GRAPHIC ANALYSIS OF TRAIT RELATIONS OF CANOLA GENOTYPES USING THE BIPLOT METHOD

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ABSTRACT

Seven genotypes of canola in two consecutive years 2019 and 2020 in a randomized complete block design with four replications were carried out at Mansoura special farm and 10 traits were measured. Correlation coefficients were computed between the seed yield and its related attributes. The genotype by trait (GT) biplot graph was used to compare genotypes based on multiple traits. The results of the experiment showed that there were significant differences among genotypes for all studied traits. The Serw 4 was superior in all traits followed by Line 1055.Highly significant and positive correlation was recorded between seed yield/plant and each of plant height, fruiting zone length, 1000-seed weight,and highly significant and negative correlation was recorded with days to 50% flowering but without significant with oil percentage. The obtained results by GT biplot graphs were coincided with those obtained by correlation matrix showing 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.

Key Words: Canola genotypes, simple correlation, GT biplot.

INTRODUCTION

Canola (*Brassica napus* L.) is a high-value crop due to its high edible oil content and good quality animal meal protein (**Wu and Ma 2018**). Improvement of seed yield in canola has been the primary objective of canola breeders for many years. Seed yield is a quantitative trait, which is largely influenced by the environment and hence has a low heritability (**Brandle and Mcvetty 1989**). 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 olates, and a 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 agronomic ally sustainable choice (**Tomm** *et al.,* **2010**), which plays a starring role in the oilseed crops business currently, rapeseed oil (*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 2.3 to 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 indata were recorded on a sample of ten individual plants/plot. The traits were days to 50% flowering, plant height, 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 identify the traits having the greatest influence on yield and their relative contributions in yield variation. This is useful in designing planned 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**).

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 I.R. Rajcan 2002 ;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 seven canola genotypes (*Brassica napus* L.) which were selected based on diversity of agronomic traits. The genotypes were evaluated based on randomized complete block design with four replications at Mansoura special farm in 2018/2019 and 2019/2020. The material under study consisted of seven canola (*B. napus* L.) genotypes including three introduced ;(NA1, NA2 and NA3), three French cultivar (Pactol, Line1055 and Line1056) as well as the local commercial cultivar Serw4. Each entry consisted of five rows 4m long. Spacing between rows and paints within the row was keep at 60 cm and 15 cm, respectively. Thinning was done at one plant/hill after 18 days of planting.

The aim of this study was studying the relation between yield and its components in seven canola genotypes, (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 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 fruit branches, number of pods/plants, first fruit branch height (cm), fruiting zone length (cm),1000 seed weight, oil content and seed weight /plant. The background of the used entries is shown in the Table (1).

Statistical Analysis

Analysis of variance

Analysis of variance of RCBD as outlined by **Gomez and Gomez (1984)** was conducted for each year. 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 traits (as casual variables) were studied using simple correlation coefficients between all pairs of traits as suggested by **Steel** *et al.,* **1997**.

GGE biplot (Genotype main effect and Genotype X Environment interaction Scatter plot that plots both genotypes and environments in the same plot) and could be used for all types of two-way data set such as

genotypes with multiple traits. **Gabriel, (1971) ; 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.

Table 1:Cultivars and produced used in the evaluation trial

Cultivars and mutants	Origin
Pactol	French
Serw 4	Local variety (Egypt)
Line 1055	French
Line 1056	French
NA 1	Unknown
NA 2	Unknown
NA 3	Unknown

RESULTS AND DISCUSSION

Mean performance of Traits in each year:

Mean performance of grain yield and its attributes for the seven canola genotypes resulted from each year is shown in the Table (2).

The **NA1** was the earliest genotype for days to 50% flowering (67.33and 67days) in the 1st and 2nd seasons, On the other hand, **NA2** showed the reverse trend, it was the latest canola genotype considering days to 50% flowering (129.33 and 131.33days) in the 1st and 2^{nd}seasons. 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 (92.7to 179.7cm) in the 1st and from (92.67to 176.3 cm) in the 2^{nd}season. The canola genotypes with maximum value for plant height were **Serw 4** in the 1st season and **Line 1055**in the in the 2nd seasons, while the shortest plants had recorded in **NA1** in the $1s^{t}$ and the 2nd season.

Results indicated that the number of fruit branches, number of pods /plants, fruit zone length (cm), seed weight /plant and % oil for **Serw 4** was the heaviest over all canola genotypes for the 1st and 2nd season. It recorded the maximum value (11.33, 422gm, 168.7, 49.3 gm and 44. 9 7%), (12.33, 406.7, 161, 48 and 45.177%) respectively while the lowest value belonged to **NAI.** It recorded the minimum value (67.33 days, 92.7 cm, 9.33,83.3 cm,47.7 and 27.473%), (67 day, 92.6 cm,10.33,82.33 cm,7,46.7 and 27.52%) for seven traits in the first and second season, respectively.

Mean performance of fruiting zone Length in the 1st and 2nd seasons is shown in Table (2). **Serw 4** gave the highest values (168.7and 161cm) in the 1st and 2nd seasons.

On the other hand, **NA1** recorded the minimum value (83.3and 82.33 cm) in the 1st and 2nd seasons with significant differences with genotypes Pactol, Mutant1, Serw 4, Mutant 3and line1056.

Data are presented in Table (2) observed that Canola plants have a high seed oil content (up to 36%), except genotype No 5 (**NA1**) was recorded the lowest value of % of Oil content (27.473 and 27.552%) respectively, in the 1st and 2nd seasons. On the other hand, two genotypes significantly surpassed all other genotypes genotype No 2 Serw 4 (44.97and 45.177%) in the 1st and 2nd seasons and genotype No 4 (line 1056) recorded (44.313 and 44.48) in the 1st and 2nd seasons. These results confirm the finding of **El-Nenny *et al.,* (2020) and Mehmet *et al.,* (2021)**.

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 (2). The elite genotypes No. 2 and 5 (**NA1** and Serw 4) surpassed all genotypes ranged from (46.67 to 49.3 g/plant) in the 1st and 2nd seasons, whereas genotype No 7 (**NA 3**) recorded the lowest values for seed yield with without significant differences with genotype No.6 (**NA 2**) in the 1st season.concerning the seed yield /feddan the highest value was obtained by NA 1 in the 1st and the 2nd season 1992 and 2112 kg/feddan respectively followed by line 1056,1055 and serw 4 in the two season.

Table 2: Mean performance of yield and the other traits of ten canola genotypes in the 1st and 2nd seasons

Genotypes	DF	PH	FFBH	FZL	NFBRA	NPODS	1000SW	Oil%	SWG	SY (kg /fed.)
1st season (2019)										
Pactol	83.67	131.7	14.67	117	7.67	315.3	5	43.32	36.7	948
Serw 4	80	179.7	11	168.7	11.33	422	4.743	44.97	49.3	1276
Line 1055	100.67	175	20.67	154.3	10.33	129	5.337	43.707	43	1317
Line 1056	109	143.3	20.33	123	10.67	79.7	6.593	44.313	34	1630
NA 1	67.33	92.7	9.33	83.3	7	47.7	6.58	27.473	47	1992
NA 2	129.33	102.7	13.33	89.3	7	340.3	4.043	37.583	25.3	680
NA 3	127	106.7	13.33	96.7	9	216.3	3.94	36.477	18.3	475
L.S.D 0.05	3.508	10.19	2.465	9.39	1.677	38.12	0.339	0.4939	8.99	462.7
2nd season (2020)										
Pactol	85.67	132.3	13	119.3	8	301.3	4.997	43.837	38.33	1007
Serw 4	82	172.3	11.33	161	12.33	406.7	4.84	45.177	48	1304
Line 1055	102	176.3	22.67	153.7	11.67	135	5.467	43.427	42	1013
Line 1056	111	142	21.33	120.7	11.33	89	6.587	44.48	28.67	1007
NA 1	67	92.67	10.33	82.33	7	46.7	6.837	27.52	46.67	2112
NA 2	131.33	100	14.33	85.67	7.67	320.7	4.457	37.76	25.67	674
NA 3	126	106.7	13.33	93.33	9	231	3.877	36.85	20	528
L.S.D 0.05	2.207	2.75	1.729	3.621	1.207	16.19	0.169	0.2093	3.863	192

Days to 50% flowering (DF), plant height (PH), first fruit branch height (FFBH), fruiting zone length (FZL)Number fruit branch (NFBRA), No. of Pods (NPODS), 1000-seed weight (g) (1000SW), oil Percentage (% of oil content), seed weight plant/g (SW)and seed yield/kg feddan (Sy)

Correlation matrix

Simple correlation coefficients among seed yield and its related attributes estimated across two seasons with row data are given in Table (3).

Results showed that the positive relationship between seed weight/plant, plant height, fruit zone length and 1000 seed weight. negative relationship with days to 50% flowering, and highly significant, while first fruit branch height, number fruit branch, number of pods, and oil % that was insignificant.

Insignificant oil% showing that this trait may be independent in their genetic behavior under the tested genotypes.

Data showed that days to 50% flowering, plant height, fruiting zone length, 1000-seed weight had the greatest influence on seed weight/plant with r values of 0.859**, 0.439**, 0.481****, 0.498**, also days to 50% flowering, , 1000-seed weight ,oil% and seed weight /plant had the greatest influence on seed yield/feddan with r values of 0.442**, 0.49**,-0.377* and 0.532** respectively. It is suggested that seed yield of these canola genotypes may be raised through selection for plants had more 1000 seed weight. These results confirm the finding of **Singh (1974) ; Çalışkan *et al.,* (1998) ; Özer *et al.,*(1999) ; Algan and Aygün (2001) ; El-Nenny, *et al.,* (2020).**

Yield components exhibited various trends of associations among themselves. Highly significant and positive associations were observed among number fruit branch, fruiting zone length and plant height and between plant height and fruiting zone length (correlation coefficients > 0.60) reporting that the tallest genotypes were lately flowering and increase number of fruit branch.

The tallest fruiting zone length genotypes produced a greater number of branch and more seed weight according to the significant and positive associations between fruiting zone length and each of the number fruit branch /plant (0.746**) and 1000sw (0.481**).

It is worthy to understand the negative associations between oil % and 1000 seed weight and insignificant., highly significant positive associations were observed among oil % and each of most traits (plant height, first fruit branch height, fruiting zone length, number fruit branch and number of pods). **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).**

Table 3: Correlation coefficients between seed yield and its related attributes computed from 10 canola genotypes evaluated across two seasons

Traits	DF	PH	FFBH	FZL	NFBRA	NPODS	1000SW	OIL%	SWG	SY
DF	1									
PH	-0.199	1								
FFBH	0.367*	0.484**	1							
FZL	-0.256	0.991**	0.369*	1						
NFBRA	0.036	0.771**	0.528**	0.746**	1					
NPODS	0.132	0.227	0.378*	0.297	0.018	1				
1000SW	-0.557**	0.034	0.228	-0.009	0.111	-0.740**	1			
% OIL	0.164	0.812**	0.544**	0.784**	0.661**	0.430**	-0.198	1		
SWG	-859**	0.439**	-0.164	0.481**	0.101	0.065	0.498**	0.016	1	
SY	-0.442**	-0.135	-0.222	-0.123	-0.283	-0.261	0.49**	-0.377*	0.532**	1

Days to 50% flowering (DF), plant height (PH), first fruit branch height (FFBH), fruiting zone length (FZL),number fruit branch (NFBRA), number of Pods (NPODS), 1000-seed weight (g) (1000SW), oil percentage (% of oil content), seed weight plant/g (SW), and seed yield kg /feddan (SY)

GT Biplot graph

1-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 traits) and to identify genotypes that are particularly good in certain part or side in canola breeding program **(Yan and Tinker 2005 ; Yan, 2014).**

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 76.28% of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 40.20% and 36.07%, respectively.

This relatively moderate proportion reflects the complexity of the relationships among the genotypes and the measured traits. Yan and Kang [24] 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 neighbouring vertex genotypes. It is obvious that genotype Serw 4 recorded high values of plant height, fruiting zone length, first fruit branch height, number fruit branch and oil content and followed byline 1055, line1065 and pactol located high values of sector with reflected similar behavior toward the same 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.

NA2 and NA3 were the worst genotypes with days to 50% flowering and gave the highest value to latest agronomy. NA1 were located far from most studied traits indicating to their poor performance toward these traits. The current results are in harmony with those obtained by **Farrag** *et al.,* **(2019)**.
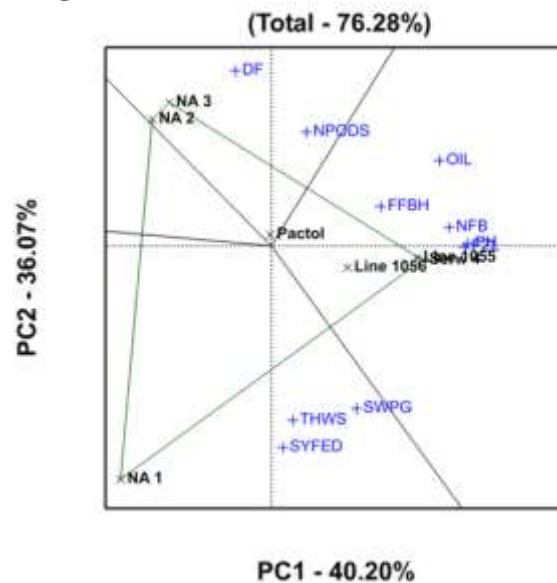

Fig. (1). Polygon view genotype by trait (GT) biplot showing which genotype had the highest values for which traits for 7 canola genotypes

2-Trait relations (vector graph): Fig. 2 is a GT biplot with a polygon view and it presents the data of seven canola genotypes with 10 traits in two years: (DF) Days to 50% flowering, (PH) Plant height, (FFBH) First fruit branch height, (FZL) Fruiting zone Length, (NFBRA) number fruit branch, (NPODS) Number of Pods, (W1000s)1000-seed weight (g), (% Oil) oil percentage ,(SW/P) seed weight plant/g and seed yield /feddan.

In this graph of GT biplot (Fig. 2), a vector is drawn from the biplot origin to each marker of the traits to visualise the relationships among them. The vector length of the trait measures the magnitude of its effects on the yield **[10]**. 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 [24]. 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 (3).

Results revealed that the most prominent relations in Fig. (2) are: A strong positive association between seed weight/plant (g), plant height, fruiting zone length, number fruit branch,1000-seed weight. In addition, there were strong and positive associations among between plant height and fruiting zone length has showed by the small acute angles between their vectors (r = cos 0 = +1). Meanwhile, there were very weak associations among each of fruiting zone length, plant height and days to 50% flowering as showed by the small obtuse angles between their vectors (r = cos 180 = -1).

Oil % also did not show any association with days to 50% flowering, 1000-seed weight, and seed weight. This is in agreement with **Sadaqat *et al.,* (1999)**.

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).**
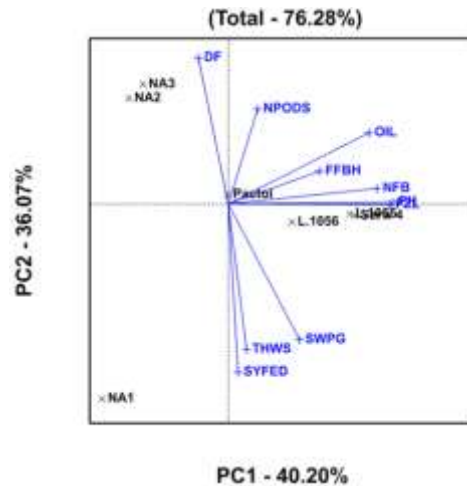
Fig. (2). Vector view genotype by trait biplot, showing the interrelationship among measured traits for 7canola genotypes

CONCLUSIONS

The best performance cross in terms of yield production was Serw 4 and Line 1055. The advantageous agronomic traits which strongly correlated to yield and yield component were frond production plant height, fruit zone length and 1000 seed weight. Furthermore, the tallest fruiting zone length genotypes produced a greater number of branch and more seed weight according to the significant and positive associations between fruiting zone length and each of the number of branch/plant and 1000seed weight. The GT biplot is a useful statistical tool for visualizing comparison crosses on the basis of multiple traits and revealing more information of interrelationships among genotypes and traits in canola.

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التحليل البيانى للعلاقات بين الصفات والتراكيب الوراثية
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1- قسم بحوث المحاصيل الزيتية– معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية – الجيزة – مصر

2- المعمل المركزي لبحوث التصميم والتحليل الاحصائى – مركز البحوث الزراعية – الجيزة – مصر

تم تتفيذ تجربة لتقييم سبعة تراكيب وراثية من الكانولا خلال موسمى زراعة متتاليين 2019 و2020 وكان تصميم التجربة فى قطاعات كاملة العشوائية فى أربعة مكررات في مزرعة خاصة بالمنصورة وكانت القياسات المستخدمة على 10 صفات. وتم دراسة العلاقات المتداخلة بين محصول الحبوب ومكوناته بإستخدام معامل الإرتباط البسيط كذلك تم ايضا إستخدام تحليل المحاور الثنائية والأشكال البيانية فى المقارنة بين التراكيب الوراثية المختبرة على أساس الصفات المدروسة. أظهرت نتائج التجربة وجود فروق معنوية بين التراكيب الوراثية لجميع الصفات المدروسة في كلا الموسمين. . وقد أعطى الصنف سرو 4 و السلالة 1055 أعلى محصول حبوب مما يشير إلى أهمية استخدامها في برامج التربية لتحسين صفة المحصول. أوضحت نتائج تحليل معامل الارتباط وجود ارتباط موجب عالي المعنوية بين محصول الحبوب / نبات وكل من ارتفاع النبات ، طول المنطقة الثمرية ، وزن 1000 حبة كما أوضحت النتائج وجود ارتباط سالب عالى المعنوية مع عدد أيام 50٪ تزهير ولكن بدون معنوية مع نسبة الزيتمما يعكس وجود ظاهرة العلاقات التعويضية بين مكونات المحصول.

تشابهت نتائج طريقة المحاور الثنائية باستخدام الرسوم البيانية (GT) Biplot مع النتائج التي تم الحصول عليها عن طريق مصفوفة الارتباط مشيرا إلى أن الرسوم البيانية Biplot (GT) تعتبر طريقة ناجحة وفعالة بجانب أو بدلا من هذه التحليلات. ومما لا شك فيه أنه يفضل إستخدام الرسوم البيانية لأنه من السهل تفسيرها ومن خلالها يمكن إظهار مزيد من المعلومات.