



Evaluation of some indigenous rapeseed genotypes for adaptability and yield traits in the agro-climatic conditions of Mansehra

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Abstract

The present study was undertaken to evaluate some indigenous rapeseed genotypes for adaptability and yield traits in the agro-climatic condition of Mansehra. These genotypes were evaluated in randomized complete block design with three replications. The experimental materials were consisting of 23 genotypes of national uniform yield trial (NUYT). Data was recorded on ten randomly selected plants from each genotype for six different characters. The six characters were studied viz., days to maturity, plant height, pods plant⁻¹, pod length, yield plant⁻¹, 1000-seed weight. Analysis of variance revealed significant differences ($P \leq 0.05$) among the genotypes for the all traits, which confirm the presence of genetic diversity. On average, the NIFA-6 showed best performance than remaining genotypes for yield attributing traits and eventually increased yield per plant. Heritabilities (broad sense) were moderate to high in magnitude for all traits. Major yield components viz., days to maturity, pods per plant and pod length revealed positive correlation with yield per plant. However, plant height showed significant ($P \leq 0.01$) negative correlation with yield per plant due to lodging. Overall, the genotypes viz., NIFA-6, 19-H and Bulbul-98 exhibited maximum yield per plant. Results revealed that the studied genotypes with larger genetic potential, positive relationship between yield and yield contributing traits and moderate to high heritability could guide intensive selection and improvement and could further be studied to identify better performing lines for Mansehra division.

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Introduction

The genus *Brassica* L. holds the most economically valuable position in the tribe Brassiceae, which is a part of family Brassicaceae (Rakow, 2004). This genus consists of a versatile batch of species that includes major oilseed crops and vegetables (Rich, 1991; Christopher *et al.*, 2005). This family comprises of 338 genera and 3709 species (Warwick *et al.*, 2006). The species of genus *Brassica* are generally classified into two main groups commonly known as rapeseed and mustard. It also contains six economically valuable species with huge genetic and morphological variation and is cultivated in all over the world (Shah *et al.*, 2008). Among these, three species are diploid (*Brassica oleracea*, $2n = 18$; *Brassica rapa*, $2n = 20$; *Brassica nigra*, $2n = 16$), and three are amphidiploid (*Brassica napus*, $2n = 38$; *Brassica juncea*, $2n = 36$; *Brassica carinata*, $2n = 34$). Rapeseed-mustard (*Brassica napus*, *Brassica campestris* and *Brassica juncea*) are grown all over the world as an important source of edible oil (Downey and Rakow, 1987).

During 2010-11, in Khyber Pakhtunkhwa canola was on 0.3 thousand hectares which produced 0.2 thousand tons seeds. Punjab is leading both in terms of acreage and production (area=9.6 thousand hectares, production =11.9 thousand tons). In Sindh and Balochistan it was grown on 3.8 and 3.5 thousand hectares with the production of 4.2 and 2.3 thousand tons respectively. Khyber Pakhtunkhwa, Punjab, Sindh and Balochistan have 450, 918, 1016 and 812kg ha⁻¹ average yield respectively (Agriculture Statistics of Pakistan 2010-11). During 2011-12 canola was grown on 90 ha (233 acres) which produced 131 thousand tons seed and 50 thousand tons oil (Economic Survey of Pakistan 2011-12). Currently, total requirement of edible oil in the country is 3.079 million tons out of which 0.696 million tons is provided by local production (34% of the demand); while remaining demand was met fulfilled by import of 2.383 million ton. The estimated cost of imports was Rs. 224 billion (US\$ 2.611 billion) in 2010-11(PBS, 2012).

World's leading producers of rapeseed are India, China, Canada, and Northern Europe. All over the world manifold increase in production has been recorded during last decade predominantly by the use of modern and conventional plant breeding approaches. According to the reports of United Nation Food & Agriculture Organization's reports, World production of rapeseed may be expected to increase further upward over between 2010 and 2015 (FAO, 2012).

For improving seeds yield and adaptability of rapeseed and other brassica species, important breeding strategies are; understand and utilization of genetic, physiological and morphological basis of yield linked traits in different environmental conditions. Determining conducive planting date plays vital role in conformation of plant growth steps with desirable environmental conditions which results in maximum yield. Planting date has a considerable effect on seed yield and adaptability by influencing the yield components so that late planting decreases the most important traits i.e. days to flowering, duration of flowering, plant height and pods plant⁻¹ which cause a remarkable reduction in seed yield. (Sharief and Keshta, 2002; Siadat and Hemayati, 2009).

The term correlation is a statistical measurement of the association between two variables. Statistical correlation refers to a quantifiable relationship among two variables. Moreover, its measure of the power and route of that relationship. For plant breeders it is thus essential to learn the relationships among pairs of characters in order to make a decision on the proper selection criteria for a breeding program (Engqvist and Becker, 1993).

Information about genetic variability gives a dependable tool to the breeder for improvement in crops. Higher genetic variability and correlation of yield with yield components are serious requirements of breeders who wish to improve production and quality of brassica (Abbas *et al.*, 2013). So, in plant breeding, the detection and utilization of genotypes

with best genetic potential is a permanent pre-requisite for production of physiologically efficient and genetically enhanced genotypes showing promise for improved production per unit area under a given set of environmental circumstances. Hence, a thorough study of the genetic mechanism of the plant characteristics is required. Considering the importance of edible oil in country, an experiment was carried out which had two fold objectives.

To evaluate genetic variability among different populations of *Brassica napus* L.

To estimate correlation coefficient for different important traits in *Brassica napus* L.

Materials and methods

Research area

The research work under consideration was carried out at Agricultural Research Station, Baffa, Mansehra, during Rabi season (2012-13) to evaluate the indigenous rapeseed genotypes for adaptability and yield traits in agro-climatic conditions of Mansehra.

Materials

The experimental materials were consisting of 23 genotypes of national uniform yield trail (NUYT). Row length was maintain as 5 m having row to row distance of 75 cm. Experimental plot was thoroughly prepared and was laid out in Randomized Complete Block Design (RCBD) with three replications. All the cultural practices were carried out as recommended.

Traits measurement and statistical analysis

Data were recorded on days to maturity, plant height, number of pods per plant, pod length, yield per plant and 1000-seed weight. All the data were subjected to analysis of variance (ANOVA) according to Steel *et al.* (1997). After getting the significant variations among genotypes performance for various parameters, the means for each parameter were further separated and compared by using the least significant difference (LSD) test at 5% level of probability. Genotypic (GCV) and phenotypic coefficients of variance (PCV) and heritability (broad sense) were computed according to

Burton and Devane (1953), Johnson *et al.* (1955) and Singh and Chaudhary (1985).

Results and discussion

Days to maturity

Analysis of variance for days to maturity revealed highly significant differences. Mean values ranged from 186.64 to 212.90 days to maturity. Many researchers have reported significant differences for days to maturity including; Sinha *et al.*, (2001), Zare and Sharafzadeh (2012). Among the tested genotypes DUNKLED took maximum days to maturity (212.90 days) followed by NIFA-6 (209.54) and NIFA-3 by taking (208.67) days to maturity. Minimum days to maturity (186.64 days) were recorded for the genotype 19-H. However, the overall mean was 198.09 for days to maturity. Genotypic (GCV) and phenotypic coefficients of variation (PCV) values for days to maturity were 5.84% and 7.38%, respectively. Broad sense heritability was 63% (Table 3). Positive significant correlation was observed between days to maturity and yield plant⁻¹ ($r= 0.279$) as well as with 1000-sw ($r= 0.057$). However, correlation was negative significant with plant height ($r= -0.185$), pod plant⁻¹ ($r= -0.091$) and pod length ($r= -0.018$). The differences in the data may be due to difference in the environment where the experiment was conducted, genetic makeup of the genotypes which perform differentially in different environments and the maturity groups.

Plant height

Data pertaining to plant height manifested significant ($p \leq 0.01$) between the accessions and ranges were 164.14 to 194.00 cm (Table 1). Greater variability among the accessions for plant height was observed (Cheema *et al.*, 2001; Sinha *et al.*, 2001; Sana *et al.*, 2003; Mansoor *et al.*, 2003; Inayat *et al.*, 2009; Ali *et al.*, 2011); Zare & Sharafzadeh, 2012 and Bashir *et al.*, 2013). Maximum plant height (194.00 cm) was recorded by genotype Abasin followed by CODED-D (193.43 cm). Least plant height (164.14 cm) was observed by genotype NIFA-4. However, the overall mean values for the said trait were 182.19 cm. Genotypic (GCV) and phenotypic coefficients of

variation (PCV) for plant height were 6.27% and 8.02%, respectively. Broad sense heritability was 61% (Table 3). High broad sense heritability coupled with moderate GCV and PCV were observed (Tariq *et al.*, 2003; Khan *et al.*, 2006; Dar *et al.*, 2010; Emrani *et al.*, 2012; Shehzad & Farhatullah, 2012). Genetic characteristics as well as environmental conditions have a significant role in the determining plant height. Negative significant correlation was observed

between plant height and pods plant⁻¹ (-0.092), pod length (r= -0.205), yield plant⁻¹ (r= -0.334**) and 1000-seed weight (r= -0.141). Zajac *et al.*, (2011) found similar results between the mentioned attributes. The variations among the genotypes for this character may be attributed to the differences in the genetic makeup of the genotypes and the environment where these genotypes were tested.

Table 1. Mean values for different genotypes of Brassica napus L.

Genotypes	DTM	PH	PPP	PL	YLPP	1000-SW
19-H	187.10±4.65h	185.42±3.22ab	304.23±2.99a/e	8.10±0.06a/e	17.43±0.79b	7.55±0.33a
DUNKLED	212.90±1.50a	191.82±1.89ab	294.74±4.14de	8.08±0.04a/f	13.38±1.10c/e	7.07±0.03b/e
BULBUL-98	207.20±4.75a/e	171.18±0.92c/e	309.57±7.59de	8.21±0.11a/f	16.69±4.05b/e	7.12±0.02b/e
RAINBOW	204.87±4.22a/g	177.67±1.33b/e	282.57±3.24e	7.90±0.10a/e	10.52±0.41c/e	7.23±0.07b/e
ABASIN	195.77±2.43b/h	194.00±1.53a	293.78±6.42e	8.13±0.07f	15.87±0.34bc	7.08±0.04b/e
NIFA-1	191.87±4.71f/h	190.06±4.49ab	309.67±6.33a	8.26±0.18c/f	12.14±1.19b/e	7.17±0.03b/e
NIFA-2	195.43±7.73b/h	183.62±0.87a/d	302.68±1.54c/e	7.81±0.26b/f	14.10±0.78b/e	7.35±0.05ab
NIFA-3	208.67±5.70ab	192.44±0.56ab	287.33±6.33e	7.47±0.12d/f	15.93±0.89b/d	7.15±0.06b/e
NIFA-4	207.87±4.64a/d	164.14±13.87a/e	315.90±7.49a/c	7.97±0.23a/e	13.30±1.63b/e	7.07±0.04b/e
NIFA-5	206.43±3.77a/f	188.00±4.36b/e	296.33±3.67d/e	7.21±0.01ab/f	11.47±1.05c/e	7.33±0.20a/c
NIFA-6	209.54±6.13a/g	184.16±5.47a/d	315.67±17.33d/e	9.07±0.43a/e	21.12±1.12a	7.64±0.31a/d
NIFA-7	194.20±1.73b/h	165.38±5.45e	320.57±2.89ab	8.05±0.05a/e	14.30±1.35c/e	7.04±0.04d/e
NIFA-8	208.33±2.48a/c	169.16±14.58a/d	295.14±5.43c/e	7.22±0.14c/f	11.95±0.41b/e	7.00±0.12e
NIFA-9	197.43±0.87b/h	183.82±2.93a/d	301.00±11.46b/e	7.57±0.23b/f	10.68±0.80c/e	7.06±0.07c/e
NIFA-10	193.20±2.11d/h	182.00±0.58a/d	313.03±6.23a/e	7.50±0.40a/f	10.65±0.78e	6.97±0.24e
NIFA-11	192.33±11.74f/h	186.40±5.21ab	302.11±1.16c/e	8.05±0.30a/c	10.93±1.65c/e	7.13±0.03b/e
NIFA-12	193.77±2.36c/h	169.15±7.07de	307.78±6.46a/e	7.82±0.18a/e	10.33±1.39c/e	6.99±0.04e
CODED-A	191.87±2.80f/h	180.40±0.87a/e	296.37±6.69b/e	8.30±0.15ab	11.47±0.15c/e	7.07±0.03b/e
CODED-B	192.47±11.86f/h	182.40±7.80a/d	292.77±5.85c/e	8.02±0.06ef	9.67±0.68e	7.07±0.03b/e
CODED-C	186.64±8.75b/h	188.67±4.91ab	301.00±0.58b/e	8.13±0.09a/d	11.31±0.21c/e	7.13±0.03b/e
CODED-D	192.87±2.23c/h	193.43±3.79ab	305.58±4.00de	7.67±0.20a/f	9.80±0.38 c/e	7.10±0.03b/e
CODED-E	191.43±3.27gh	182.55±5.64a/d	293.00±6.43de	7.85±0.26a/c	10.60±0.42c/e	7.05±0.03c/e
CODED-F	193.87±1.79c/h	184.42±4.31a/c	311.10±6.00a/d	7.43±0.17a	14.22±0.52c/e	7.04±0.03de
LSD _(0.05)	15.105	16.553	18.618	0.5815	3.3371	0.3396

Where, DTM= Days to maturity, PH=Plant height (cm), PPP=pods per pod, PL= pod length (cm), YLPP=yield per plant (gm) and 1000-SW= seed weight (gm).

Number of pods plant⁻¹

Data concerning number of pods plant⁻¹ showed significant ($p \leq 0.05$) differences amongst the accessions. The data ranged from 282.57 to 320.57 for pods plant⁻¹. Number of pods plant⁻¹ varied significantly among the studied rapeseed accessions. Several workers have previously reported similar significant differences for this character including

Cheema *et al.*, (2001), Ali *et al.*, (2002), Sana *et al.*, (2003), Cheema and Sadaqat (2004), Ivanovoska *et al.*, (2005), Tuncturk M and Ciftci V (2007), Inayat *et al.*, (2009), and Zare and Sharafzadeh., (2012). Maximum pods plant⁻¹ (320.57) was recorded for the genotype NIFA-7 followed by NIFA-4 (315.90). Minimum value for said trait was exhibited by genotype RAINBOW (282.57). However, overall

mean values were 302.26 for number of pods plant⁻¹. Genotypic (GCV) and phenotypic coefficients of variation (PCV) values for number of pods plant⁻¹ were 6.76% and 8.66%, respectively. Broad sense heritability was 61% (Table 3). Significant positive correlation was found among pod plant⁻¹ and 1000-seed weight ($r= 0.251^*$), while positive association with pod length ($r= 0.033$), yield plant⁻¹ ($r= 0.023$). The number of pods plant⁻¹ is known as a key and major determining component of Brassica species and has a substantial contribution towards seed yield depending upon the factors like variety, environmental condition and suitable soil. Number of

pods plant⁻¹ revealed positive significant correlation with 1000-seed weight and positive correlation with pod length, number of seeds pod⁻¹, yield plant⁻¹. Sana *et al.*, (2003) manage to find positive significant correlation between pods plant⁻¹ and seed yield. Inayat *et al.*, (2009) found positive correlation between number of pods plant⁻¹ and yield plant⁻¹. Similarly, positive significant correlation was also noticed between pods plant⁻¹ and seed yield (Rameeh *et al.*, 2011). These differences among the accessions may be due the differences in the genetic makeup, genetic potential of the genotypes and the environment where these genotypes were tested.

Table 2. Phenotypic correlations among important traits in Brassica napus L.

Genotypes	DTM	PH	PPP	PL	YPP	1000-SW
DTM	-	-0.185	-0.091	0.081	0.279*	0.057
PH		-	-0.092	-0.205	-0.334**	-0.141
PPP			-	0.033	0.023	0.251*
PL				-	0.102	0.160
YPP					-	0.008
1000-SW						-

Where, ** = highly significant, * = significant.

DTM= Days to maturity, PH=Plant height (cm), PPP=pods per pod, PL= pod length (cm), YLPP=yield per plant (gm) and 1000-SW= seed weight (gm).

Pod Length

The data recorded for pod length exhibited significant ($P \leq 0.01$) differences. The mean values ranged from 7.21 to 9.07 cm for pod length. The results obtained from the experiment are in confirmaty with the previous results obtained by several researchers including Islam *et al.*, (2004), Ahmad *et al.*, (2008), Inayat *et al.*, (2009) and Zare and Sharafzadeh., (2012) reported significant differences among the genotypes for pod length. The data for the character varied among the genotypes confirming the presence of the genetic variability among the accessions. Maximum pod length (9.07 cm) was exhibited by the genotype NIFA-6, followed by the genotype CODED-A (8.30 cm) and NIFA-1 (8.26 cm). NIFA-5 revealed the minimum value (7.21 cm) pod length. The overall mean shown by the said trait was of 7.80 cm. Genotypic (GCV) and phenotypic coefficients of variation (PCV) values for pod length said trait were

6.72% and 8.71%, respectively. Broad sense heritability was 59% (Table 3). Pod length showed positive association with yield plant⁻¹ ($r= 0.102$) and 1000-seed weight ($r= 0.160$). Wang *et al.*, (2007) revealed positive correlation with pod length and yield plant⁻¹, where as Nasim *et al.*, (2013) reported positive correlation between pod length and 1000-seed weight. These differences among the genotypes may be due the differences in the genetic makeup, genetic potential of the genotypes and the environment where these genotypes were tested.

Yield plant⁻¹

Data pertaining to yield pod⁻¹ revealed significant differences among the accessions. The ranges for mean values were 9.67 to 21.12 g. Similar results has been reported by many workers which reveal sufficient variability in their mean values including; Cheema *et al.*, (2001), Sana *et al.*, (2003), Inayat *et al.*,

(2009) and Zare and Sharafzadeh., (2012), Bashir *et al.*, (2013) reported considerable differences among the genotypes for seed yield pod⁻¹. Maximum yield per pod (21.12 g) was exhibited by the genotype NIFA-6. Coded-B revealed the minimum value (9.67 g) for said attribute. The overall mean was 12.95 g was recorded for yield plant⁻¹. Genotypic (GCV) and phenotypic coefficients of variation (PCV) values for the yield pod⁻¹ were 42.16% and 50.09%, respectively.

Broad sense heritability was 71% (Table 3). Yield pod⁻¹ exhibited positive (0.003) correlation with 1000-seed weight. This type of correlation is in conformity with the research works of other investigators (Ghobadi *et al.*, 2006 and Inayt *et al.*, 2009). These differences among the genotypes may be due the differences in the genetic makeup, genetic potential of the genotypes and the environment where these genotypes were tested.

Table 3. Genetic, environmental and phenotypic variances with heritability for various morpho yield traits of Brassica napus L.

TRAITS	GMS	EMS	V _g	V _p	h ²	GCV (%)	PCV (%)
DTM	160.53	79.64	133.98	213.62	0.63	5.84	7.38
YLPP	30.75	11.13	27.04	38.17	0.71	42.16	50.09
PH	158.94	83.41	131.13	214.55	0.61	6.27	8.02
PPP	487.64	257.55	401.79	659.34	0.61	6.76	8.66
PL	0.34	0.19	0.27	0.46	0.59	6.72	8.71
TSW	0.06	0.03	0.05	0.08	0.60	3.03	3.91

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, V_g = Genetic variance, V_e = Environmental variance, V_p = Phenotypic variance, h² = Heritability (bs).

1000-seed weight

The perusal of the data pertaining to 1000-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions. Greater variability among the accessions for 1000-seed weight was observed (Cheema *et al.*, 2001; Akbar *et al.*, 2003; Mansoor *et al.*, 2003; Ivanovska *et al.*, 2005; Akbar *et al.*, 2007; Kumar and Misra, 2007; Aytac & Kinaci, 2009; Inayt-ur-Rahman *et al.*, 2009; Zare & Sharafzadeh, 2012 and Bashir *et al.*, 2013). The data recorded for this character ranged from 6.97 g to 7.64 g. Maximum 1000-seed weight (7.64 g) was observed in genotype NIFA-6 followed by 19-H (7.55 g) and NIFA-2 (7.35 g). Minimum seed weight (6.97 g) was recorded in genotype NIFA-10. However, the overall mean value for the said trait was 7.15 g. Genotypic (GCV) and phenotypic coefficients of variation (PCV) values for 1000-seed weight were 3.03% and 3.91%, respectively. Broad sense heritability was 60% (Table 3). The seed weight expresses the magnitude of seed development that tells us of the potential of seed yield of a variety. These differences among the genotypes

may be due the differences in the genetic makeup, genetic potential of the genotypes and the environment where these genotypes were tested.

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