



Biochemical and stability analysis of variations of indigenous *Brassica juncea* genotypes in different agro-climatic environmental conditions of Pakistan

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Abstract

Stability and biochemical analysis give the information about the genetic diversity of plants, which further help the scientists and breeders for the cultivation of plants in different climatic conditions. The local indigenous species collection from the different environments are the best for researcher because these local varieties have many resistant genes against environmental disasters. Reproducible and diverse genotypes are very important for the successful plant breeding. Therefore, this study was designed to analyse the stability and biochemical profiling of different locally collected genotypes of *Brassica juncea*. For this purpose, 25 genotypes of *B. juncea* along with one check cultivar were obtained from various regions of Pakistan. Stability was investigated using Randomized Complete Block Design (RCBD) and ANOVA while biochemical analysis was performed using Near Infra-Red (NIR) spectroscopy. ANOVA results showed highly significant differences in the all studied parameters for genotypes, genotypes x year, location x year, genotypes x location x year except location which was no significant with an overall (cv) coefficient of variance was 3.37 for days to flower completion, 7.05 for seed silique, 4.25 for protein content, 5.06 for glucosinolates and 4.57 for erucic acid. Stability analysis showed that 1611, 1616 and 1617 were the most stable varieties in adverse environmental condition because they have less b regression coefficient and S²d deviation from regression. Current findings revealed that among all checked genotypes, some remained stable under different harsh environmental conditions for abiotic factors further no effect of these adverse conditions was observed on biochemical profiling.

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Introduction

Stability plays very important role for the healthy growth of plants in adverse environmental conditions. Harsh environmental conditions can affect the growth of plants from many aspects, favourable environment can become harsh due to different abiotic factors like temperature, pH and salinity. Stability and biochemical analysis give the information about the genetic diversity of plants, which further help the scientists and breeders for the cultivation of plants in different climatic conditions. Stable and biochemically identified indigenous plants are considered to be best for researcher. The local indigenous species collection from the different environments are considered to be the best for plant breeders because these local varieties have many resistant genes against environmental disasters. Reproducible and diverse genotypes are very important for the successful plant breeding (Zada *et al.*, 2013; Naushad *et al.*, 2015). Favourable environment promotes the best growth of genotypes so genotypes and the interaction of the environment Genotype (G) and Environmental Interactions (EI) is the major concern to the plant breeder. G x EI further defined two types of variations, quantitative (absolute difference between genotypes) and qualitative (rank changes). So, due to the lots of G and EI will make the difficulties for the plant breeder to select the best and the stable variety (Li and Yau, 1995). The diverse climatic conditions and the different soil types will produce the problems to genotypes and environmental interaction and to resolve these problems the scientist and researchers used the latest tools for the selection of best genotypes and performed the new experiments on diverse environments for many years to check the stability of genotypes on different location, and its yield related properties. The production of best genotypes also depends on the Genotypes x Location x Year (G x L x Y) (Lin and Binns 1988a).

Brassica species are very important economically crop cultivated all over the world. In Asia, *Brassica* grown species are related with vegetables like mustard leaf, broccoli and cabbages while in Europe

Brassica species are related with the oilseed crops. *Brassica* is the important part of humans' diet throughout the world. To improve the techniques for the collection, characterization and evaluation of germplasm will help to increase the utilization of the plant genetic resources (Mukhlesur and Hirata, 2004). In Pakistan, *Brassica* contributed to fulfil the edible requirements grown in both traditional (mustard rapeseed, groundnuts and cabbages) as well as non-traditional (sunflower & soybean oil seeds). (Bakht *et al.*, 2010a and b; Siddique *et al.*, 2012; Taran *et al.*, 2013) Indian Mustard (*Brassica juncea*) has economically important place among all *Brassica* species and grown in large area of Indian subcontinent and in Pakistan for many years. *B. juncea* considered to be most resistant to drought and shattering than *B. campestris* and *B. napus* due to its rigidity. Indian or oriental mustard (*B. juncea* L.) is the most extensively cultivated and well adapted of the five oilseed *Brassica* species grown in Pakistan. It has a high seed yield potential coupled with early maturity and is known to be more drought tolerant and shattering resistant than *B. napus* and *B. campestris* (Woods *et al.*, 1991; Chen *et al.*, 1997). *B. juncea* out-yielded *B. napus* by 12% and *B. campestris* by more than 16%. Similarly, seed yield of *B. juncea* was higher than that of *B. campestris* and *B. napus* (Munir, 1987). Moreover, it was harder and more tolerant to some insects as compared to the other two rapeseed species. *B. napus* very important but *B. campestris* is also considering important as it is the progenitor of *B. juncea* and *B. napus*. *B. juncea* can be grown in semiarid conditions (Woods *et al.*, 1991; Getinet *et al.*, 1999).

Rapeseed is a big source of protein and oil. The rapeseed is the second largest imported crop of Pakistan to fulfil the oil deficiency in Pakistan. The rapeseed contains 50 % oil content and the seed meal has 44 % protein and has a complete profile of essential amino acids like cystine, methionine and lysine etc (Anonymous, 2002). The regular cooking oil of mustard and rapeseed is not considered to be edible if it consists of more than 100 μMg^{-1} and more than 40 % high erucic acid. High concentration of

glucosinolates will produce the nutritional disorders and also affect the reproduction and growth of animals, while the high concentration of erucic acid affects the taste and flavour (Vermorel *et al*, 1986). In Canada, researchers and scientists develop the breeding programmes to improve the rapeseed canola with low erucic acid and glucosinolates concentration, and if in Pakistan breeders provide the favourable environment and use the latest techniques to cultivate the canola rapeseed will increase the yield per unit area will overcome the deficiency of edible oil in Pakistan (Baranyk and Zukalova 2000).

The oil is presently processed as a renewable energy in the petrochemical industry for production of biodiesel. Morphological and biochemical changes are most important because they are the direct gene products (Perry and McIntosh, 1991). Keeping all these considerations in view, this study was designed to identify the genotypes *B. juncea* based on stability and biochemical analysis so that these genotypes of can efficiently cultivated under different harsh climatic conditions.

Materials and methods

Experimental material

A total of 25 different indigenous lines of *Brassica juncea* were collected from different locations of Pakistan. After their characterization on the field level, the best confirmed 25 genotypes from *B. juncea* along with one check cultivar Canola Mustard CM (Bj) was selected for further studies (Table 1).

Experiments

All genotypes of *B. juncea* along with one check, were evaluated at two different locations for two years to check their stability based on morphological markers. These locations included University of Haripur (UOH) and Bafa Research Centre Mansehra during the crop growing seasons of 2014-15 and 2015-16.

In 2014, experimental materials were sown on September 15, University of Haripur (UOH) and October 10, Bafa Research centre Mansehra. In 2015, same sets of experimental materials were planted on

September 10, UOH and on October 12, Bafa Research Centre Mansehra.

Randomized Complete Block Design (RCBD) & ANOVA

Experiments were laid down with randomized complete block design (RCBD) with three replications having row length of 4 m each. Each genotype had two rows. Row to row distance was 30 cm with a plant to plant distance of 10 cm. For seed bed preparation, field was irrigated 14 days prior to sowing to get favourable moisture conditions. Basic dose of fertilizer @ 90 kg N and 60 kg P₂O₅ was applied at the time of land preparation. Sowings were done with the help of hand drill having depth of 3-4 cm.

In order to maintain optimum plant population thinning was done after 1st irrigation of sowing. Weeds were controlled manually. No insecticide or pesticides were applied. Harvesting of the experimental material was done when more than 75% of the plants in each genotype turned yellowish in colour. Significance of plants were analysed by (ANOVA) Statistix version 8.1.

According to Finlay and Wilkinson 1963, if the regression coefficient (b) is equal to unity (b=1), then it means that genotypes have same performance in all environment, if b value is more than unity then the genotypes have good performance in favorable environments and if b value is less than unity, it means the genotype have good performance in poor environment.

Studied parameters

Data were recorded on five selected plants for the following parameters:

Days to flower completion: Data was recorded in days from seed sowing till the flower completion were initiated in each genotype.

Seeds siliquae⁻¹: Number of seeds siliquae⁻¹ was recorded by counting seeds from sample of 25

randomly selected siliques of each selected plant in every genotype.

Biochemical analysis: Seed sample from each genotype was taken to determine fatty acids composition using NIR (Near Infra-Red) Spectroscopy System FOSS 6500 equipped with ISI version 1.02a software of Infra Soft International according to the manufacturer's protocol. During this process well cleaned dried seed samples of 2-5g were used. Biochemical analyses were carried out at Biochemical Lab, Crop Breeding Section, Nuclear

Institute for Food and Agriculture (NIFA), Peshawar for protein content (%), glucosinolates content ($\mu\text{M g}^{-1}$), and erucic acid content (%).

Results

Genetic diversity analysis

Highly significant differences in terms of analysis of variance of *B. juncea* were observed for important traits like days to flower completion, days to maturity, seed silique, protein content, glucosinolates content, and erucic acid.

Table 1. Collected *Brassica* indigenous germplasm of *B. juncea* for analyses of genetic diversity based on morphological, biochemical markers.

<i>Brassica juncea</i>					
S. #	Genotypes Number	Location of collections	S. #	Genotype Number	Location of collections
1	1600	Haripur (KP)	14	1613	Mung
2	1601	Panain	15	1614	Sarai Salah
3	1602	Jarikas	16	1615	Sarikot 1
4	1603	Peshawar	17	1616	Fateh Jang
5	1604	Labmail	18	1617	Bannue
6	1605	Sarikot	19	1618	Hangu
7	1606	Panain1	20	1619	Peshawar (KP)
8	1607	Buldhar	21	1620	Islamabad (PP)
9	1608	Ghazi	22	1621	Haripur (KP)
10	1609	Attock	23	1622	Qila Abdull
11	1610	Kohat	24	1623	Sawabi
12	1611	Taxila	25	CM(Bj)	
13	1612	KotNajeeb			

* Check cultivar

KP= Khyber Pakhtunkhwa

NA= Northern Areas,

FATA= Federally Administered Tribal Areas

PP= Punjab Province.

Results of ANOVA for days to flower completion showed the highly significant differences for genotypes, genotypes x location, genotypes x year, location x year, genotypes x location x year while non-significant results were recorded for locations with an overall (cv) coefficient of variance 3.37%. Data recorded for seed silique is highly significant for genotypes, years, genotypes x location, genotypes x year, location x year, genotypes x location x year while

nonsignificant for location with an overall (cv) coefficient of variance was 7.05% (Table 2). Significant differences were recorded for protein content for genotypes, genotypes x year, location x year, genotypes x location x year except location which was nonsignificant with an overall (cv) coefficient of variance was 4.25%. Glucosinolates values were recorded highly significant for genotypes, location, year, genotypes x year, location x year,

genotypes x location x year with an overall (cv) coefficient of variance was 5.06. Data recorded for erucic acid were highly significant for genotypes, year, genotypes x year, location x year, genotypes x location

x year among all these highly significant values only genotypes x location was nonsignificant and total of the (cv) coefficient of variance for erucic acid was 4.57 (Table 2).

Table 2. Mean square values for indicating plant traits days to flower completion, seed silique, protein content, glucosinolates content and erucic acid of *B. juncea* evaluated for two years at two different locations.

S.V	Df	days to flower completion	seed silique	protein content	Glucosinolates	Erucic acid
Replications	2	18.92	4.17	0.82	20.74	18.2
Genotypes	24	625.85**	8.44**	9.28**	1045.9**	572.34**
Locations	1	5.07 ^{ns}	8.33*	2.01 ^{ns}	78.54 ^{ns}	578.24**
Years	1	274.56**	141.45**	77.01**	206.84**	173.12**
G*L	24	29.47**	3.93**	6.941**	185.8**	8.44 ^{ns}
G*Y	24	46.04**	2.65*	8.37**	74.08**	40.08**
L*Y	1	5572.83**	133.33**	547.83**	2171.37**	692.20**
G*L*Y	24	101.33**	5.45**	8.765**	552.4**	276.67**
Error	198	13.24	1.65	1.115	37.24	7.779
Grand Mean		108	18.24	24.83	120.54	61.03
CV		3.37	7.05	4.25	5.06	4.57

Stability analysis

During 2014-2015 *B. juncea* data recorded in Mansehra for days to flower completion were in range from 84 (CM(Bj)) to 126 (1600) and the mean value was 111 while in Haripur data ranges from 80 ((CM(Bj)) to 120 (1600) mean value was 103. During 2015-2016 in Mansehra data was in the range of 81 (CM(Bj)) to 121 (1600) with mean value was 105 while in Haripur data was in the range of 83 (CM(Bj)) to 129 (1616) and the mean value was 113. For days to flower completion in *B. juncea* showed the significant

differences. Regression coefficient (b) values for days to flower completion were in the range of minimum 0.20 for the genotype 1607 to maximum 2.70 for the genotype 1619, check cultivar CM(Bj) had $b > 1$ (1.57), among 25 genotypes of *B. juncea* 5 genotypes (1600, 1603, 1612, 1618 and 1623) b values were near to unity. S²d values for days to flower completion were in the range of minimum 4.93 for the genotype 1611 to 11.40 for the genotype 1612, all 25 genotypes of *B. juncea* none had S²d less than 1, the check cultivar CM(Bj) showed the 5.30 S²d (Table 3).

Table 3. Mean values, regression coefficient (b) and deviation from regression (S²d) of *B. juncea* for Days to Flower completion (DFC) in two years.

Genotypes	2014-2015		2015-2016		Mean	Stability	
	Mansehra	Haripur	Mansehra	Haripur		b	S ² d
1600	126	120	121	120	122	0.94	5.60
1601	113	104	108	115	110	1.30	9.36
1602	121	115	112	116	116	1.65	6.80
1603	104	99	103	114	105	0.60	5.34
1604	110	102	105	115	108	1.71	7.60
1605	112	100	109	112	108	1.95	5.32
1606	113	97	108	113	108	0.55	8.90
1607	103	99	109	112	106	0.20	7.17
1608	115	103	114	116	112	1.64	6.30
1609	119	112	112	117	115	1.40	5.44
1610	112	102	103	112	107	1.20	7.30
1611	124	105	97	126	113	2.43	4.93
1612	100	105	99	106	103	0.70	11.40
1613	119	104	101	116	110	2.17	5.88

1614	106	99	104	114	106	1.70	6.90
1615	118	101	106	120	111	1.96	6.32
1616	123	107	106	129	116	2.40	7.40
1617	104	99	102	107	103	0.47	7.84
1618	112	105	97	115	107	0.75	6.40
1619	102	101	106	112	105	2.70	6.11
1620	120	105	105	116	112	2.10	5.40
1621	101	99	102	108	103	0.49	5.94
1622	101	103	101	106	103	1.90	6.40
1623	120	106	103	116	111	0.50	6.87
CM(Bj)	84	80	81	83	82	1.57	5.30
Mean	111	103	105	113	108	1.40	6.73

Data recorded for seed siliques of *B. juncea* for the year 2014-2015 in Mansehra was in the range from 14 (1622) to 21 (1601) and the mean value was 17 while in Haripur data recorded in the range from 16 (1608) to 21 (1614) mean value was 18, for the year 2015-2016 in Mansehra data ranges from 17 (CM)Bj) to 22 (1617) mean value was recorded 20, while in Haripur data ranges from 15 (1615) to 20 (1605, 1609, 1610 and 1613) and the mean value was 18. For seed siliques in *B. juncea* showed considerable amount of variations in studied traits. Regression coefficient

(b) values for seed siliques were in the range of minimum 0.31 for genotype 1617 to maximum 1.93 for genotype 1605, among 25 genotypes of *B. juncea* 7 genotypes (1600, 1608, 1609, 1611, 1616, 1621 and 1622) were near to unity. The check cultivar had $b < 1$ (0.71). While the values of S^2d for seed siliques were in the range of minimum 1.13 for the genotype 1611 to maximum 3.13 for the genotype 1602. Among all genotypes of *B. juncea* none had S^2d less than 1. The check cultivar CM (Bj) had 1.21 S^2d value (Table 4).

Table 4. Mean values, regression coefficient (B) and deviation from regression (S^2d) of *B. juncea* for Seed siliques (SS) in two years.

Genotypes	2014-2015		2015-2016		Mean	Stability	
	Mansehra	Haripur	Mansehra	Haripur		B	S^2d
1600	18	17	19	16	18	0.67	2.41
1601	21	19	21	19	20	0.44	1.99
1602	20	19	19	19	19	1.34	3.13
1603	17	19	20	17	18	1.51	1.21
1604	18	17	19	19	18	0.32	1.97
1605	19	18	19	20	19	1.93	2.13
1606	15	20	21	16	18	0.45	2.18
1607	18	19	20	19	19	1.87	1.23
1608	17	16	21	18	18	0.67	1.31
1609	17	18	19	20	18	0.98	2.17
1610	16	17	19	20	18	1.23	1.32
1611	17	17	19	19	18	0.99	1.13
1612	15	18	20	17	18	0.54	2.15
1613	19	20	19	20	19	1.21	1.67
1614	17	21	21	19	19	0.33	2.34
1615	16	18	18	15	17	1.25	1.39
1616	16	18	21	18	18	0.76	2.15
1617	18	18	22	19	19	0.31	2.21
1618	17	17	20	18	18	1.12	2.14
1619	17	17	19	17	18	0.32	1.23
1620	18	17	21	16	18	1.21	2.11
1621	17	17	19	17	18	0.91	1.46
1622	14	18	19	17	17	0.66	1.29
1623	17	19	20	19	19	0.39	1.37
(CM)Bj	15	17	17	17	16	0.71	1.21
Mean	17	18	20	18	18	0.88	1.79

Protein content percentage of *B. juncea* in 2014-2015 in Mansehra were ranged from 22.3 (1604) to 29.3 (1613) and the mean value was 25.8 %, while in Haripur data ranged from 21.3 (1603) to 25.6 (1605) and the mean value was 25.6%, during 2015-2016 in

Mansehra data ranges from 21.6 (1610) to 28.5 (1619) and the mean value was 24.1%, while in Haripur data ranges from 24.1 (1611) to 28.5 (1617) and the mean value was 26.6%.

Table 5. Mean values, regression coefficient (B) and deviation from regression(S²d) of *B. juncea* for Protein Content (PC) in two years.

Genotypes	2014-2015		2015-2016		Mean	Stability	
	Mansehra	Haripur	Mansehra	Haripur		B	S ² d
1600	24.3	22.8	22.3	25.3	23.7	1.23	4.69
1601	26.2	25.3	23.4	27.2	25.5	0.77	3.88
1602	27.3	23.7	23.2	27.2	25.4	0.38	1.87
1603	24.2	21.3	22.4	27.5	23.8	0.97	3.79
1604	22.3	21.8	23.6	26.2	23.5	1.96	4.99
1605	25.7	21.8	23.4	25.4	24.1	2.89	2.99
1606	24.6	24.0	23.3	25.6	24.4	1.33	7.54
1607	27.5	23.0	24.3	26.5	25.4	0.91	4.56
1608	21.5	24.5	24.5	27.3	24.5	1.23	3.46
1609	26.3	23.2	23.2	26.4	24.8	1.54	4.78
1610	24.7	21.6	21.6	24.2	23.0	0.88	3.21
1611	27.4	22.0	22.0	24.1	23.9	0.21	1.67
1612	25.4	23.2	23.2	26.6	24.6	0.66	4.56
1613	29.3	22.0	22.0	28.2	25.4	0.51	3.22
1614	27.5	21.7	21.7	26.7	24.4	0.84	6.54
1615	24.7	24.5	24.5	24.9	24.7	1.66	4.56
1616	28.4	23.7	24.5	27.5	26.0	1.91	3.83
1617	27.3	89.1	28.0	28.5	43.2	2.77	3.40
1618	27.1	19.6	28.3	27.7	25.7	1.56	4.00
1619	22.9	23.3	28.5	26.8	25.4	1.64	6.99
1620	27.4	21.8	27.2	28.0	26.1	2.32	2.75
1621	25.3	23.4	22.6	27.9	24.8	1.57	6.41
1622	24.3	24.2	24.3	26.2	24.8	2.31	2.76
1623	25.1	25.5	24.5	26.2	25.3	2.12	4.98
CM(Bj)	27.3	22.0	25.4	27.1	25.5	1.44	3.33
Mean	25.8	25.6	24.1	26.6	25.5	1.42	4.19

In *B. juncea* protein content (PC) showed significant differences in studied traits. Regression coefficient (b) values for total protein content were in the range of (0.21 to 2.89) 1611 and 1605 respectively, among 25 genotypes of *B. juncea* 6 genotypes (1601, 1603, 1607, 1610, 1612 and 1614) have the values near to unity.

The check variety CM(Bj) had $b > 1$ (1.44). On the other hand, the values recorded for deviation from

regression (S²d) were in the range of 1.67 (1611) to 6.99 (1619). Among all the genotypes none had S²d less than 1, for check variety CM(Bj) S²d value was 3.33 (Table 5).

Quantities of glucosinolates ($\mu\text{M g}^{-1}$) of *B. juncea* in Mansehra during 2014-2015 were ranged from 13.9 (1621) to 131.7 (1616) mean value was $123.5 \mu\text{M g}^{-1}$, while in Haripur data ranges from 68.4 (1605) to

147.1 (1613) and the mean value was $119.2 \mu\text{M g}^{-1}$, during 2015-2016 in Mansehra the data ranges from 72.9 (1606) to 141.1 (1613) mean value was $116.5 \mu\text{M g}^{-1}$, in Haripur data ranges from 98.9 (1605) to 136.1 (1616) mean value was $122.9 \mu\text{M g}^{-1}$. For glucosinolates (GSL) in *B. juncea* showed the significant differences. Regression coefficient (b) values for glucosinolates were in the range of minimum 0.21 for the genotype 1617 to maximum

3.21 for the genotype 1611, check cultivar CM(Bj) had $b > 1$ (2.64), among 25 genotypes of *B. juncea* 2 genotypes (1600 and 1622) b values were near to unity. S²d values for glucosinolates were in the range of minimum 2.15 for the genotype 1623 to 5.98 for the genotype 1619, all 25 genotypes of *B. juncea* none had S²d less than 1, the check cultivar CM(Bj) showed the 3.76 S²d (Table 6).

Table 6. Mean values, regression coefficient (B) and deviation from regression (S²d) of *B. juncea* for Glucosinolate (GSL) in two years.

Genotypes	2014-2015		2015-2016		Mean	Stability	
	Mansehra	Haripur	Mansehra	Haripur		B	S ² d
1600	114.0	125.5	118.5	122.9	120.2	0.54	3.33
1601	122.4	135.9	120.8	127.8	126.7	0.32	2.85
1602	124.3	130.6	124.2	127.1	126.6	0.45	3.12
1603	127.8	131.6	131.2	130.1	130.1	1.54	4.67
1604	125.8	87.5	98.4	124.2	109.0	1.89	3.77
1605	122.4	68.4	92.4	98.9	95.5	2.32	4.23
1606	114.2	109.8	72.9	112.0	102.2	2.43	3.24
1607	121.8	87.4	101.0	121.9	108.0	0.23	4.22
1608	124.3	117.5	105.4	123.3	117.6	0.41	2.98
1609	121.4	121.3	112.1	123.4	119.6	2.36	4.12
1610	124.8	133.4	124.1	128.7	127.7	1.76	3.98
1611	125.6	133.0	132.8	120.3	127.9	3.21	3.35
1612	123.9	96.5	102.2	122.1	111.2	1.55	2.67
1613	125.3	147.1	141.1	123.6	134.3	1.35	2.13
1614	124.3	118.2	116.5	120.7	120.0	2.13	3.15
1615	128.4	128.5	120.9	134.4	128.0	1.36	3.98
1616	131.7	122.8	118.3	136.1	127.2	0.34	2.56
1617	130.7	122.3	120.7	131.1	126.2	0.21	3.21
1618	127.4	129.3	122.3	133.7	128.2	0.33	4.35
1619	128.4	126.3	121.1	132.0	126.9	1.65	5.98
1620	116.2	117.9	125.4	115.2	118.7	1.64	3.25
1621	113.9	121.0	123.6	100.4	114.7	1.87	4.35
1622	124.1	123.7	123.8	114.6	121.6	0.65	4.12
1623	122.1	121.5	123.9	126.8	123.6	1.65	2.15
CM(Bj)	123.4	122.9	119.1	121.3	121.7	2.64	3.76
Mean	123.5	119.2	116.5	122.9	120.5	1.39	3.58

Erucic acid percentage in 2014-2015 of *B. juncea* in Mansehra data ranges from 33.4 (1605) to 69.0 (1612) mean value was 60.4, while in Haripur data ranged from 47.0 (1602) to 67.2 (1621) mean value was 60.1 %, during 2015-2016 in Mansehra data ranged from 44.0 (1601) to 68.9 (1612) mean value was 58.9 %, while in Haripur data ranges from 31.3 (1605) to 76.8

(1611) mean value was recorded as 64.7 %. For erucic acid in *B. juncea* showed considerable amount of variations in studied traits. Regression coefficient (b) values for erucic acid were in the range of minimum 0.13 for genotype 1616 to maximum 1.56 for genotype 1614, among 25 genotypes of *B. juncea* 7 genotypes (1601, 1605, 1606, 1609, 1611, 1621, 1622, 1623 and

CM(Bj) were near to unity. The check cultivar had $b < 1$ (0.98). While the values of S^2d for erucic acid were in the range of minimum 1.45 for the genotype 1621 to

maximum 8.67 for the genotype 1614. Among all 25 genotypes of *B. juncea* none had S^2d less than 1. The check cultivar CM(Bj) had 4.13 S^2d value (Table 7).

Table 7. Mean values, regression coefficient (B) and deviation from regression (S^2d) of *B. juncea* for Erucic acid content in two years.

Genotypes	2014-2015		2015-2016		Mean	Stability	
	Mansehra	Haripur	Mansehra	Haripur		B	S^2d
1600	68.2	55.3	48.5	69.7	60.4	1.11	1.98
1601	53.2	54.2	44.0	59.2	52.7	0.60	1.78
1602	61.2	47.0	44.4	62.2	53.7	1.07	2.46
1603	80.1	48.0	44.3	83.0	63.9	1.28	2.66
1604	38.3	52.9	45.9	39.8	44.2	1.17	2.98
1605	33.4	53.0	47.4	31.3	41.3	0.94	6.14
1606	61.0	64.7	63.3	66.1	63.8	0.54	2.54
1607	61.2	57.5	57.5	65.3	60.4	1.21	4.13
1608	55.3	60.1	58.9	59.8	58.5	1.30	3.88
1609	60.6	60.6	63.3	64.7	62.3	0.93	3.76
1610	63.2	62.1	66.3	71.4	65.7	1.45	4.21
1611	62.2	64.0	68.6	76.8	67.9	1.36	4.34
1612	69.0	66.4	68.9	74.1	69.6	0.34	5.45
1613	65.2	63.2	65.4	73.2	66.8	0.31	3.83
1614	57.2	60.0	61.5	65.3	61.0	1.56	8.67
1615	56.3	62.2	59.2	59.9	59.4	1.29	2.56
1616	68.1	65.7	66.7	73.1	68.4	0.13	1.68
1617	60.9	64.3	54.6	56.0	59.0	0.23	2.43
1618	64.9	61.6	59.4	62.5	62.1	1.24	2.36
1619	61.3	61.2	63.8	64.5	62.7	0.37	4.56
1620	62.3	62.4	64.2	67.3	64.0	0.32	1.89
1621	66.2	67.2	68.5	73.3	68.8	0.67	1.45
1622	61.9	62.4	61.5	70.2	64.0	0.71	2.34
1623	60.5	63.4	62.3	65.7	63.0	0.75	3.45
CM(Bj)	58.3	64.2	63.9	63.1	62.4	0.98	4.13
Mean	60.4	60.1	58.9	64.7	61.0	0.9	3.43

Discussion

Means of all the studied parameters of the *Brassica* species across two years and two locations along with stability analysis showed significant differences. Days to flower completion and seed siliques were showed highly significant results for G x L, These findings were supported by the earlier work of Ali *et al.* (2008) who also obtained same results. Seed siliques similarly, the findings of Volker *et al.* (2004) and Salem (2005) also

supported our results. Protein content, glucosinolates and erucic acids were observed significant for location and G x L while highly significant for G x L x Y. These results further supported by the earlier findings of Kakani (1989) and Meena (1997) who also found significant different G x E interaction for most of the traits in taramira.

According to Finlay and Wilkinson (1963), model a stable genotype should have a high mean yield, $b =$

1.0 and $S^2d = 0$. It is however specifically the deviation from the regression (S^2d) which is used as a measure of a genotype's stability across environments the genotypes having regression coefficients (b) value near to 1.0 signify average stability, but that should be allied with high value of mean yield establish the stability of that genotype. When the regression coefficients are approximating 1.0 and are linked with high yield mean, genotypes are adapted to all environments. On the other hand, those genotypes which have low mean yields, then other genotypes are poorly adapted to all environments. Those genotypes which have regression coefficients above 1.0 show the increased sensitivity of the genotypes to the environmental change, as a result showing below average stability and great specific adaptability to high yielding environments. Regression coefficients decreasing below 1.0 provide a measure of greater resistance to environmental change, having above average stability but showing more specific adapted to low yielding environments. Therefore, there was a need for assessing stability of performance of the twenty-five genotypes of *B. juncea* species in order to identify genotypes having superior attributes. Protein content percentage was less than 1 for genotype 1611 were stable for harsh environment. These results were strengthened by the earlier findings of Singh and Chaudary (1985b), Koanwar and Talukdar (1986) and Bhatnagar and Tiwari (1989) who also obtained significant differences for genotype x environment interaction. Similar results were obtained earlier by Majid *et al.* (2007) who also got the similar results for most of the quantitative traits in wheat. Glucosinolates b value recorded less than 1 for genotype 1617 so it is considered to best in adverse environmental conditions. Deviation from regression S^2d value was greater than unity for some genotypes means these genotypes were considered to be best even for poor environments. The divergence from regression for most of the genotypes was highly significant which showed that these genotypes were unstable at all the locations. As these are local collections so we can get best results if we use that in our regular breeding programmers (Arshad *et al.*, 2003).

Erucic acid percentage b regression coefficient value was recorded less than 1 of genotype 1616 indication for stable variety, and deviation from regression value showed more than 1 for are studied genotypes. So, these genotypes are better for poor environments as well. Combined analysis of variance of oil content showed highly significant difference between the genotypes, locations and GEI, suggesting differential response of genotypes across testing locations. The results obtained by Setegn and Habtu (2003) are also supported our findings. Present studies further supported by the earlier research of Zenebe and Hussien (2009) who studied stability analysis for oil content in sesame indicum 20 genotypes tested at six locations.

The bottom line of this study is that ANOVA and stability analysis of morphological and biochemical traits of 25 *B. juncea* genotypes showed highly significant results for selected locations while among them 3 genotypes including 1606 Panain, 1607 Buldhair and 1611 Kohat were the most stable varieties for different climatic conditions. Thus, it can be suggested that most of the indigenously collected genotypes from Pakistan were stable and hence they can be considered to be the best varieties for plant breeders as they can be easily cultivated in agro-climatic conditions and improves the national economy.

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