 (-19.2)	74.9 (-17.5)	79.1 (-12.8)	75.9 (-15.8)
40	18.5 (+ 4.9)	20.1 (+23.3)	16.5 (+1.8)	18.0 (+10.4)	12.2 (-16.4)	12.5 (15.7)	13.0 (-11.6)	13.4 (-8.8)	66.0 (-27.2)	62.2 (-31.5)	78.8 (-13.1)	74.4 (-17.5)
60	19.2 (+ 9.2)	21.2 (+30.1)	18.9 (+16.7)	20.2 (+23.9)	10.3 (-29.4)	11.2 (-24.6)	11.6 (-21.1)	12.2 (-17.0)	53.8 (-40.7)	52.8 (-41.8)	61.4 (-32.3)	60.4 (-33.0)
80	15.2 (-5.6)	16.5 (+1.2)	14.5 (-10.5)	16.5 (+1.2)	8.3 (-43.1)	8.7 (-41.8)	9.2 (-37.4)	10.1 (-31.3)	54.5 (-39.9)	52.7 (-41.9)	63.4 (-30.1)	61.9 (-31.4)
100	13.5 (-16.1)	14.3 (-12.3)	12.7 (-21.6)	14.5 (-11.0)	7.5 (-48.6)	8.2 (-45.2)	8.6 (-41.5)	9.6 (-34.7)	55.6 (-38.7)	57.3 (-36.9)	67.7 (-25.3)	66.2 (26.6)
CD at 5%	0.47	0.70	0.89	0.62	0.66	0.61	0.57	0.61	3.46	4.85	6.61	4.67

Data in parenthesis indicate percent stimulation (+)/ inhibition (-) over Control.

Phytohormones induced promotion in seed germination of Indian mustard (*Brassica juncea* L. Czern & Coss.) under water stress conditions.

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Introduction

India is one of the largest among rapeseed mustard growing countries in the world ranking second in area and third in production after China and Canada. The production of rapeseed-mustard in India is lower than the world's average (1730 kg/ha) due to large number of factors viz. its cultivation under marginal conditions and losses caused by various biotic and abiotic stresses (Toor and Atwal, 2007). *Brassica juncea* (L.) (Czern & Coss.) (Indian mustard) commonly known as *raya* is one of the most important oilseed crop of rapeseed-mustard group and grown in northern and north east part of India. Abiotic stresses such as drought, salinity, extreme temperature and chemical toxicity are serious threats to agriculture and significantly diminish the plant productivity. Drought is one of the most important stresses which can strike crop and affects the growth and development.

Brassica being a crop of arid and semi arid region, its sowing depends upon rain. Under such conditions the farmers have no option except sowing the crop early in the season on the conserved moisture. Early sowing of *Brassica* implies many important advantages (Bapu, 2010). Firstly, early harvest of *Brassica* is desirable to avoid disease infestation and aphid attack that normally coincides with the flowering stage. Secondly, shattering of siliquae can be avoided during the time of harvest when crop encounters high temperature. But, high temperature along with water stress prevailing at that time of sowing reduces seed germination and even causes seedling mortality (Chhabra *et al.* 2007). Therefore crop is to be re sown many a time before a final successful crop is taken. This causes a lot of economic loss to farmers. This necessitates the need of seed priming that could improve seed germination under water stress conditions. Keeping in view this problem, the effect of priming seeds with various hormonal concentrations was examined to see their effect on germination and seedling survival under water stress conditions.

Materials and Methods

Two hundred counted seeds of Var. RH 8812 of *B. juncea* were soaked in water (as water soaked control) and various hormonal concentrations viz: Naphthyl Acetic Acid (NAA) 200, 100 and 20 μ M, Gibberallic Acid (GA) 200, 100 and 20 μ M and Kinetin (Kin). Unsoaked control (C) was also taken. Soaking was done in test tubes with just enough water to dip the seeds. Soaking was done for 2 hours. Seeds were thoroughly rinsed with distilled water and then filter dried before sowing in the field. Recommended dose of fertilizer (80 kg/ha) was

used. Sowing was done in 2 rows x4 m plot. Field contained loam soil and was under water stress i.e. with water poor water status than required for optimum germination. Fifteen days after sowing plant count was recorded and per germination was calculated.

Results and Discussion

In unsoaked control (C), the germination was 37 per cent. The poor germination was because the soil was under water stress condition. Soaking seeds with water for 2 hours increased the germination to 50.5%. Just soaking seeds in water for 2 hours resulted an additional 12.5% germination over unsoaked control, is an important observation.

Soaking seeds in NAA 200 μM caused 62.0 per cent germination (25.0% increase over unsoaked control). Germination with NAA 100 and 20 μM was though higher than unsoaked control but lesser than NAA 200 μM . Germination also improved with GA treatments. Among various concentrations of GA used, GA100 μM was most effective in this regard. GA 200 and GA 20 were statistically at par with each other. Among various concentrations of KIN used, KIN 100 μM was most effective. It increased 23.5% germination over unsoaked control (C) followed by KIN 100 μM which increased 21.6% germination.

On an overall NAA was most effective at 200 μM concentration while GA and Kinetin were most effective at 100 μM concentrations. Among the three hormones used NAA 200 μM was most effective in increasing germination. It increased 25 per cent germination over unsoaked control whereas it improved 11.5 per cent over water soaked control. On an overall soaking seed in NAA 200 μM for 2 hours is a commercially viable project. Kin 20 μM was least effective among various concentrations of kinetin used.

On an overall NAA 200 μM was most effective followed by KIN 100, GA 100 and KIN 200 μM .

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Table 1. Effect of soaking *Brassica juncea* seeds in various hormonal concentrations on per cent germination under water stress conditions.

S. No.	Hormonal Concentration (μM)	Per cent seed germination	Per cent Increase over unsoaked control
1	NAA 200	62.0	25.0
2	NAA 100	48.2	11.2
3	NAA 20	47.2	10.2
4	GA 200	48.3	11.3
5	GA 100	58.6	21.6
6	GA 20	51.0	14.0
7	KIN 200	58.6	21.6
8	KIN 100	60.5	23.5
9	KIN 20	50.5	13.5
10	Water soaked (WS)	50.5	13.5
11	Unsoaked Control(C)	37.0	-
	CD (%)	3.2	

Allelopathic influence of basil extracts on *Brassica rapa* L. : IV. Plant height, branches/plant and silique/plant

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Abstract

Ocimum sanctum L. and *O. canum* Sims. plant extracts had stimulating effect on plant height, number of branches/plant and number of silique/plant of turnip (*Brassica rapa* L.). 80% concentration of the plant extract was found most effective in this regard. Relatively, *O.canum* treatment had more stimulating effect than *O. sanctum* at all the used concentrations.

Keywords

Basil, extracts, turnip, fertilization value, allelopathy

Introduction

Allelopathy is a kind of plant – plant interaction mediated through the release of chemical substances by one plant, which is detrimental to the other growing nearby. All types of crops of our use have more or less allelopathic function, especially the weeds and the medicinal plants. Biochemical interactions occur when allelochemicals (secondary plant metabolites) produced by one plant escape into environment and influence the growth and development of organisms growing in the vicinity (1, 10, 11, 13, 18, 21). The genus *Ocimum*, collectively called basil of family Lamiaceae, has long been recognized as a diverse and rich source of essential oils. Frequent interspecific hybridizations and polyploidy have created great taxonomic confusion and challenges, further complicated by the existence of chemotypes which do not differ much in morphology. The essential oils of basil contain biologically active constituents that are insecticidal (2, 4, 5), nematocidal (3), fungistatic (17) and antimicrobial properties (12). Extensive researches have been done on agricultural crops for getting superior varieties in order to obtain high yield, disease resistance and better quality, but virtually no works have been done to know the allelopathic influence of drug-yielding or medicinally important plants on the yield and yield-components of our valuable crops. Keeping this in view, present study was undertaken to know the allelopathic impact of *O. sanctum* and *O. canum* on plant height, branches/plant and silique/plant of turnip (*Brassica rapa* L.).

Materials and Methods

'Rose Red' cultivar of turnip constituted the material for present investigation. The method of preparing solutions of different concentrations of *Ocimum sanctum* and *O. canum*, mode of treatment and raising the plants were the same as described earlier (7). The height of 25 randomly selected natured plants in each case

under both kinds of treatment along with Control, was measured simultaneously with the help of a scale and thread to score mean plant height. The secondary branches developing from the primary axis in each of the 25 randomly selected matured plants in each concentration of both kinds of treatment, including control, were counted to score mean number of siliqua/plant. To compute mean number of siliqua/plant, all the siliqua attached on each of the 25 plants in each case, along with the control, were counted under both kinds of treatment. The treatments were replicated four times in Complete Randomized Design. The data were analyzed statistically using Critical Difference (CD) at 5% level of significance. All the results are presented in Table 1.

Results and Discussion

Both kinds of treatment, *O. sanctum* as well as *O. canum*, exhibited stimulating effect on plant height, branches/plant and siliqua/plant of turnip. There was a gradual increase in all the three parameters from 20% to 80% concentrations, followed by a sharp decrease at 100% in M_1 generation. Maximum stimulation was demonstrated at 80% concentration under both kinds of treatment. A further increase took place in M_2 in these traits at all the used doses. Remarkably, *O. canum* treatment had more stimulating effect than *O. sanctum* in all the cases.

Moderate higher doses of the leaf extract of periwinkle (*Catharanthus roseus* Don.) exhibited deleterious effect on plant height, branches/plant and siliqua/plant of turnip (15). Carrot weed (*Parthenium hysterophorus* L.) leaf and flower extracts had retarding effect on these traits of turnip (16). *O. canum* is very effective against obnoxious carrot weed (*Parthenium hysterophorus* L.) harmful to human beings, crops and a real curse for the bio-diversity (8). The lower doses of the leaf extract of neem (*Azadirachta indica* A. Juss.) and azadirachtin - based biopesticide had inducing effect on plant height, branches/plant and siliqua/plant of turnip of *Brassica rapa* L., but their higher doses were harmful (14). The crude neem oil treatment exhibited inducing effect on the above said traits of turnip (9).

Study of plant height, number of branches/plant and number of siliqua/plant bears special significance in relation to yield. Basil contains a strong-scented volatile oil composed primarily of terpenoids particularly eugenol, thymol, and estragole. The exact components of basil oil vary widely. It also depends on the time of day of harvest (6). The biochemical interactions occurred when the allelochemicals present in the plant extracts of the basil species came in contact with the embryo of the seeds during treatment which ultimately influenced the growth and development of turnip plants raised from these. At present it is difficult to ascertain out of various constituents present in the basil plant extracts which one, or a group of these, is causal factor for stimulation or inhibition of the concerned traits of turnip. Obviously, it requires further biochemical investigations. It is invariably believed that the medicines of botanical origin are safe and can be consumed without any special care, but it is not so. Sometimes they have serious side effects (19). Ocimum-based medicines and extracts too, may be toxic. Hence their use in large amount, particularly at higher concentrations, may prove hazardous.

It is expected that in near future the knowledge of allelopathy will play a vital role in crop production and protection, agro forestry and horticultural practices in the developed as well as developing countries. Besides it has potentiality to emerge as one of the strategic sciences to reduce the environmental pollution. The rich plant diversity in India offers a great potential for future research in this field. Present studies on allelopathy are focusing mainly on ecophysiology. In future molecular or gene-level studies will help in explaining the mechanisms of allelopathy more accurately that will facilitate the production of desired transgenic allelopathic plants (20).

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Table 1. Effect of basil extracts on yield components of turnip.

Dose (%)	Plant height (cm)				Number of branches/plant				Number of silique/plant			
	<i>O. sanctum</i>		<i>O. canum</i>		<i>O. sanctum</i>		<i>O. canum</i>		<i>O. sanctum</i>		<i>O. canum</i>	
	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)	M ₁ (Mean)	M ₂ (Mean)
Control	71.1	72.1	72.5	72.4	8.2	8.1	8.6	8.1	66.4	66.1	66.3	67.0
20	73.7 (+3.6)	80.3 (+11.4)	82.7 (+14.1)	83.4 (+15.2)	9.5 (+15.8)	10.1 (+24.7)	9.9 (+15.1)	11.2 (+38.3)	68.0 (+2.4)	69.8 (+5.6)	75.6 (+14.0)	76.3 (+13.9)
40	80.9 (+13.8)	82.6 (+14.6)	87.5 (+20.7)	89.7 (+23.9)	10.9 (+32.9)	12.4 (+53.0)	11.4 (+32.5)	12.1 (+49.4)	72.7 (+9.5)	76.7 (+16.0)	81.4 (+22.8)	85.0 (+26.9)
60	87.4 (+22.9)	88.9 (+23.3)	90.5 (+24.8)	92.6 (+27.9)	11.7 (+42.7)	13.0 (+60.5)	12.6 (+46.5)	13.2 (+62.9)	82.7 (+24.5)	86.0 (+30.1)	91.1 (+37.4)	102.9 (+53.6)
80	92.8 (+30.5)	94.5 (+31.1)	105.9 (+46.1)	107.4 (+48.3)	14.3 (+74.4)	15.5 (+91.3)	16.4 (+90.7)	17.1 (+111.1)	91.7 (+38.1)	92.1 (+39.3)	105.6 (+59.3)	111.5 (+66.4)
100	74.3 (+4.5)	82.4 (+14.3)	75.5 (+4.1)	86.8 (+19.9)	12.1 (+47.6)	13.3 (+64.2)	14.7 (+70.9)	15.4 (+90.1)	72.8 (+9.6)	74.3 (+12.4)	80.1 (+20.8)	82.7 (+23.4)
CD at 5%	3.10	2.70	2.79	2.96	0.54	0.54	0.30	0.49	2.53	3.07	4.29	2.99

Data in parenthesis indicate percent stimulation (+)/ inhibition (-) over Control.

Diversification of CMS system in snowball cauliflower through introgression of *Trachystoma ballii* sterile cytoplasm

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Abstract

In vegetable *brassicas* 'Ogura' cytoplasm from Japanese Radish is the only source of male sterility used world wide for production of F₁ hybrid seeds. Monoculture may result in any epidemic of biotic agents. In the present study, we have made attempt to transfer *Trachystoma ballii* sterile cytoplasm from *Brassica juncea* into cauliflower variety, Pusa Snowball K-1. Successful embryo rescue have been done to generate F₁ and BC₁ plants. All the F₁ and BC₁ plants had male sterile flowers. The morphological traits of F_{1s} were intermediate between the parents. These populations are in use in recurrent back-crossing programme involving embryo rescue for development of cauliflower lines with sterile 'Trachy' cytoplasm.

Introduction

Snowball cauliflower is grown through out the Indian sub-continent during the Rabi season. In cauliflower, F₁ hybrids are advantageous especially in uniform maturity, high early and total yield, better curd quality with respect to compactness and color, resistance to insect pests, diseases and unfavorable weather conditions (Kucera et al, 2006). Two pollination control mechanisms viz. self-incompatibility (SI) and male sterility (particularly CMS) are used widely for production of F₁ hybrid seeds. So far, majority of cruciferous hybrid cultivars have been developed by using SI system (Watanabe and Hinata, 1999). However, SI system has several disadvantages like, possibility of sibs in the hybrids and multiplication of SI parents through tedious bud pollination or CO₂ and NaCl spray (Sharma et al, 2004). In case of snowball cauliflower, self incompatibility system is very weak or not present at all (Watts 1963; Niewhoff 1963). In such a situation, CMS system offers a good alternative (Kucera, 2006; Sharma et al. 2004) for production of F₁ hybrid seeds. Unlike in genetic male sterility (GMS) system, this system does not require roguing out of fertile individuals from the female line at the time of anthesis.

Sterile cytoplasm (Ogura) from Japanese radish is the only source of male sterility used in vegetable brassicas, worldwide. Thus, diversification of CMS system is immediately needed to avoid any imminent epidemic of biotic agent. The present study was therefore undertaken to transfer sterile cytoplasm from *Trachystoma ballii* into snowball/late cauliflower (*Brassica oleracea* var. *botrytis*) using embryo rescue.

Materials and Methods

Interspecific crosses: Plants of *Brassica juncea* (AABB; 2n=4x=34) with *Trachystoma ballii* sterile cytoplasm and *Brassica oleracea* var. *botrytis* (2n=2x=18) were raised at Office field of IARI-Regional Station, Katrain,

Himachal Pradesh. The crosses were attempted between CMS lines as female and cauliflower (var. Pusa Snowball K-1) as male parent during 2008 and first backcross was made in the following year in both the cases and population assessed during 2010.

In vitro embryo rescue techniques: Two embryo rescue techniques viz. ovule and ovary culture were used for recovery of hybrid plants. For ovule culture, pods were harvested after 4, 6, 8, 10, 12, 15 and 20 days after pollination. They were surface sterilized with 70% alcohol for 30 seconds followed by mercuric chloride (0.1%) for 5 minutes. After sterilization ovules were excised and cultured on MS media containing casein hydrolysate (100mg l⁻¹), BAP (0.1mg l⁻¹) and NAA (0.1 mg l⁻¹). For sequential ovary culture, pods were excised and cultured after 5-10 days after pollination. The cultures were maintained at 25±1°C temperature under fluorescent white light (47µ mol/m²/s) at a photoperiod of 16:8 hours light and dark cycles.

Shoot multiplication and rooting: The germinated shoots were excised and cultured and maintained on MS media containing kinetin (1 mg l⁻¹) + GA (0.1mg l⁻¹). Rooting of individual shoots were obtained on ½ MS media with 0.5 mg l⁻¹ NAA, 100 mg l⁻¹ activated charcoal and 45 g l⁻¹ sucrose.

Hardening: The rooted plantlets were carefully removed from flasks, washed free of the agar sticking to the roots. The roots were then treated with Bavistin (0.1%) for few seconds and then transferred to the hardening media consisting of sterilized peat and soilrite mixture saturated with ½ strength MS medium containing only macro- and micro- salts. Hardening was done in plastic pots covered with polythene.

Raising of F₁ and BC₁ plants: The hardened F₁ plants were transferred to 12" pots and crosses were attempted to obtain BC₁ were raised in similar fashion. BC₁ were obtained in similar fashion as F₁.

Results and Discussion

For the introgression of diverse sterile cytoplasm into snowball cauliflower from *Trachystoma ballii* via *Brassica juncea*, embryo rescue was employed for obtaining F₁ and backcross (BC₁) plants. The percentage of developed embryos obtained and their germination percentage in F₁ and BC₁ is given below in the table 1. The percentage of germinated embryos was in the range of 1.1-2.0% while developed embryos were in the range of 2.4-3.9%.

Attempt was made to transfer sterile cytoplasm of *Trachystoma ballii* into one genotype of cauliflower, namely, Pusa Snowball K-1 through hybridization assisted with embryo rescue. The morphological features of F₁ and BC₁ generations are presented in Table 2 and Figure 2. Different stages of embryo culture are presented in Figure 1. The F₁ plants developed were morphologically similar among themselves.

As the wild relatives of the crop plants are an important source of genetic variability various economic traits including male sterility, the scope of using these germplasm for crop improvement is limited by hybridization barrier. These barriers operate during pollen germination, fertilization or hybrid development and prevent gene transfer. In the present study for the introgression of sterile cytoplasm from diverse sources into snowball cauliflower was carried out with the help of embryo rescue to overcome the problem of post-fertilization barrier in F₁ and BC₁. The sterile cytoplasm sources namely, *Trachystoma ballii* (via *Brassica juncea*) was employed for transferring sterile cytoplasm into cauliflower (*B. oleracea* var. *botrytis* L.) background. Sterile plants with rudimentary stamens and shriveled anthers were pollinated with cauliflower pollen.

Morphologically, F₁s were of intermediate type in leaf characteristics, whereas for flower characteristics and bolting behaviour these were like that of sterile source.

The F₁ and BC₁ generations developed using *Trachystoma ballii* sterile cytoplasm and cauliflower as pollen parent were completely sterile with flowers having rudimentary stamen and shriveled anthers and pollen viability test also confirmed sterility.

The BC₁ plants developed using the cytoplasm sources in cauliflower background were closer to recurrent parent with respect to leaf length, breadth and waxiness of leaves. The BC₁ plants had the bolting inflorescence like that of broccoli emerging head the delay however was unlike that of sterile cytoplasm sources. For sterility pattern in F₁s and BC₁s, our findings are in corroboration with those of Celis et al. (1991),

Momtaz et al. (1998), Hinata and Kano (1979), Vyas et al. (1995) and Bang et al. (2007). This study needs to be furthered with continued backcrossing using cauliflower as recurrent parent for complete introgression of sterile cytoplasm into cauliflower background for facilitating heterosis breeding and affordable hybrid seed production.

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Table 1. Developed embryo (%) obtained and the germination (%) in *Trachystoma ballii* derived F1 and BC1

SI No.	Number of ovule cultured	Developed embryo obtained (%)	Germinated embryo (%)
1	210	2.4	1.4
2	190	2.6	1.6
3	207	3.8	2.0
4	178	3.9	1.7
5	184	3.3	1.1

Table 2. Morphological features of F1 and BC1 derived from *Trachystoma ballii* cytoplasm

Characters	Female parent	Male parent	F ₁ hybrids	BC ₁
Leaf length	25-30	45-55	30-35	33-40
Leaf width	8-15	24-30	12-18	12-20
Plant height	85-110	50-65	100-120	90-110
Leaf margin	Variously lobed	Variously lobed	Variously lobed	Variously lobed
Leaf shape	Ovate to obovate	Broad elliptic	Narrow elliptic	Narrow elliptic
Texture	Rough and hairy	Smooth and waxy	Moderate smooth	Moderate smooth
Flower	Yellow and stamenless with nectarines	Creamish with well developed stamen and nectarines	Yellow with shriveled rudimentary stamen and nectarines	Yellow with rudimentary shriveled stamen and nectarines



Figure 1. Embryo rescue techniques via ovule culture in cauliflower.

- a: Hybrid embryo germinating on MS medium.
- b: Embryo rescued hybrid seedlings growing *in vitro* on solid MS medium
- c: *In vitro* rooting of hybrid seedling on liquid medium.
- d: Hardening of hybrid seedlings in glass jars.
- e: F₁ hybrid obtained through embryo rescue .



Figure 2. Comparison of F1 (a) and BC1 (b) plants obtained via embryo rescue

Nutritional quality evaluation of new varieties/strains of Indian mustard (*Brassica juncea* L. Czern & Coss)

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Introduction

Among the oilseed *Brassica* crops, Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is an important source of oil from nutritional point of view (Ahuja, *et al.* 1984). The nutritional value of oil and cake quality is governed mainly by the composition of its fatty acids, iodine value, saponification, acid value, glucosinolates, crude fibre, protein and limiting amino acids, respectively. Meal cake is a protein supplement in animal diet. The high amount of glucosinolates in meal and erucic acid in oil may create health problems *viz.* lipidosis in young animals, fibrosis in older animals, reduced food intake, causes goiter, stroma and cancer (Kumar, 2005).

In *Brassica* breeding, considerable emphasis is being laid to develop the varieties with high oil content, low glucosinolates and better oil quality characteristics. Keeping this in view, the present study was undertaken to work out the nutritional quality of *Brassica juncea* genotypes in terms of their contents such as oil per cent in seed, iodine value, saponification value, acid value in oil and glucosinolate in cake.

Materials and Methods

Seeds of twenty six varieties/strains of Indian mustard were obtained from AICRP on Rapeseed-mustard, Department of GPB, N.D. Univ. of Agric. and Tech., Kumarganj, Faizabad. The seeds were sun dried followed by oven drying and used as the experimental materials in the present investigation for chemical composition analysis during 2006-07. The chemical analysis of the experimental material was carried out in the laboratory of Chemistry Department, KNIPPSS, Sultanpur.

The oil content was determined by Soxhlet Extraction Procedure using petroleum ether (boiling point range 40-60 °C) as described by Annon (1975). The iodine value of oil was determined by Wij's solution (Sawhney, 2001). The saponification value of oil sample was determined by Hart and Fisher (1971) and glucosinolate was estimated by the method given by Annon (1970).

For analysis of acid value, 0.5 g filtered oil was weighted in a 250 ml of conical flask. 10 ml of petroleum ether was added to the flask in order to dissolve the oil. The content of flask was then kept on a boiling water bath. It was titrated against N/10 Sodium hydroxide by putting few drops of phenolphthalein indicator. The end point was recorded when light pink colour was obtained. From these readings calculation was done.

Results and Discussion

The oil content, Iodine value, saponification value, acid value and glucosinolate value in different *Brassica juncea* genotypes varied from 36.15 to 42.14%, 105.47% to 118.26%, 156.08 to 175.28%, 0.203 to 0.997% and 0.243 to 0.357%, respectively (Table-1). Oil content was higher in varieties/strains Varuna, Vardan, RGN-152, JGM-03-02 and Krishna being 42.10%, 42.0%, 41.83%, 41.65% and 41.1, respectively. The oil content in seed differed significantly among different genotypes.

The iodine value in different varieties/strains differed numerically. The lowest value of iodine was recorded in strain KLM-287 (105.47), followed by Basanti (105.94), Varuna (106.04), Vardan (106.05), Rohini (106.21), NDYR-8 (106.43). The increase in iodine value of oil might be due to the increase in unsaturated fatty acids. The increase in essential fatty acids is desirable to improve the quality of oil. The results are in accordance to Indian Standard Institute (1984).

The minimum saponification value was found in strain RGN-152 (156.08) followed by NDYR-8 (156.60), Varuna (157.22) and Rohini (157.25). This might be due to increase in unsaturation of fatty acids and reduction in saturation of oil. The low saponification value of oil also improves the quality of oil as indicated by Downey (1993), Appleqvist (1972) and Indian Standard Institute (1984). The acid value was maximum in strain RK-05-2 (0.997) and Varuna (0.993), while minimum acid value was recorded in strain RK-05-1 (0.203) followed by RGN-152 (0.283), RB-50 (0.403), LET-20 (0.447) and TERI-LGM-06 (0.453).

The minimum glucosinolate content (%) was recorded in genotypes TERI-LGM-06 (0.243) followed by RB-50 (0.267) and PQR-2001 (0.267). The content of glucosinolate increases with increase in content of sinigrin in seed. Minimum glucosinolate in cake indicates superior meal quality of mustard (Bhowmic, 2003 and Singh *et al.* 2007).

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Table 1. Variation in oil (%) and oil quality in different genotypes of Indian mustard

varieties/strains	Oil content in seed (%)	Iodine Value	Saponification Value	Acid Value	Glucosinolate (%)
LET-17	37.07	112.74	175.28	0.853	0.277
LET-18	36.97	118.12	173.01	0.797	0.347
PQR-9701-46	39.47	118.26	171.42	0.647	0.300
PQR-2001	39.43	112.98	160.90	0.783	0.267
VARUNA	42.14	106.04	157.22	0.993	0.273
ROHINI	38.60	106.21	157.25	0.673	0.350
BIO-Q-108-2000	36.15	113.66	174.24	0.840	0.307
TERI-LGM-06	38.65	116.22	171.37	0.453	0.243
TERI-LGM-08	37.88	115.61	170.20	0.547	0.283
SKM-450	40.67	107.92	158.50	0.787	0.307
RB-50	39.63	106.27	162.36	0.403	0.267
RK-05-1	39.75	114.77	164.15	0.203	0.327
RK-05-2	40.24	109.05	160.28	0.997	0.280
JGM-3-02	41.18	106.76	158.06	0.693	0.307
RGN-152	41.47	107.59	156.08	0.283	0.343
PAC-432	40.95	106.44	157.18	0.953	0.270
BASANTI	41.35	105.94	158.28	0.843	0.357
NARENDRA RAI	40.23	108.20	157.40	0.953	0.313
NDYR-8	40.45	106.43	156.91	0.947	0.293
NDRE-4	41.20	106.47	158.37	0.597	0.280
KRANTI	39.82	109.11	162.16	0.957	0.317
VARDAN	41.99	106.05	159.62	0.903	0.268
LET-20	39.44	109.17	173.26	0.447	0.283
KRISHNA	40.66	108.09	157.32	0.847	0.287
KLM-287	37.88	105.47	158.01	0.953	0.303

Fatty acid composition of Indian mustard (*Brassica juncea* L. Czern & Coss)

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Introduction

Among the oilseed *Brassica* crops, Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is an important source of oil from nutritional point of view (Ahuja, *et al.* 1984). The nutritional value of oil is governed mainly by the composition of its fatty acids *viz.* Palmitic acid, Stearic acid, Oleic acid, Linoleic acid, Linolenic acid, Eicosenoic acid, Erucic acid along with anti nutritional factors (Bhowmic, 2003).

The high amount of glucosinolates in meal and erucic acid in oil may create health problems *viz.* lipidosis in young animals, fibrosis in older animals, reduced food intake, causes goiter, stroma and cancer (Kumar, 2005). In India till date, the main emphasis has been to improve the rapeseed-mustard seed yield and oil content. It is necessary that seed oil quality especially the fatty acid composition also be improved wherever possible. Keeping this in view there is a need to screen/develop Indian mustard varieties having low erucic acid.

Materials and Methods

Seeds of thirty one varieties/strains of Indian mustard were obtained from All India Coordinated Research Project on Rapeseed-mustard, Department of Genetics and Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad. The seeds were sun dried followed by oven drying and used as the experimental materials in the present investigation for chemical composition analysis during 2006-07.

Methyl-esters of fatty acids were prepared from the oil obtained using Soxhlet apparatus. The method used for preparation of methyl esters is described in "A manual of laboratory technique" published from Nutritional Institute of Nutrition, Hyderabad (AP) India. The major fatty acids namely palmitic, stearic, oleic, linoleic, linolenic, eicosenoic and erucic acid were analysed using Perkin Elmer Autosystem XL Gas liquid chromatography (GLC). The carrier gas was nitrogen (20 ml/minute nitrogen). Flame ionization detector (FID) was used. The calculations were done using the standard fatty acids.

Results and Discussion

The results (Table 1) indicated that the major saturated fatty acids *viz.*, palmitic and stearic acids along with mono and poly-unsaturated fatty acids like oleic, eicosenoic, erucic, linoleic and linolenic acids were found in

the oil. The range of different fatty acids is given in Table-1. The range for palmitic acid was [1.26% (PAC-432) to 4.45% (LET-17)], stearic acid [1.14% (Kranti) to 3.58% (PAC-432)], oleic acid [2.91% (PAC-432) to 45.02% (PQR-2001)], linoleic [6.30% (Vardan) to 41.80% (LES-1-27)], linolenic acid [7.35% (NDYR-8) to 29.85% (LET-3)]. The zero per cent eicosenoic and erucic acid were found in the genotypes viz., LES-1-27, LET-3, PQR-9701-46, and PQR-2001 except KLM-287 which observed zero per cent erucic acid and lowest eicosenoic acid (2.41%). Erucic acid is a typified fatty acid of *Brassica* oil and ranged from 0 to 52.56%. The variations of different fatty acids showed conformity with those reported by several scientists (Nagraj, 1990 and Banga and Banga, 2002). Indian mustard oils are inferior in quality as they contain high amount of erucic (28.0-53.0 %) and linolenic (8.5-22.7%) acids although they also contain linoleic (12.0-21.0 %) and oleic (10.0-24.0 %) acids which are nutritionally good (Bhowmic, 2003).

Among the various fatty acids recorded in Indian mustard oil, palmitic, stearic, oleic and linoleic acids are nutritionally desirable whereas, linolenic, eicosenoic and erucic acids are undesirable. Among the undesirable fatty acids, erucic acid is typified fatty acid whose concentration is comparatively higher as compared to other acids in toria and mustard. Intake of lower amount of mustard oil having 40% erucic acid would be safe for consumption as reported by Appelqvist (1972). However, several workers have reported that, by and large, due to higher intake of mustard oil having high concentration of more than 40% erucic acid may cause some health problems like absorption, lipidosis in children and myocardial fibrosis in adults (Banga and Banga, 2002; Kumar, 2005).

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Table 1. Fatty acid composition in different varieties/strains of Indian mustard

varieties/strains	16:0	18:0	18:1	18:2	18:3	20:1	22:1
PQR-9701-46	4.11	2.54	41.74	33.42	18.12	0.00	00.00
CS-234-2	2.79	3.41	7.20	10.15	16.50	8.41	51.44
LES-1-27	2.88	1.45	40.09	41.80	13.26	0.00	00.00
LET-3	4.03	3.28	25.00	37.04	29.85	0.00	00.00
LET-17	4.45	2.61	35.30	33.32	15.45	4.54	3.50
LET-18	3.24	1.80	23.53	33.28	18.39	5.42	13.54
TERI-LGM-08	2.85	1.62	8.41	19.25	16.78	17.61	32.82
PQR-2001	4.15	2.53	45.02	34.60	12.85	0.00	00.00
RB-50	2.03	2.19	7.19	12.31	16.24	7.38	52.56
ROHINI	2.54	2.02	7.57	12.83	15.50	9.48	49.74
TERI-LGM-06	3.40	1.66	3.57	26.08	18.48	14.55	31.70
RGN-152	2.60	2.25	7.76	14.74	16.78	9.75	45.95
SKM-450	2.77	3.35	9.32	8.58	16.20	9.71	50.01
SKM-425	2.03	3.03	8.52	14.35	14.57	8.27	49.21
BASANTI	2.97	2.78	4.70	13.47	12.34	10.59	52.32
RK-05-1	3.26	3.20	6.55	11.62	16.02	7.61	51.22
RK-05-2	1.29	2.10	12.2	13.51	15.34	9.48	45.78
JGM-3-02	2.69	2.33	7.99	12.34	14.51	7.83	51.50
NARENDRA RAI	2.05	2.60	9.59	8.11	15.55	12.35	49.59
PAC-432	1.26	3.58	2.91	17.37	15.65	12.09	46.54
VARDAN	2.30	2.55	12.80	6.30	18.27	10.56	47.06
KLM-287	4.11	2.18	42.44	34.01	14.50	2.41	00.00
NDYR-8	2.08	2.02	14.36	15.42	7.35	7.19	50.93
NDRE-4	2.01	2.04	11.75	12.25	10.62	8.80	51.82
KRANTI	2.16	1.14	12.34	7.46	17.10	9.10	50.12
RL-2047	2.20	2.57	8.38	14.36	14.61	8.77	49.06
LET-20	3.52	2.50	35.60	26.25	14.37	7.27	10.26
PBG-1188	2.25	1.93	6.38	16.13	15.94	10.30	47.01
BIO-Q-108-2000	3.05	2.48	13.48	18.14	16.23	9.43	36.75
KRISHNA	2.47	3.22	6.53	10.29	18.53	9.18	49.75
VARUNA	3.75	2.23	7.54	12.00	14.32	7.51	52.45
General Mean	2.81	2.44	15.67	18.74	15.81	7.92	36.21
CD at 5 %	0.163	0.242	0.578	0.350	0.308	0.364	0.562

16:0=Palmitic acid, 18:0=Stearic acid, 18:1=Oleic acid, 18:2=Linoleic acid, 18:3=Linolenic acid, 20:1=Eicosenoic acid, 22:1= Erucic acid

Secondary metabolites in different species of Brassica vegetables grown in greenhouse

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Introduction

In Galicia (northwestern Spain), different *Brassica* species are used as leaf vegetable products for human and also for animal consumption. Kales (*Brassica oleracea acephala* group), cabbages (*B. oleracea capitata* group), leaf rape (*B. napus pabularia* group), and turnip tops and turnip greens (*B. rapa rapa* group) are the most important Brassica crops in this region. At the Misión Biológica de Galicia (CSIC, Spain), a collection of local varieties of these species is kept in a Germplasm Bank. The glucosinolate and phenolic profile, metabolites related with human health, has been previously studied in this collection (Padilla et al., 2007b; Velasco et al., 2007;2008; Cartea et al., 2008a; 2008b; Francisco et al., 2009) under field conditions. Nevertheless, due to the yield losses caused by several pests and the adverse weather conditions throughout the growing season, these crops are increasingly being cultivated under cover or greenhouse conditions. In these conditions, the content in secondary metabolites may be quite different and it has not been studied yet. For this reason, the objective of this work was to quantify the glucosinolate and phenolic content of four different crops: kale, cabbage, leaf rape and turnip greens grown under greenhouse conditions in two different times and to compare them with the same varieties studied in the field in different experiments.

Materials and Methods

Eight local varieties, currently kept in the Germplasm Bank at the 'Misión Biológica de Galicia' were evaluated in this study: two kale varieties (BOA) named 'MBG-BRS0468' and 'MBG-BRS0476' (*B. oleracea acephala*), two white cabbage varieties (BOC) named 'MBG-BRS0057' and 'MBG-BRS0074' (*B. oleracea capitata*), two leaf rape varieties (BN) named 'MBG-BRS0035' and 'MBG-BRS0063' (*B. napus pabularia*), and two turnip greens varieties (BR) named 'MBG-BRS0132' and 'MBG-BRS0401' (*B. rapa rapa*). The populations were planted in multipot-trays and seedlings were transplanted to bigger pots at the five or six leaves stage. Populations were evaluated in a randomized design with nine replications and 10 plants per replication. Leaf material was collected at two times (two and three months after transplanting). The third leaf of each plant was collected to extract and analyze glucosinolates and phenolic compounds. Greenhouse conditions were: light 16h/8h, maximum temperature 25 °C, minimum temperature 10 °C. The protocol for extraction and metabolite identification was followed as described by Francisco et al. (2009). Analyses of variance were made for each compound to compare species and varieties. Comparison of means was made by Fisher's protected least significant difference (LSD) at P=0.05 (Steel et al., 1997). All statistical analyses were made using SAS (SAS

Institute, 2007).

Results and Discussion

Twenty six compounds were found in the species studied, nine glucosinolates (GL), nine hydroxycinnamic acids (HA), and eight flavonoids (F). There were significant differences among species for total GL, HA and F ($P < 0.05$; data not shown). BR was the species with the highest GL concentration followed by BN, BOC, and BOA. BR showed also the highest HA concentration followed by BOA, BN, and BOC. Finally, BN and BOA had the highest concentration of F, followed by BR and BOC (Table 1). Regarding the variation of secondary metabolites over sampling times, the concentration of F decreased for BR and BOC in 14% and 5% and increased for BN and BOA in 30% and 18%, respectively. HA concentration decreased a 9% in BR while increased in the other species from 15% in BN to 61% in BOA. Concentration of aliphatic GL increased in all species from 38% in BR to 93% in BN. In the other side, indolic GL decreased from 6% in BOC to 26% in BOA. The only aromatic GL decreased in all species from 1% in BOA to 26% in BOC.

When comparing the GL composition of these varieties grown in greenhouse conditions with the GL content of the same varieties grown in the field (Padilla et al., 2007b; Cartea et al., 2008a; 2008b), the greatest differences on GL content were found in BN and BOC. In BN proportions of aliphatic and indolic GL were 92% and 7% in field conditions, and 73% and 22% in greenhouse conditions. BOC showed more indolic GL (52%) in greenhouse than aliphatic GL (42%). In the field these varieties showed 43% of indolic GL and a 58% of aliphatic GL. Besides, total GL concentration of the species grown in the field was, as a mean, 2.5 times higher than in the greenhouse, showing a better development of these species in field conditions. For phenolic compounds, we could only compare BR species (Francisco et al., 2009). In field conditions, F concentration was a 40% of total phenolics and HA the 60%. In greenhouse conditions, F were the 27% of total phenolics and HA the 73%.

Conclusion

These results showed that different crop conditions results in different concentrations of secondary metabolites. As GL, HA and F are metabolites with implications in human health (i.e. anticarcinogenic or antioxidant), it is necessary to establish the best conditions in the cultivation of these species to obtain the highest concentration of healthy compounds.

Acknowledgements

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Table 1. Mean ($\mu\text{mol g}^{-1}$ dw) for total glucosinolate content and phenolic compounds found in the four *Brassica* species evaluated at two sampling dates.

	<i>Brassica rapa</i>	<i>Brassica napus</i>	<i>Brassica oleracea acephala</i>	<i>Brassica oleracea capitata</i>
Aliphatic GL	25.90	11.23	4.59	4.94
Indolic GL	2.37	3.33	4.08	6.20
Aromatic GL	0.88	0.92	0.92	0.87
Total Glucosinolates	28.90	15.93	8.97	11.88
Total Hydroxycinnamic acids	28.79	20.45	22.78	14.37
Total Flavonoids	10.38	11.92	10.82	9.47
Total Phenolics	39.17	32.37	33.60	23.84

Consideration for metabolomic studies regarding glucosinolates in brassica oilseeds

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Introduction

Glucosinolates and transformation products of glucosinolates are key factors for the nutritional value of cruciferous oilseed crops and for the value of products produced from them. Considering the physiological effects of glucosinolates and glucosinolate products it seems to be possible to use appropriate structural types in concentrations of the compounds where they can function as food, feed and plant protection agents and/or as chemoprotection or health beneficial compounds without reaching the toxic levels of the compounds (Bellostas et al. 2007). This study aims to perceive the effect of different idiosyncratic environments (altitude and growth season) on synthesis of glucosinolate (GSL) in oilseed rape (*Brassica napus* L.) using metabolomics approaches such as vibrational spectroscopy, 'Near Infrared Spectroscopy' (NIR) coupled with multivariate statistical analysis such as 'Principal Component Analysis' (PCA).

Materials and Methods

Intake GSL of 125 seed samples of variety 'Abasin-95' obtained from two environments; one was Kaghan, Lesser Himalayan region (altitude of 2039m) and second was Peshawar, Hindu Kush region (altitude of 510m). One set of plant samples of one season (summer) was collected from Kaghan while two sets of plant samples were developed for two consecutive seasons (winter 1 and winter 2) at Peshawar. GSL of all 125 seed samples for three seasons of two environments were determined by NIR (FOSS 6500) at NIFA, Peshawar (William and Norris, 2001). Preliminary PCA analysis with mean centering was performed on all samples (Johnson and Wichern., 1998).

Results and Discussion

As shown in the Figure 1-A, the two extracted components of Principal Component Analysis explained 72.58% of sum of squares from the GSL data developed through NIR. Principal Component (PC)-1 score plot explained 42.34% of the total variance (R^2) As a result, GSL in seed samples from Kaghan and Peshawar were clearly separated by PC-2 (30.24%) The GSL synthesized at Peshawar during normal winter growth period (October to April) produced variances with the eigenvalue of 1.26 in PC-1 for the both seasons. The maximum variance of 2 was observed in PC-1 in both sets of data from Peshawar. The GSL determined in the plants at high altitude of Kaghan during summer growth period (May to August) attained maximum variance in PC-2 with an eigenvalue of 0.92. The low variance of -1 observed in PC-2 of data from Kaghan (Figure-1-B). This NIR analysis based on intake GSL concentration in seeds of rapeseed revealed compositional differences of this

secondary metabolite synthesized at different agro-climatic environs. The knowledge of heredity and variability in conjunction with metabolism studies through latest techniques in cruciferous oilseed crops is therefore of great relevance in order to explore health promoting effects of transformation products of GSL (Bellostas et al. 2007).

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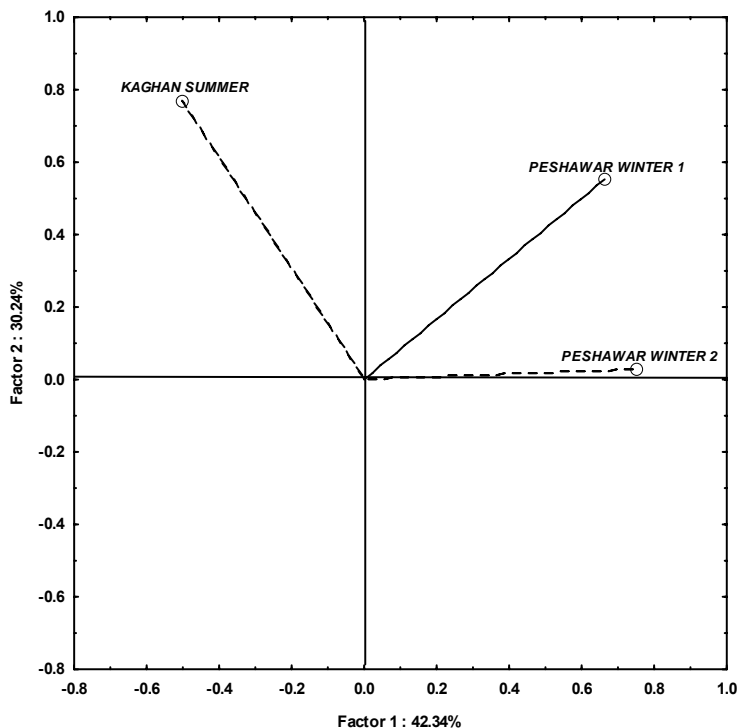
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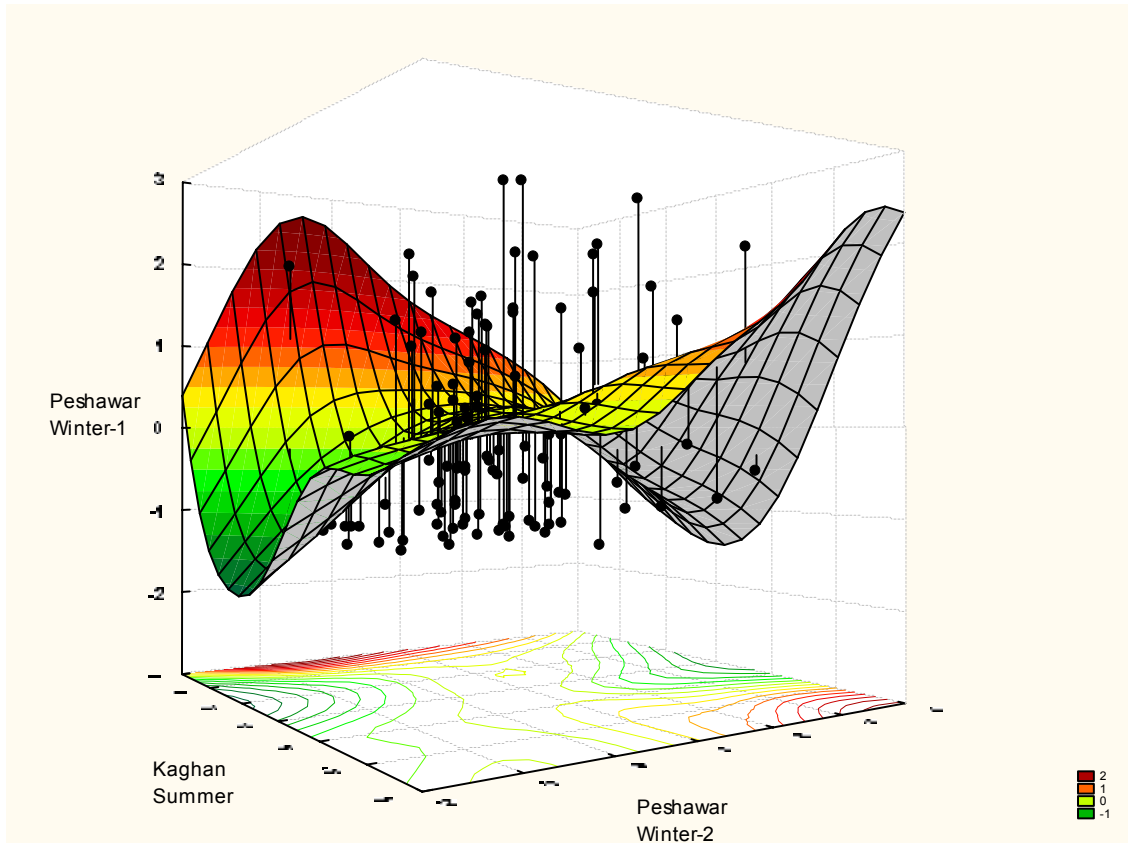
Figure 1.

A- Factor plot of first two principal components derived from near infrared (NIR) absorbance spectra of GSL concentration in rapeseed (*Brassica napus* L.) from low altitude region 'Peshawar' and high altitude region 'Kaghan'.

B- 3D surface projection of GSL concentration score loading of 125 rapeseed (*Brassica napus* L.) plant samples at three environments.

A





B

Assessment of genetic variability and correlation analysis in sprouting broccoli

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Abstract

Variability and correlation studies were undertaken in 22 genotypes of sprouting broccoli under the temperate climatic conditions of India. Considerable amount of variation was observed for different traits. Head weight ranged from 200 g to 680 g. Estimates for phenotypic coefficients of variation were higher than the genotypic coefficients of variation. Heritability estimates were high (>80%) for all the 6 traits studied whereas estimates for genetic advance were high (>70%) for head weight and plant weight. All the traits were significantly and positively correlated with head weight except number of leaves. Path coefficient analysis revealed that direct selection for plant weight and indirect selection for plant height, plant spread and number of leaves in the positive direction may lead to increased head weight.

Introduction

Broccoli (*Brassica oleracea* var. *italica*) is believed to be the first of the cole crops to evolve from the wild species of kale or cabbage. It is a relatively recent introduction to India and now gaining popularity due to its rich nutraceutical properties. The edible parts of broccoli plant are unopened flower buds and tender stem. They are good source of vitamin A, riboflavin or B₂ and calcium. Broccoli and cauliflower are quite similar morphologically but broccoli produces a green head with longer and more slender floret stalk than cauliflower. The purpose of the study was to determine the amount of variability present in the broccoli materials and to find out the interrelationship of various traits to chalk out an effective breeding strategy.

Materials and Methods

Materials for the study comprised of 22 genotypes of broccoli which were evaluated at the IARI, Regional Station, Katrain (H.P.) India located at 1467 m above msl, 32° 05.898 N latitude and 077° 08.160 E longitude. The experiment was laid out in a randomized complete block design with 2 replications maintaining row-to-row and plant-to-plant spacing at 45 cm. Observations were recorded on 5 randomly selected plants in each replication for plant height, plant spread, number of leaves per plant, plant weight, harvest index and head weight. Analysis of variance and components of variability were computed using standard statistical methods by Gomez and Gomez (1984). Genotypic and phenotypic variances were worked out following Burton and De Vane (1953). Heritability and genetic advance were calculated according to Johnson *et al.* (1955) and Robinson *et al.* (1949). The genotypic and phenotypic coefficients of variation were calculated according to Al-Jibouri *et al.* (1958). Path coefficients of various characters were calculated as suggested by Wright (1921).

Results and Discussion

Variances due to genotypes were found to be significant for all the six characters as revealed by the analysis of variance. The extent of variability measured in terms of mean and range, genotypic and phenotypic coefficients of variation, heritability and expected genetic advance as per cent of mean are presented in Table 1. Plant height and plant spread exhibited a similar range between 30.0-68.0 cm and 37.5-66.0 cm, respectively. Number of leaves ranged from 9.8-18.4 and harvest index between 40-85%. A wide range for plant weight and head weight was observed between 580-1400 g and 200-680 g, respectively. Estimates for phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) as also reported by Rattan *et al.*, (2006) indicating the role of environment in the expression of characters. The GCV estimates were maximum for head weight (48.35%) followed by plant weight (36.36%) and harvest index (29.12%). Broad sense heritability (H^2) estimates were high (>80%) for all the six characters. Genetic advance expressed as per cent of mean (GA as % of mean) was observed maximum for head weight (97.9%) followed by plant weight (72.7%) and harvest index (58.8%). Rest of the characters exhibited less than 50% values for GA as % of mean. Only two characters, plant weight and head weight exhibited high heritability along with high genetic advance indicating the role of additive gene action for these traits (Kalia and Shakuntla, 2002).

Phenotypic correlation coefficient as presented in Table 2 revealed that plant height had significant and positive correlation with all the characters except plant weight. Plant spread had significant and positive correlation with plant weight and head weight. Number of leaves did not show significant correlation any of the characters. Plant weight and harvest index were significantly and positively correlated with head weight. Path coefficient analysis was also performed to know the true nature of cause and effect relationship. Partitioning the correlation coefficient into direct and indirect effects (Table 3) revealed that plant weight had maximum direct effect (0.8167) on head weight followed by harvest index (0.6173). So, direct selection for plant weight may be important for increasing yield as it has also shown maximum significant and positive correlation with head weight (0.7798). Plant spread has shown maximum indirect effect (0.4774) followed by plant weight (0.2751) and number of leaves (0.2142) via plant weight. Harvest index has shown negative indirect effect (-0.0172) via plant weight. Therefore, it may be concluded that for increasing head weight direct selection for plant weight and indirect selection for plant height, plant spread and number of leaves may be effective.

Acknowledgements

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Table 1. Estimates of different parameters of variability for various quantitative traits in broccoli

Sr. No.	Character	Mean \pm SE	Range	GCV (%)	PCV (%)	H ²	GA as % of mean
1.	Plant height (cm)	47.7 \pm 3.1	30.0-68.0	17.65	18.78	0.88	34.1
2.	Plant spread (cm)	53.2 \pm 2.2	37.5-66.0	13.24	13.89	0.92	26.2
3.	No. of leaves	13.1 \pm 0.6	9.8-18.4	12.36	13.40	0.85	23.4
4.	Plant weight (g)	647.1 \pm 40.2	580-1400	35.82	36.36	0.97	72.7
5.	Harvest Index (%)	41.7 \pm 2.41	40-85	29.12	29.69	0.96	58.8
6.	Head weight (g)	269.9 \pm 24.8	200-680	48.35	49.23	0.97	97.9

GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation
 GA = genetic advance, H² = heritability coefficient

Table 2. Estimates of phenotypic correlation coefficients among different traits in broccoli

Character	Plant spread	Number of leaves	Plant weight	Harvest index	Head weight
Plant height	0.7259*	0.5202*	0.3369	0.5134*	0.5796*
Plant spread		0.3584	0.5233*	0.3386	0.6038*
No. of leaves			0.2622	0.1997	0.2888
Plant weight				-0.0211	0.7798*
Harvest Index					0.5994*

*Significant at P \leq 0.05

Table 3. Path coefficient analysis showing direct (diagonal) and indirect (off-diagonal) effects of 5 traits on Head weight in broccoli

Character	Plant height	Plant spread	No. of leaves	Plant weight	Harvest Index	Correlation with Head weight
Plant height	0.0563	-0.0380	-0.0307	0.2751	0.3169	0.5796
Plant spread	0.0409	-0.0523	-0.0212	0.4274	0.2090	0.6038
No. of leaves	0.0293	-0.0188	-0.0591	0.2142	0.1232	0.2888
Plant weight	0.0190	-0.0274	-0.0155	0.8167	-0.0130	0.7798
Harvest Index	0.0289	-0.0177	-0.0118	-0.0172	0.6173	0.5994

Development of low erucic acid mustard (*Brassica juncea* L.) mutants

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Introduction

Cruciferous crops including rapeseed and mustard are broadly cultivated throughout Pakistan, and the largely for edible vegetable oil production. In cool temperate climates with good moisture availability, rapeseed (*Brassica napus* L.) is preferred and is the most productive. But where moisture availability is not appropriate, most of the area is cultivated to mustard crop (*Brassica juncea* L.). Indigenous available mustard germplasm possess desirable agronomic characteristics but possess high-erucic and high-glucosinolate contents. Breeding through induction of mutations using gamma irradiation for low-erucic acid germplasm of *B. juncea* is attempted to develop canola quality mustard in Pakistan.

Materials and Methods

Gamma irradiated mutagenized population of mustard crop (*Brassica juncea* L.) at doses of 0.8, 1.0 and 1.2 Gys was raised using standard "induced mutation techniques" and "pedigree method" (IAEA, 1997). Mutant plants were grown to produce modified levels of erucic acid and isolated plants with the desired modified level of erucic acid through Near Infrared Reflectance Spectroscopy (Reinhardt and Röbbelen, 1992). Two selection cycles in $M_{2,4}$ had to be made to recover a true breeding mutant line that exhibited the modified erucic acid level in a genetically stable manner. The agronomic performance and seed quality attributes of selected mutant lines was evaluated in field trials at the Experimental Research Farm at Nuclear Institute for Food and Agriculture (NIFA), Peshawar, Pakistan.

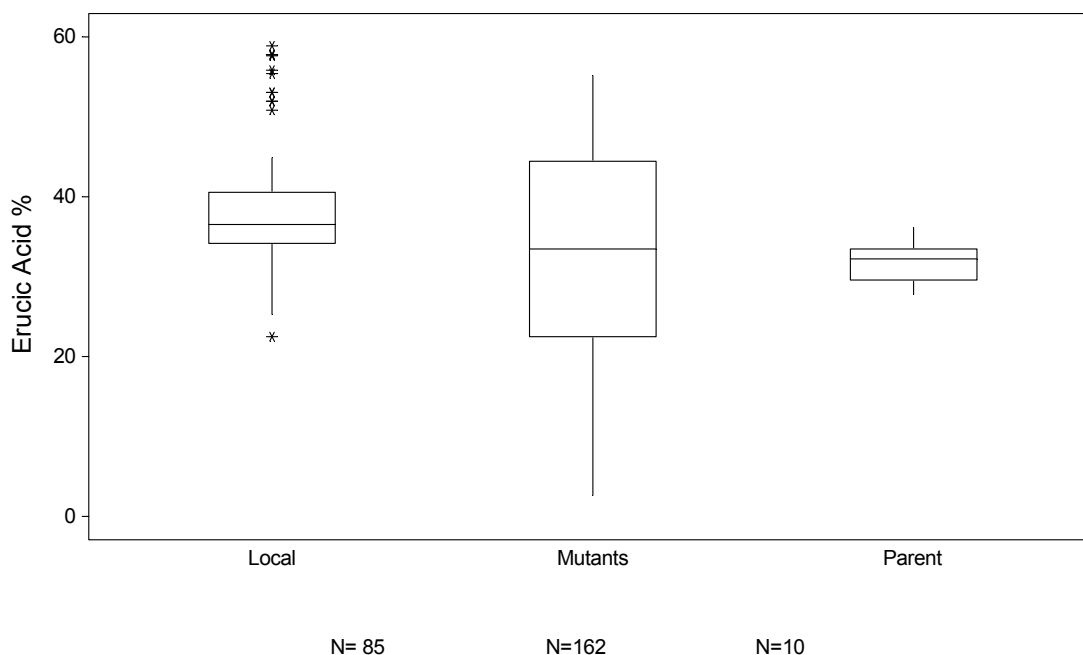
Results and Discussion

The average erucic acid content (31.9%) of the parent lines was typical. The erucic acid level content, which was determined in selfed seed material from individual plants of 85 accessions of local germplasm showed considerable variation ranging 22.5 to 58.9% (Fig. 1). The group of 162 mutant progenies in M_4 generation obtained an average erucic acid content of 34.1%. The minimum low concentration of erucic acid was determined up to 2.7% in seeds of some mutant progenies, while maximum (55.2%) high erucic acid content was observed in some other mutant progenies. The gamma radiation doses, induced mutations for erucic acid content in mustard crop with effective and competent magnitude is reported earlier (Syed and Rehman, 2009). The two-way mutation spectrum for erucic acid level was observed with a variance of 192.77 in the mutant population. The present findings confirmed the expediency of induced mutations for the development of canola type mustard crop through selection of mutant lines with low erucic acid content (Bhatia et al, 1999).

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Figure 1- Variation of Erucic Acid levels in local germplasm, mutant progenies and parent line (N = number of individual plants)



Evaluation of SI and CMS systems based F₁ hybrids of cabbage under temperate conditions of India

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Abstract

Self incompatibility (SI) and cytoplasmic male sterility (CMS) are important pollination control mechanisms used for commercial production of F₁ hybrid seeds in cole crops. Six SI and one CMS (Ogura) lines of cabbage developed at our station were used as female parents for developing 49 F₁ hybrids including one identified F₁ hybrid, KGMR-1 as check. These hybrids were evaluated for 8 important horticultural traits. Among these the hybrids KTCBH-4 and KTCBH-6 had highest yield (50.3 t/ha) followed by KTCBH-2 (49.9 t/ha). The hybrids, KTCBH-25 and KTCBK-28 were earliest in maturity (72.5 days) whereas, KTCBH-35 took maximum time for maturity (112.5 days). Among the hybrids evaluated few had more yield potential and better for yield as well as other traits as compared to the check, KGMR-1 indicating potentiality of the systems in the development of F₁ hybrids in cabbage.

Introduction

Among the vegetable *brassic* grown in India, F₁ hybrids are highly popular in cabbage (*Brassica oleracea* var. *capitata*) because of uniform maturity, better head quality, early maturity and resistance to biotic stresses besides, higher yield. Two pollination control mechanisms viz., self-incompatibility (SI) and male sterility (particularly CMS) are used for commercial hybrid seed production of cabbage. As self-incompatibility widely exists in cabbage, stable self-incompatible lines are used as the parents to produce hybrids (Fang *et al.*, 2004; Watanabe and Hinata, 1990). Until now all cabbage hybrid seeds have been produced using self-incompatible lines all over the world (Fang *et al.* 2004). However, SI system has several disadvantages like, possibility of sibs in the hybrids and multiplication of SI parents through bud pollination or CO₂ and NaCl spray (Kucera, 1990). Hence, CMS system offers a suitable alternative for F₁ hybrid seed production (Kucera *et al.* 2006). Presently, the Ogura cytoplasm from Japanese radish is the only source of male sterility used in cole group of crops for development of F₁ hybrid seeds. Initially the system suffered from low temperature chlorosis. However, protoplast fusion was successful in replacing the defective chloroplast of Japanese radish by *Brassica oleracea* chloroplast. In our station six SI lines were developed after proper screening for effective SI system. The CMS line developed after BC₉ was free from chlorosis at low temperatures and any floral deformities. So, these lines were suitable as female parents for development of F₁ hybrids. Present study was conducted to evaluate the potentiality of these CMS and SI lines for their utilization in heterosis breeding programme.

Materials and Methods

Six SI lines (S-621, S-624, S-645, S-208, S-691 and S-696) and one CMS (Ogura) line (GA-804) were utilized for development of 48 F₁ hybrids during 2008. These hybrids were evaluated along with an identified F₁ hybrid, KGMR-1 as check during rabi season of 2009 at IARI, Regional Station, Katrain. Each entry was replicated twice in a randomized block design. Row to row and plant to plant distance was maintained at 45 cm each in 3m × 3m plot size. All the recommended cultural practices were adopted to raise a successful crop. Data were recorded for 8 horticultural important traits viz. frame size (cm), numbers of leaves, head size index (cm), gross weight (kg), net weight (kg), harvest index (%), yield (q/ha) and days to maturity. Five plants were randomly selected among 18 plants for recording of data and statistical analysis was conducted as per Sukhatme and Amble (1995).

Results and Discussion

Frame size is an important trait determining commercial acceptability of cabbage in large scale. Cultivar with larger frame size increases the planting distance thus reducing the total yield per unit area. Thus, smaller frame size is desirable for cabbage cultivars. The hybrid, KTCBH-28 had lowest frame size (40.4 cm) where as the commercial check KGMR-1 had frame size of 40.7 cm (Table 1). Cultivars with lower number of non wrapper leaves and with higher yield are more desirable. The hybrid, KTCBH-6 had lowest number of leaves (11.6) followed by KTCBH-39 (12.5). Harvest index is very important which determines the ability of a cultivar to divert total energy towards the development of the economically important parts. Among the 49 hybrids harvest index was highest in KTCBH-31 (81.9%) followed by KTCBH-19 (70.3%) and KTCBH-41 (70.2%). A large number of the evaluated hybrids had significantly higher yield than the commercial check, KGMR-1, indicating good scope in utilizing these SI and CMS lines for the development of heterotic hybrids. Yield was highest in the hybrids KTCBH-4 and KTCBH-6 (50.3 t/ha) followed by KTCBH-2 (49.9 t/ha) and KTCBH-34 (49.1 t/ha). The hybrids showing earliest maturity were, KTCBH-25 and KTCBK-28 (72.5 days) whereas, KTCBH-35 took maximum time for maturity (112.5 days).

From the evaluation data it was clear that there was large number of F₁ hybrids based on SI and CMS systems which had better yield and related traits. Thus, these SI and CMS lines can be utilized in the development of F₁ hybrids in cabbage. Moreover, SI lines had strong and stable self incompatibility reaction. Easier maintenance of the SI lines through CO₂ or NaCl treatment would be highly useful for use of these lines in the development of F₁ hybrids in cabbage. The presently used CMS line was free from chlorosis at low temperatures and any floral deformities (Chander parkash and Verma, 2002). Thus, proper maintenance of this line and its use in the development of F₁ hybrids through honeybees is to be standardized.

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Table1. Mean performance of 48 cabbage hybrids for various quantitative traits

S. No.	Hybrids	Frame size (cm)	No. of non wrapper leaves	Head size index (cm)	Gross wt. (kg)	Net head wt. (kg)	Harvest index (%)	Yield (t/ha)	Days to maturity
1.	KTCBH-2	57.1	14.5	291.6	2.350	1.280	54.3	49.9	92
2.	KTCBH-3	54.5	13.9	245.7	2.070	1.060	51.2	41.3	102
3.	KTCBH-51	51.4	15.6	225.8	1.830	1.180	64.3	46.0	82
4.	KTCBH-4	52.5	13.9	253.2	2.050	1.290	63.8	50.3	92
5.	KTCBH-5	58.7	16.2	237.9	2.150	1.100	51.0	42.9	92
6.	KTCBH-6	50.8	11.6	248.4	1.880	1.290	68.6	50.3	92
7.	KTCBH-7	47.9	14.8	212.7	1.690	1.110	65.9	43.2	82
8.	KTCBH-8	51.3	13.3	197.2	1.580	1.020	64.3	39.7	97
9.	KTCBH-9	53.1	15.6	235.9	1.880	1.130	60.0	44.0	92
10.	KCH-5	52.2	17.4	224.9	2.110	1.260	59.8	49.1	79
11.	KTCBH-10	49.0	15.1	225.2	1.720	1.040	60.5	40.5	79
12.	KTCBH-11	50.1	14.9	210.7	1.827	1.055	57.6	41.1	92
13.	KCH-9836	49.6	14.3	225.5	1.800	1.110	61.8	43.2	82
14.	KTCBH-12	44.1	15.0	163.1	1.250	0.810	64.5	31.5	82
15.	KTCBH-13	47.5	21.6	192.0	1.640	0.940	56.9	36.6	84
16.	KTCBH-14	46.6	16.0	172.6	1.560	0.870	57.6	33.9	87
17.	KTCBH-15	44.2	15.2	157.6	1.330	0.790	59.2	30.8	92
18.	KTCBH-84	48.3	15.1	189.0	1.530	1.010	66.0	39.3	76
19.	KTCBH-16	46.7	14.5	190.5	1.650	0.970	58.7	37.8	82
20.	KTCBH-86	48.8	15.9	199.2	1.620	0.880	54.3	34.3	79
21.	KTCBH-17	44.9	15.4	165.0	1.330	0.840	63.1	32.7	79
22.	KTCBH-18	41.8	16.3	188.0	1.330	0.760	57.5	29.8	82
23.	KTCBH-19	43.0	13.9	189.0	1.220	0.860	70.3	33.5	79
24.	KTCBH-20	41.7	13.1	157.1	1.090	0.720	66.0	38.0	72.5
25.	KTCBH-21	47.2	18.5	209.9	1.540	0.840	54.5	32.7	87
26.	KTCBH-22	46.1	16.9	174.3	1.520	0.730	47.6	28.4	87
27.	KTCBH-23	42.9	15.0	160.1	1.110	0.680	61.6	26.5	82
28.	KTCBH-24	42.1	17.3	178.3	1.240	0.830	66.9	32.3	82
29.	KTCBH-25	45.3	15.2	172.5	1.260	0.840	66.5	32.7	72.5
30.	KTCBH-26	53.15	15.0	193.1	1.945	1.007	51.7	39.2	101
31.	KTCBH-27	47.5	16.8	174.8	1.580	0.910	57.5	35.4	84
32.	KTCBH-28	40.4	14.5	169.5	1.100	0.710	64.5	27.6	72.5
33.	KTCBH-29	51.4	15.3	197.1	1.620	0.970	59.9	37.8	82
34.	KTCBH-30	52.5	15.9	180.2	1.630	0.850	52.1	33.1	87
35.	KTCBH-31	45.1	14.2	189.3	1.190	0.975	81.9	38.0	87
36.	KTCBH-32	48.3	12.6	234.1	1.695	1.115	65.8	43.4	87
37.	KTCBH-33	50.1	16.1	201.9	1.560	0.975	62.5	38.0	79
38.	KTCBH-34	49.4	18.8	226.8	1.980	1.260	63.6	49.1	87
39.	KTCBH-35	52.9	17.9	205.2	1.980	0.990	50.0	38.6	112.5
40.	KTCBH-36	51.5	13.9	273.9	1.590	0.870	54.7	33.9	92
41.	KTCBH-37	46.7	15.5	161.6	1.260	0.780	61.9	30.4	97
42.	KTCBH-38	48.3	19.0	214.4	1.860	1.180	63.3	46.0	82
43.	KTCBH-81	48.7	13.5	228.7	1.690	1.180	68.6	46.0	76
44.	KTCBH-39	57.0	12.5	217.3	2.145	1.132	52.8	44.1	97
45.	KTCBH-41	46.0	12.6	189.3	1.390	0.980	70.2	38.2	76
46.	KTCBH-42	53.95	15.4	190.0	1.765	0.925	51.9	36.0	97
47.	KTCBH-43	51.8	13.9	211.0	1.920	1.040	54.4	40.5	82
48.	KTCBH-85	51.8	14.8	195.5	1.560	0.880	56.4	34.3	84
49.	KGMR-1 (C)	40.7	17.6	170.5	1.240	0.910	75.4	35.4	72.5
	CD at P≤0.05	6.09	2.38	57.13	0.510	0.340	9.89	13.4	13.3

Introgression of osmotin gene leads to enhanced drought tolerance in *Brassica juncea*

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Introduction

In nature, plants encounter different environmental stresses. Out of these drought is one of the most serious yield-reducing stress in agriculture. To counter the effects of stress, plants undergo a process of stress acclimation. This process may require changes in the flow of metabolites through different pathways, the suppression of pathways that may be involved in the production of RO during stress, and the induction RO scavenging enzymes (Dat et al., 2000) and expression of specific genes and synthesis of a large number of stress-related proteins. Osmotin is stress responsive proteins which comes under pathogenesis related protein but express in response to abiotic stress also (Parkhi et al, 2009).Osmotin, play important role in maintaining osmotolerance by facilitating the compartmentation of solute (Barthakur et al, 2001).

We transferred osmotin gene under the control of CaMV 35 promoter in Brassica and used here as model plant (data not shown). In the present investigation, effect of water stress at different time intervals was studied using both non-transformed and transformed plant as study material.

The accumulation of free proline in the tissue of several plant species is regarded as a general response to various kind of abiotic stress (Nayar and Walia, 2003; Delauney and Verma, 1993). Hanson, Nelson & Everson (23) considered proline accumulation to be a symptom of damage.

Materials and Methods

Estimation of proline, H₂O₂ and free radical level: The procedure of Bates *et al.* (1973) was used for determination of proline content. The H₂O₂ level was measured colorimetrically as described by Jain and Choudhury (1980). Malondialdehyde (MOA) was extracted with trichloroacetic acid and determined according to Heath and Packer (1968).

Estimation of leaf relative water content: Relative water measurements were made on fully expanded young leaf from each plant according to the method of Bansal and Nagarajan (1987) after 3, 4, 5, 7 and 10 days of water stress.

Results

Water stress was imposed in two transformed and three non-transformed Brassica plant hardened and grown in poly house by withholding water for 10 days. Proline, H₂O₂ and free radical accumulation and relative water content (RWC) was recorded on 0, 3, 4, 5, 7 and 10 days (Fig 1).

Proline accumulation: The proline content increased marginally in transformed plant whereas non-transformed plant accumulated higher levels of proline when subjected to water stress. The proline content was 625 and 740 μg in OsmG1 and OsmG2 on 10th day of water stress, whereas non-transformed plant accumulated more than ten times i.e., 7800, 9850 and 7450 μg proline/g fresh weight on 10th day of water stress (Fig. 2).

H₂O₂ accumulation: The basal level of H₂O₂ was more or less similar in both transformed and non-transformed plant. A 3 and 3.77 fold increase in H₂O₂ production was observed in OsmG1 and OsmG2 at 10th day from the basal level whereas non-transformed plant (C1, C2 and C3) exhibited 4, 3.57 and 4.36 fold increase in H₂O₂ accumulation at 10th day of water stress from the basal level. The H₂O₂ production was 42.85, 44.63 and 42.85 n mol in C1, C2 and C3 plants whereas OsmG1 and OsmG2 accumulated 27.67 and 30.35 n mol/g fresh weight on 10th day of water stress (Fig 3).

Free radical accumulation: Free radical accumulation was high in transformed plant in comparison to non-transformed plant with time. Free radical production was observed with 3.43, 6.5, 3.3, 3 and 3.3 fold increase at 10th day of stress in OsmG1, OsmG2, C1, C2 and C3 from the basal level. The free radical production was 3548, 3725 and 3548 n mol in C1, C2 and C3, respectively, whereas in transformed plant OsmG1 and OsmG2 showed 2129 and 2306 n mol/g fresh weight at 10th day at stress, respectively (Fig. 4).

Relative water content: One of the transformed plants maintained significantly higher RWC as compared to the non-transformed plants. The RWC at 10 day was 42.32, 26.68 and 43.69% in non-transformed plant whereas in transformed plant it was 87.58 and 58% (Table 1).

Discussion

Many plant systems can survive dehydration, but to different extents. In response to cellular dehydration, many plants and microorganisms accumulate compatible solutes, irrespective of whether the dehydration is brought about by drought, freezing or osmotic shock. Among them are proline, glutamate, glycine, betaine, carnitine, mannitol, sorbitol, fructans, polyols, trehalose, sucrose and oligosaccharides. The accumulation of free proline in plants may be part of a general adaptation to water stress (Hare et al., 1998). Our results also showed that dehydration increases the proline accumulation in non-transformed plant.

The free radical and H₂O₂ accumulation was seen in both transformed and non-transformed plant under water stress. The level of free radical and H₂O₂ was higher in non-transformed plant.

At low concentrations, AOS induce genes and adaptive responses. Sub-lethal levels of AOS are able to acclimate plants to biotic and abiotic stress conditions and reduce plant growth, probably as part of an additional response (Breusegen *et al.*, 2001). At higher concentrations AOS trigger a genetically controlled cell death programme. Our results also are consistent with this hypothesis. The non-transformed plant show severe wilting and senescence of leaves (at 10 day of water stress high level of AOS) which is a type of cell death. While transformed plant does not show wilting and senescence of leaves (low level of AOS). The results of this study confirm the reports of others that there is an increase in the proline concentration of water stressed plants. The water stress result confirmed that osmotin provide protection against dehydration conditions which may be due to drought.

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Table 1. Effect of water stress on RWC (%) in leaves of transformed and non-transformed *Brassica* plants

	0 day	3 rd day	4 th day	5 th day	7 th day	10 th day
C1	97.3	89.5	95.35	81.5	58.39	42.32
C2	94.5	84.0	84.5	68.0	41.0	26.68
C3	94.5	81.5	76.0	56.5	57.8	43.69
Osm G1	97.0	93.0	92.0	90.5	88.73	87.58
Osm G2	95.0	89.5	84.5	83.5	80.74	58.0

CRUCIFERAE NEWSLETTER Nr. 31

Instructions to the authors – 2011

Deadline for contribution submission: December 1st 2011

The current issue of the Cruciferae Newsletter (vol. 31) will be published online at the beginning of year 2012 from the Brassica website (<http://www.brassica.info/info/publications/cruciferae-newsletter.php>). Online process will ensure rapid publication of your contribution. Therefore, we should be grateful if you would, please, follow the instructions below.

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2- Authors should submit manuscripts only by email to cruciferaenewsletter@rennes.inra.fr. A manuscript file in Microsoft Word (or some other word processing format) is required. The manuscript file must be named as following: **Full name of the first author_Year of submission.doc or .rtf**.

3- As previously contributions must not exceed **2 pages**, including tables, figures and photographs. **Arial 10** character is expected with single spacing (**please use the submission form below**).

4- The heading of the paper must be written in boldface letters and must include the title (1st line), followed by the author names (lines below) and their address (3rd lines) with the email address of the corresponding author.

5- Tables, figures and photographs must be included in, or at the end of the text.

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Table 1. Title

Figure 1. Title