

Research Article

Genetic variability for biochemical traits among advanced lines of Brassica

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Abstract

To investigate genetic variability, heritability and correlation among different biochemical traits, six advanced lines (F_{10:11}) of *Brassica rapa* were studied at New Developmental Research farm, Faculty of Agriculture, Peshawar university during 2012-13. The experiment was carried out in randomized complete block design with three replications. Significant differences were observed for glucosinolate, oil content, protein content, oleic acid, linolenic acid and erucic acid. The advanced line, AUP-05 produced the maximum gluconsinolates (75.35 $\mu\text{mol g}^{-1}$), protein content (24.56%). Advanced line AUP-04 had the highest erucic acid (50.31) and linolenic acid (10.60%). Advanced line AUP-06 produced the high oil content (48.83%). Genotypic variances were greater than the environmental variances for majority of the traits. Ranges for genotypic and phenotypic coefficient of variation were 2.01 to 96.92% and 2.99 to 33.22%, respectively. Majority of the traits exhibited high heritability. The maximum heritability was recorded for erucic acid (0.78), protein content (0.77), glucosinolate (0.76), oleic acid (0.70). Oil content and linolenic acid exhibited moderate heritability with a value of 0.58 and 0.45, respectively. Overall the studied parameters indicate significantly varied results among the advanced lines. AUP-05 and AUP-06 showed promising results for maximum traits. Due to the presence of high genetic variability for glucosinolate content, protein content, oleic and erucic acid, these lines could be used in future breeding programs for the improvement of the biochemical attributes.

Keywords: Heritability; Brassica advanced lines; genotypic variances; Phenotypic coefficient of variances

Introduction

The genus Brassica L. is the most economically important genera in the tribe Brassiceae, belonging to the family Brassicaceae [1], which is further divided into 338 genera and 3709 species [2].

Diversity of this genus can be judged by the presence of the major vegetable and oil seed crops [3, 4]. Rapeseed and mustard are the two major groups which together make the genus brassica along with the presence of worldwide grown six economic species,

which have great genetic and morphological diversity [5]. Both Mustard and Rapeseed are widely grown as a rich source of edible oil [6]. In Pakistani rapeseed-mustard are economically important and high yielding oil seed varieties grown from long time that is why it is needed to produce improved oilseed brassica varieties for successful expansion of cultivation of oilseed crops [7]. In Pakistan rapeseed was cultivated over an area of 219 thousand hectare and produced 158 thousand tons seeds which in turn produced 51 thousand tons of edible oil during 2012-13 [8]. Cost price of oil is the 2nd largest imported commodity of Pakistan after the petroleum and is the single largest cost price imported commodity in food products [9]. Due to provision of energy, delicious taste and palatability of Oil and fats are key items in human diet. Pakistan is continuously facing deficiency in the production of edible oils and increasing continuously because of fast growth in population and rise in people's living standards. Classical breeding and genetic techniques are the sources of modifying the quality traits in brassica e.g., oil, protein and glucosinolates content. Production of high quality edible oil for humans and high quality protein meals for feeding animals was made possible by the genetic improvement in the seed quality of oilseed rape. Detergents, lubricants, cosmetics, hydraulic oils or biodiesel accounts for non-edible products of seed [10, 11]. Beside the direct consumption of humans and animals, brassica biomass is also used for production of bio energy [12]. A sulphur compound is present in glucosinolate, a sulphur containing compounds, makes the brassica species unfit for food and feed purposes [13]. Presence of 2% erucic acid and 30 $\mu\text{mol g}^{-1}$ glucosinolate in brassica oil are known as double zero or double low cultivars, which are good for both humans and animals use [14]. Future edible oil

requirement can only be achieved through the improvement of seed quality by breeding brassica [15, 16]. Estimation of the relationship between two variables is known as correlation. Measurable association alludes to a quantifiable relationship between two variables. Moreover, it is a quality's measure between two variables. For plant breeders it is necessary to concentrate on the relationship between sets of characters keeping in mind the end goal to settle on the proper determination criteria for a breeding program [17]. Therefore, the main objective of this study was to evaluate potential lines in agro-climatic conditions of Peshawar on the basis of biochemical attributes and to quantify the heritability and association of biochemical attributes in brassica.

Materials and methods

During 2012-13 six advanced lines (F_{10:11} families) of brassica were evaluated for Genetic variability of biochemical attributes at New Developmental form (NDF), The University of Agriculture, Peshawar Khyber Pakhtunkhwa.

Oil quality analysis

Quality of brassica is assessed on the basis of low percentage of glucosinolates (GSL), erucic acid and linolenic acid with a high percentage of oleic acid, oil, and protein. Near Infrared Reflectance Spectroscopy (NIRS) was used for screening the genotypes against these traits. The screening procedure was carried out at Nuclear Institute for Food and Agriculture (NIFA), Tarnab, Peshawar.

Estimation of genetic parameters

Genotypic and phenotypic variances, genotypic (GCV) and phenotypic coefficients of variance (PCV), heritability (broad sense) and genetic advance were computed according to Burton [18, 19, 20, 21]. The genotypic, phenotypic and environmental variances and heritability were calculated by the following formulas

$$V_g = \frac{GMS - EMS}{r}$$

Where

V_g= Genetic variance

GMS= Genotypic mean square

EMS= Error mean squares

r=Number of replication

Environmental variance (V_e) = Error mean squares(EMS)

$$V_p = V_g + V_e$$

Heritability broad sense (H²) on entry mean basis was calculated as:

$$\text{Heritability} = v_g / v_p$$

The expected response to selection (Re) for each trait was calculated as under:

$$Re = k \sqrt{vp} H^2$$

Where

k= 1.40 at 20% selection intensity for a trait

V_p= Phenotypic variance for a trait.

H² = Broad sense Heritability for a trait.

Genotypic coefficient of variation (GCV) = $\sqrt{V_g}/GM \times 100$

Phenotypic coefficient of variation (PCV) = $\sqrt{V_p}/GM \times 100$

Where

V_g= Genotypic variance

V_p= phenotypic variance

GM= Grand mean of the trait

Results and discussions

Glucosinolates is the 2nd major unwanted constituent of brassica which have adverse effects on human beings as well as animals. Therefore, preference is given to low contents of glucosinolate (GSL), for this purpose breeders are trying to develop such varieties possessing low content of glucosinolates. Brassica genotypes showed highly significant differences ($p \leq 0.01$) for glucosinolates ($\mu\text{mole g}^{-1}$) among the brassica genotypes (Table 1), exhibiting similar significant status in *brassica napus* studied by [22, 9]. Maximum of 75.35 ($\mu\text{mole g}^{-1}$) glucosinolates were recorded for genotype AUP-05, while minimum of 48.96 ($\mu\text{mole g}^{-1}$) for AUP-03 with an average of 66.75 ($\mu\text{mole g}^{-1}$) in advanced lines (Table 2). Variances for both the Environment and

genotypes were 24.71 and 79.39 for glucosinolates content and phenotypic coefficient of variation (11.99%) was lower than genotypic coefficient of variation (96.92%). Glucosinolates exhibited high broad sense heritability of 0.75 (Table 3). F_{2:3} introgressed population of brassica exhibited high heritability [23]. *B. napus* genotypes and Inter specific brassica population manifested high heritability for GLS contents [24, 25] whereas, low heritability for GSL in winter oil seed rape [26]. Glucosinolates revealed positive significant correlation with protein (0.56*) and positive non-significant with erucic acid ($r=0.35^{\text{NS}}$) and linolenic acid ($r=0.43^{\text{NS}}$). However, glucosinolates established negative but significant association with oil percent ($r=-0.52^*$) and oleic acid ($r=-0.52^*$) (Table 4). These results were supported by [9, 27]. They also postulated positive significant correlation of glucosinolate with protein, linolenic acid and erucic acid and negative association with oleic acid.

Data pertaining to oil content showed highly significant ($p \leq 0.01$) differences for genotypes among the advance lines (Table 1). The interspecific hybrids of brassica had 21.27% protein content [28], whereas lower protein content of 18% was observed in rapeseed genotypes [29]. Minimum oil content of 45.62% was recorded for genotype AUP-01, while maximum of 49.52% for genotype (AUP-03) with an overall mean of 47.78% in advanced lines (Table 2). Variances for genotypes (V_g), environment (V_e) were 1.58 and 5.93, respectively, whereas genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV) were 2.63%, 3.47%, respectively. Heritability h² (bs) were 0.58 for the said trait (Table 3). [30, 31] also reported similar genetic variability. Positive and non-significant association of oil content with oleic acid ($r=0.29^{\text{NS}}$) and erucic acid ($r=0.30^{\text{NS}}$) was observed. Negative but

significant correlation of Oil content with protein content ($r=-0.64^{**}$) and glucosinolates ($r=-0.52^*$). However, negative and non-significant correlation with linoleic acid ($r=-0.19$) (Table 4). Similar findings were also reported by [32, 31, 9].

Results regarding protein content were highly significant ($p\leq 0.01$) which coincide with the results of [33], who also recorded highly significant results in *Brassica napus* for protein contents (Table 1). Maximum oil content (24.56%) was recorded for genotype AUP-05, while minimum of 19.71% for AUP-06 with an average of 22.93% in advanced lines (Table 2). Environmental and genotype variance was 1.06 and 4.61, respectively. Similarly, genotypic coefficients of variation (9.36%), phenotypic coefficients of variation (10.40%) and broad sense heritability (0.77) were recorded for protein content, respectively (Table 3). [33] reported medium heritability for protein content in brassica, in contrast [30] recorded high heritability in rapeseed genotypes. Positive significant correlation was observed between protein content and glucosinolates ($r=0.56^*$) these findings are at par with the results of [27, 31, 9]. Positive and non-significant correlation of protein content with linoleic acid ($r=0.31^{NS}$) and erucic acid ($r=0.06^{NS}$) was observed, whereas negative significant with oil content ($r=-0.64^{**}$) and negative non-significant with oleic acid ($r=-0.28^{NS}$) (Table 4). These results show similarity with the previous results documented by [34].

Highly significant differences ($p\leq 0.01$) were observed among the advance lines of brassica for oleic acid (Table 1). [24] have also found confirming results for oleic acid. Maximum (55.53%) oleic acid was recorded for genotype AUP-03, while minimum of 46.89% for AUP-02 with an average of 50.63% in advanced lines (Table 2).

Phenotypic and genotypic coefficients of variation were 12.95% and 6.29%, respectively. High heritability of 0.70 was estimated which indicates the genetic control of the trait (Table 3). Higher heritability estimates for the said attribute tally with the results of [26]. Positive and non-significant correlation of oleic acid with oil content ($r=0.29^{NS}$) and linoleic acid ($r=0.39^{NS}$). However, negative but non-significant association with protein content ($r=0.28^{NS}$) and erucic acid ($r=-0.42^{NS}$). However, significant negative correlation with glucosinolates ($r=-0.52^*$) (Table 4). The findings of [35, 9] are in close conformity, who reported positive association between oleic acid and linolenic acid contents in brassica genotypes. Similarly, some other findings were in close agreement with our results, showing strong negative correlation between linolenic acid and oleic acid [36].

Brassica genotypes exhibited significant values ($p\leq 0.05$) for linolenic acid (Table 1), exhibiting similarity with the findings of [24, 9]. Maximum linolenic acid (10.60%) was recorded for genotype AUP-04, while minimum (7.35%) AUP-03 with an average of 9.19% in advanced lines (Table 2). Genotypic variance (1.03), environmental variance (1.27), genotypic (2.01%) and phenotypic coefficients of variation (2.99%) was observed for linolenic acid with a moderate heritability (0.45) (Table 3), the existing findings for heritability are in line with the results observed [33] and in contrast with the high heritability for linolenic acid reported by [24, 30]. Positive and non-significant correlation of linoleic acid with protein content ($r=0.31^{NS}$), glucosionate ($r=0.43^{NS}$), and oleic acid ($r=0.39^{NS}$). However, negative but non-significant association with oil content ($r=-0.19$). Linolenic acid revealed positive and significant relationship with erucic acid ($r=0.72^{**}$) (Table 4). Linolenic acid and

erucic acid exhibited negative non-significant correlation [9, 24], while [36] observed highly significant between linolenic acid and oleic acid.

Erucic acid is a problematic and unwanted constituent of oil seed brassica. Prime focus of this study was the assessment of promising genotypes for low erucic acid among the advance lines. Erucic acid manifested highly significant differences ($p \leq 0.01$) in these genotypes [24, 9] (Table 1). Maximum erucic acid 50.31% was recorded for genotype AUP-04, while minimum of 30.15% for AUP-03 with an average of 40.01% in advanced lines (Table 2). Environmental and genotypic variance was 12.52 and 45.51, respectively. Whereas genotypic coefficient of variation and

phenotypic coefficient of variation 29.41% and 33.22%, respectively. Similarly, high broad sense (0.78) was observed indicating sufficient genetic control on the mentioned trait (Table 3). These high estimates for the genetic components are in line with those of [9]. Erucic acid showed positive significant association with linolenic acid ($r=0.72^{**}$), and positive but non-significant with oil content ($r=0.30^{NS}$), protein content ($r=0.06^{NS}$) and glucosinolate ($r=0.35^{NS}$). However, erucic acid established negative correlation with oleic acid ($r=-0.42$) (Table 4). Our findings are in contrast with the results of [24, 9], who recorded a negatively non-significant association of linolenic acid with erucic acid.

Table 1. Mean Squares for various biochemical attributes among advance lines of brassica, during 2012-13

Traits	Glucosinolate	Oil content	Protein content	Oleic acid	Linolenic acid	Erucic acid
Replications	39.461	0.351	0.822	1.047	0.583	1.491
Genotypes	262.838**	5.929*	14.888**	31.035**	4.362*	149.049**
Error	24.706	1.166	1.064	3.907	1.269	12.524
CV %	7.451	2.27	4.501	3.901	12.251	8.841

Table 2. Mean values for various biochemical attributes among brassica advanced lines, during 2012-13.

Genotypes	Glucosinolate ($\mu\text{mol g}^{-1}$)	Oil Content (%)	Protein Content (%)	Oleic acid (%)	Linolenic acid (%)	Erucic acid (%)
AUP-01	68.02	45.62	24.55	47.85	9.89	36.73
AUP-02	72.62	47.56	24.30	46.89	8.16	39.84
AUP-03	48.96	48.73	20.41	55.53	7.35	30.15
AUP-04	65.60	48.76	23.90	51.85	10.60	50.31
AUP-05	75.35	46.25	24.56	52.31	9.69	37.67
AUP-06	69.95	48.83	19.71	49.34	9.46	45.38
Mean	66.75	47.62	22.91	50.63	9.19	40.01
LSD (0.05)	9.04	1.96	1.88	3.59	2.04	6.43

Table 3. Genetic components for various biochemical traits of advanced lines of brassica, during 2012-13

Traits	Glucosinolate	Oil content	Protein content	Oleic acid	Linolenic acid	Erucic acid
GMS	262.84	5.93	14.88	31.03	4.36	149.05
EMS	24.71	1.16	1.06	3.91	1.27	12.52
VG	79.38	1.58	4.61	9.04	1.03	45.51
VP	104.08	2.74	5.97	12.95	2.3	58.03
GCV	96.92	2.63	9.36	6.29	2.01	29.41
PCV	11.99	3.47	10.4	7.53	2.99	33.22
H ² (bs)	0.76	0.58	0.77	0.7	0.45	0.78

Vg = Genotypic variance, EMS = Ve = Environmental variance, Vp = Phenotypic variance

Table 4. Phenotypic correlations among biochemical traits in advance lines of brassica, during 2012-13

Traits	OIL	PRO	GSL	OLEIC	LINO	ERUCIC
OIL	--	-0.64**	-0.52*	0.29	-0.19	0.30
PRO		--	0.56*	-0.28	0.31	0.06
GSL			--	-0.52*	0.43	0.35
OLEIC				--	0.39	-0.42
LINO					--	0.72**
ERUCIC						--

OIL: Oil Contents, PRO: Protein contents, GSL: Glucosinolates, OLEIC: Oleic acid, LINO: Linolenic acid and ERUCIC: Erucic acid

Conclusion

The aim of the breeders is to enhance oil content of a variety to meet the need of end users. Overall the studied parameters indicate significantly varied results among the advanced lines. AUP-05 and AUP-06 showed promising results for maximum traits. Due to the presence of high genetic variability for glucosinolate content, protein content, oleic and erucic acid, these lines could be used in future breeding programs for the improvement of the biochemical attributes.

Authors' contributions

Conceived and designed the experiments: N Ullah, IU Jan, Z Rahman & F Ali, Performed the experiments: J Khan & MW Khan, Analyzed the data: H Ullah & I Hussain, Contributed reagents/ materials/

analysis tools: M Alam, Wrote the paper: H Raza.

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