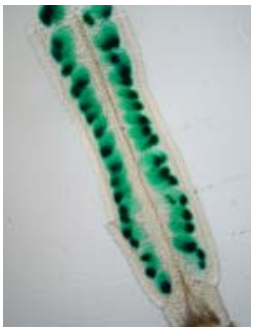
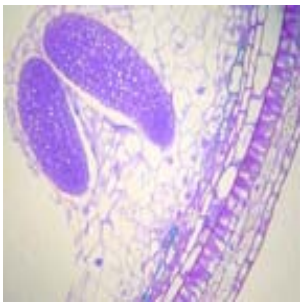
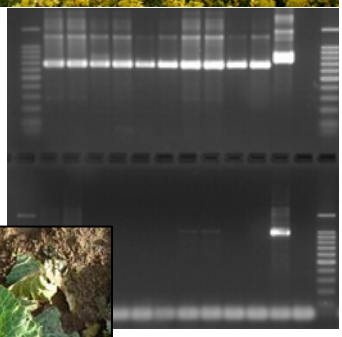
Cruciferae Newsletter



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On behalf of the editing group,

Dr. Nathalie NESI, Dr. Anne-Marie CHEVRE,

Dr. Maria MANZANARES-DAULEUX, Asma ALLEE

Contact:

UMR 118 INRA-Agrocampus Ouest-Univ. Rennes1

Plant Genetics and Biotechnology Laboratory

BP 35327, 35653 Le Rheu cedex, France

http://www.rennes.inra.fr/apbv/index.htm

email: cruciferaenewsletter@rennes.inra.fr

Pictures of the cover page are generous gifts from the Brassica team of Rennes.

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Karyotypic variation in some cultivated species of *Brassicaceae*

Nandjee Kumar*, S. R. Choudhary and R. B. Kumar
Department of Botany, Magdh University, Bodhgaya-824234, INDIA
*Corresponding author: kumarnandjee@rediffmail.com

Abstract
Karyotypic studies were made in five cultivated species of *Brassicaceae* viz *Iberis amara* L., *Brassica campestris* L., *Brassica rapa* L., *Brassica oleracea* L. and *Raphanus sativus* L. The somatic chromosome number was determines as 2n=14 in *Iberis amara*, 2n=20 in *Brassica campestris* and *Brassica rapa* while 2n=18 in *Brassica oleracea* and *Raphanus sativus*. A significant interspecific variation of mean chromosome size and total chromatin was noted. Obviously *Iberis amara* and *Raphanus sativus* had symmetrical while *B. campestris, B. rapa* and *B. oleracea* had asymmetrical karyotype.

Introduction
Brassicaeae is a large family with many economically important short cycled oleiferous cultivated species of which *Brassica* ranks fifth among the oilseed crops with high protein and erucic acid content. The present study constitutes a comparative karyotypic analysis in some cultivated crucifers with a view to understand the interspecific relationship and evolutionary trend amongst *Brassica* species.

Material and methods
The materials used in the present investigation include five species of *Brassicaeae* viz *Iberis amara* L., *Brassica campestris* L., *Brassica rapa* L., *Brassica oleracea* L. and *Raphanus sativus* L. The seeds were obtained from the courtesy of the Department of Genetics and Plant Breeding Rajendra Agriculture University, Pusa, and were germinated on separate Petri dishes lined with moist blotting paper for germination. The pretreated root tips were stained and squashed in 2 % acetocarmine and the karyotypic analysis was done as described by Huziwara (1962).

Results and discussion
In general mitosis was almost normal with variation in chromosome number, size and chromatin length and TF (%). The somatic chromosome number varied from 2n=14 in *Iberis amara*, 2n= 18 in *B. oleracea* and *Raphanus sativus* and 2n=20 in *B. campestris* and *B. rapa* which might have been caused by aneuploidy or mutation.
On the basis of total chromatin length the cultivated crucifer may be categorized as *rapa-oleracea* group with maximum chromatin length, *campestris-raphanus* group with minimum chromatin length and *Iberis* group with intermediate chromatin length (table 1). Such karyotypic variations constitute potential evolutionary units to form species and sub-species. When differences between the length of smallest and the longest pair of chromosomes are large, the karyotype is symmetrical and the species is more evolved than those having symmetrical karyotype (Levitzky, 1931; Stebbins, 1971). Conspicuously the *Brassicas* are more evolved than *Iberis* and *Raphanus*. Further the cultivated crucifers varied significantly in mean chromosome size and chromatin length (table 2).

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Table 1. Somatic chromosome number, length of chromosome pairs, total chromatin length and karyotypic formula of some cultivated crucifers.

Species	Chromosome number (2n)	Chromosome length (µm)	Total chromatin length (µm)	Total form (%)	Karyotypic formula
Iberis amara	14	2.81 ± 0.18	39.36	36.43	$C_2 + D_{12}$
B campestris	20	1.82 ± 0.13	36.56	43.65	$D_2 + E_4 + F_{14}$
B rapa	20	2.54 ± 0.11	44.46	39.00	$D_6 + E_6 + F_8$
B oleracea	18	2.70 ± 0.13	48.60	41.55	$C_4 + D_{10} + E_2 + F_2$
R sativus	18	2.09 ± 0.25	37.74	42.44	$D_{12} + E_2 + F_4$

Table 2. Analysis of variance of mean length of chromosome and total chromatin length in some cultivated crucifers.

Source of variation	Parameter	SS	df	MS	F	P
Between species	ML	1.307	4	0.326	81.50	0.001
	TL	452.48	4	113.12	251.37	0.001
Within species	ML	0.001	1	0.001	0.25	NS
	TL	0.004	1	0.004	0.008	NS
Residual	ML	0.016	4	0.004	-	-
	TL	1.80	4	0.450	-	-

ML, mean chromosome length

TL, total chromatin length

Hybridization of Ethiopian mustard (*Brassica carinata*) and *Brassica napus* assisted through cytogenetic studies

F.A. Sheikh[1], Shashi Banga, S.S. Banga, S. Najeeb[1], G.A. Parray [1] and A.G. Rather[1]
Department of Plant Breeding, Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, 141 004, INDIA
[1] Rice Research & Regional Station (SKUAST-K), Khudwani, Anantnag-192102
Correspondence: sfaroq4@rediffmail.com

Abstract
The present study was undertaken to develop agronomically superior genotypes of *Brassica carinata* (BBCC, 2n=34) with improved oil and meal quality through interspecific hybridization using elite genotypes of *B. napus* (AACC, 2n=38) as donor parents. The cytogenetic studies were carried out in each segregating populations to select and advance genomically stable *B. carinata* genotypes which saved time and resources.

Keywords: *B. carinata,* interspecific hybridization, autosyndetic pairing, allosyndetic pairing

Introduction
Brassica carinata (BBCC, 2n=34) is the most neglected species in terms of crop improvement. The naturally high levels of erucic acid and very low levels of oil content as well as the restricted amount of genetic variability available in natural *B. carinata* for these traits require use of new sources of variability for broadening the genetic base of source population. Interspecific hybridization has a great potential and is widely used to expand gene sources and to introduce exogenous genes in crop *Brassica* species (Inomata, 1992).

Material and Methods
Brassica carinata cv. PC5 was crossed as a male with different elite cultivars *Brassica napus (*AACC, 2n=38). The interspecific nature of hybrids was confirmed on the basis of morphological and cytological basis. The flower buds were fixed in Carnoy's solution II. After 48 hours of fixing, the young anthers were crushed in 2 % acetocarmine to study the chromosome number and pairing behaviour of chromosomes. The F_1 plants were backcrossed to *B. carinata* to improve fertility and seed setting. The BC_1 plants that showed the maximum bivalents, had high pollen fertility and were morphologically similar to *B. carinata* were backcrossed to give the BC_2 generation. These BC_2 plants were further subjected to cytological analysis and the plants showing high pollen fertility, genomic stability (2n=34) and morphological akinness to *B. carinata* were tagged and subjected to fatty acid, oil and glucosinolate analyses as per the standard procedures.

Results and discussion
The cytological studies on the pollen mother cells (PMCs) of *B. napus* x *B. carinata* hybrid (ABCC) revealed a somatic chromosome number of 2n=36 with occurrence of up to 12 bivalents and 10 univalents coupled with one trivalent and one quadrivalent in most of the cells (Table 1). The occurrence of high number of bivalents and

multivalents in the hybrid is expected due to homologous pairing between the chromosomes belonging to the common C genome, intragenomic autosyndetic pairing due to inherent homologies in A, B and C genomes (Roebbelen, 1960) and to some extent allosyndetic pairing between A and B chromosomes. In BC_1 plants of *B. napus* x *B. carinata* with *B. carinata*, the somatic chromosome number varied from 29 to 41 with 2II+17I as the predominant meiotic configuration at a frequency of 45 %. However, the occurrence of trivalents and quadrivalents in many cells might have resulted from the allosyndetic pairing (Attia and Roebbelen, 1986), which could increase the variability in *B. carinata* through introgression of desirable genes from A genome of *B. napus* (Prakash, 1973). Those BC_1 plants, which were morphologically similar to *B. carinata* and had high pollen grain stainability, were backcrossed to raise the BC_2. In BC_2, 17II being the predominant meiotic configuration configurations with frequency 0.66. The cytogenetic studies helped in selection and advancing of genomically stable *B. carinata* genotypes in segregating populations derived from the interspecific cross and saved time and resources.

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Roebbelen G (1960). Beitrage Zur Analyse des Brassica–Genome. Chromosome II: 205-228

Table 1. Meiotic studies in F_1 and backcross progenies of (*B. napus* x *B. carinata)* x *B. carinata*

Combination	Generation	PMCs	Meiotic Profile		Mean frequency		
			Configuration	Proportio	II	III	IV
B. napus x B. carinata	F1	97	11 II + 1 IV + 10I 12II + 1III + 9I	0.57 0.43	11.4	0.4	0.6
	BC1	144	10II + 9I 11II + 13I 11II + 10I + 1 IV 12II + 17I 12II + 1III + 1IV + 5I 13II + 10I	0.06 0.06 0.11 0.45 0.22 0.10			
	BC2	81	15II + 5I 16II + 3I 17II	0.20 0.14 0.66	16.4	-	-

Cytogenetic studies of F_1 and backcross generations of Ethiopian mustard (*Brassica carinata*) and Indian mustard (*Brassica juncea).*

F.A. Sheikh[1], Shashi Banga, S.S. Banga, S. Najeeb[1], G.A. Parray [1] and A.G. Rather[1]
Department of Plant Breeding, Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, 141 004, INDIA
[1] Rice Research & Regional Station(SKUAST-K), Khudwani, Anantnag-192102
Correspondence: sfaroq4@rediffmail.com

Abstract
The present study was undertaken to develop agronomically superior genotypes of *Brassica carinata* (BBCC, 2n=34) with improved oil and meal quality through interspecific hybridization using elite genotypes of *Brassica juncea* (AABB, 2n=36) as donor parents. The cytogenetic studies were carried out in each segregating populations to select and advance genomically stable *B. carinata* genotypes which saved time and resources.

Keywords: *B. carinata,* interspecific hybridization, autosyndetic pairing, allosyndetic pairing

Introduction
Brassica carinata (BBCC, 2n=34) is the most neglected species in terms of crop improvement. The naturally high levels of erucic acid and very low levels of oil content and the restricted amount of genetic variability available in natural *B. carinata* for these traits require use of new sources of variability for broadening the genetic base of source population. Interspecific hybridization has a great potential and is widely used to expand gene sources and to introduce exogenous genes in crop *Brassica* species (Inomata, 1992).

Material and Methods
Brassica carinata cv. PC5 was crossed as a male with different elite cultivars *Brassica juncea (*AABB, 2n=36). The interspecific nature of hybrids was confirmed on the basis of morphological and cytological basis. The flower buds were fixed in Carnoy's solution II. After 48 hours of fixing, the young anthers were crushed in 2 % acetocarmine to study the chromosome number and pairing behaviour of chromosomes. The F_1 plants were backcrossed to *B. carinata* to improve fertility and seed setting. The BC_1 plants that showed the maximum bivalents, had high pollen fertility and were morphologically similar to *B. carinata* were backcrossed to give the BC_2 generation. These BC_2 plants were further subjected to cytological analysis and the plants showing high pollen fertility, genomic stability (2n=34) and morphological akinness to *B. carinata* were tagged and subjected to fatty acid, oil and glucosinolate analyses as per the standard procedures.

Results and discussion
The cytological studies on the pollen mother cells (PMCs) of *B. juncea* x *B. carinata* hybrid (ABCC) revealed a

somatic chromosome number of 2n=36 with occurrence of up to 12 bivalents and 13 univalents with the mean bivalent frequency of 11.3 (Table 1). The occurrence of high number of bivalents and multivalents in the hybrid is expected due to homologous pairing between the chromosomes belonging to the common B genome, intragenomic autosyndetic pairing due to inherent homologies in A, B and C genomes (Roebbelen, 1960) and to some extent allosyndetic pairing between A and C chromosomes. In BC_1 plants of *B. juncea* x *B. carinata* with *B. carinata* the somatic chromosome number varied from 28 to 35. Up to 17 IIs were observed with 12II +1III + 3I the predominant meiotic with the frequency of per cent. However, the occurrence of trivalents and quadrivalents in many cells might have resulted from the allosyndetic pairing (Attia and Roebbelen, 1986), which could increase the variability in *B. carinata* through introgression of desirable genes from A genome of *B. juncea* (Prakash, 1973). In BC_2, 17II being the predominant meiotic configuration configurations with mean bivalent frequency of 16.88. The cytogenetic studies helped in selection and advancing of genomically stable *B. carinata* genotypes in segregating populations derived from the interspecific cross and saved time and resources.

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Roebbelen G (1960) Beitrage Zur Analyse des Brassica–Genome. Chromosome II: 205-228

Table 1. Meiotic studies in F_1 and backcross progenies of (*B. juncea* x *B. carinata)* x *B. carinata*

Combination	Generation	PMCs	Meiotic Profile		Mean frequency		
			Configuration	Proportio	II	III	IV
B. juncea x B. carinata	F1	62	11II + 13I 12II + 1IV + 7I	0.68 0.32	11.3	-	0.3
	BC1	122	10II + 2III + 2I 11II + 1IV + 5I 12II + 1III + 3I 13II + 1IV + 4I 14II + 1III + 3I 16II + 1III 16II + 3I 17II + 1I 17II	0.04 0.17 0.34 0.14 0.12 0.09 0.05 0.03 0.02	-	-	-
	BC2	85	16II + 2I 17II	0.12 0.08	16.9	-	-

Induction of genetic variability in Ethiopian mustard (*Brassica carinata*) for quality traits through interspecific hybridization.

F.A. Sheikh[1], Shashi Banga, S.S. Banga, S. Najeeb[1], and A.G. Rather[1]
Department of Plant Breeding, Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, 141 004, INDIA
[1] Rice Research & Regional Station(SKUAST-K), Khudwani, Anantnag- 192102
Correspondence: sfaroq4@rediffmail.com

Abstract
Interspecific hybridization was used to enhance the spectrum of genetic variability in *Brassica carinata* (BBCC, 2n = 34*)* cv. PC5 for oil and meal quality traits from quality lines of *Brassica juncea* (AABB, 2n = 36).

Keywords: *B. carinata,* interspecific hybridization, fatty acid, oil content

Introduction
The natural Ethiopian mustard (*Brassica carinata*) has high levels of erucic acid and very low levels of oil content and the restricted amount of genetic variability available in natural *B. carinata* for these traits requires use of new sources of variability for broadening the genetic base of the crop. Interspecific hybridization is an attempt in this direction.

Materials and Methods
Brassica carinata cv. PC5 (BBCC, 2n = 34) was crossed as a male with different elite lines *Brassica juncea* (AABB, 2n = 36) with the objective of substituting B genome of *B. carinata* with B genome of *Brassica juncea,* in addition to cytoplasmic substitution (Table 1). The F_1 plants were backcrossed to *B. carinata* with the objective to eliminate unwanted A chromosomes and improve fertility and seed setting. *Brassica carinata* type BC_1 selected on the basis of morphology and cytology were raised to BC_1F_2 generation through selfing. The BC_1F_2 *Brassica carinata* type plants showing complete genomic stability (2n = 34) and complete pollen fertility were tagged and were subjected to fatty acid analysis as per the standard procedure of ethyl ester preparation followed by gas liquid chromatography, oil content estimation using nuclear magnetic resonance and meal glucosinolate estimation (Kumar *et al.* 2004).

Results and Discussion
The fatty acid profile of BC_1F_2 plants from (*B. napus* x *B. juncea*) x *B. juncea* cross (Table 2) revealed that besides increase in the mean value, range of variability also enlarged for each trait. Individual plants were identified with up to 24.3% oleic acid and 31.6% linoleic acid in comparison to 11.2% and 18.2% respectively for the control (PC5). The significant decrease in mean erucic acid content (24.2±1.7 %) over the control (45.9%) with individual plants with decrease down to 18.5 per cent erucic acid was identified. This clearly indicated stable expression of introgressed genes for low erucic acid content. The erucic acid content in *B. juncea* is controlled by two

independent genes which act in an additive manner and one gene could be present in each of A and B genomes (Kirk and Hurlstone, 1983). There is also excellent variability for oil content with some plants showing as high as 39.5% oil content, indicating a clear effect of gene introgression. Glucosinolate content recorded a significant decrease on the mean basis (82.8±5.2 µmoles/g defatted meal) as well as the excellent variability for low glucosinolate was also present (63.1 µmoles/g defatted meal). Getinet *et al.* (1997) were successful in identifying plants that contained only 20 µmole of 2-propenyl glucosinolate from (*B. carinata* x *B. juncea*) x *B. carinata* combination. The desired variability introgressed from elite, related species for fatty acid composition, oil content and meal quality may result in the development of canola quality cultivars of *B. carinata* having high oil content and desired morphotypes.

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Table 1. Genotypes of *Brassica juncea* and *B. carinata* used in the hybridization.

Species	Genotypes	Particularities
B. napus	NUDH YJ-4	Canola
B. *carinata*	PC5	High C22:1

Table 2. Mean and range of fatty acid composition, oil and glucosinolate content of *B.napus* x *B. carinata*) x *B. carinata* BC_1F_2 plants

Generation	Fatty acid composition (%)							Oil content (%)	Glucosinolate (µ moles / g defatted meal)
	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Linolenic acid	Eicosenoic acid	Erucic acid		
BC_1F_2	5.6±0.4 (4.0-8.1)	0.5±0.2 (0 – 1.5)	17.0±1.2 (12-24.3)	25.8±1.1 (23.1-31.6)	14.2±0.4 (11.3-16.9)	8.9±0.4 (6.9-10.8)	27.3±1.6 (18.5-36.6)	34.5±1.7 (31.3-39.5)	82.8±5.2 (63.1-99.9)
PC5 (control)	3.5	0.6	11.2	18.1	11.1	9.6	45.9	34.3	107.5

Figures in parenthesis indicate range

Introgression of lipid and meal quality traits to Ethiopian mustard (*Brassica carinata*) from elite lines of *Brassica napus.*

F.A. Sheikh[1], Shashi Banga, S.S. Banga, S. Najeeb[1], Asif B. Shikari [1] and A.G. Rather[1]
Department of Plant Breeding, Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, 141 004, INDIA
[1] Rice Research & Regional Station(SKUAST-K), Khudwani, Anantnag- 192102
Correspondence: sfaroq4@rediffmail.com

Abstract
Interspecific hybridization was used to successfully introgress genes into *Brassica carinata* (BBCC, 2n = 34*)* cv. PC5 for low erucic acid, high oleic acid and high oil content from quality lines of *Brassica napus* (AACC, 2n = 38).

Keywords: *B. carinata,* interspecific hybridization, fatty acid, oil content

Introduction
The natural Ethiopian mustard (*Brassica carinata*) has high levels of erucic acid and very low levels of oil content and the restricted amount of genetic variability available in natural *B. carinata* for these traits requires use of new sources of variability for broadening the genetic base of the crop. Interspecific hybridization is an attempt in this direction.

Material and Methods
Brassica carinata cv. PC5 (BBCC, 2n = 34) was crossed as a male with different elite lines *Brassica napus* (AACC, 2n = 38) with the objective of substituting the C genome of *B. carinata* with the C genome of *Brassica napus,* in addition to cytoplasmic substitution (Table 1). The F_1 plants were backcrossed to *Brassica carinata* with the objective to eliminate unwanted A chromosomes and improve fertility and seed setting. *Brassica carinata* type BC_1 selected on the basis of morphology and cytology were raised to BC_1F_2 generation through selfing. The BC_1F_2 *Brassica carinata* type plants showing complete genomic stability (2n = 34) and complete pollen fertility were tagged and subjected to fatty acid analysis as per the standard procedure of ethyl ester preparation followed by gas liquid chromatography, oil content estimation using nuclear magnetic resonance and meal glucosinolate estimation (Kumar *et al*. 2004).

Results and Discussion
The fatty acid profile of BC_1F_2 progenies from (*B. napus* x *B. carinata*) x *B. carinata* cross (Table 2) revealed a significant increase in the mean value and range of variability. Individual plants were identified with up to 24.1% oleic acid and 28.3% linoleic acid in comparison to 11.2% and 18.2% respectively for the control (PC5). The significant decrease in erucic acid content over the control revealed successful introgression of genes from *B. napus* parent for low erucic acid content. Individual plants with a decrease down to 15.6% erucic acid were identified. Erucic acid content in *B. napus* is controlled by two genes, one gene in each of it's A and C genomes

which act in additive manner (Harvey and Downey, 1964). Interspecific hybrid between high erucic acid *B. carinata* parent ($B^+B^+C^+C^+$) and zero erucic acid *B. napus* parent ($A^-A^-C^-C^-$) would be of the genome constitution ($A^-B^+C^+C^-$). Normally A and B genomes do not show allosyndetic pairing in haploid state (Mizushima, 1950; Olsson, 1960). When such hybrids are selfed after one backcross, BC_1F_2 plants of constitution $B^+B^+C^+C^-$, $B^+B^+C^-C^-$ with C genome free of erucic acid are possible. The oil content of the progenies showed an increase in the mean value with individual plants with high oil content of 36.9% that were identified. Though mean glucosinolate content was at par with the control, however individual plants with very low glucosinolate content (95.4 µmoles/g of defatted meal) have been identified. Previously successful introgression of desirable alleles for low glucosinolate in mustard (*Brassica juncea*) from turnip rape (*Brassica rapa*) was made through hybridization followed by backcross and selfing (Banga, 1996). The desired variability introgressed from elite, related species for fatty acid composition, oil content and meal quality may result in the development of canola quality cultivars of *B. carinata* having high oil content and desired morphotypes.

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Table 1. Genotypes of *B. napus* and *B. carinata* used in the hybridization.

Species	Genotypes	Particulars
B. napus	NHO 7-10	'0' C22:1
	MHO 18-1-36	Canola
B. *carinata*	PC 5	High C22:1

Table 2. Mean and range of fatty acid composition, oil and glucosinolate content in (*B. napus* x *B. carinata*) x *B. carinata* BC_1F_2 plants

Generation	Fatty acid composition (%)							Oil content (%)	Glucosinolates (µ moles / g defatted meal)
	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Linolenic acid	Eicosenoic acid	Erucic acid		
BC_1F_2	6.3±0.3 (5.3-7.8)	0.9±0.3 (0.1 – 2.2)	19.8±1.4 (15.7-24.1)	25.5±0.9 (22.9-28.3)	13.1±0.6 (11.4-15.6)	10.1±0.5 (8.4-11.9)	22.2±2.2 (15.6-28.0)	35.3±0.4 (33.4-36.9)	107.7±6.0 (95.4-121.20)
PC5 (control)	3.5	0.6	11.2	18.1	11.1	9.6	45.9	34.3	107.5

Figures in parenthesis indicate range

Genetic analysis in rapeseed (*B. napus* L.)

S.M. Razvi*, S.K. Gupta and S. Najeeb
Division of Plant Breeding & Genetics, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Main Campus, Chatha, Jammu, INDIA
Corresponding author: m.razvi@rediffmail.com
Other address: najeeb_sofi2006@yahoo.co.in

Abstract
The knowledge of gene action is required before initiating a breeding strategy for improvement of a crop. Hence present investigation was taken up to understand the nature of gene effects involved in the inheritance of various quantitative characters in *B. napus*. The experiment material consisted of two crosses viz., GSG-9107 x RSPN-25 and KG-G-6 x DGS-1 whose parents were primarily selected on the basis of their genetic diversity for different traits. Different scaling tests revealed that in both crosses, the non-epistatic model failed for all the characters. On the basis of six parameter model, the three epistatic components were found to be significant for almost all characters in both the crosses. Duplicate type of epistasis was manifested for most of the characters in both crosses. Potence ratio of more than one and high heterotic effect in F_1 were not always associated with high inbreeding depression in the F_2 generation.

Keywords: *B. napus*, gene action, scaling tests, six parameter model, epistasis

Introduction
To breed an efficient genotype the knowledge of nature of gene action is required before hand to design a breeding scheme. Hence present investigation was taken up to understand the nature of gene effects involved in the inheritance of various quantitative characters in *B. napus*.

Materials and Methods
The experimental material consisted of two crosses viz., GSG-9107 x RSPN-25 and TKG-G-6 x DGS-1 whose parents were selected primarily on the basis of their genetic diversity for different agronomic and yield traits. The two F_1 crosses made during rabi 2004-05 at the Experimental Farm of the Division of Plant Breeding & Genetics, SKUAST-Jammu, Chatha were advanced to the F_2 generation as well as BC_1 and BC_2 to constitute a complete set of six basic generations viz. P_1, P_2, F_1, F_2, BC_1 and BC_2. All these six basic generations were sown in a complete randomised block design with three replications during rabi 2005-2006 at Main Campus Chatha. Data for nine quantitative traits were taken from ten competitive plants randomly selected in each generation except in F_2 where 25 plants were selected. Row to row and plant to plant distance were kept at 45 cm and 15 cm respectively. The recommended package of practices were adopted to raise the crop. 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 and then tested for non-allelic interactions by individual scaling tests of Mather (1949) and by joint scaling test of Cavalli (1952).

Results and Discussion

Analysis of variance conducted for different characters indicated highly significant differences (P<0.01) for all the characters under study. Mean sum of squares among the different generations within a cross revealed highly significant differences for both the crosses for all the characters, thereby suggesting the presence of enough genetic variability in the material under investigation. Generation mean analysis revealed that the mean of F_1 progenies produced the highest value for both crosses for all the traits and mean of F_2 generation were considerably lower than the F_1 generation. The backcross families behaved more or less like their recurrent parents.

Different scaling tests revealed that in both the crosses, the non-epistatic model failed for all the characters. Therefore, six parameters viz., m, (d), (h), (i), (j) and (l) were estimated from the basic six generations i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2. In the present investigation the additive gene effects were significant for all the characters in both of these crosses thus playing an important part in the inheritance of these traits (Table 1). The dominance effects too were significant for all the characters, however, the relative contribution of dominance gene effects was higher than the additive gene effects in both crosses for almost all characters studied.

Based on the six parameter model, the three epistatic components were found to be significant for almost all characters in both the crosses (Table 1). However, the type and magnitude of these three epistatic effects vaired in two crosses for the same character. In both the crosses all the three types of interaction components viz., additive x additive (i), additive x dominance (j) and dominance x dominance (l) were significant for all the characters. It therefore, clearly indicated that all the three interactions were equally important. The dominance (h) and dominance x dominance (l) gene effects were of opposite sign in all the characters thus revealing duplicate type of epistasis except for 1000 seed weight and seed yield per plant in cross GSG-9107 x RSPN-25 (complementary type of epistasis). Indu Varsha *et al.* (1999) demonstrated non-alleic 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 siliquae/main receme, 1000 seed weight, secondary branches/plant and seeds/siliqua and seed yield per plant. Duplicate type of epistasis was also reported by Indu Varsha *et al.* (1999) in the inheritance of seed yield.

In the present study the potence ratio, heterosis and inbreeding depression were also estimated for all characters. The potence ratio was more than one for all characters except for number of days to bloom and number of primary and secondary branches in the cross TKG-G-6 x DGS-1. However, 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 over estimated when (d) components is underestimated due to the dispersion of genes in the parents.

Significant heterosis (over better parent) was observed in the characters like days to bloom, number of primary and secondary branches and seed yield per plant in the cross-GSG-9107 x RSPN-25, whileas for 1000-seed weight and number of siliquae per plant heterosis manifested non-significance in TKG-9-6 x DGS-1. Inbreeding depression was found significant for seed yield per plant and number of primary branches in GSG-9107 x RSPN-25 while for the other traits it was non-significant, however, for other cross it proved non-significant for pod length, 1000 seed weight and number of siliquae per plant. The results further indicated that high heterotic effects in the F_1 generation for various characters were not always associated with high inbreeding depression in the F_2 generation. This suggests the importance of non-alleic interaction in the manifestation of the heterosis. Heterosis is maximum when dispersed genes show maximum unidirectional dominance and there is no internal cancellation of h's of different signs. Heterosis is maximum when complementary epistasis [h] and [l] of the same sign combines with dispersion (rd = 0 and ri = -1) and is minimised in presence of duplicate epistasis and complete association. Epistasis causes bias in the estimation of the degree of dominance if it is estimated from the analysis of six basic families. Dispersed complementary genes inflate the ratio leading to its misinterpretation as overdominance. On the other hand, overdominance may be misinterpreted as complete or partial dominance due to associated complementary or dispersed duplicate genes. Thus in the present investigation it was observed that seed yield and

major yield traits showed the significance of both additive and non-additive type of gene effects suggesting that part of heterosis could be fixed in the segregating generations. The preponderance of non-additive gene action, however, revealed that heterosis could be exploited by hybrid breeding in *B. napus*. However, biparental cross approach appears to be more useful in *B. napus* breeding owing to the importance of additive and non-additive gene effects. The advantage of this procedure is to capitalize both additive and non-additive genetic variance simultaneously for affecting improvement in the population.

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Table 1. Estimates of genetic components based on generation means (six parameters model), heterosis, potence ratio and inbreeding depression for maturity, morphological, yield and yield attributing traits in *B. napus*

Parameters	No. of days to bloom	No. of primary branches/plant	No. of secondary branches/plant	Pod length (cm)	No. of seeds/ siliqua	1000-seed weight (g)	No. of siliquae per plant	Seed yield per plant (g)	Harvest index (%)
GSG-9107 x RSPN-25									
(m)	97.73±0.25	4.80±0.18	5.53±1.81	7.33±0.14	30.60±0.02	4.62±0.018	737.55±1.55	25.56±0.11	19.19±0.01
(d)	-6.77±0.02**	-1.11±0.01**	4.67±0.01**	0.37±0.02**	1.07±0.01**	0.09±0.002**	63.46±0.26**	0.67±0.009**	-0.12±0.01**
(h)	-115.7±0.60**	6.09±0.42**	-118.82±3.6**	-3.15±0.03	-24.5±0.06**	1.27±0.37**	-1087.49±3.29**	4.71±0.031**	-10.12±0.05**
(i)	-43.12±0.29**	5.29±0.18**	-29.69±1.81**	-0.37±0.13**	-7.29±0.02	0.82±0.0018**	-126.49±1.53**	2.36±0.11**	-3.49±0.01**
(j)	-3.99±0.15**	1.86±0.11**	-11.94±0.05**	-0.32±0.07**	-0.08±0.02**	-0.06±0.005**	-565.65±0.64**	0.41±0.09**	0.66±0.02**
(l)	71.69±0.36**	-1.7±0.26**	79.33±1.81**	2.64±0.17**	17.24±0.05**	0.08±0.02*	813.62±1.97**	2.14±0.22**	10.28±0.03**
Type of epistasis	D	D	D	D	D	C	D	C	D
Potence ratio	17.09	5.48	25.44	8.51	22.96	14.11	17.13	7.00	87.50
Heterosis over a better parent	0.122±0.04**	-0.18±0.03**	-0.47±0.04**	-0.06±0.04	-0.04±0.02	0.07±0.00	-0.31±0.48	0.133±0.05**	0.19±0.01**
Inbreeding depression	-0.07±0.06	0.19±0.04**	0.005±0.45	0.005±0.04	0.02±0.01	0.11±0.00	0.14±0.60	0.122±0.05**	0.12±0.00
TKG-G-6 x DGS-1									
(m)	55.01±0.15	8.54±0.14	28.84±0.38	3.57±0.45	9.17±0.03	4.33±0.005	188.05±2.11	43.72±0.05	13.61±0.07
(d)	-14.60±0.03**	2.99±0.03**	2.89±0.03**	-0.16±0.008**	-0.38±0.005**	-0.04±0.001	-46.47±0.008**	0.24±0.02**	-0.09±0.006**
(h)	-14.12±0.43**	-1.83±1.38**	-42.15±0.81**	7.52±0.91**	28.81±0.08**	2.31±0.013**	640.65±4.26**	-50.28±0.13**	-9.93±0.18**
(i)	20.67±0.15**	4.14±0.13**	-16.44±0.38**	3.33±0.45**	14.40±0.03**	1.18±0.005	338.62±2.11**	-16.70±0.04**	1.552±0.07**
(j)	-24.03±0.14**	-11.43±0.12**	-10.80±0.13**	0.39±0.05**	2.10±0.02**	0.31±0.04**	-699.9±0.29**	-6.69±0.05**	-0.85±0.05**
(l)	42.62±0.58	1.82±0.24	21.86±0.51	214.68±0.51	-12.68±0.05	-456.44±2.1	-0.40±0.011	30.12±0.09	14.06±0.12
Types of epistasis	D	D	D	D	D	D	D	D	D
Potence ratio	0.967	0.61	0.61	47.00	75.81	57.75	13.78	209.5	-
Heterosis over a better parent	0.362±0.04**	-0.45±0.05**	-0.45±0.05**	0.05±0.01**	0.05±0.01**	0.12±0.00	-0.35±0.22	-0.135±0.04**	0.16±0.02**
Inbreeding depression	0.298±0.044**	0.05±0.02*	6.54±0.001**	0.14±0.11	0.19±0.01**	0.13±0.00	-0.5±0.54	-0.108±0.02**	0.31±0.03**

*, **, significant at 5 and 1 per cent level of significance

Green forage yield components in white mustard (*Sinapis alba* L. subsp. *alba*)

A. Mikić[1,*], V. Mihailović[1], S. Petrović[2], M. Dimitrijević[2], S. Vasiljević[1], Đ. Karagić[1], I. Pataki[1]

[1]Institute of Field and Vegetable Crops, Forage Crops Department, Maksima Gorkog 30, 21000 Novi Sad, SERBIA

[2]University of Novi Sad, Faculty of Agriculture, Department of Field and Vegetable Crops, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia

* Corresponding author: mikic@ifvcns.ns.ac.yu

Introduction

Although white mustard (*Sinapis alba* L. subsp. *alba*) is dominantly used for various industrial purposes, it is known that it can be cultivated as a forage crop as well. Majority of white mustard cultivars grown for green forage are sown in early spring and are characterised by a considerably brief period between sowing and cutting of about 60 days (Vučković, 1999).

Breeding white mustard for forage is aimed at high and stable green forage yields, early maturity and increased resistance to late spring frosts.

The goal of the study was to examine the variability and the inter-relationship of green forage yield components and green forage yield in white mustard lines.

Materials and Methods

A small-plot trial has been carried out in 2007 and 2008 at the Experimental Field of the Institute of Field and Vegetable Crops at Rimski Šančevi. It included ten white mustard lines of Serbian origin, namely BS-01, BS-02, BS-03, BS-04, BS-05, BS-06, BS-07, BS-08, BS-09 and BS-10.

All ten lines were sown in early March, at a seeding rate of 50 viable seeds m^{-2}, with a plot size of 5 m^2 and three replicates, and were cut in the stages of full budding and beginning of flowering (Mihailović *et al.*, 2007). There were monitored plant height (cm), number of lateral branches (plant^{-1}), number of internodes (plant^{-1}), stem mass (g plant^{-1}), leaf mass (g plant^{-1}) and green forage yield (g plant^{-1}). The study results were processed by analysis of variance (ANOVA) with the Least Significant Difference (LSD) test applied. There were calculated simple correlation coefficients (*r*) between each of the monitored characteristics.

Results and Discussion

There were significant differences at both levels in forage yield components between the examined white mustard lines (Table 1). The greatest plant height was in the line BS-05 (112 cm). The lines BS-08 and BS-09 had the greatest number of lateral branches (17 plant^{-1}), while the line BS-03 had the greatest number of internodes (35 plant^{-1}). The line BS-08 had the highest green forage yield (64.61 g plant^{-1}). It was confirmed that white mustard may produce high green forage yields (Schuchert, 2006).

As shown in Table 2, green forage yield was in high positive correlations with stem mass (r = 0.990), number of lateral branches (r = 0.891) and leaf mass (r = 0.857). Number of lateral branches was in high positive correlations with both stem mass (r = 0.878) and leaf mass (r = 0.780). Stem and leaf masses were in a high positive correlation (r = 0.777).

Conclusions

There are promising lines of white mustard that can be developed into first Serbian cultivars suitable for green forage production. Such cultivars should be characterised by an optimal relationship between single green forage yield components and thus have improved potential for high green forage yield.

Acknowledgements

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Table 1. Average values of green forage yield components and green forage yield in white mustard lines for 2007 and 2008 at Rimski Šančevi

Genotype	Plant height (cm)	Number of lateral branches (plant^{-1})	Number of internodes (plant^{-1})	Stem mass (plant^{-1})	Leaf mass (plant^{-1})	Green forage yield (g plant^{-1})
BS-01	92	6	25	22.03	5.80	27.83
BS-02	89	4	23	21.10	8.28	29.38
BS-03	98	6	35	35.96	10.25	46.21
BS-04	110	7	22	19.64	5.00	24.64
BS-05	112	15	26	41.10	11.73	52.83
BS-06	83	10	33	25.22	13.17	38.39
BS-07	102	15	26	38.53	13.35	51.88
BS-08	105	17	29	50.80	13.81	64.61
BS-09	100	17	29	50.01	12.93	62.94
BS-10	110	14	24	37.10	9.73	46.83
Average	100	11	27	34.55	10.61	45.15
$LSD_{0.05}$	14	4	5	4.41	1.53	6.02
$LSD_{0.01}$	19	6	7	6.38	2.11	8.74

Table 2. Simple correlation coefficients (*r*) between green forage yield components and forage yield in white mustard lines

	Number of lateral branches	Number of internodes	Stem mass	Leaf mass	Green forage yield
Plant height	0.517	-0.337	0.473	0.047	0.398
Number of lateral branches		0.122	0.878**	0.780**	0.891**
Number of internodes			0.352	0.549	0.410
Stem mass				0.777**	0.990**
Leaf mass					0.857**

* - significant at 0.05; ** - significant at 0.01

Green forage yield components in fodder kale (*Brassica oleracea* L. var. *viridis* L.)

V. Mihailović[1], A. Mikić[1,*], M. Dimitrijević[2], S. Petrović[2], S. Katić[1], D. Milić[1], Đ. Krstić[2]
[1]Institute of Field and Vegetable Crops, Forage Crops Department, Maksima Gorkog 30, 21000 Novi Sad, SERBIA
[2]University of Novi Sad, Faculty of Agriculture, Department of Field and Vegetable Crops, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia
* Corresponding author: mikic@ifvcns.ns.ac.yu

Introduction
Fodder kale (*Brassica oleracea* L. var. *viridis* L.) represents the most important forage brassica species in many regions of Europe, including Serbia (Erić *et al.*, 2006). It is highly appreciated for its high green forage yields and is considered one of the best preceding crops in diverse farming systems.
Modern fodder kale breeding programmes are directed towards the development of cultivars with high, quality and stable green forage yields, improved tolerance to low temperatures and early maturity.
The goal of the study was to examine the variability and the inter-relationship of green forage yield components and green forage yield in fodder kale genotypes.

Materials and Methods
A small-plot trial has been carried out in 2007 and 2008 at the Experimental Field of the Institute of Field and Vegetable Crops at Rimski Šančevi. It included ten fodder kale genotypes, that is, three fodder kale cultivars, namely NS-Bikovo (Serbia), Perast (Serbia) and Maksimirski Visoki (Croatia), and seven Serbian fodder kale lines, namely K-021, SK-01, SK-02, SK-03, SK-04, SK-05 and SK-06.
All ten genotypes were sown in early September, at a seeding rate of 50 viable seeds m^{-2}, and were cut in the stages of full budding and beginning of flowering (Erić *et al.*, 2007).
There were monitored plant height (cm), number of lateral branches (plant^{-1}), number of internodes (plant^{-1}), stem mass (g plant^{-1}), leaf mass (g plant^{-1}) and green forage yield (g plant^{-1}). The study results were processed by analysis of variance (ANOVA) with the Least Significant Difference (LSD) test applied. There were calculated simple correlation coefficients (*r*) between each of the monitored characteristics.

Results and Discussion
There were significant differences in forage yield components between the examined fodder genotypes (Table 1). The cultivar Perast had the greatest plant height (105 cm), number of internodes (23), stem mass (87.36 g plant^{-1}), leaf mass (58.68 g plant^{-1}) and green forage yield (146.04 g plant^{-1}), while the genotype SK-01 had the greatest number of lateral branches (8). In average, it was confirmed that fodder kale has a great potential for green forage yields (Mihailović *et al.*, 2008).
As shown in Table 2, green forage yield was in high positive correlations with leaf mass (r = 0.839), stem mass (r = 0.801) and plant height (r = 0.661). The highest among the correlations between single forage yield components was between number of lateral branches and number of internodes (r = 0.873).

Conclusions
The examined genotypes have great potential for green forage yield production. Green forage yield is in highest positive correlations with plant height, stem mass and leaf mass.

Acknowledgements
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Table 1. Average values of green forage yield components and green forage yield in fodder kale genotypes for 2007 and 2008 at Rimski Šančevi

Genotype	Plant height (cm)	Number of lateral branches (plant^{-1})	Number of internodes (plant^{-1})	Stem mass (g plant^{-1})	Leaf mass (g plant^{-1})	Green forage yield (g plant^{-1})
NS-Bikovo	87	4	18	75.00	57.48	132.48
Perast	105	7	23	87.36	58.68	146.04
K-021	78	3	12	65.84	46.08	111.92
Maksimirski Visoki	78	4	13	61.36	42.36	103.72
SK-01	83	8	22	56.28	44.76	101.04
SK-02	80	5	17	67.52	36.60	104.12
SK-03	61	3	11	45.44	21.00	66.44
SK-04	66	5	15	64.76	30.60	95.36
SK-05	86	3	14	64.40	26.76	91.16
SK-06	86	4	10	57.32	15.24	72.56
Average	81	5	16	64.53	37.96	102.48
$LSD_{0.05}$	16	2	6	8.12	4.25	12.43
$LSD_{0.01}$	21	3	8	11.03	5.78	16.24

Table 2. Simple correlation coefficients (*r*) between green forage yield components and forage yield in fodder kale genotypes

	Number of lateral branches	Number of internodes	Stem mass	Leaf mass	Green forage yield
Plant height	0.458	0.594	0.769**	0.549	0.661*
Number of lateral branches		0.873**	0.350	0.470	0.305
Number of internodes			0.616	0.731*	0.493
Stem mass				0.744*	0.801**
Leaf mass					0.839**

* - significant at 0.05; ** - significant at 0.01

Evaluation of non-heading Chinese cabbage (*Brassica campestris* ssp *chinensis* L.) lines for their bolting and yield behaviour during summer in Highlands of North Western Himalayas

Sonia Sood[1*] and J.J. Sharma[2]
[1] Department of Vegetable Science
[2]. Department of Agronomy, CSK Himachal.Pradesh Agricultural University, Palampur -176 062, INDIA
*Corresponding author e-mail: soniasood2005@rediffmail.com

Abstract
A field experiment was conducted to evaluate seven lines of Chinese cabbage for their bolting and yield behaviour at Highland Agricultural Research and Extension Centre, Kukumseri (Lahaul) situated at an elevation of 2772 m asl for two years during summer seasons. The results revealed that on an average first harvesting which was done 25 days after transplanting (DAT) contributed 17.32 to 32.5 per cent towards total marketable yield in different lines. Comparatively lower average temperature 21.2 ^{0} C during first year than 24.9^0 C in second year accelerated bolting. Mean data showed line PVCH-VI (6.3%), PVCH-V (15.8%) and PVCH-III (39.3%) to be less prone to bolting up to 60 DAT. The line PVCH-I having yellowish green, thin and spreading leaves though recorded significantly higher yield but was found to be highly susceptible (90.3%) to bolting. The lines PVCH-V and PVCH-III having dark green, succulent, fleshy and semi erect leaves with consumers' acceptability showed delayed bolting with high yield were found promising lines for summer cultivation in highlands.

Introduction
Lahaul valley in Himachal Pradesh, India consists of rugged mountainous terrain and represents temperate dry climate. The area remains cut off from rest of the part during winter due to heavy snow fall. Therefore, there is only one cropping season (April-September) and all the crops are taken only under irrigated conditions. Non – heading Chinese cabbage is a valuable source of calcium, crude fibre and vitamin C. Because of sensitivity to high temperature, its cultivation is confined to cooler month in low and mid-hills. However, due to congenial climatic conditions, the crop is grown on limited scale during summer in highlands and is consumed as *saag.* Also, the leaves are dried by inhabitants and used during winter when no vegetables are available. High altitude, cold climate, great variation in temperature and long day length are conducive to high rates of bolting (Du *et a*l., 1995). For summer cultivation late bolting is a highly desirable character. Hence, a field experiment was undertaken to identify promising lines with delayed bolting, consumer's acceptability and higher yield which can be grown under long day summer conditions.

Materials and Methods
A field trial was conducted at Highland Agricultural Research and Extension Centre, Kukumseri (Lahaul) situated at an 32° 42' 32" N latitude, 76°41' 29" E longitude and at elevation of 2772 m asl. The soil was loamy sand in texture, neutral in reaction, medium in available N and K and high in P. Seven lines of Chinese cabbage (Table 1) were evaluated in a randomized block design with 3 replications for two years. Twenty five days old seedlings were transplanted at a spacing of 45cm x 30cm in the first fortnight of June each year. Irrigation was applied through sprinkler system as per need of the crop. The harvesting was initiated 25 days after transplanting. The observations on per cent of total crop harvested and plants bolted were recorded at an interval of 10 days. The data were subjected to arc sin transformation.

Results and Discussion
The visualized data on characteristic features of different lines has been given in Table 1. The data (Table 2) revealed that 25 DAT, on an average different lines contributed 17.3 to 32.5 per cent towards their total marketable yield, the highest being in PVCH-I which showed initial faster growth as compared to other lines. But the difference amongst the lines became narrower with successive harvest intervals. At 45 DAT the variation was 62.1 (PVCH-VI) to 72.8 (PVCH-III) per cent indicating faster growth of PVCH-III between 25 to 45 DAT. The maximum harvest in all the lines was obtained up to 55 DAT. However, being only one cropping

season harvesting was continued till 85 DAT after which the growth ceased due to abrupt decline in temperature, in spite of 8.9, 29.0 and 50.6 per cent bolting in PVCH-VI, PVCH-V and PVCH-III, respectively at 70 DAT.

The lines PVCH-I and PVCH-II behaved differentially in two years. Line PVCH-I showed greater sensitivity to low temperature where as PVCH-II was sensitive to both low as well as high temperatures. The per cent bolting at 40 DAT ranged between 0 to 32.1 and 0 to 48.5 while it was 8.9 to 98.1 and 3.6 to 76.3 at 60 DAT during first and second year, respectively. Comparatively lower average temperature 21.2°C during first year than 24.9°C in second year accelerated pre mature bolting, resulting in development of flower stalk and flower bud formation. Kalisz and Cebula (2001) also obtained unfavorable effect of low air temperature which increased the percentage of bolting in Chinese cabbage plants. Two years mean data (Table 3) showed significantly lower bolting in PVCH-VI (ornamental) at all the stages. However, PVCH-V (15.8%) and PVCH-III (39.3%) were also less prone to bolting till 60 DAT. The line PVCH-III, if planted earlier may also prove to be higher yielder. The line PVCH-I though recorded significantly higher yield and was at par with PVCH-V but was found to be highly susceptible (90.2%) to bolting. Therefore, lines PVCH-V having broader leaves as compared to PVCH-I and line PVCH-III which has dark green, succulent, freshly leaves with consumers more acceptability were found most promising lines for summer cultivation in highland area of temperate dry regions.

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Table 1. Characteristic features of different lines.

Lines	Features
PVCH-I	Leaves yellowish green, thin, spreading
PVCH-II	Leaves medium green, semi erect, serrated margins
PVCH-III	Leaves dark green, succulent, fleshy and semierect
PVCH-IV	Like PVCH-III but pubescence on leaves
PVCH-V	Like PVCH-I but broader leaves
PVCH-VI &VII	Ornamental type

Table 2. Per cent crop harvested at different intervals.

Lines	Days after transplanting																				
	25			35			45			55			65			75			85		
	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean
PVCH-I	36.5	28.5	32.5	57.0	46.2	51.6	67.9	63.4	65.7	97.1	78.7	87.9	98.8	85.3	92.1	100.0	96.3	98.2	100.0	100.0	100.0
PVCH-II	31.8	29.4	30.6	52.6	45.0	48.8	68.7	61.3	65.0	95.8	86.0	90.9	97.5	95.0	96.3	99.8	98.0	98.9	100.0	100.0	100.0
PVCH-III	22.5	24.6	23.6	55.6	40.8	48.2	84.1	61.5	72.8	97.7	77.3	87.5	99.0	88.5	93.8	100.0	96.3	98.2	100.0	100.0	100.0
PVCH-IV	14.2	24.4	19.3	45.8	39.8	42.8	80.0	58.1	69.1	94.6	76.9	85.8	96.3	84.6	90.5	98.5	93.2	95.9	100.0	100.0	100.0
PVCH-V	15.3	33.0	24.2	44.4	49.7	47.1	78.8	63.4	71.1	92.4	81.5	87.0	95.0	88.5	91.8	99.0	96.3	97.7	100.0	100.0	100.0
PVCH-VI	16.3	18.3	17.3	43.3	33.2	38.3	68.4	55.8	62.1	90.0	76.4	83.2	92.5	85.0	88.8	92.5	93.0	92.8	98.0	100.0	99.0
PVCH-VII	25.2	20.2	22.7	52.8	32.4	42.6	81.1	53.4	67.3	95.9	72.1	84.0	97.3	86.5	91.9	94.0	97.0	95.5	97.5	100.0	98.8

Table 3. Per cent bolting at different stages and yield (t/ha) of different lines of Chinese cabbage.

Lines	Days after transplanting												Yield (t/ha)		
	40			50			60			70					
	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean	I Year	II Year	Mean
PVCH-I	16.7	0.0	8.4	23.3	10.5	16.9	96.7	63.6	75.1	98.3	82.2	90.2	18.9	22.9	20.9
	(24.1)	(0.4)	(12.2)	(28.8)	(18.4)	(23.6)	(81.3)	(47.1)	(64.2)	(83.7)	(65.6)	(74.7)			
PVCH-II	32.1	48.5	40.3	62.3	68.7	65.5	98.1	76.3	87.2	100.0	86.6	93.3	14.0	16.3	15.1
	(34.5)	(44.1)	(39.3)	(52.2)	(56.1)	(54.1)	(82.2)	(60.9)	(71.6)	(89.6)	(68.7)	(79.1)			
PVCH-III	4.8	5.2	5.0	17.7	11.8	14.8	58.1	20.4	39.3	71.0	30.9	50.6	13.1	17.4	15.2
	(12.6)	(13.2)	(12.9)	(24.8)	(20.1)	(22.4)	(49.8)	(26.8)	(38.3)	(57.6)	(32.3)	(45.0)			
PVCH-IV	9.8	7.9	8.8	16.4	18.0	17.2	50.8	37.7	44.3	67.2	41.0	54.1	12.5	14.8	13.6
	(18.2)	(19.3)	(17.3)	(23.8)	(25.0)	(24.4)	(45.4)	(37.8)	(48.6)	(55.1)	(39.8)	(47.5)			
PVCH-V	1.9	4.4	3.2	1.9	6.3	4.1	15.1	16.5	15.8	22.6	35.3	29.0	15.4	20.5	18.0
	(7.9)	(11.4)	(9.7)	(7.9)	(14.4)	(11.2)	(22.8)	(23.9)	(23.3)	(28.3)	(36.3)	(32.3)			
PVCH-VI	0.0	3.6	1.8	0.0	3.6	1.8	8.9	3.6	6.3	10.7	7.1	8.9	15.6	16.0	15.8
	(0.4)	(9.1)	(4.7)	(0.4)	(9.1)	(4.7)	(17.3)	(9.1)	(13.2)	(19.1)	(14.6)	(16.8)			
PVCH-VII	14.2	16.1	15.2	21.3	20.3	20.8	44.3	47.2	45.8	59.0	57.4	58.2	14.4	16.3	15.4
	(22.1)	(23.5)	(22.8)	(27.4)	(26.7)	(27.1)	(41.7)	(43.4)	(42.5)	(50.2)	(49.3)	(49.8)			
C.D.(P=0.05)	**1.98**	**6.85**	**3.38**	**3.25**	**8.40**	**4.26**	**9.56**	**7.98**	**5.89**	**8.13**	**10.13**	**6.15**	**4.19**	**4.14**	**3.95**

Figures in parentheses are arc sin transformed values

Characterization of Indian mustard (*Brassica juncea* L.) germplasms for economic traits

A.K. Misra* and A. Kumar
National Research Centre on Rapeseed-Mustard, Bharatpur, 321 303 (Rajasthan) INDIA
*Corresponding author: akmisra@yahoo.com

Introduction

The *Brassica* groups of oilseed crops, commonly known as rapeseed-mustard are the second largest oilseed crop next to groundnut in terms of area and production ii India. Indian mustard is the predominant crop among the *Brassica* oilseeds occupying near 90% of the total area amongst other six cultivated species of *Brassica* group (Kumar & Misra 2007). The low productivity can be considerably increase by the use of high yielding varieties/hybrid which in turn serve as potential donors for various quantitative and qualitative traits. Beside this plant morphology has been an important criterion for identification, classification and documentation of species and cultivars. It plays an important role in studying of genetic and breeding behaviour of plants. But, science morphology reflects interaction of genotypes with its environments, it is inappropriate to compare morphological data for cultivars that have been collected across different years and / or locations. In the present study, an attempt has been made to establish the relationship among *Brassica* genotypes and identify the divergent genotypes though seed yield.

Materials and Methods

The experimental material consisting of seventy five diverse genotypes of Indian mustard (*Brassica juncea* L.) were grown during *rabi* season 06-07 at the National Research Centre on Rapeseed–Mustard, Bharatpur, Rajasthan. Theses genotypes, along with three checks (BIO 902, PCR 7 and RH 30) were sown in an Augmented Complete Block Design. Each genotype was sown in two rows of 3m length with row to row distance of 30 cm and plant to plant distance of 10 to 15 cm was maintained by thinning. Random samples of five plants were selected at appropriate growth stages of crop to record observations on 15 morphological. 1000-seed was counted by electronic seed counter (Contador, Germany) and weighed by electronic balance. Further, protein and oil content were analyzed by NIR. Range, mean, and coefficient of variation were computed using standard statistical methods (Gomez and Gomez 1984).

Results and Discussion

The evaluated germplasm showed considerable variability for majority of the traits as indicated by coefficients of variation (CV) present in Table 1, Seed yield per plant and siliquae on main shoot had the highest variability (CV 36.3%) and (CV 26.2%), respectively and lowest variability had observed for maturity period (CV 1.7%) and oil content (CV 2.7%) correspondingly. On the basis of coefficient of variation the highest (CV >35%) was recorded for seed yield per plant (36.3%), while moderate (CV 20-35 %) were observed for siliquae on main shoot (26.2%), secondary branches per plant (21.6%), harvest index (20.5%) and 50% flowering (21.2%) however, lowest coefficient of variation were recorded (<20%) initiation of flowering (19.2%), main shoot length (17.5%), seeds

per siliqua (17.3%), 1000-seed weight (16.7%), primary branches per plant (12.7%), siliqua length (10.6%), plant height (10.5%), protein content (4.7%), oil content (2.7%) and maturity period (1.7%). Similar finding were also reported by Ghosk *et al.* (2001), Singh *et al.* (2003), Misra *et al.* (2004, 2007). Promising donors were identified for various economically useful traits which can be used as donors in the cultivar development (Table 2).

In plant breeding study of correlation is essential because knowledge of relationship between yield and its components is essential as this may help in constructing suitable selection criteria for seed yield. In the present study, the seed yield per plant was positively and significantly correlated with plant height, main shoot length, oil content, harvest index and maturation period (Table 3). Similar observations for correlations with seed yield were reported by Dubey *et al.* (1996), Misra *et al.* (2005, 2008). Protein content showed positive and significant correlations with initiation of flowering, 50% flowering, siliquae on main shoot and main shoot length. Significant positive correlations of harvest index with siliqua length, seeds per siliqua and main shoot length; siliquae on main shoot with main shoot length; seeds per siliqua with siliqua length. The present study indicated the presence of wide range of variability for plant height, primary branches per plant, seeds per siliqua, harvest index and seed yield per plant. Therefore, selection should be based on these characters in order to achiever productivity in this crop.

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Table 1. Range, Mean and Coefficients of Variation for different agro-morphological traits in Indian mustard

Characters	Range	Mean ± SEm	CV (%)	Mean values of checks		
				BIO 902	PCR 7	RH 30
Initiation of flowering (days)	39-121	49.2 ± 1.1	19.2	51	50	51
50 % flowering (days)	44-136	56.6 ± 1.4	21.2	56	54	57
Maturity (days)	133-147	137.2 ± 0.3	1.7	136	134	137
Primary branches per plant	3.6-6.8	5 ± 0.1	12.7	6	5.6	5.8
Secondary branches per plant	3-7.6	4.8 ± 0.1	21.6	5	5	5.2
Siliquae on main shoot	15.2-47	28.1 ± 0.9	26.2	25.8	34.2	36.6
Seeds per siliqua	6.5-18.1	13.8 ± 0.3	17.3	15.4	16.5	16.2
Main shoot length (cm)	32.4-72	48 ± 1.0	17.5	45	43	68
Plant height (cm)	106-172.5	131 ± 1.6	10.5	114	128	123
Siliqua length (cm)	2.6-4.8	3.7± 0.1	10.6	4.01	3.9	4.2
Protein content (%)	17.3-23.6	20.5 ± 0.1	4.7	19.6	19.8	20.5
Oil content (%)	37.7-42.9	40.5 ± 0.1	2.7	40.1	39.9	39.1
Harvest index (%)	8.9-31.8	21.8 ± 0.5	20.5	17.4	26.1	18.3
1000-seed weight (g)	2.9-5.8	4.2 ± 0.1	16.7	3.68	4.15	4.02
Seed yield per plant (g)	2.1-19.5	10.0 ± 0.4	36.3	12.4	13.9	9.5

Table 2. Promising donors of Indian mustard germplasm for important traits.

Characters	Promising Accessions
Initiation of flowering	**≤ 50:** NPJ 108, SAL 9, PBR 306, TNM 17, RH 0023
50 % flowering	**≤ 54:** NPJ 108, RGN 145, PAC 432, SKM 149
Plant height (cm)	**≤ 114:** RRN 299, LET 3, PBG 1188, KLM 145
Siliqua length (cm)	**≥ 4.1:** PBR 2004-06, BPR 560-11-B, RGN 145, RH 9902,
Secondary branches per plant	**≥ 5.2:** SKM 425, NRCDR 507, HUJM 03-05, NDRH 2008, NDR 05-02
Siliquae on main shoot	**≥ 37.0:** NRCDR 509, BIOHY 19-04, ELM 079, LET 17
Seeds per siliqua	**≥ 16.5:** SKM 425, RKM 1, CS 700-2-1-1, PUJ 02-402
1000-seed weight (g)	**≥ 4.8:** RH 216, BBM 05-01, RH 317, Bio 169-96
Harvest index (g)	**≥ 26.02 :** RGN 73, BIOHY 19-04, RH 213,
Seed yield per plant (g)	**≥13.9:** PBR 306, PBR 290, RK 05-1, RH -02-02
Oil content (%)	**≥ 40.12:** RH 0023, RGN 145, NRC 323-1, RRN 598, RK 05-01
Protein content (%)	**≥ 20.5:** KLM 145**,** PR 2004-11, LES 1-27, CS 52-24

Table 3. Correlations among the different agro-morphological traits in Indian mustard

Characters	IF	FF	PH	PB	SB	MSL	SMS	SL	SPS	1000-SW	PC	OC	HI	DM
50% flowering (FF)	0.82*													
Plant Height (PH)	0.26*	0.37*												
Primary per branches (PB)	0.20*	0.04	0.08											
Secondary per branches (SB)	-0.04	-0.03	0.25*	0.20*										
Main shoot length (MSL)	-0.04	-0.04	0.25*	0.09	0.07									
Siliquae on main shoot (SMS)	-0.01	0.07	0.15	0.00	-0.03	0.69*								
Siliqua Length (SL)	-0.10	-0.09	0.07	-0.22*	-0.20*	-0.06	0.00							
Seeds per siliqua (SPS)	-0.08	-0.11	-0.15	-0.33*	-0.23*	-0.06	0.07	0.33*						
1000 seed weight (1000 SW)	-0.09	-0.21*	-0.05	-0.10	-0.12	-0.15	-0.09	0.10	0.04					
Protein Content (PC)	0.36*	0.44*	0.05	0.06	-0.10	0.26*	0.38*	-0.12	-0.03	-0.10				
Oil Content (OC)	-0.23*	-0.15	0.11	-0.16	0.05	-0.24*	-0.24*	0.13	-0.03	0.11	-0.55*			
Harvest Index (HI)	-0.26*	-0.22*	0.00	-0.37*	-0.18	0.23*	0.19	0.31*	0.22*	0.08	-0.11	0.15		
Days to maturity (DM)	-0.05	-0.06	0.11	-0.21*	0.14	-0.25*	-0.25*	0.07	0.08	0.06	-0.17	0.18	0.21*	
Seed yield per plant (SYP)	-0.09	0.03	0.50*	-0.22*	0.06	0.23*	0.09	0.18	0.03	0.05	-0.26*	0.30*	0.50*	0.24*

**Significant at 5 per cent level*

Nitrogen economy through biofertilizers in cabbage (*Brassica oleracea* var *capitata*)

Ruchi Sood*, Vidyasagar and Amit Sharma
Department of Vegetable Science and Floriculture, CSKHPKV, Palampur 176 062 (HP) INDIA
*Corresponding author: ruchi_sood17@rediffmail.com

Introduction

During the last decades there is spectacular break through in the consumption of nitrogenous fertilizers leading to imbalance of nutrients in soil thus affecting the soil health. Moreover, the use of expensive commercial fertilizers as per the requirement of the crop is not much affordable to the average farmer, being costly and at times not readily available. Therefore, the importance of integrated nutrient supply in sustaining productivity is emphasized to restore and sustain soil health and productivity in the long run which otherwise is likely to deteriorate due to continuous and intensive cultivation without adequate nutrient management. An investigation was therefore, undertaken to explore the possibility of integrating nitrogen fertilizer with biofertilizers for getting yields higher or atleast comparable with the recommended dose of chemical fertilizers.

Materials and methods

The present investigation was carried out at Vegetable Research Farm, Palampur of the University being located at 32°6´ N latitude and 76°3´ E longitude and 1290.8 m altitude. The soil of the experimental site was silty clay loam, high in organic carbon, medium in available nitrogen, phosphorus and potash and acidic in reaction (5.7). The experiment was laid out in randomized block design with three levels of nitrogen (80, 60 and 40% of recommended nitrogen dose), two biofertilizers (*Azotobacter* and *Azospirillum*) and two methods of biofertilizer application (Soil and seed) along with recommended dose of chemical fertilizers (125, 100, 50 kg/ha NPK and 10t/ha FYM) replicated four times in 2.7 x 2.7 m^2 plot size at 45 x 45 cm spacing during consecutive two rabi seasons (2002-03 and 2003-04). The fertilizers used were calcium ammonium nitrate, single super phosphate and muriate of potash for nitrogen, phosphorus and potash, respectively. Full doses of phosphorus, potash, FYM and one third nitrogen treatment wise were applied in pits prior to transplanting. The remaining dose of nitrogen was top dressed equally at weeding, hoeing and earthing up. Manual weeding and other recommended agronomical practices were followed time to time in order to raise an ideal crop. Observations relating to number of non wrapper leaves, gross head weight, net head weight, head compactness were recorded on ten randomly selected plants. Marketable yield obtained from plot was utilized for computing marketable yield per hectare. The data recorded was subjected to statistical analysis and critical difference was worked out at 5% probability level to find out the difference among treatments (Panse and Sukhatme, 1978).

Results and discussion

The marketable yield was significantly influenced by the interaction nitrogen x biofertilizer x methods of biofertilizer application and nitrogen levels in the first and second year, respectively. The application of 80% nitrogen + *Azospirillum* as soil application resulted in the highest marketable yield of 357.53q/ha which was

significantly superior to the control (285.28 q/ha) (Table 1). Higher marketable yield can be attributed to the favorable response of this treatment on the yield attributes viz., gross head weight, net head weight, heading percentage, and non wrapper leaves (Table 2) which were either at par or better than the control. In the second year, the nitrogen levels alone proved significant and 80% nitrogen irrespective of biofertilizer and methods of biofertilizer application gave marketable yield of 194.94 q/ha which was significantly lower than the control (244.20 q/ha). Although the three way interaction was not significant for the yield attributes but the two way interaction revealed that biofertilizer *Azospirillum* as soil application in combination with 80% nitrogen gave favorable response in respect of the traits, gross head weight and net head weight comparable to the control (Table 2). The *Azospirillum* in the presence of inorganic nitrogen might have helped in the improvement of the over all nutritional environment of the rhizosphere which resulted in greater uptake of nutrients and there by exercised a favourable influence on plant metabolic activities appearing finally in the improvement of yield and yield contributing traits in cabbage.

Conclusion

The yield and yield attributing traits of cabbage could be enhanced significantly by the application of 80% nitrogen + *Azospirillum* as soil or seed application resulting in economizing the recommended dose of nitrogen upto 20% under agroclimatic conditions of Palampur.

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Table 1. Effect of interactions between nitrogen levels, biofertilizers and methods of biofertilizer application on marketable yield of cabbage

Nitrogen/biofertilizers		Marketable head yield (q/ha)					
		Methods of biofertilizers application					
		M_1		M_2		Mean (NxB)	
		2002-03	2003-04	2002-03	2003-04	2002-03	2003-04
N_1	B_1	305.13	320.90	200.34	200.00	313.01	200.16
	B_2	357.55	254.10	182.18	197.26	305.83	189.71
N_2	B_1	233.23	235.45	135.25	139.38	234.59	137.31
	B_2	214.40	172.60	142.78	152.05	193.50	154.25
N_3	B_1	140.75	189.73	124.65	115.40	165.24	120.03
	B_2	167.13	168.85	129.78	134.59	167.99	136.11
N x M	N_1	331.34	191.25	287.50	198.63	309.42	194.94
	N_2	223.81	139.01	204.28	152.55	214.04	145.78
	N_3	153.94	127.21	179.29	128.93	166.61	128.07
B x M	B_1	226.37	153.41	248.86	151.59	237.61	152.50
	B_2	246.36	151.58	198.52	168.48	222.44	160.03
Mean		236.36	152.49	223.69	160.04	-	-
Control mean		285.28	244.20				
Others mean		230.03	156.26				

For comparing means of	2002-03	2003-04
Nitrogen levels (N)	12.56	14.02
Biofertilizers (B)	10.25	NS
Methods of biofertilizer application (M)	10.25	NS
Interactions:		
Nitrogen x Biofertilizers	17.76	NS
Nitrogen x Methods of biofertilizer application	17.76	NS
Biofertilizer x Methods of biofertilizer application	14.50	NS
Nitrogen x Biofertilizers x Methods of biofertilizer application	25.11	NS

Table 2. Effect of nitrogen levels, biofertilizers and methods of biofertilizer application on yield attributes

Treatments	Gross head weight (g)		Net head weight (g)		Heading Percentage (%)		Number of non-wrapper leaves	
	2002-03	2003-04	2002-03	2003-04	2002-03	2003-04	2002-03	2003-04
N_1 (80% of RDN)	1520.94	1166.09	902.91	511.72	77.53(61.92)	87.15(69.48)	12.32	12.92
N_2 (60% of RDN)	1240.16	904.38	720.34	461.88	59.33(50.43)	77.28(62.01)	10.92	11.83
N_3 (40% of RDN)	1244.69	839.50	682.66	404.38	50.18(45.10)	83.26(66.08)	10.56	11.57
CD (P=0.05)	**88.21**	**38.08**	**32.59**	**38.07**	**1.40**	**4.14**	**0.62**	**0.59**
B_1 (*Azotobacter*)	1334.58	962.40	780.15	448.85	54.20(65.05)	64.82(81.13)	11.10	12.11
B_2 (*Azospirillum*)	1335.94	977.58	757.13	469.79	50.77(59.64)	66.90(84.00)	11.43	12.10
CD (P=0.05)	**NS**	**NS**	**NS**	**NS**	**1.15**	**NS**	**NS**	**NS**
M_1 (Soil application)	1338.33	1003.13	801.31	450.83	61.35(52.01)	81.38(65.07)	11.22	12.13
M_2 (Seed application)	1332.19	936.85	753.25	446.88	63.33(52.96)	83.74(66.64)	11.31	12.08
CD (P=0.05)	**NS**	**31.09**	**26.61**	**NS**	**NS**	**NS**	**NS**	**NS**
Interactions								
N x B	NS	53.85	46.08	53.84	1.98	NS	NS	NS
N x M	124.75	53.85	46.08	NS	1.98	NS	0.87	NS
B x M	101.86	43.97	NS	NS	1.62	NS	0.71	NS
N x B x M	176.42	NS	64.17	NS	2.81	NS	NS	NS

Note: RDN: Recommended dose of nitrogen Values in the parenthesis are the transformed values

Allelopathic influence of basil extracts on *Brassica rapa* L.: II. root weight and days to flower

M.K.A. Durrani and Chandreshwar Prasad*
Department of Botany, Vinoba Bhave University, Hazaribag – 825 301, INDIA
*Corresponding author: c.prasad@yahoo.com

Abstract
Ocimum sanctum L. and *O. canum* Sims plant extracts have stimulating effect on root weight of turnip (*Brassica rapa* L.). 80% concentration of the plant extract is the most effective in this regard. Contrary to this, there is gradual delay in the time of flowering from lower to higher doses. Increase in root weight associated with late flowering is beneficial from agricultural point of view.

Keywords: Basil, extracts, turnip, root weight, allelopathy.

Introduction
Allelopathy refers any process involving secondary metabolites produced by vascular plants, bryophytes, algae, bacteria and fungi that influence the growth and development of agricultural and biological systems. 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, 20). The genus *Ocimum*, collectively called basil of family Lamiaceae, has long been recognized as a diverse and rich source of essential oils. Frequent interspecific hybridization and polyploidy have created great taxonomic confusion and challenges, further complicated by the existence of chemotypes that do not differ much in morphology. The essential oils of basil contain biologically active constituents that are insecticidal (2, 4, 5), nematicidal (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 yield and yield-components of economically important crops. Keeping this in view, present study was undertaken to know the allelopathic impact of *O. sanctum* and *O. canum* on root weight and days to flower of 'Rose Red' cultivar of turnip (*Brassica rapa* L.).

Material and methods
To make the plant extracts field grown *Ocimum sanctum* L. and *Ocimum canum* Sims. were harvested. 250 g. sample was dried at 60^0C. Then it was grinned to pass through 1mm screen and was stored at room temperature. Sterilized distilled water was used to make aqueous plant extract in 40:1 (V/W) water: plant sample ratio. It was kept in refrigerator for 18 hours. The suspension was centrifuged at 900 x g for 15 minutes and then vacuum filtered through 0.4µm polycarbonate filters 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. The seeds were thoroughly washed in double distilled water and sown immediately in different pots having homogenous soil along with control to raise M_1 plants. M_2 populations were grown from the seeds collected from M_1 through selfing. 25 randomly selected plants in each concentration and control, under both kinds of treatment, were pulled out from the soil just before emergence of the flowering shoot and their weight was taken separate by with the help of a single pan balance to score mean root weight. The additional plants were grown for this purpose. The appearance of the first flower and its difference from the date of sowing gave the number of days to flower in each case. 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 root weight of turnip. There was a gradual increase in root weight 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. Noticeably a further increase took place in M_2 at all the doses under both kinds of treatment. Remarkably, *O. canum* treatment demonstrated more stimulating effect than *O. sanctum* at all concentrations. Contrary to this, gradual delay in the time of flowering occurred from lower to higher concentrations under both kinds of treatment in M_1 generation. Some earliness in this regard was noted in M_2 in both the cases at all the doses.

Moderate higher doses of the leaf extract of periwinkle (*Catharanthus roseus* Don.) exhibited effect on root weight (15). Carrot weed (*Parthenium hysterophorus* L.) leaf and flower extracts had deleterious effect on root weight of turnip (16). The lower doses of the leaf extract of neem (*Azadirachta indica* A. Juss.) and azadirachtin - based biopesticide had inducing effect on root weight of *Brassica rapa* L., but their higher doses were harmful (14). The crude neem oil treatment exhibited inducing effect on root weight of turnip (9). However, all the treatments caused delay in the time of flowering (9, 14, 15, 16,)

Molisch (10) coined the term allelopathy which refers to all stimulatory and inhibitory biochemical interactions between the plants including microbes. However, all plants do not have allelopathic tendencies. Allelopathic plants control the environment in which they live. Allelopathic compounds and interactions are much more common in terrestrial plants. 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 germination, survival, 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.

Present investigation reveals that the medicinal plants like *O. sanctum* and *O. canum* have inducing effect on root weight of turnip. First and foremost goal of a plant breeder at least in a developing country like India is to achieve higher yield in any crop. Turnip is a root crop plant. It looses its commercial value after the emergence of the flowering short. Hence delay in flowering associated units increase in root weight is beneficial from agricultural point of view. The time of flowering is also regarded as on important partner in any crop plant species since it is concerned with the earliness and lateness of a variety. 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. *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).

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Table 1. Effect of basil extracts on root weight and days to flower of turnip.

Dose (%)	Root weight (g)				Days to flower			
	O. sanctum		**O. canum**		**O. sanctum**		**O. canum**	
	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	162.0	163.8	162.0	161.7	72.7	73.0	73.7	73.5
20	169.1 (+4.4)	173.9 (+6.17)	174.0 (+7.4)	176.1 (+8.9)	75.7 (+4.1)	73.7 (+0.9)	76.0 (+3.1)	74.7 (+1.6)
40	263.1 (+62.4)	266.2 (+62.5)	301.6 (+86.2)	313.2 (+93.7)	79.5 (+9.3)	75.0 (+2.7)	81.5 (+10.6)	76.2 (+3.7)
60	283.9 (+75.2)	299.7 (+82.9)	311.7 (+92.4)	317.7 (+96.5)	81.5 (+12.1)	77.0 (+5.5)	84.7 (+14.9)	81.2 (+10.5)
80	294.0 (+81.5)	304.1 (+85.6)	314.9 (+94.4)	318.6 (+97.0)	84.0 (+15.5)	76.5 (+4.8)	86.7 (+17.6)	83.7 (+13.9)
100	189.2 (+16.8)	187.2 (+14.3)	221.8 (+36.9)	243.5 (+50.6)	86.2 (+18.6)	81.5 (+11.6)	88.2 (+19.7)	85.5 (+16.3)
CD at 5%	4.96	10.22	5.38	9.72	1.59	1.57	1.81	1.77

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

CRUCIFERAE NEWSLETTER Nr. 29

Instructions to the authors – 2009

Deadline for contribution submission: **December 15th 2009**

The current issue of the Cruciferae Newsletter (vol. 29) will be published online at the beginning of year 2010 from the Brassica website (http://www.brassica.info/information/cn/newsletter.htm). Online process will ensure rapid publication of your contribution. Therefore, we should be grateful if you would, please, follow the instructions below.

1- All contributions should be written in **English**.

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.

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.

6- While submitting their contributions, authors should mention **one of the listed topics** that is the most relevant to their work (see the list below), in order to facilitate the editing process.

7- All papers are published on their author's responsibility.

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Developmental and reproductive biology
Functional genomics: from model to crop
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Genetic transformation and biotechnologies
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Other topics (please give two keywords)