ASSESSMENT OF QUANTITATIVE AGRO-MORPHOLOGICAL VARIATIONS AMONG BRASSICA RAPA DIVERSE POPULATIONS

SOHAIL AHMAD JAN^{1,3*}, ZABTA KHAN SHINWARI^{1, 2}, MALIK ASHIQ RABBANI³, IFTIKHAR AZIM NIAZ⁴ AND SABIR HUSSAIN SHAH⁵

¹Department of Biotechnology, Quaid-i-Azam University, Islamabad, Pakistan
²Pakistan Academy of Sciences, Islamabad, Pakistan
³Plant Genetic Resources Institute, National Agricultural Research Centre, Islamabad, Pakistan
⁴Department of Computer Science, COMSATS Institute of Information Technology, Islamabad, Pakistan
⁵Department of Agricultural Sciences, Allama Iqbal Open University, Islamabad-Pakistan
*Corresponding author's email: sjan.parc@gmail.com

Abstract

Brassica rapa is one of the important oilseed crops and commonly grown all over the world for multiple purposes. The present study was designed to study intra-specific quantitative characters among 253 *B. rapa* genotypes. The two years mean morphological data were recorded for all these characters under field condition. Significant variations were recorded among genotypes for days to flower initiation, days to 50% flowering completion, days to flowering completion, days to maturity, leaf length and width, plant height, primary branches plant⁻¹, main raceme length, pod length, pod width, stem thickness, thousand seed weight, seed yield plant⁻¹ and pod shattering (stage I-IV). Many elite lines such as Br-505, Br-512, Br-536, Br-547, Br-560, Br-760, etc. had excellent morphogenic responses in both years. The present early flowering and maturity lines, pod shatter resistant and maximum yielding genotypes give unique opportunity to enhance the quality and production of this important crop.

Key words: Brassica rapa, Quantitative traits, Pod-shattering, Plant yield, Early flowering.

Introduction

Brassica rapa is one of the important vegetable oil crop species, belong to important family Brassicaceae. It consists of wide ranges of leafy or root vegetables types such as Chinese cabbage, pak-choi etc. that used as human diet (Zhao *et al.*, 2005). The main aim of plant breeders is to study the genetic variability of new genotypes of important crop species and to screen best genotypes for efficient utilization or varieties development. Estimation of various qualitative and quantitative traits provides a clear picture of improve diverse genotypes. Among these characters the yield parameter plays a vital role for new variety development (Ali *et al.*, 2013; Azam *et al.*, 2013).

It has been reported that more than 70% flowering plants undergoes genome polyploidizations. This process is also common in important Brassicaceae family. The crop such as cabbages, turnip and Chinese cabbage are diploid in nature (Zhang et al., 2016). Yu et al. (2010) study intraspecific variation among various genotypes of B. rapa ssp. chinensis Makino. Genetic association study was conducted for 29 morphological characters along with 20 different simple sequence repeats (SSR) markers. Five diverse groups were produced on the basis of correlation and similarity coefficient values. Significantly variation was observed for both morpho-molecular associations. Padilla et al. (2005) found morphological based variation in B. rapa ssp. rapa that including turnips, both green, and turnip tops. The agro-morphological based diversity of 134 different landraces was evaluated. All the genotypes were grouped in five major groups. Considerable variations for both qualitative and quantitative characters were observed. Iqbal et al. (2014) studied the genetic diversity often locally B. rapa genotypes for quantitative characters and maximum variation were recorded. The traits likes' 1000seed weight, seed yield/plant, plant height, main raceme length etc. showed maximum polymorphism except for the trait of silique width. No such report is available for some

diverse genotypes of *B. rapa*. Therefore the present study was attempted to study agro-morphological based variation among different local and exotic genotypes of *B. rapa* for economically important quantitative traits.

Materials and Methods

Plant Material: The plant materials contained 253 local and exotic genotypes (251 new accessions with two check varieties) of *Brassica rapa*. The experimental seed materials were provided by Plant Genetic Resources Institute (PGRI), National Agricultural Research Centre (NARC), Islamabad, Pakistan. The detailed information of *B. rapa* genotypes is given in Table 1.

Agro-morphological characterization and crop management: Two years experiment was conducted in experimental field of PGRI, NARC, Islamabad, Pakistan. The inter-row to row distance of 60cm and inter-path distance of 30 cm was maintained. The plot size was 2 rows of 5 m length for each genotype. The field was irrigated in order to provide maximum moisture before one week of sowing and after the field was maintained under rain-fed condition by withholding water.

The seed were sown in the field with the help of single row hand drill. Once germination occur the excess of weeds were removed and pesticides were sprayed in whole field. Phenotypic data of five selected plants was taken regularly and its various important quantitative agro-morphological traits were studied such as days to flower initiation (DFI), days to 50% flower (50% DF), days to flower completion (DFC), leaf length (LL), leaf width (LW), pod shatter resistance-I-IV, plant height (PH), main raceme length (MRL), pods per main raceme (P/MR), stem thickness (ST), pod length (PL), pod width (PW), seeds per pod (S/P), seed yield per plant (SY/P) and 1000 seeds weight.

					Tab	le 1. List	of accession	s and its	Table 1. List of accessions and its origin of diverse <i>B. rapa</i> population	verse B. ra	<i>pa</i> populat	ion.					
Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin	Acc#	Origin
Br-501	Pakistan	Br-531	Netherlands Br-561	Br-561	Germany	Br-591	Germany	Br-621	Germany	Br-651	Pakistan	Br-681	Pakistan	Br-711	Pakistan	Br-741	Pakistan
Br-502	Pakistan	Br-532	Netherlands Br-562	Br-562	Germany	Br-592	Germany	Br-622	Germany	Br-652	Pakistan	Br-682	Pakistan	Br-712	Pakistan	Br-742	Pakistan
Br-503	Pakistan	Br-533	Netherlands Br-563	Br-563	Germany	Br-593	Germany	Br-623	Germany	Br-653	Pakistan	Br-683	Pakistan	Br-713	Pakistan	Br-743	Pakistan
Br-504	Pakistan	Br-534	Br-534 Netherlands Br-564	Br-564	Germany	Br-594	Germany	Br-624	Germany	Br-654	Pakistan	Br-684	Pakistan	Br-714	Pakistan	Br-744	Pakistan
Br-505	Pakistan	Br-535	Br-535 Netherlands Br-565	Br-565	Germany	Br-595	Germany	Br-625	Sweden	Br-655	Pakistan	Br-685	Pakistan	Br-715	Pakistan	Br-745	Pakistan
Br-506	Pakistan	Br-536	Br-536 Netherlands Br-566	Br-566	Germany	Br-596	Germany	Br-626	Sweden	Br-656	Pakistan	Br-686	Pakistan	Br-716	Pakistan	Br-746	Pakistan
Br-507	Pakistan	Br-537	Br-537 Netherlands Br-567	Br-567	Germany	Br-597	Germany	Br-627	Sweden	Br-657	Pakistan	Br-687	Pakistan	Br-717	Pakistan	Br-747	Pakistan
Br-508	Pakistan	Br-538	Br-538 Netherlands Br-568	Br-568	Germany	Br-598	Germany	Br-628	Sweden	Br-658	Pakistan	Br-688	Pakistan	Br-718	Pakistan	Br-748	Pakistan
Br-509	Pakistan	Br-539	Br-539 Netherlands Br-569	Br-569	Germany	Br-599	Germany	Br-629	Sweden	Br-659	Pakistan	Br-689	Pakistan	Br-719	Pakistan	Br-749	Pakistan
Br-510	Pakistan	Br-540	Br-540 Netherlands Br-570	Br-570	Germany	Br-600	Germany	Br-630	Sweden	Br-660	Pakistan	Br-690	Pakistan	Br-720	Pakistan	Br-750	Pakistan
Br-511	Pakistan	Br-541	Br-541 Netherlands Br-571	Br-571	Germany	Br-601	Germany	Br-631	Sweden	Br-661	Pakistan	Br-691	Pakistan	Br-721	Pakistan	BSA	Pakistan
Br-512	Pakistan	Br-542	Br-542 Netherlands Br-572	Br-572	Germany	Br-602	Germany	Br-632	Sweden	Br-662	Pakistan	Br-692	Pakistan	Br-722	Pakistan	Toria	Pakistan
Br-513	Pakistan	Br-543	Br-543 Netherlands Br-573	Br-573	Germany	Br-603	Germany	Br-633	Sweden	Br-663	Pakistan	Br-693	Pakistan	Br-723	Pakistan	TS1	Pakistan
Br-514	Pakistan	Br-544	Br-544 Netherlands Br-574	Br-574	Germany	Br-604	Germany	Br-634	Sweden	Br-664	Pakistan	Br-694	Pakistan	Br-724	Pakistan		
Br-515	Pakistan	Br-545	Br-545 Netherlands Br-575	Br-575	Germany	Br-605	Germany	Br-635	Sweden	Br-665	Pakistan	Br-695	Pakistan	Br-725	Pakistan		
Br-516	Pakistan	Br-546	Br-546 Netherlands Br-576	Br-576	Germany	Br-606	Germany	Br-636	Sweden	Br-666	Pakistan	Br-696	Pakistan	Br-726	Pakistan		
Br-517	Pakistan	Br-547	Br-547 Netherlands Br-577	Br-577	Germany	Br-607	Germany	Br-637	Sweden	Br-667	Pakistan	Br-697	Pakistan	Br-727	Pakistan		
Br-518	Pakistan	Br-548	Br-548 Netherlands Br-578	Br-578	Germany	Br-608	Germany	Br-638	Sweden	Br-668	Pakistan	Br-698	Pakistan	Br-728	Pakistan		
Br-519	Pakistan	Br-549	Br-549 Netherlands Br-579	Br-579	Germany	Br-609	Germany	Br-639	Sweden	Br-669	Pakistan	Br-699	Pakistan	Br-729	Pakistan		
Br-520	Pakistan	Br-550	Br-550 Netherlands Br-580	Br-580	Germany	Br-610	Germany	Br-640	Sweden	Br-670	Pakistan	Br-700	Pakistan	Br-730	Pakistan		
Br-521	Pakistan	Br-551	Br-551 Netherlands Br-581	Br-581	Germany	Br-611	Germany	Br-641	Sweden	Br-671	Pakistan	Br-701	Pakistan	Br-731	Pakistan		
Br-522	Pakistan	Br-552	Netherlands Br-582	Br-582	Germany	Br-612	Germany	Br-642	Sweden	Br-672	Pakistan	Br-702	Pakistan	Br-732	Pakistan		
Br-523	Pakistan	Br-553	Br-553 Netherlands Br-583	Br-583	Germany	Br-613	Germany	Br-643	Sweden	Br-673	Pakistan	Br-703	Pakistan	Br-733	Pakistan		
Br-524	Pakistan	Br-554	Br-554 Netherlands Br-584	Br-584	Germany	Br-614	Germany	Br-644	Sweden	Br-674	Pakistan	Br-704	Pakistan	Br-734	Pakistan		
Br-525	Pakistan	Br-555	Br-555 Netherlands Br-585	Br-585	Germany	Br-615	Germany	Br-645	Unknown	Br-675	Pakistan	Br-705	Pakistan	Br-735	Pakistan		
Br-526	Netherland	s Br-556	Netherlands Br-556 Netherlands Br-586	Br-586	Germany	Br-616	Germany	Br-646	Unknown	Br-676	Pakistan	Br-706	Pakistan	Br-736	Pakistan		
Br-527	Netherland	s Br-557	Netherlands Br-557 Netherlands Br-587	Br-587	Germany	Br-617	Germany	Br-647	Sweden	Br-677	Pakistan	Br-707	Pakistan	Br-737	Pakistan		
Br-528	Netherlands Br-558	s Br-558	Germany	Br-588	Germany	Br-618	Germany	Br-648	Sweden	Br-678	Pakistan	Br-708	Pakistan	Br-738	Pakistan		
Br-529	Br-529 Netherlands Br-559	s Br-559	Germany	Br-589	Germany	Br-619	Germany	Br-649	Pakistan	Br-679	Pakistan	Br-709	Pakistan	Br-739	Pakistan		
Br-530	Br-530 Netherlands Br-560	s Br-560	Germany	Br-590	Germany	Br-620	Germany	Br-650	Pakistan	Br-680	Pakistan	Br-710	Pakistan	Br-740	Pakistan		

In present study the morphological based variation was studied in 253 *B. rapa* genotypes including two check varieties (TS-1 and BSA). All the genotypes showed maximum phenotypic variations for all quantitative characters. Total of twenty different agro-morphological parameters were recorded for important quantitative traits like days to flower initiation (DF-I), days to 50% flowering (DF50%), days to flowering completion (DFC100%), days to maturity, leaf length and width, plant height, primary branches/plant, main raceme length, pod length, pod width, stem thickness, thousand seed weight, seed yield/ plant and pod shattering (stage I-IV).

Days to flower initiation (DFI), days to 50% flowering (DF50) and days of flower completion (DFC) response of B. rapa genotypes: The days to flower initiation is the numbers from sowing to appearance of initial flower. Among all genotypes the accession Br-536 showed very early days to flower initiation (DFI) (35 days) followed by Br-707 and Br-712 (36 days). The DFI, DF50% and DFC response was maximum in genotypes Br-505, Br-707, Br-716, Br-718 and Br-747 each as compared to check variety TS1 (41, 50 and 57 days) and BSA (54, 60 and 66 days). The genotype Br-548 gave very late DFI, DF50% and DFC (160, 164 and 167 days) followed by Br-619 (155, 157 and161 days). The very early flowering genotypes are very useful for breeding program as they shows maximum early maturity. The maximum genotypes showed early DFI, DF50% and DFC as compared to late flowering genotypes (Figs.1A-C).

Days to maturity based variations among *B. rapa* **genotypes:** The days to maturity is directly correlated with DFI, DF50% and DFC. The genotypes showing early flowering matured earlier than late flowering. The genotype Br-512 (149 days) gave very early maturity followed by Br-647, Br-692 and Br-693 (150 days) each as compared to TS-1 (153 days) and BSA (159 days each). The genotype Br-571 had very prolonged maturity period (184 days) followed by Br-550 (182 days). Overall 61 genotypes were found novel that gave very early maturity (160 days) as compared to others late mature germplasms (Fig. 1D).

Screening of pod shattering resistance lines of *B. rapa*: In present study maximum *B. rapa* genotypes showed resistance to pod shatter except for only few genotypes. The genotype Br-748 showed susceptibility to pod shattering at stage-I-IV (11, 24, 28 and 31%) followed by Br-728 (9, 15, 24 and 26%) and Br-724 (7, 13, 18 and 25%) respectively. Both check varieties (TS-1 and BSA) showed pod shatter resistance at all stages with slightly lower at stage IV (14 and 13%). Our findings showed that 6 genotypes out of 253 gave low to moderate level of pod shatter resistance (21-31%) as compared to other resistant experimental genotypes (Figs. 1E-H).

Leaf length/width (LL/LW) based agro-morphological based diversity among diverse *B. rapa* genotypes: The leaf length and width mean were almost similar for both years. However considerable variations were observed

among genotypes. The vegetable Chinese cabbage genotypes showed the highest leaf length and width as compared to other non-vegetable types. The highest leaf length was calculated for genotypes Br-555 (55.2 cm) followed by Br-652 (55cm) and Br-541 (51cm) as compared check varieties TS-1 and BSA (20.5 and 13.2 cm respectively). The lowest leaf length was noted for genotype Br-607 (6.3cm) followed by Br-605 (6.8cm). The maximum broad leaves were observed for genotype Br-555 (27.5 mm) followed by Br-568 (24.2 mm) as compared to TS-1 and BSA (11.2 and 6.6mm). Maximum genotypes (152) showed leaf length at ranges of 21-30cm as compared to three lengthy leafy genotypes (>50cm) (Fig. 1I). The twenty broad Chinese cabbage vegetable types showed very broad leaves (>20 mm) (Fig. 1J).

Screening of short, medium and tall plants among *B. rapa* genotypes: A wide range of phenotypic intra-specific variability was observed among genotypes for plant height. The mean plant height of genotypes varies from 101.7 to 230.2cm. The genotype Br-520 was the tallest (230.2cm) followed by Br-646 (227.6cm) as compared to the most dwarf accession Br-728 (101.7cm). Both the check varieties showed moderate height (150.3 and 147.2 cm) as compared to other tested genotypes. The frequency distribution data showed that maximum genotypes (78) have plant height in range of 161-180 cm. While only two genotypes have plant height greater than 220 cm as compared to 13 dwarf genotypes (<120cm) (Fig. 1R).

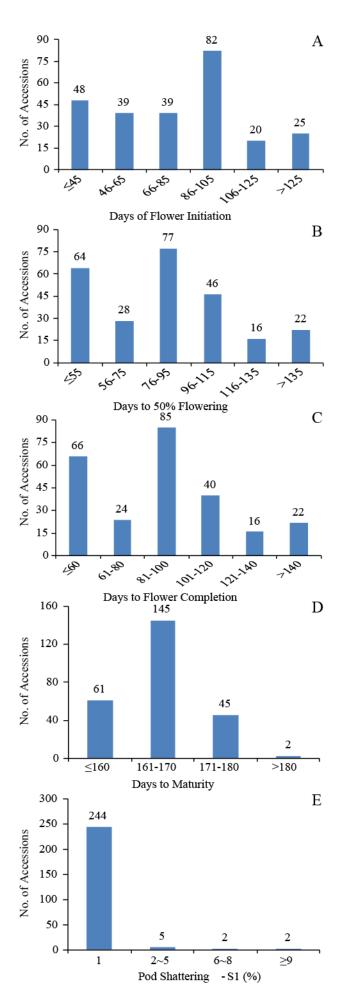
Primary branches/plant (PB/P) based intra-specific variations among *B. rapa* germplasm: The average PB/P varies from 4.8 to 28. The maximum PB/P were recorded in genotype Br-587 (16), followed by Br-695 (14), Br-731 (13) and Br-539 (13). The lowest PB/P was observed in Br-508 (4.6) as compared to TS-1 and BSA (9.6 and 6.4). The majority of genotypes (174) showed maximum PB/P at range 6.1-9 (Fig. 1K). The genotype Br-587 was selected an elite line as compared to others due to more than 15 PB/P.

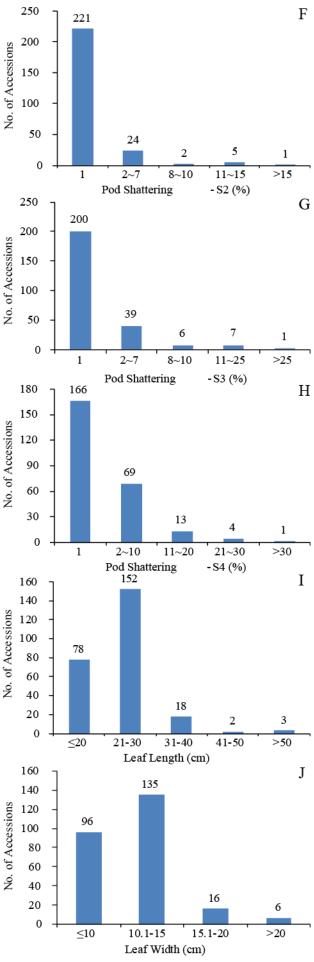
Main raceme length (MRL) based variability among *B. rapa* genotypes: The mean raceme length varies among genotype and it is genotype dependent. The genotypes Br-668 and Br-692 have maximum MRL (79 and 75.8) as compared to check varieties TS-1 and BSA (46.2 and 58.2cm). The lowest MRL value was recorded for genotype Br-506 (19.2cm) followed by Br-725 and Br-714 (24.8 and 25cm). The highest number of genotypes (107) showed the lowest MRL (<40cm) as compared to the two elite lines MRL (>70cm) (Fig. 1L).

Presence of low to maximum number of pod/main raceme (P/MR) among *B. rapa* **genotypes:** In present experiment maximum variation was observed for pods/main raceme (P/MR) among different genotypes and its values ranged from 12.8 to 62.2. Maximum P/MR was recorded for accession Br-396 (62.2) followed by Br-395 (59.2) as compared to check varieties TS-1 and BSA (48.2 and 50.4). The genotype Br-533 gave very poor response of P/MR (12.8) followed by Br-535 (14). Maximum number of genotypes (157) had P/MR less than 30 cm. The other 16 genotypes had the highest P/MR (>45 cm) (Fig. 1M).



SOHAIL AHMAD JAN ET AL.,





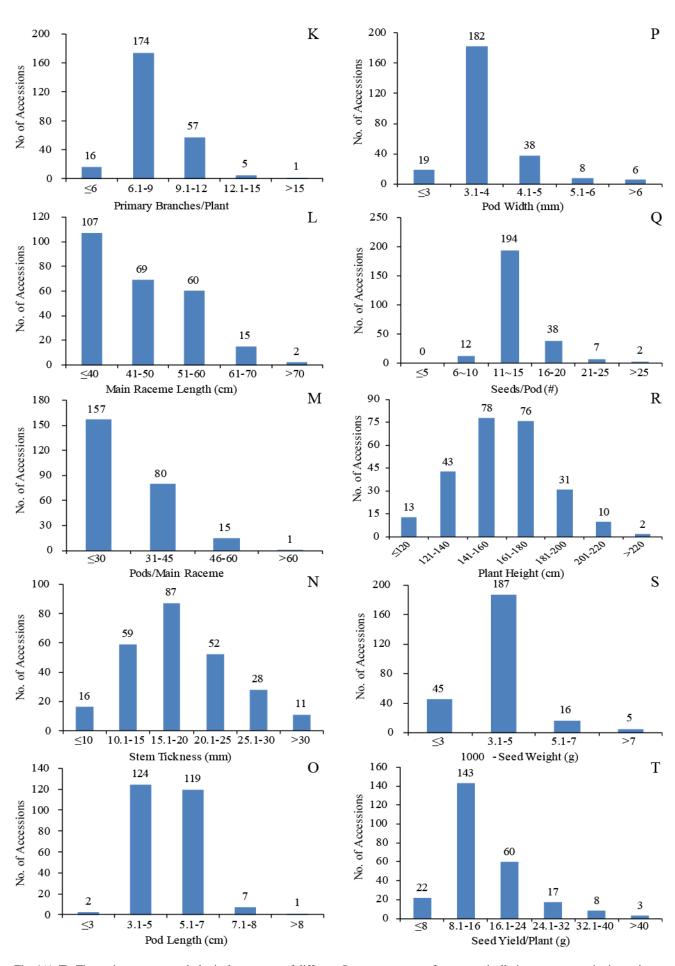


Fig. 1(A-T). The various agro-morphological responses of different B. rapa genotypes for economically important quantitative traits.

Stem thickness (ST) based selection of vegetable and non-vegetable *B. rapa* species: Significant mean differences were noted for stem thickness among vegetable type and non-vegetable type sarson. The vegetable type sarson have very thick stems as compare to other type. The maximum ST was recorded for genotype Br-555(47.2cm) followed by Br-652 (41.3cm) as compared to TS-1 and BSA (21.3 and 17.5cm). The lowest ST values were noted for genotypes Br-501 and Br-512 (5.6 and 6.2mm) (Fig. 1N). Among 253 genotypes, 87 showed ST value range from 15.1 to 20mm. Our finding showed that maximum genotypes have narrow and thin stem.

Pod Length (PL) based morphological variations among *B. rapa* genotypes: In present study different size of pods (small, medium and long) were noted among *B. rapa* genotypes. The pods length values ranged from 2.4 to 8 cm. The genotype Br-650 gave maximum PL (8cm) as compared to TS-1 (5.1cm) and BSA (4.5cm). The minimum PL values were noted for genotype Br-512 (2.4cm) followed Br-556 (2.7cm). The large number of genotypes gave PL ranges from 3.1-5cm as compared to other 119 germplasm PL (5.1-7cm) (Fig. 1O).

Pod width (PW) based genetic differences among three sub-species of *B. rapa*: The three different sub-species of *B. rapa* have different pod width (PW). Among these three types the yellow sarson have minimum broad pods as compare to other brown saron and toria type. The maximum PW was observed for genotype Br-531 (8.5mm) followed by Br-592 (7.1mm) as compared to check varieties TS-1 (4.6mm) and BSA (3.6mm). On the basis of this character these two genotypes are highly diverse from the rest ones. The narrow and the lowest PW were noted in genotype Br-606 and Br-638 (2.5 and 2.7mm). Maximum number of genotypes (182) gave PW value between 3.1-4mm (Fig. 1P).

Selection of low to high number of seeds/pod (S/P) among different *B. rapa* genotypes: The average number of seeds per pod (S/P) response varies with genotype and its value ranges from 8.6 to 31.3. The maximum S/P (31.3) was recorded in genotype Br-693 followed by Br-695 (30) as compared to check varieties TS-1 and BSA (17.1 and 14.8). The minimum S/P (8.6) were noted in genotype Br-529 followed by Br-522 (9.3). The 194 genotypes have 11-15 S/P as compared the two genotypes that have more than 25 S/P (Fig. 1Q).

Yield based differences among *B. rapa* genotypes: Seed yield/plant is one of the important quantitative characters for crop improvement. The genotypes BR-547 and Br-560 had excellent SY/P, and these are very useful for breeding point of view. In present study the genotype Br-547gave excellent average SY/P (61.6g) response followed Br-560 (41.2g) as compared to the yield of TS-1 and BSA (31.8 and 20.9g). The yield of genotype Br-547 is almost double of TS-1 and triple as compare to BSA. The lowest SY/P (3.8g) was recorded for genotype Br-705 followed by Br-501 (5.8gm). From frequency distribution table we noted that maximum number of genotype (143) have 8.1-16g SY/P (Fig. 1T). Only three genotypes had excellent

SY/P and these were highly diverse from the rest of genotypes.

Intra-specific based diversity among diverse *B. rapa* genotypes for important quantitative character of thousand seed weight: Thousand seed weight is also an important quantitative character that depends also on seed size. The genotypes having big seed size have more TSW as compared to small seeded plants. In present germplasms the genotype Br-705 had excellent TSW (8.9 gm) followed by Br-692 (8.5g) as compared to TS-1(3.9g) and BSA (3.6g). The genotype Br-524 have minimum TSW (1.8g) followed by Br-631 (2.2g). From Fig IS we noted that majority of genotypes (187) had TSW ranging from 3.1-5g. The five diverse genotypes had TSW higher than 7g (Fig. 1S).

Discussion

Agro-morphological based variation is important to screen best genotypes in field experiment. The diverse agro-morphological based genotypes are useful for further biochemical and molecular evaluation. Genetic diversity study is used for efficient utilization and for development of improved cultivar/varieties (Shinwari et al., 2014; Shinwari et al., 2013; Jan et al., 2016^{a-d}). Morphological based screening of different crop species/sub-species is therefore so much important for all plant breeders (Martins et al., 2006; Iqbal et al., 2015). Therefore proper strategies and planning is needed to evaluate local and exotic germplasm and to screen best genotypes among these for both qualitative and quantitative characters (Balkaya & Ergun, 2008). The conservation strategies are important for many reasons as it is best source to conserve threaten/endangered species, for further crop improvement through new morphological techniques and to develop new breeding cultivars/varieties (Baranger et al., 2004).

The present experiment was attempted to screen the important Brassica rapa L. genotypes for important quantitative agro-morphological characters including pod shattering resistance. Various agro-morphological parameters were taken such as days to flower initiation (DF-I), days to 50% flowering, days to flower completion, days to maturity, leaf length, leaf width, leaves plant⁻¹, plant height, primary branches plant⁻¹, main raceme length, pod length and width, stem thickness, seeds /pod, thousand seed weight, seed yield/plant and pod shattering resistance stage I-IV. Significant variations were observed among all genotypes for all quantitative characters. All the genotypes had distinct characters from one another as compared to TS-1 and BSA (Figs. 1A-T). Our results are in line with the findings of Zada et al. (2013), who recorded diverse Brassica carinata L. genotypes for both qualitative and quantitative characters. They found maximum variations for important quantitative characters such as main raceme length, plant height, leaf length, DF50%, DF100%, plant maturity and seed yield. Our findings are also very close with the results of Ali et al. (2003) who noted maximum variation in 1000 seed weight and seed yield/plant among different Brassica napus L. germplasm. The yield response varies with type of genotypes used. The different local and

exotic Brassica napus genotypes showed significant variations from one another for both quantitative traits such as 100 seed weight and seed yield/plant (Abideen et al., 2013; Rameeh, 2013). The Number of primary branches and main raceme length have impressive role in richness of diversity (Murty & Quadri, 1966). Ali et al. (2003) noted maximum morpho-molecular based interspecific variations among 25 rapeseed accessions important quantitative traits. All the genotypes have different pods length, pods/plant and plant height. The 52 diverse local Pakistani B. juncea genotypes showed different response for leaf length/width, days to flowering and silique length (Rabbani et al., 1998). Our findings are in line with Bhajan et al. (2013) that reported that brown sarson genotype Lotni gives better yields in Kashmir and Himachal Pradesh regions. The yield of genotype varies with change of environmental condition.

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References

- Abideen, S.N.U., F. Nadeem and S.A. Abideen. 2013. Genetic variability and correlation studies in *Brassica napus* L. genotypes. Int. J. Innov. Appl. Stud., 2(4): 574-581.
- Ali, Y., Farhatullah, H. Rahman, A. Nasim, S.M. Azam and A. Khan. 2013. Heritability and correlation analysis for morphological and biochemical traits in *Brassica carinata*. *Sarhad J. Agric.*, 29(3): 359-369.
- Ali, N., F. Javed, J.Y. Elmira and M.Y. Mirza. 2003. Relationship among yield and components and selection criteria for yield improvement in winter rape seed (*Brassica napus* L.). *Pak. J. Bot.*, 35: 167-174.
- Azam, S.M., Farhatullah, A. Nasim, S. Shah and S. Iqbal. 2013. Correlation studies for some agronomic and quality traits in *Brassica napus* L. Sarhad J. Agric., 29(4): 547-550.
- Balkaya, A. and A. Ergun. 2008. Diversity and use of pinto bean (*Phaseolus vulgaris*) populations from Samsun, Turkey. N. Z. J. Crop Hort. Sci., 36: 189-197.
- Baranger, A., G. Aubert, G. Arnau, A. Laine, G. Deniot, J. Potier, C. Weinachter, I.L. Henaut, J. Lallem and J. Burstin. 2004. Genetic diversity within *Pisum sativum* using protein and PCR-based markers. *Theor. Appl. Genet.*, 108: 1309-1321.
- Bhajan, R., U. Pant, R.K. Khulbe and A.K. Singh. 2013. New sources of variability for restructuring *Brassica rapa*. J. Oilseed Brassica., 4(1): 53-56.
- Iqbal, J., Z.K. Shinwari and M.A. Rabbani. 2015. Maize (Zea mays L.) germplasm agro-morphological characterization based on descriptive, cluster and principal component analysis. Pak. J. Bot., 47(SI): 255-264.

- Iqbal, S., Farhatullah, S. Shah, M. Kanwal, L. Fayyaz and M. Afzal. 2014. Genetic variability and heritability studies in indigenous *Brassica rapa* accessions. *Pak. J. Bot.*, 46(2): 609-612.
- Jan, S.A., Z.K. Shinwari and M.A. Rabbani. 2016^a. Agromorphological and physiological responses of *Brassica* rapa ecotypes to salt stress. *Pak. J. Bot.*, 48(4): 1379-1384.
- Jan, S.A., Z.K. Shinwari, M. A. Rabbani. 2016^b. Determining genetic divergence among *Brassica rapa* ecotypes through electrophoretic mobility of total seed proteins. *The J. Anim. Plant Sci.*, 26(6): 1758-1764.
- Jan, S.A., Z.K. Shinwari And M. Ashiq Rabbani. 2016^c. Morpho- biochemical evaluation of *Brassica rapa* subspecies for salt tolerance. *Genetica.*, 48(1): 323-338.
- Jan, S.A., Z.K. Shinwari, M.A. Rabbani, S.H. Shah, M.I. Ibrahim and M. Ilyas. 2016^d. Optimization of an efficient SDS-PAGE protocol for rapid protein analysis of *Brassica rapa. J. Bio. Env. Sci.*, 9(2): 17-24.
- Padilla, G., M.E. Cartea, V.M. Rodriguez and A. Ordas. 2005.Genetic diversity in a germplasm collection of *Brassica rapa* subsp *rapa* L. from northwestern Spain. *Euphytica*, 145: 171-180.
- Martins, S.R., F.J. Vences, L.E. Miera, M.R. Barrosa and V. Carnide. 2006. RAPD analysis of genetic diversity among and within Portuguese landraces of common white bean (*Phaseolus vulgaris* L.). Sci. Hort., 108: 133-142.
- Murty, B.R. and M.I. Quadri. 1966. Analysis of divergence in some self- compatible forms of *Brassica campestris* var. brown sarson. *Indian J. Genet.*, 26: 45-48.
- Rabbani, M.A., A. Iwabuchi, Y. Murakami, T. Suzuki and K. Takayanagi. 1998. Phenotypic variation and the relationships among mustard (*Brassica juncea* L.) germplasm from Pakistan. *Euphytica*, 101: 357-366.
- Rameeh. V. 2013. Multivariate analysis of some important quantitative traits in rapeseed (*Brassica napus* L.) advanced lines. J. Oilseed Brassica, 4(2): 75-82.
- Shinwari, Z.K., H. Rehman and M.A. Rabbani. 2014. SDS-PAGE based genetic divergence in safflower (*Carthamus tinctorius* L.). *Pak. J. Bot.*, 46(3): 811-815.
- Shinwari, S., A.S. Mumtaz, M.A. Rabbani, F. Akbar and Z.K. Shinwari. 2013. Genetic divergence in Taramira (*Eruca sativa* L.) germplasm based on quantitative and qualitative characters. *Pak. J. Bot.*, 45(SI): 375-381.
- Yu, S., F. Zhang, X. Wang, X. Zhao, Z. Deshuang, Y. Yu and J. Xu. 2010. Genetic diversity and markertrait associations in a collection of Pakchoi (*Brassica rapa L. ssp. chinensis* Makino) accessions. *Genes & Genomics*, 32: 419-428.
- Zada, M, N. Zakir, M.A. Rabbani and Z.K. Shinwari. 2013. Assessment of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. *Pak. J. Bot.*, 45(S1): 583-593.
- Zhang, X., T. Liu, X. Li, M. Duan, J. Wang, Y. Qiu, H. Wang, J. Song and D. Shen. 2016. Interspecific hybridization, polyploidization, and backcross of *Brassica oleracea var. alboglabra* with *B. rapa* var. *purpurea* morphologically recapitulate the evolution of *Brassica* vegetables. *Sci. Report*, 6: 186-188.
- Zhao, J.J., X.W. Wang, B. Deng, P. Lou, J. Wu, R.F. Sun, Z.Y. Xu, J. Vromans, M. Koornneef and G. Bonnema. 2005. Genetic relationships within *Brassica rapa* as inferred from AFLP fingerprints. *Theor. Appl. Gen.*, 110: 1301-1314.

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