

Research Article

Genetic variability and correlation studies for biochemical traits in *Brassica juncea* L.

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Abstract

Brassica juncea germplasm was evaluated to estimate divergence, associations among traits and heritability for various bio-chemical traits in RCB design having three replications at the University of Agriculture, Peshawar during 2011-12. Data were recorded on six bio-chemical traits viz., oil content, erucic acid content, glucosinolate content, protein content, oleic acid content and linolenic acid content. Highly significant variations were recorded for all the studied bio-chemical traits. Maximum heritability was observed for glucosinolate content (0.90), protein content (0.80) and erucic acid content (0.82), whereas moderate heritability was recorded for oil content (0.54), oleic acid content (0.33) and linolenic acid (0.43). The high heritability was coupled with appreciable selection response. Negative associations were recorded among oil content and protein content ($r = -0.419^{**}$). Protein content showed positive associations with glucosinolate content ($r = 0.678^{**}$) and erucic acid content ($r = 0.481^{**}$).

Keywords: *Brassica Juncea* L.; Heritability; Correlation; Selection response

Introduction

Brassica belongs to family Brassicaceae, an important genera of this group [1]. Family Brassicaceae consists of about 338 genera and 3709 species [2]. *Brassica juncea* generally known as Indian mustard is cultivated on about 70% of the area devoted to rapeseed and mustard. *Brassica juncea* is an important species among the six most

cultivated species of brassica worldwide. The most suited qualities of *Brassica juncea* are early ripening, pest resistance, heat tolerance and non-shattered pods. Cultivation of *Brassica juncea* cultivar are reducing day by day due low seed yield and is one of the most dangerous threat to it. Pakistan spent a huge amount of money on oil import after petroleum. It could be only

saved by producing oilseed cultivars having high yield and better quality [3]. To fulfill the demand and needs of future oil consumption of Pakistan, the oilseed having high quality must be one of the key objectives of brassica breeding [4, 5]. Both conventional and genetic engineering methods are used to improve quality traits of brassica. Correlation analysis is a useful tool to determine the relationship between different pairs of traits. In the genetic context, there is little likelihood of separate control for any pair of characters [6]. Genetic divergence, heritability and associations among traits are important to develop effective criteria for selection in a breeding programs [6-8]. New cultivars development with better performance is the paramount goal of a plant breeder in a breeding program. To run an effective breeding program, the available local germplasm must be evaluated for variability and heritability to know their actual potential. These local germplasms will be used as a source to design a breeding programme [9].

Materials and methods

Brassica juncea germplasm was evaluated to estimate divergence, associations among traits and heritability for various biochemical traits in RCB design with three replications at the University of Agriculture, Peshawar during 2011-12. Row length was 5 meter while distance between adjacent rows and plants were 30 and 20 cm, respectively. Each entry had two rows per genotype in a replication. Total area of the experiment was 9 m². Ten plants were selected for data recording per genotype in each replication.

Statistical analysis

MSTAT-C computer software was used for the analysis. Broad sense heritability was estimated from their expected means squares [10]. Components of variance including genotypic, phenotypic and error variances were computed according to [11].

Genetic variance = $V_g = (GMS-EMS)/r$

Environmental variance = $V_e = EMS$

Phenotypic variance = $V_p = V_g + V_e$

Heritability = $h^2_{BS} = V_g/V_p$

Selection response was determined using the following formula [12].

$$Re = k \times \sqrt{V_p} \times h^2$$

Where;

K = A constant value at a specific selection intensity, $k=1.40 @ 20\%$.

Results and discussion

An oilseed having high oil content with better quality is the end goal of each grower. Analysis of variance showed highly significant ($P \leq 0.01$) differences for oil content [13, 14] (Table 1). Oil content ranged from 43.60 to 50.70 %. Maximum oil content was observed in genotype 619 (50.70 %) followed by genotypes 618 (50.60 %), 616 (50.20 %), 615 (49.80 %). Whereas minimum values were found in genotype 610 (43.60 %) followed by 606 (45.00 %), 611 (45.80 %) and 608 (46.10 %) (Table 2). Genetic variance (2.88) was greater than environmental variance (2.47) for oil content. Moderate broad sense heritability (0.54) and the selection response (1.74) were recorded for said trait, which suggested that genetic variance could play an important role in the inheritance and improvement of the said trait (Table 3). However high magnitude of heritability (bs) for oil percent were recorded in rapeseed [15]. Oil content showed highly significant negative correlation with protein content ($r = -0.419^{**}$), whereas non-significant with rest of the traits (Table 4). These findings are in conformity with [14, 16, 17] who observed negative correlations among oil content and protein content. However, [18] reported positive associations among oil content and protein content.

For protein content highly significant ($P \leq 0.01$) differences were observed (Table 1). Our findings are similar with the results of [6, 19]. They noted significant differences

for protein content in *Brassica napus* and *Brassica juncea*. The ranges for the mean were 26.20 to 20.6 % for protein content. Maximum (26.20 %) protein content was observed in genotype 606 followed by genotypes 605 (25.60 %), 608 (25.20 %), 610 (25.00 %). Whereas minimum protein content (20.60 %) was revealed by genotype 615, this genotype was found at par with 603 (20.80 %), 601 and 617 both with the mean value of 21.60% (Table 2). Genetic variance (2.33) was greater in magnitude than environmental variance (0.58) for protein content. High heritability (bs) and the selection response 0.80 and 1.91 found in protein content, respectively (Table 3). These results suggested that genetic variance could play an important role in the inheritance and improvement of the said trait. Similarly, high heritability with high selection response was also reported by [6] during his study of rapeseed. While low heritability was observed by [14] in brassica for the said trait. Protein content showed highly significant positive correlation with glucosinolate content ($r = 0.678^{**}$) and erucic acid content ($r = 0.481^{**}$) (Table 4). [20] reported positive correlation among protein content, glucosinolate content, erucic acid content, oleic acid content and linolenic acid content which confirmed our findings. Highly significant ($P \leq 0.01$) variations were recorded from ANOVA (Table 1) for glucosinolates and the mean values varied between 107.40 to 144.40 (μgMg^{-1}). [21, 22] supported our findings by reporting highly significant variations for the said trait. Significant variations were also observed among the studied brassica genotypes [23]. Maximum glucosinolate content was observed in genotype 608 ($144.40\mu\text{gMg}^{-1}$). This genotype was found equal in performance with 605 ($143.10\mu\text{gMg}^{-1}$), 606 ($139.20\mu\text{gMg}^{-1}$) and 610 ($133.40\mu\text{gMg}^{-1}$). However minimum values performance was shown by genotypes 611 ($107.40\mu\text{gMg}^{-1}$)

followed by 617 ($110.60\mu\text{gMg}^{-1}$), 604 ($117.00\mu\text{gMg}^{-1}$) and 615 ($117.80\mu\text{gMg}^{-1}$) (Table 2). Genetic variance (93.03) was greater than environmental variance (9.69) for glucosinolate content. High broad sense heritability (0.91) with maximum selection response (12.85) was computed for glucosinolates, which suggested that the inheritance and improvement of the said trait could be due to genetic variance (Table 3). High heritability for glucosinolate content with moderate selection response was in similarity with the findings of [14, 24]. Glucosinolate content revealed highly significant positive correlation with erucic acid content ($r = 0.377^{**}$), while non-significant correlation was revealed with rest of the traits (Table 4). Positive correlation among glucosinolate content, linolenic acid content and erucic acid content were observed [14].

Highly significant ($P \leq 0.01$) differences were resulted for oleic acid content (Table 1) which were further strengthened by the results of [14] who also reported significant variations among different genotypes oleic acid content ranged from 33.30 to 39.80 %. Maximum oleic acid content was observed in genotype 603 (39.80 %) followed by genotypes 601 (39.50 %), 619 (38.90 %) and 610 (38.70 %). Whereas minimum values were found in genotype 609 (33.30 %) followed by 615 (34.20 %), 605 (35.30 %) and 614 (35.40 %) (Table 2). Genetic variance (1.88) was smaller than environmental variance (3.71) for oleic acid content. Moderate broad sense heritability (0.34) and the selection response (1.11 %) were recorded for said trait (Table 3). However, our findings are discouraged by [25] who estimated high heritability with high selection response. Oleic acid content showed non-significant positive correlation with linolenic acid content ($r = 0.011$) and erucic acid content ($r = 0.159$) (Table 4). [26] negative correlation between linolenic acid

content and oleic acid content which is in dissimilarity to our results.

For linolenic acid content manifested highly significant ($P \leq 0.01$) differences (Table 1) and ranged between 9.60 to 12.00 %. Our results are in agreement with the result of [14, 6]. They also reported significant differences for linolenic acid in brassica genotypes. Highly significant variations were also observed by [27] for the said trait. Maximum linolenic acid content (11.80 %) was observed in genotype 603 and was found at par with genotypes 606 (11.70 %) and 602 (11.60 %). However minimum values were found in genotype 610 (9.60 %) and were found in performance equal with 611 (9.90 %), 614 (10.20 %); while genotypes 613, 615 and 617 exhibited same mean value of 10.30 % (Table 2). Genetic variance (0.35) was lower than environmental variance (0.46) for linolenic acid content. Moderate broad sense heritability (0.43) and the selection response (0.54 %) were recorded for said trait (Table 3). However, contrasted results have been reported by [6] having high heritability with moderate selection response. Linolenic acid content showed non-significant positive correlation with all the studied traits (Table 4). Positive correlations were reported among glucosinolate content, protein content, linolenic acid content, protein content and erucic acid content by [28, 18]. [29] reported contrast results by negative associations between oil content and linolenic acid content.

Highly significant ($P \leq 0.01$) differences were observed for erucic acid content from analysis of variance (Table 1). The findings of [30, 14] are in similarity to our results by reporting significant variations for erucic acid content. Erucic acid content ranged from 30.10 to 65.80 %. Maximum erucic acid content was observed in genotype 605 (65.80 %) followed by genotypes 602 (62.30 %), 600 (60.90 %), 612, 616 and 620 (60.80 %). Whereas minimum values were found in genotype 615 (30.10 %) followed by 603 (50.00 %), 617 (55.00 %) and 601 (56.20 %) (Table 2). Genetic variance (49.60) was greater than environmental variance (10.74) for erucic acid content. High broad sense heritability (0.82) and the selection response (8.94) were recorded for said trait, which suggested that genetic variance could be helpful in the inheritance and improvement of the said trait (Table 3). These observations are in similarity with the findings of [31]. They estimated high broad sense heritability for erucic acid content in *Brassica juncea*. Erucic acid content showed highly significant positive correlation with protein content ($r = 0.481^{**}$) and glucosinolate content ($r = 0.377^{**}$), whereas non-significant with rest of the traits (Table 4). Our results are similar with the result of [23]. He suggested that some of the linked parameters i.e. protein content, glucosinolate content and erucic acid content showed significantly positive associations among each other.

Table 1. Mean squares table of brassica genotypes evaluated for some important biochemical traits during 2011-12

Traits	Replications	Genotypes	Error	CV %
Oil content	2.118	11.092**	2.465	3.26
Protein content	4.245	7.567**	0.579	3.31
Glucosinolates content	176.663	288.776**	9.691	2.47
Oleic acid content	88.35	9.343**	3.711	5.21
Linolenic acid content	0.206	1.517**	0.464	6.34
Erucic acid content	110.382	159.525**	10.736	5.64

Table 2. Mean squares table of *brassica* genotypes evaluated for some important bio-chemical traits during 2011-12

S.NO	Codes	Oil content (%)	Protein content (%)	Glucosinolate content (μgMg^{-1})	Oleic acid content (%)	Linolenic acid content (%)	Erucic acid content (%)
1	600	48.9	23.2	128.7	35.9	11.4	60.9
2	601	49.7	21.6	132.1	39.5	10.5	56.2
3	602	48.1	22.7	124.1	35.7	11.6	62.3
4	603	49.6	20.8	119.0	39.8	12.0	50.0
5	604	49.7	21.9	117.0	36.0	10.3	60.0
6	605	48.3	25.6	143.1	35.3	11.5	65.8
7	606	45.0	26.2	139.2	37.5	11.8	58.8
8	608	46.1	25.2	144.4	36.9	11.2	60.9
9	609	48.4	22.6	118.0	33.3	11.7	60.4
10	610	43.6	25.0	133.4	38.7	9.6	59.1
11	611	45.8	22.8	107.4	37.7	9.9	57.5
12	612	48.3	23.5	125.2	36.5	9.9	60.8
13	613	48.6	22.8	122.8	35.7	10.3	60.1
14	614	48.2	24.4	130.5	35.4	10.2	60.6
15	615	49.8	20.6	117.8	34.2	10.3	30.1
16	616	50.2	22.6	125.1	38.4	10.6	60.8
17	617	46.5	21.6	110.6	37.9	10.3	55.0
18	618	50.6	21.7	123.5	38.5	10.4	60.4
19	619	50.7	21.8	129.4	38.9	10.9	60.7
20	620	48.0	23.7	131.2	37.2	10.6	60.8
LSD_(0.05)		2.595	1.257	5.146	3.184	1.126	5.416

Table 3. Genetic variance, environmental variance, heritability and selection response of various *brassica* genotypes

Traits	Vg	Ve	Vp	h^2	R_e (20%)
Oil content	2.876	2.465	5.341	0.538	1.742
Protein content	2.329	0.579	2.908	0.801	1.912
Glucosinolate content	93.028	9.691	102.719	0.906	12.850
Oleic acid content	1.877	3.711	5.588	0.336	1.112
Linolenic acid content	0.351	0.464	0.815	0.431	0.544
Erucic acid content	49.596	10.736	60.332	0.822	8.939

Vg= Genotypic variance; Ve= Environmental variance; Vp=Phenotype variance; h^2 = Heritability; R_e =Selection response

Table 4. Correlations among six bio-chemical traits of various *brassica* genotypes tested during 2011-12

Traits	Oil content	Protein content	Glucosinolates	Oleic acid content	Linolenic acid	Erucic acid
Oil content	1	-0.419**	-0.129	0.040	0.158	-0.052
Protein content		1	0.678**	0.066	0.106	0.481**
Glucosinolates			1	0.179	0.225	0.377**
Oleic acid				1	0.011	0.159
Linolenic acid					1	0.098
Erucic acid						1

Conclusions

It is concluded from the above results that highly significant variations were observed for all the bio-chemical parameters. Highest heritability and selection response were recorded for glucosinolate content followed by erucic acid content while lowest heritability and selection response were obtained for oleic acid content. Oil content showed negative associations with protein content, glucosinolate content and erucic acid content, while rest of all the associations were positively associated with each other. Genotypes 606 (oil content), 619 (protein content) and 603 (oleic acid and linolenic acid contents) were superior, while genotypes 617 (glucosinolate content) and 615 (erucic acid content) were inferior and should be recommended for use in future breeding programs.

Authors' contributions

Conceived and designed the experiments: Fawad Ali, Junaid Khan, Performed the experiments: Haneef Raza, Ijaz Naeem, Analyzed the data: Murad Khan, Naila Nawaz Khan, contributed reagents/materials/analysis tools: Anwar Rashid, Mohammad Wasiullah Khan, Wrote the Paper: Jawad Ali, Abdul Saboor Khan

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