Assessment of some Canola genotypes based on genotype by Trait (GT) Biplot Analysis

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ABSTRACT

This investigation was conducted at Giza Research Station, Agricultural Research Center (ARC), during 2016/17 and 2017/18 growing seasons, to study the behavior of eight canola genotypes including four promising mutants population, three French cultivar and one Local variety (Serw 4). A randomized complete block design with four replications was used. Correlation coefficients were computed between grain yield and its related attributes as well as factor analysis. The genotype by trait (GT) biplot graph was used to compare genotypes based on multiple traits. Results revealed significant differences among genotypes for all studied characters. The inbreed line 1055 was superior in all characters flowed by inbreed line 1056 and Mutant 39. Highly significant and positive correlation was recorded between seed yield/plant and each of days to 50% flowering, plant height , first racemes height , fruiting zone Length, number of racemes /plant , 1000-seed weight (g) but without significant with oil percentage. Factor analysis divided the studied variables into three factors that contributed (77.30%) of the total variability. First factor included, days to 50% flowering, first racemes height and fruiting zone Length that accounted for (31.34%) of the total variability. Second factor consisted of plant height, number of racemes /plant and 1000-seed weight that accounted for (29.78%) and the third factor endued only oil percentage that accounted for (16.18%) of the total variability. The obtained results by GT biplot graphs were coincided with those obtained by correlation matrix indicating that GT biplot graph is considered a successful and effective technique beside or instead of these analyses. Undoubtedly, GT biplot graph is preferred because it is easy to interpret and gave more information.

Worldwide *Brassica* species are the third most important source of oils and their production has viewed a steady rising movement through modern and conventional plant breeding approaches. The main rapeseed-producing countries of the world are Canada, China, India and France FAO STAT (2012). It contains 40-45% oil and 36-40% protein. Canola oil has low content of erucic acid and glucose in oblates and high content of omega 3 and vitamin E which is also considered one of the healthier oils for human consumption, being recognized by medicine as a functional food (Brown *et al.*, 2008).

Rapeseed *(Brassica napus* L.) has the third rank in production of vegetable oil in the world. It is also the second leading source of protein meals (Azizinia, 2012). Canola seeds contain an average content of 38% oil, which may represent an agronomically sustainable choice (Tomm *et al.*, 2010), which plays a starring role in the oilseed crops business currently, oil seed rape (*Brassica napus* L.) is one of the most important vegetable oil crops in the word, although the planted cultivars are capable of achieving high oil content, but further improvement of grain yield and percentage of oil through different breeding activities is required.

It has been reported that one percentage increase in canola seed oil is equivalent to 2.3~2.5 percentage increase in seed yield accordingly, a lot of effort has been put to breed high oil yield canola cultivars around the globe. Selected genotypes may be used directly as new varieties or they may be used indirectly as sources of new genes to improve the commercial genotypes. Several investigations had been conducted canola genotypes evaluation experiments (Nasr and Omar, 1999). They posted significant differences among either introduced or landrace genotypes in data were recorded on a sample of ten individual plants/plot. The traits were days to 50% flowering, plant height , number of racemes, height of first raceme ,fruiting zone length,1000 seed weight, oil content and seed yield/ plant.

Yield is a complex character determined by several variables. Hence, it is essential to indentify the characters having the greatest influence on yield and their relative contributions in yield variation. This is useful in designing planed breeding programs. Increasing canola production is one of the major targets of the agricultural policy that can be achieved by increasing both canola genotypes area and unit area productivity. Breeding decisions based only on correlation coefficients may not always be effective since they provide only one-dimensional information neglecting the complex interrelationships among plant traits (Kang, 1994).

The factor analysis procedure basically reduces along number of correlated variables to a small number of uncorrelated factors. The present study was conducted to evaluate eight canola genotypes for yield and its components and to assess the inter relationships among them (Thompson *et al.,* 2003). Genotype x trait (GT) biplot permits the visualization of the real correlation among traits and understanding of relationships that facilitate the identification of traits that can be used in indirect selection for a grain yield (Yan and Rajcan, 2002; Yan and Tinker, 2005, Yan, 2014). In addition, GT biplot gives information on the usefulness of cultivars for production as well as information that helps detect less important (redundant) traits. Swelam (2012) used GT biplot graph to visualize the relationships among genotypes, traits and among them. In this investigation GT biplot graph could be successfully used for multi-traits selection in canola breeding programs.

Despite the recent interest shown in GT biplot graph to interpret the two-way table of genotype and traits, it is rarely used in the yield trials in Egypt. Few references were found concerning this technique. The objectives of this work were (1) to determine the way in which yield components related to each other (2) to identify genotype and trait relationships using correlation coefficient to discuss whether GT biplot graph is possible to be a good alternative procedure for correlation coefficient.

Materials and Methods

The experimental material for the present investigation comprised of 8 rapeseed (*Brassica napus* L.) genotypes which were selected based on diversity of agronomic characters. The genotypes were evaluated based on randomized complete block design with four replications at Giza Research Station in 2016/2017 and 2017/2018, Agricultural Research Center (ARC). The material under study consisted of eight rapeseed (*B. napus* L.) genotypes including four promising mutants population; (36, 37, 38 and 39), three French cultivar (Pactol, G1055 and G1056) as well as the local commercial cultivar Serw-4. Each entry consisted of five rows 4m long. Spacing between row and plants within the row was keep at 60 cm and 15 cm, respectively. Thinning was done at one plant/hill after 18 days of planting.

Table 1. Cultivars and mutants used in the evaluation trial

Cultivars and Mutants	Origin
Mutant (36)	Cursor variety treated with 300 Gry.
Mutant (37)	Cursor variety treated with 300 Gry.
Mutant (38)	Cresol variety treated with 300 Gry.
Mutant (39)	Cursor variety treated with 300 Gry.
Pactol	French
Inbreed line 1055	French
Inbreed line 1056	French
Serw (4)	Local variety (Egypt)

The aim of this study was study the relation between yield and its components in eight canola (*Brassica napus*, L.) genotypes namely Pactol, Serw 4, Mutant 36, Mutant 37, Mutant 38, Mutant 39 and two local Local varieties (G1055 and G1056). and to compare genotypes on the basis of multiple traits (seed yield and its related characters); (I) to identify genotypes that are particularly good in certain part or side in canola breeding program and to visualize

the relationships among them, (II) to identify genotype and trait relationships using correlation coefficient and GT biplot graph and can graphically display the interrelationships among traits and facilitate visual comparison of treatments.

Agronomic Traits

Data were recorded on a sample of ten individual plants/ plot. The traits were days to 50% flowering, plant height (cm), number of racemes, height of first raceme (cm), fruiting zone length (cm), 1000 seed weight, oil content and seed yield/ plant. The obtained date were statistically analysis and difference among entries were done using the Duncan multiple rang method. The background of the used entries is indicated in table 1.

Statistical Analysis

Analysis of Variance

Analysis of variance of RCBD as outlined by (Gomez and Gomez, 1984) was conducted for each year. Levene test (1960) was run prior to the combined analysis to test the homogeneity of individual error terms. Least significant difference (LSD) test was used to detect the significant differences among genotype means at 0.05 probability level. Simple correlation coefficients between grain yield (as resultant variable) and its related characters (as casual variables) were studied using simple correlation coefficients between all pairs of traits as suggested by (Steel *et al.*, 1997). Factor analysis method as applied by (Cattle, 1965) was also used. This method basically reduces a large number of correlated variables to a small number of uncorrelated factors. When the contribution of a factor to the total percentage of the trace was less than 10%, the process stopped. After extraction, the matrix of factor loading was submitted to a varimax orthogonal rotation, as applied by (Kaiser, l958).

The effect of rotation is to accentuate the larger loading in each factor and to suppress the minor loading coefficient and in this way to improve the opportunity of achieving a meaningful biological interpretation of each factor. Thus, factor analysis indicates both grouping and contribution percentage to total variation in the dependence structure, since the objective was to determine the way in which yield components related to each other. GGE biplot could be used for all types of two-way data set such as genotypes with multiple traits.

Gabriel, K. R. (1971) and Yan and Rajcan (2002) used the genotype by trait (GT) biplot, which is an application of the GGE biplot to study the genotype by trait data. Because the traits were measured in different units, the biplot procedure was generated using the standardized values of the trait means.

Results and Discussion

Before operated combined analysis of variance, using of (Levene test, 1960) proved the homogeneity of separate error variances for all studied character.

Earliness and Other Traits

Results in table 2 exhibited that mean squares due to season, genotype and interaction between them were significant or highly significant (0.05 or 0.01 probability levels) for all characters, except for days to 50% flowering, plant height, first racemes height, fruiting zone length, 1000-seed weight, oil percentage and seed weight plant/ g and grain filling rate for seasons. The significant genotype× year interaction indicated that differences among genotypes were not stable from 1 year to another, and these interactions are unavoidable in agricultural investigations (Yan and Kang, 2003), first racemes height, number of racemes of plant and 1000-seed weight for interaction between genotype and season. When the interaction effect between genotype and season was insignificant, it is meaning that the canola genotypes had similar behavior in the two seasons. Therefore, it is enough to present the combined averages across the two seasons without showing its seasonal averages. These results reflect the different genetic backgrounds of the studied genotypes for earliness and yield characters.

Mean Performance of Traits in Each Year and Combined

Mean performance of grain yield and its attributes for the 8 canola genotypes resulted from combined analysis across the two seasons is shown in table 3. The interaction between genotype x season was highly significant for earliness mean performance in table 3 indicated that Mutant 36 was the earliest genotype for days to 50% flowering (82, 81.75 and 81.88 days) in the 1st and 2nd seasons and their combined analysis, without significant differences in with genotypes *viz,*

E. M. M. El-nenny, Suzan A. K. Ibrahim, Sahar A. Farag

Table 2. Mean squares (MS) of the studied characters combined analysis of the 8 canola genotypes using the studied yield characters 2016-17 and 2017-18

S. O. V.	df	DF	PH	FRH	FZL	NRP	1000 WS	Oil %	SW/P (g)
Seasons (S)	1	0.016	54.39	26.27	87.89	21.39**	0.022	0.023	4.47
Reps/Seasons	6	88.16	51.95	5.75	259.33	0.95	0.59	3.40	1.41
Genotypes (G)	7	1070.43**	1928.87**	99.53**	1238.91**	23.91**	5.45**	25.97**	197.52**
G x S	7	641.59**	300.21**	11.09	452.93**	1.18	0.11	25.48**	8.42**
Error	42	51.42	34.97	4.22	173.79	1.68	0.41	1.47	1.09
Total	63								

Note: *, ** = Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.
Days to 50% flowering (DF), Plant height (PH), First racemes height (FRH), Fruiting zone length (FZL), No. of racemes /plant (NRP), 1000-seed weight (g) (W1000s), Oil percentage (% of Oil content), Seed weight plant/g (sw/p (g).

Table 3. Yield and the other traits data of eight rapeseed canola genotypes in the 1st and 2nd seasons and their combined analysis

Geno-types	Days to 50% Flowering			Plant Height			First Racemes Height	Fruiting Zone Length			Number of Racemes /Plant	1000-seed Weight (g)	% of Oil Content			Seed Weight plant/g		
	1st S	2nd S	Comb.	1st S	2nd S	Comb.	Comb.	1st S	2nd S	Comb.	Comb.	Comb.	1st S	2nd S	Comb.	1st S	2nd S	Comb
Pactol	92.00	91.75	91.88	127.5	122.75	125.13	15.63	108.75	111.00	109.88	9.75	3.53	49.68	41.53	45.60	13.00	13.00	13.00
Serw 4	93.00	92.50	92.75	125	134.25	129.63	17.13	110.75	118.00	114.13	8.75	4.77	42.05	43.90	42.98	10.75	16.23	13.49
Mutant 36	82.00	81.75	81.88	108.75	124.75	116.75	11.25	101.25	110.00	105.63	7.13	3.19	38.73	40.58	39.65	7.50	6.75	7.13
Mutant 37	91.00	90.75	90.88	115	132.00	123.50	14.38	122.5	95.00	108.75	8.63	3.26	39.98	41.73	40.85	8.75	9.25	9.00
Mutant 38	83.25	83.50	83.38	128.75	117.50	123.13	12.88	101.25	116.25	108.75	8.13	3.27	40.80	40.53	40.66	8.25	7.50	7.88
Mutant 39	92.50	126.50	109.50	141.25	138.25	139.75	17.63	107.5	127.50	117.50	11.38	4.84	40.08	43.60	41.84	14.00	14.25	14.13
G1055	126.00	93.00	109.50	155	162.00	158.50	22.63	142.5	145.00	143.75	11.75	4.91	41.73	41.23	41.48	20.00	20.00	20.00
G1056	108.50	108.75	108.63	162.5	147.00	154.75	18.13	128.75	118.75	123.75	11.38	4.85	42.00	41.65	41.83	20.00	19.50	19.75
Mean	96.03	96.06	96.05	132.97	134.81	133.89	16.20	115.41	117.69	116.52	9.61	4.08	41.88	41.84	41.86	12.78	13.31	13.05
LSD 0.05	10.89	10.19	7.24	9.43	7.90	5.97	2.07	19.68	19.09	13.31	1.31	0.65	1.53	**2.00**	1.22	1.48	1.59	1.06
CV%	7.71	**7.21**	**7.47**	4.82	3.98	4.42	12.68	11.60	11.03	11.31	13.49	**15.70**	2.49	3.25	**2.89**	7.90	8.12	8.02

Note: Days to 50% flowering (DF), Plant height (PH), First racemes height (FRH), Fruiting zone length (FZL), No. of racemes /plant (NRP), 1000-seed weight (g) (W1000s), Oil percentage (% of Oil content) and Seed weight plant/g (swpg),

Pactol, Serw 4, Mutant 37, Mutant 38 and Mutant 39 in the 1st season and genotypes Pactol, Mutant 37 and Mutant 38 in the 2nd season, combined analysis for days to 50% flowering observed in significant differences in with two earliest genotype Mutant 36 and Mutant 38. On the other hand, inbreed line 1055 showed the reverse trend, it was the latest canola genotype considering days to 50% flowering (126 and 109.50 days) in the 1st and their combined analysis, with the other shape Mutant 39 was the latest canola genotype considering days to 50% flowering (126.50 and 409.50 days) in the 2nd season and their combined analysis. The observed significant variation among the genotypes might partially reflect their different genetic backgrounds. The plant height is important in terms of resistance to lodging and seed yield. Plant height ranged from (108.75 to 162.50 cm) in the 1st and from (117.50 to 162. cm) in the 2nd season and (116.75 to 158.50 cm) for combined analysis across the two seasons.

The canola genotypes with maximum value for plant height were inbreed line 1056 in the 1st season and inbreed line 1055 in the in the 2nd and combined analysis across the two seasons, while the shortest plants had recorded in Mutant 36 in the 1st and combined analysis and Mutant 38 in the 2nd season. Results indicated that the first racemes height, number of racemes /plant and weight of 1000 seed for inbreed line 1055 was the heaviest over all canola genotypes for combined analyses across the two seasons. It recorded the maximum value (22.63 cm, 11.75 cm and 4.91g), while the lowest value belonged to Mutant 36 It recorded the minimum value (11.25 cm, 7.13 cm and 3.19 g) for three characters, respectively.

Results indicated that there is insignificant between the lowest value belonged Mutant 36 and Mutant 38 for two characters first racemes height and number of racemes/ plant and there is insignificant between the maximum value inbreed line 1055 and each of Mutant 39 and inbreed line 1056 for combined analysis across the two seasons. Mean performance of fruiting zone length in the 1st and 2nd seasons and their combined analysis across the two seasons is shown in table (3). Inbreed line 1055 gave the highest values (142.5, 145 and 143.75 cm) in the 1st and 2nd and combined over two seasons, without significant differences with inbreed line 1056 in the 1st and 2nd seasons.

On the other hand Mutant 36 recorded the minimum value (101.25, 95 and 105.63 cm) in the 1st and 2nd seasons and their combined analysis across the two seasons without significant differences with genotypes Pactol, Serw 4, Mutant 38 and Mutant 39 in the1st season, Pactol and Mutant 37 in the2nd seasons and Pactol, Serw 4, Mutant 37, Mutant 38 and Mutant 39 with combined analysis across the two seasons. Data are presented in table (3) observed that Canola plants have a high seed oil content (up to 38%), while the genotype No 3 (Mutant 36) was recorded the lowest value of % of oil content (38.73 and 39.65%) respectively, in the 1st and combined over two seasons and with genotype No 5 (Mutant 38) which recorded (40.53%) in the 2nd season.

On the other hand two genotypes significantly surpassed all other genotypes Pactol No 1 (49.68 and 45%) in the 1st and combined over two seasons and (43.90%) and genotype No 2 (Serw 4) in the second season.

The seed yield is the ultimate expression of the many individual physiological processes. Variation in seed yield among studied canola genotypes was relatively high as shown in table (3). The elite genotypes No. 7 and 8 (inbreed line 1055 and1056) surpassed all genotypes ranged from (19.5 to 20 g/ plant) in the 1st and 2nd seasons and their combined analysis across the two seasons, whereas genotypes No. 3 (Mutant 36) recorded the lowest values for grain yield with without significant differences with genotypes No. 4 and 5 (Mutant 37 and 38) in the 1st season and with genotype No. 5 (Mutant 38) in the 2nd seasons and their combined analysis across the two seasons.

Correlation Matrix

Simple correlation coefficients among seed yield and its related attributes estimated across two seasons with row data are given in table (4). Results indicated that the relationship between seed yield/ plant and seven yield components was positive and highly significant, except oil% that was insignificant, with r value of 0.245 indicating that this trait may be independent in their genetic behavior under the tested genotypes. Data indicated that days to 50% flowering, plant height, first racemes height, fruiting zone length, number of racemes/ plant, 1000-seed weight had the greatest influence on seed yield with r values of 0.611**, 0.824**, 0.744**, 0.529** , 0.668** , 0.708**, respectively.

It is suggested that GY of these canola genotypes may be raised through selection for plants had more 1000 seed weight. These results confirm the finding of (Singh, 1974; Özer *et al.,* 1999; Çalışkan *et al.,* 1998, Algan and Aygün, 2001). Yield components exhibited various trends of associations among themselves. Highly significant and positive associations were observed among first racemes height and days to 50% flowering and plant height and between plant height and number of racemes/ plant (correlation coefficients > 0.60) reporting that the tallest genotypes were lately flowering and increase number of racemes/ plant. The tallest fruiting zone Length genotypes produced more number of racemes/ plant and more 1000 seed weight according to the significant and positive associations between FZL and each of NRP (0.440**) and 1000sw (0.363**).

Table 4. Correlation coefficients between seed yield and its related attributes computed from 8 rapeseed genotypes evaluated across two seasons

Characters	DF	PH	FRH	FZL	NRP	1000 SW	% of Oil	SY
DF	1							
PH	0.538**	1						
FRH	0.602**	0.760**	1					
FZL	0.559**	0.479**	0.499**	1				
NRP	0.548**	0.639**	0.586**	0.440**	1			
1000 SW	0.457**	0.531**	0.442**	0.363**	0.482**	1		
% of Oil	0.156	0.113	0.327**	-0.011	0.115	0.182	1	
SY	0.611**	0.824	0.744**	0.529**	0.668**	0.708**	0.245	1

Note: Days to 50% flowering (DF), Plant height (PH), First racemes height (FRH), Fruiting zone length (FZL), No. of racemes /plant (NRP), 1000-seed weight (g) (W1000s), Seed weight plant/g (SY) and Oil percentage (% of Oil content)

Table 5. Summary of factor loadings for seven traits of canola genotypes across 2016/17and 2017/18 seasons

Variable	Loading	Communality	Eigen Values	Variance %	Suggested Factor Name
Factor I					
DF x_1	0.743	0.695	2.194	31.339	Climatic
FRH x_3	0.637	0.776			
FZL x_4	0.869	0.789			
Factor II					
PH x_2	0.693	0.749	2.064	29.776	Growth
NRP x_5	0.678	0.667			
W1000s x_6	0.867	0.771			
Factor III					
Oil x_7	0.979	0.964	1.133	16.183	Chemical
Cumulative Variance	77.297				

It is worthy to understand the negative associations between oil % and FZL and insignificant and positive associations were observed among oil % and each of most traits (DF, PH, FRH, NRP and SY/p). Murat and Vahdettin (2007) reported that oil content was found positive but insignificant with seed yield plant. This trend of interrelationships among yield attributes sometimes called offset, buffer or compensation effects. The breeder should be aware about the nature of associations among yield components. On the other hand, the magnitude of the correlation coefficients among other traits was trivial and insignificant. These results concur with those reported by (Beeck *et al*., 2010).

Factor Analysis

The factor analysis divided the 7 studied characters into three groups or factors, which explained 77.30% of the total variability in the dependence structure. A summary of the composition of variables of the three factors with loadings is given in table (6). Factor 1 included three variables, which accounted for 31.339 % of the total variance. These variables were days to 50% flowering, first racemes height and fruiting zone length. These variables were of almost equal importance and communal with factor1, this factor may be regarded as a climatic factor. Factor 2 consisted of plant height, number of racemes/ plant and 1000-seed weight.

This factor accounted for 29.776 % of the total variability in the dependence structure, this factor may be regarded as a growth factor. Factor 3 included oil content which accounted for 16.183 % of the total variance, thus it can be called the chemical factor from the previous results and it can be concluded that, factor analysis is the one that can be used successfully for analysis for large amounts of multivariate data, and should be applied more frequently in field experiments (Hamed, 1993). The greatest benefit of factor analysis can be delineating areas of further researches designed to test the validity of the suggested factors.

GT Biplot Graph

Genotype Comparison (Polygon Graph)

Recently, the biplot graphs can be used to compare genotypes on the basis of multiple traits (seed yield and its related characters) and to identify genotypes that are particularly good in certain part or side in canola breeding program (Yan and Rajcan, 2002, Yan and Tinker, 2005). The polygon view of a genotype by trait (GT) biplot graph is the best way to visualize the interaction patterns between genotypes and traits provided the biplot should explain a sufficient amount of the total variation. The biplot graph (fig 1) presents the relationship among the aimed canola genotypes using the seed yield (g/plant) and its related attributes.

The GT biplot of the mean performance of the canola data explained 75.35% of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 52.65% and 22.70%, respectively. This relatively moderate proportion reflects the complexity of the relationships among the genotypes and the measured traits. Yan and Kang (2003) mentioned that the first two PC's should reflect more than 75 % of the total variation in order to achieve the goodness of fit for GT biplot model. The perpendicular genotypes to the polygon sides facilitate comparison between neighboring vertex genotypes. It is obvious that genotype G1056 recorded high values of oil content and fruiting zone length. Also, G1056 located high values of sector with reflected similar behavior toward the days to 50% flowering; first racemes height and plant height, number of racemes/ plant and fruiting zone Length traits.

It is noted that the points of these genotypes and traits placed into one sector and the angles among them were acute reflecting the positive associations among them. Genotype Pactol was among the best genotype in terms of oil content. Serw 4, Mutant 37 and Mutant 39 were the best genotype with 1000-seed weight (g) were spread near the original point, they had moderate values of most studied traits. Finally, the four genotypes Mutant 36 and Mutant 38 were located far from most studied traits (obtuse angles) indicating to their poor performance toward these traits. The current results are in harmony with those obtained by (Mona *et al.,* 2019).
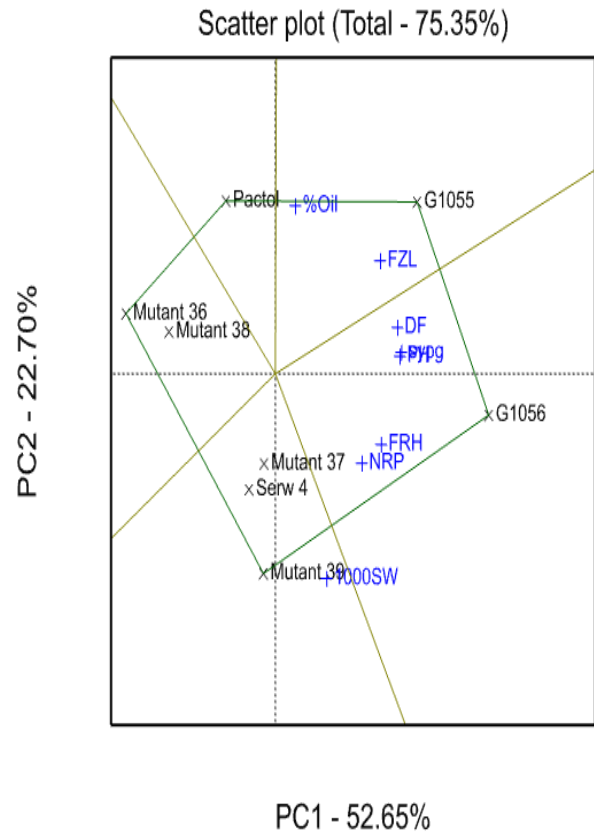

Fig 1. Polygon view genotype by trait (GT) biplot showing which genotype had the highest values for which traits for 8 canola genotypes

Trait Relations (Vector Graph)

Figure 2 is a GT biplot with a polygon view and it presents the data of eight winter rapeseed varieties with 8 traits in two years: DF, PH, FRH, FZL, NRP, W1000s, % of Oil content (g) and SW/p. In this graph of GT biplot (fig. 2), a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among them. The vector length of the trait measures the magnitude of its effects on the yield (Yan and Tinker, 2005). Accordingly, any two traits are positively correlated if the angle between their vectors is an acute angle (< 90°) while they are negatively correlated if their vectors are an obtuse angle (> 90°) and close to 90° no correlation (Yan and Kang, 2003). Hence, the associations among traits could easily be visualized from the biplot graph. These associations would be compared and confirmed by correlation coefficients between any two traits table (4). Results revealed that the most prominent relations in fig (2) are: a strong positive association between seed yield/ g,

days to 50% flowering, plant height, first racemes height, fruiting zone length, number of racemes/ plant and 1000 seed weight. In addition, there were strong and positive associations among between plant height, first racemes height, fruiting zone length, number of racemes/ plant and 1000 seed weight. As indicated by the small acute angles between their vectors (r = cos 0 = +1). Meanwhile; there were very weak associations among each of GY , PH and DF from one side and each of FRH, and NRP from the other side as indicated by near perpendicular vectors among them (r = cos 90 = 0). On the other hand, the associations between oil % and all other traits were negative as shown by the large obtuse angles among their vectors. These results coincided with those obtained by correlation matrix indicating that the GT biplot graph is a good substitute procedure for correlation coefficients for interpreting the interrelationships among the studied traits, oil % also did not show any association with GW and seed Y. This is in agreement with (Sadaqat *et al*., 1999).

Fig 2. Vector view genotype by trait biplot, showing the interrelationship among measured traits for 8canola genotypes

These results coincided with those obtained by correlation matrix indicating that the GT biplot graph is a good substitute procedure for correlation coefficients for interpreting the interrelationships among the studied traits. Furthermore, it is clear that the biplot methodology is an excellent tool for visual data analysis. Compared with conventional methods of data analysis, the biplot approach has some advantages. The first advantage of the biplot is its graphical presentation of data, which greatly enhances our ability to understand the patterns of the data. The second is that, it is more interpretative and facilitates pair-wise genotype comparisons. The third advantage of this method is that, it facilitates identification of possible genotypes or traits groups. The fourth advantage is that, it gives a complete picture about the interrelationships among genotypes and traits. The current results are in harmony with those obtained by (Swelam, 2012; Naser and Mohsen; 2014, Yan, 2014).

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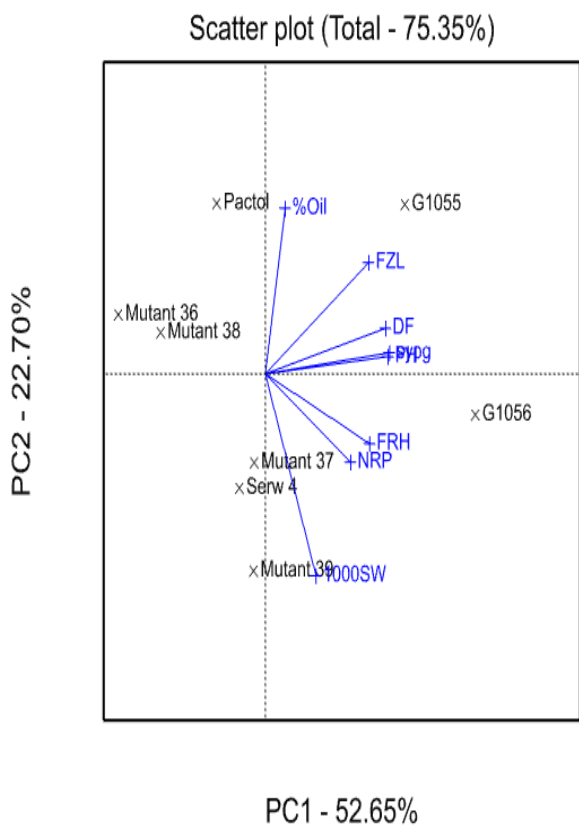
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