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GENETIC DIVERSITY ASSESSMENT IN BRASSICA GERMPLASM BASED ON MORPHOLOGICAL ATTRIBUTES

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ABSTRACT:- Genetic diversity of 28 *Brassica* genotypes was studied using different morphological attributes. Data were recorded on days to maturity (DM), plant height (PH), primary branches plant^{-1} (PBPP), pod length (PL), seed pod^{-1} (SP), 1000-seed weight (1000-SW), yield plant^{-1} (YPP) and oil (%). Three checks (Pakola, CM and TA), were used to check the performance of collected materials with already available brassica varieties. Significant statistical differences were observed among the tested genotypes based on the studied morphological traits. Among the tested genotypes, genotype Kalabat proved to be superior as compared to other studied genotypes due to maximum level of studied traits like pod length (7.03 cm), seed pod^{-1} (32.33), 1000-seed weight (5.38 g), seed yield plant^{-1}(110.8 g) and oil content (52.9%). The highest level of performance recorded by Kalabat in terms of branches plant^{-1}, pod length (cm), number of seed pod^{-1}, seed yield plant^{-1} (g), 1000-seed weight (g) and oil content (%), indicates that this genotype is genetically different and superior than the other studied genotype. Therefore, genotype Kalabat can be either used as variety after adaptability trials over a larger area or included in Brassica breeding programmes as a good source of genetic variation.

Key Words: Brassica Species; Local Accessions; Morphological Traits; Genetic Diversity; Agronomic Characters; Yield; Yield Components; Pakistan.

INTRODUCTION

The genus *Brassica* is one of the most economically important plant genera which belong to tribe Brassiceae of the family Brassicaceae (Rakow and Raney, 2003). This genus contains six important annual species which are cultivated globally as oilseed crops, condiments, fodder or vegetables. The oil obtained from these species is used for human consumption in addition to other industrial uses and the meal after the extraction of oil is used as animal feed. Three of six species are diploids (2x) viz., *B. rapa* (2*n*=20); *B. nigra* (2*n*=16) and *B. oleracea* (2*n*=18), while the remaining three (*B. juncea*, 2*n*=36; *B. napus*, 2n=38; *B. carinata*, 2*n*=34) are amphidiploids (4x) derived from chromosome doubling in the hybrids obtained from three possible crosses among the diploid species. Commonly four Brassica species have been cultivated as oilseed crops viz., *B. napus, B. rapa, B. carinata*, *B. juncea* globally (Song et al., 1990) and they are also important in Pakistani context.

Brassica, as mentioned earlier, is used as vegetable, grain, oilseed and

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green compost for soil restoration (Gomez-Campo, 1980; Williams and Hill, 1986). In Pakistan oilseed Brassica is cultivated every year on 482,000 acre with the production of 186,000 t of seed, which produced 61000 t oil (GoP, 2013). In Pakistan five species viz., *B. rapa, B. napus, B. juncea, B. carinata* and *Eruca sativa* of rapeseed and mustard are cultivated in particular (Munir and Khan, 1984). Morphological evaluation is the primary step in description and categorization of the germplasm (Taylor et al., 1991). Morphological differences in plant species are the result of long-term selection/ adaptation in different parts of the world where the species were initially cultivated. Different techniques have been effectively used to find the pattern of phenotypic diversity in species indicating genetic differences of a variety of crops (Dias et al., 1993; Amurrio et al., 1995). To expand the existing genetic pool, breeders collect and evaluate the germplasm from all over the world for their genetic diversity (Ana et al., 2009). Estimating genetic diversity among germplasm collections, enhances the efficiency of germplasm collection management (Nisar et al., 2008) as well as the genetic improvement of crops leading to the higher genetic gain (Gelet et al., 2005).

The present study was aimed to evaluate the genetic variability among different *Brassica* genotypes based on their morphological attributes for the identification of the genotypes with best genetic potential for their use in future breeding programmes.

MATERIALS AND METHOD

This study was carried out at research farm of Haripur University, Haripur, Khyber Pakhtunkhwa, Pakistan in Hazara Region, Pakistan, during 2013-14. The experiment was laid out in RCBD with three replications. The plot size was 6.75m^2. Twenty eight different genotypes, including 25 accessions and three checks (Pakola, CM and TA) were used to study genetic variation among the genotypes. These genotypes included five from *Brassica napus*, six from *B. juncea* and 15 from *B. rapa*. Seed were sown in rows with the help of hand hoe during second week of September. Row length were kept 1m with a row to row distance of 30-45 cm and plant to plant distance was 4-5 cm. Fertilizer were applied as 90N:60P:50K. Four irrigations were applied during the whole period and seed were harvested at 70% maturity.

Data were recorded on days to maturity (DM), plant height (PH), primary branches plant^{-1} (PBPP), pod length (PL), seed pod^{-1} (SP), oil%, 1000-seed weight (1000-SW) and yield plant^{-1} (YPP). The experimental data were recorded and statistically analyzed through Statistix 8.1 computer software (Analytical Software, 2005), the means were separated using least significant difference (LSD) test. All differences described in the text were significant at the 1% level of probability.

RESULTS AND DISCUSSION

The analysis of data revealed highly significant ($P \leq 0.01$) statistical differences for all the studied traits and so confirmed the presence of genetic variability. Similar results were reported by Nasim et al.(2014), Zare (2012), Ali et al. (2002), Synrem

et al. (2014), Ghosh and Gulati (2001), Azadgoleh et al. (2009) and Tahir et al. (2006).

Maximum days (181) to physiological maturity were recorded in Panyain 01 followed by genotype Sarikot 01 (170 days), whereas minimum days (131) to maturity were observed in genotype Havellian (Table 1). These results are consistent with the findings of Nasim et al.(2014) and Zare and Sharafzadeh (2012) who reported significant variations among genotypes/varieties of *Brassica* for days to maturity. Taller plants are more susceptible for lodging as compared to dwarf one, so semi-dwarf plants is ideal for plant breeder. Plant height data revealed that genotype Sarihot 03 gained maximum height (243.67 cm) against the Shayein (160.33 cm) (Table 1). Genotype Kalabat produced medium plant height (175.33 cm). Nasim et al. (2013), Ali et al. (2002) and Zare and Sharafzadeh (2012) also reported similar results showing significant differences among the genotypes for plant height. The high level of variation in plant height in the studied material could be attributed to the genetic differences among the studied genotypes (Khan et al., 1987). Genotype Kalabat recorded maximum branches per plant (17), while genotype Abbottabad produced minimum branches plant^{-1} (7) (Table 1). These results were in conformity with the findings of Synrem et al. (2014) and Nasim et al. (2013) who found significant differences among *Brassica* genotypes for primary branches plant^{-1} in their various studies. In *Brassica*, the number of primary branches plant^{-1} is directly associated with the yield of a plant and number of pods (Khan et al., 1987) and consequently, genotypes with higher number of branches and pods per plant lead higher seed yield. Similarly, maximum pod length (7.00 cm) was recorded for genotype Kalabat while minimum level of this trait was observed in genotype Qalandar Abad (2.87 cm) (Table 1). Significant variation for pod length among different genotypes of *Brassica* representing different genetic makeup was also revealed by Zare and Sharafzadeh (2012), and Aytac and Kinaci (2009). After fertilization, which is usually completed within 24 h of pollination, the syncarpous ovary elongates to form a pod (siliqua). Such variation in pod length may be due to diverse genetic makeup and environmental effects (Khan et al., 1987). Maximum number of seed pod^{-1} (32) was observed for genotype Kalabat, while minimum seed pod^{-1} (9.33) found in genotype Sarihot 03 (Table 1). It was in agreement with the results of Nasim et al. (2013), Zare and Sharafzadeh (2012) and Ghosh and Gulati (2001), who reported signifi-cant differences among the tested genotypes. The average data on seeds per pod (Table 1) showed a range of 9.33-32.33 which represents a huge variation among the genotypes regarding this variable. This shows huge genomic differences among the studied genotypes. The data regarding 1000-seed weight (g) also revealed significant genotypic differences. The maximum 1000-seed weight (5.4 g) was produced by genotype Kalabat, followed by genotypes Qalandar Abad 01 and Pakola, respectively (Table 1). For 1000-seed weight, large variations were also reported earlier (Nasim et al., 2013; Azadgoleh et al., 2009; Tahir et al., 2006). Thousand seed weight is one of the most

Table 1. Mean data values on different studied morphological traits of 28 genotypes of Brassica including 3 checks

S.No	Entry	Collection Place	Species	DM	PH	PBPP	PL (cm)	SP	Oil %	1000-SW (g)	YPP (g)
1	E1	Check (Pakola)	*B. napus*	167.67	237.00	10.66	4.70	24.67	48.77	2.69	35.10
2	E2	Mang	*B. napus*	162.33	222.67	14.00	5.23	23.33	44.40	4.57	31.00
3	E3	Havellain	*B. napus*	164.67	231.33	13.67	6.30	30.00	45.16	2.327	39.40
4	E4	Buldher	*B. napus*	166.33	223.33	9.67	6.17	28.33	43.57	3.03	38.13
5	E5	Sarikot 01	*B. napus*	170.67	215.33	10.67	7.00	28.00	44.93	4.18	32.27
6	E6	Kalabat	*B. napus*	165.00	175.33	17.33	7.03	32.33	52.93	5.38	110.83
7	E7	Panyain 01	*B. juncea*	181.33	225.67	14.33	5.70	26.33	49.50	4.71	42.73
8	E8	Panyain 02	*B. juncea*	155.33	232.33	12.67	3.87	13.33	42.53	2.93	43.03
9	E9	Saraie Ghadie	*B. juncea*	156.00	162.00	12.33	3.20	13.00	42.57	4.93	67.27
10	E10	Shayein	*B. juncea*	156.67	160.33	14.00	3.30	15.67	43.53	4.74	31.63
11	E11	Salhat	*B. juncea*	153.33	222.3	9.67	3.83	12.67	43.97	3.78	45.17
12	E12	Qalandar Abad 02	*B. juncea*	149.00	220.33	12.00	2.87	11.33	44.67	3.57	34.50
13	E13	Check (CM)	*B. juncea*	156.00	224.33	9.00	4.20	23.00	44.63	4.03	42.43
14	E14	Qalabdar Abad 01	*B. campestris*	145.00	184.00	8.00	4.87	18.67	45.27	4.82	49.07
15	E15	Panyain 03	*B. campestris*	141.00	204.67	11.67	5.23	21.67	46.70	3.00	38.60
16	E16	Panyain 04	*B. campestris*	147.00	191.00	7.333	3.93	21.333	43.300	2.3700	38.10
17	E17	Sarikot 02	*B. campestris*	142.33	178.33	8.000	5.20	21.333	43.600	4.6367	33.20
18	E18	Sarikot 03	*B. campestris*	157.00	243.67	10.33	2.90	9.33	46.033	2.58	35.53
19	E19	Saraie Sala	*B .campestris*	140.33	227.67	12.00	4.13	17.33	44.800	4.03	27.50
20	E20	Abbottabad	*B. campestris*	141.33	211.33	7.00	2.97	10.00	41.833	3.58	26.97
21	E21	Jarikas 01	*B. campestris*	146.00	169.00	12.67	3.33	14.00	46.067	3.47	34.20
22	E22	Jarikas 02	*B. campestris*	154.67	227.67	11.66	4.87	18.00	41.667	4.58	37.40
23	E23	Hattar	*B. campestris*	158.33	197.67	12.67	6.47	22.67	41.833	3.00	29.57
24	E24	Baffa	*B. campestris*	132.67	189.00	9.00	6.03	31.00	49.267	2.67	45.97
25	E25	Havellain	*B. campestris*	131.00	175.67	12.33	4.40	20.67	47.500	3.74	36.20
26	E26	Swat Chowk	*B. campestris*	137.00	181.33	15.00	4.60	21.67	49.033	3.54	23.87
27	E27	Qalandar Abad 03	*B. campestris*	152.00	181.33	16.33	4.80	15.33	46.433	3.94	30.57
28	E28	Check (TA)	*B. campestris*	148.67	186.67	15.00	5.47	21.33	43.833	2.52	41.20
LSD				4.71	34.92	3.62	1.05	10.72	1.11	0.85	21.45
SD				29.90	51.98	3.54	1.53	6.36	2.71	0.88	16.23
SE				8.63	15.01	1.02	0.44	1.84	0.78	0.25	4.69

important yield contributing factors in Brassica. The difference between 1000-seed weights of different genotypes may be attributed to the variation in size and quality of seed in different genotypes as reported by Khan et al. (1987).

Seed yield plant^{-1}, an important trait contributing to the per unit area yield in Brassica varieties, also showed significant variation in this study which may be due to the genetic variation among the genotypes (Khan et al., 1987). Maximum seed yield plant^{-1} (110.8 g) was obtained for genotype Kalabat against the minimum seed yield plant^{-1} (23.87 g) for genotype Swat Chowk (Table 1). These results regarding genetic variation for seed yield among the studied genotypes were in agreement with those of Nasim et al. (2013), Sadat et al. (2010) and Tahir et al. (2006). Seed yield has been the major objective of most breeding programmes on *Brassica* like any other crop cultivated for seed as major economic product. Therefore, vigorous efforts are required to boost up the yield vertically by evolving varieties with genetic potential for higher yield. Late maturing genotypes frequently produced higher seed yield, but may also be exposed to numerous climatic hazards i.e., frost, drought or heat damage causing significant yield losses .

Oil content (%) is the most important component of the seed, having a monetary value of 2 to 3 times that of the remaining high protein meal. As brassica species are mostly cultivated for oil obtained from its seed so higher seed oil content (%) has been a prime breeding objective. Highly significant variations were observed in the present study for oil content (%) among the studied genotypes. These significant differences among the studied Brassica genotypes for oil (%) represent genetic differences in the studied accessions. Comparatively higher oil content (%) was recorded in genotype Kalabat, while lowest oil content was found in genotype Jarikas 02. These results are also consistent with those of Ali et al. (2013) and Azam et al. (2013), who reported significant differences among *Brassica* genotypes for oil content (%).

It is thus concluded that genotype Kalabat of Brassica napus recorded higher level of different yield contributing factors among the tested genotypes against *B. rapa* and *B. juncea*. Therefore, genotype Kalabat is recommended for inclusion in *Brassica* breeding or releasing it directly as commercial variety in trial area after further necessary evaluation and formalities.

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AUTHORSHIP AND CONTRIBUTION DECLARATION

S. No	Author Name	Contribution to the paper
1.	Mr. Israr Ali	Data collection
2.	Dr.Naushad Ali	Conceived the idea
3.	Dr. Riffat Tahira	Technical input at every step
4.	Mr. Sardar Ali	Overall management
5.	Mr. Izhar Hussain	Germplasm collection
6.	Dr. Sher Aslam Khan	Data entry and analysis

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