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COMPREHENSIVE AGRONOMIC AND MOLECULAR EVALUATION OF BREAD WHEAT GENOTYPES IN VARIOUS EGYPTIAN ENVIRONMENTS

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One of the main objectives of Egyptian agriculture in relation to food production is to increase the amount of wheat produced in a country in order to meet the food needs created by a constantly increasing population of people (Morsy *et al.*, 2021). As a result, it is necessary to develop more productive

methods for growing wheat and bridging the gap between production and consumption of wheat within Egypt. The additional need to produce an increasing quantity of wheat is also true if we are to feed the predicted 9 billion people in the world by the year 2050 (Ray *et al.*, 2012). In order to accomplish this goal, two

strategies must be employed; First, expanding the amount of land available for cultivation of wheat crops and secondly, increasing the productivity of wheat crops through the evaluation and exploitation of the genetic diversity present in existing wheat germplasm, in conjunction with the development of genetically improved varieties of wheat, and the use of best management practices (Philipp *et al.* 2019).

Both correlation and path analysis are used to provide information about the cause-and-effect relationship between traits. The genotypic and phenotypic correlation coefficient determines the relationship between a grain yield trait and other associated traits, while the path coefficient divides the correlation between traits into direct and indirect effects. This helps plant breeders in successful selection. Therefore, studying correlation and path coefficients helps in understanding the relationship between grain yield and its associated traits. Furthermore, the path coefficient aids in indirect selection for traits most strongly associated with grain yield, while direct selection for grain yield traits with lower heritability is less efficient Ali *et al.* (2024) and Kumar *et al.* (2024).

Molecular markers allow a more accurate analysis of genetic diversity, which is essential for future breeding and greater utilization of different genetic resources (Shaygan *et al.* 2021). Molecular breeding with SCoT markers is a reliable approach for assessing the

genetic differences among wheat cultivars (Hamidi *et al.* 2014) and selecting preferable cultivars for further breeding programs (Yalinkilic *et al.* 2024). Recently, various investigations worldwide have reported the application of SCoT markers test the diversity in wheat germplasm (Abd El-Moneim *et al.* 2020; Shaban *et al.* 2022 and Abouseada *et al.* 2023). Moreover, Shaban *et al.* (2022), Abouseada *et al.* (2023) and Fouad *et al.* (2024a) assessed the genetic diversity in Egyptian wheat genotypes using ISSR, SCoT and SDS-PAGE techniques.

Genetic diversity plays a crucial role in mitigating global concerns, including climate change and population expansion, which pose significant threats to food production and sustainability. Altaf *et al.* (2024) revealed that, through the utilization of the valuable data obtained from SCoT markers, scholars and decision-makers can make substantial advancements in strengthening food security, ultimately ensuring a more resilient and productive agricultural future.

This study aimed to evaluate the growth and yield of twelve distinct lines of Egyptian wheat cultivated under varying Egyptian environmental conditions, estimate the correlation and direct and indirect effects using path analysis, as well as to assess the genetic variability of these lines using SCOT molecular markers to facilitate the selection of the most appropriate variety

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for enhancing wheat crop productivity through breeding.

MATERIALS AND METHODS

Agronomical studies

Wheat genotypes

Twelve bread wheat genotypes included (ten lines developed by Prof. Dr. Ezzat E. Mahdy, Agronomy. Dept., Fac. Agric., Assiut Univ. and two cultivars Giza 164 and Sids 4 (Table 1) were evaluated during the 3 environments; 1st environment of 2021/2022 at the experimental farm, Fac. Agric., Assiut Univ. (27°11'08.0"N 31°09'42.7"E), 2nd and 3rd environments of seasons 2022/2023 and 2023/2024, respectively at the experimental farm, Fac. Agric., Minia Univ. (28°07'04.7"N 30°44'02.4"E). All the 12 genotypes were evaluated in 3 environments as shown in (Table 2).

Experimental design

The experimental design was a randomized complete blocks design with 3 replications at each environment. The plot size was three rows, 2 m in length, and 0.2 m in width. Seeding rate was 60 kg/fed. Seeds were sown by hand drill 5 cm. apart. The sowing dates were 25th, 20th and 22nd November for the 1st, 2nd and 3rd environment, respectively. Other recommended cultural practices were applied for wheat production throughout the growing season. Data were taken on 1 m middle row on the following traits: Days to 50% heading (DH), plant height

(PH) in cm, spike length (SL) in cm, biological yield per row BY/Row in gm, number of spikes row⁻¹ (NS Row⁻¹), grain yield per row (GY/Row) in gm and 100 grain weight (100GW) in gm. Phenotypic and genotypic correlation coefficients were calculated as outlined by Johnson *et al.* (1955), as follows: Phenotypic correlation $r_{p_{xy}} = \text{cov } p_{xy} / (\sigma p_x \cdot \sigma p_y)$ and genotypic correlation $r_{g_{xy}} = \text{cov } g_{xy} / (\sigma g_x \cdot \sigma g_y)$. Path-analysis was done for grain yield/plant as dependent variable (effect) affected by remained independent variables (causes) according to method of Deway and Lu (1959). Metrological analysis of weather of the three environments are shown in Table (3).

Molecular studies

Molecular studies were conducted at Molecular Genetics Laboratory, Genetics Department, Faculty of Agriculture, Minia University, Egypt.

Genomic DNA isolation

Genomic DNA isolation was carried out on a total of 200 mg of the young plants belonging to 12 different Egyptian bread wheat genotypes. The plant samples were ground to a fine powder in liquid nitrogen and the DNA was isolated from the sample using a Cornel Extraction Buffer consisting of: 500 mM NaCl, 100 mM Tris-HCl (PH 8.0), 50 mM EDTA, and 0.84% SDS. The amount and quality of the extracted genomic DNA were determined using a 1% agarose Gel and the concentration using a Nano-spectrophotometer at the

Central Laboratory of the Faculty of Agriculture at Minia University.

PCR condition for SCoT primers analysis

The SCoT (Start Codon Targeted) primers provide an opportunity to investigate the genetic diversity between the twelve Egyptian bread wheat genotypes. Ten SCoT primers were used for this purpose (see Table 4). The PCR amplification using each SCoT primer was conducted in a PCR reaction volume of 25 µl for each SCoT primer with the following components: 12.5 µl of PCR Master Mix, 2.5 µl of primer, 6 µl of distilled water, and 4 µl of Genomic DNA. The PCR amplifications were conducted using a Multigene Thermal Cycler as follows: one cycle of 4 minutes at 94 °C, followed by 35 cycles of 50 seconds at 94 °C, one minute at 50 °C, and 2 minutes at 72 °C, followed by a final extension for 7 minutes at 72 °C.

The PCR products were gel electrophoresed on a 2% agarose gel, and a stain of Ethidium bromide (0.1g of Ethidium bromide was dissolved in 10ml of 1X TAE Buffer) was used to visualize the DNA samples after electrophoresis. The sizes of the DNA fragments in the samples were determined by comparing them to a standard marker (100 bp ladder) that was included on the same gel. GBOX 230V was used for documentation of photographs.

PCR methods detected gels were analysed for all of the detected PCR

products, including molecular sizes of the PCR products produced (1) and (0), frequency of PCR products produced across PCR run samples, and polymorphism type(s) for each sample (e.g., monomorphic or polymorphic), as well as the mean and polymorphism % for all primer, using the software GelAnalyzer3 found on the internet (<http://www.geocities.com/egygene>) (GelAnalyzer Version 3, 2007). The data created by the similarity matrix were analysed by cluster analysis using software SPSS Ver. 1.

Statistical analysis

The Revised Least Significance Difference (RLSD) method was utilized as the basis for adopting statistical Analysis of Variance (ANOVA) with respect to genotype to compare the means of individual genotypes. A variance analysis of genotypes (square means) utilizing ANOVA was performed using the guidelines established by Gomez and Gomez, (1984). The form of analysis of variance genotypes square expectations are presented in Table (5).

RESULTS AND DISCUSSIONS

Agronomical evaluation

Analysis of variance (Table 6) showed significant ($P < 0.05$ or 0.01) difference among three environments, twelve genotypes and their interaction except biological yield / row, number of spikes / row and 100 grain weight of environments. The results indicating

genetic diversity among the studied genotypes and its response to different environments. Significance of genotypes x environments interaction is referring to inconsistency of genotypes in response to change environments. Similar results were reported by Naheed (2021), Fouad (2024b) and Khare *et al.* (2024).

Mean performance

Means of the studied traits for the genotypes in the three environments are shown in Tables (7 and 8). For the environments, the 3rd environment (Minia 2023/2024) recorded the earliest days to 50% heading followed by E2 then E1 by 77.78, 78.64 and 80.89 days, respectively. The difference between E2 and E3 in days to heading -0.86 days was insignificant. Similar results were reported by Fouad, (2019) and Zhang *et al.* (2023). The highest values for plant height and biological yield / row and grain yield per row were observed for the first environment by 112.00 cm and 504.72 gm. and 182.55 gm., respectively. While, the second environment E2 recorded the highest values for spike length, number of spikes per row and 100 grain weight by 13.44 cm and 83.22 and 5.72 gm, respectively. Indicating E1 and E2 were the most suitable environments for these traits.

For genotypes, mean days to 50% heading ranged from 71.33 of line 1 to 87.22 of Giza 164 with average 79.10 days. The two lines no. 1 and 2 recorded the significant early by -2.00 and -1.55 days compared to the earlier parent Sids

4. While, most of the remained genotypes were late in earliness. For plant height, the three lines 13, 27 and 37 gave significant increase in plant height compared to the tallest parent Sids 4 (94.89 cm) by 10.87, 7.33 and 10.33 cm., respectively. The three lines no. 23, 27 and 32 showed significant increase in spike length by 20.35, 7.64 and 10.18%, respectively compared to the highest parent Sids 4.

Mean biological yield per row was ranged from 322.17 to 776.33 gm. for line 13 and line 1 with average 499.64 gm. Seven lines no. 1, 2, 21, 23, 35, 37 and 38 recorded significant increase in BY/Row compared to the highest parent Giza 164. Three lines from them no. 1, 2 and 35 gave significant increase in number of spikes per row compared to the highest parent Giza 164 by 20.61, 19.50 and 16.00 spikes, respectively, (Table 7)

For grain yield per row, data in **Table (8)** showed that the means of the genotypes ranged from 111.35 of line 13 to 264.56 gm. for line 1 with average 172.30 gm. Six lines no. 1, 2, 13, 35, 37 and 38 recorded high grain yield by 264.56, 211.72, 179.72, 206.00, 176.00 and 190.83 gm. Grain yield per row for these six lines showed significant increase compared to the high-yielding parent Giza 164 by 69.28, 35.46, 15.00, 31.81, 12.62 and 22.11%, respectively. The four lines no. 1, 2, 35 and 38 recorded the highest 100 grain weight by 6.95, 6.73, 6.39 and 6.03 gm., respectively compared to the highest parent Sids 4 (5.34 gm.).

Genotypic and phenotypic correlation coefficients among the studied traits over three environments are presented in Table (9). Days to 50% heading showed insignificant or significant negative genotypic and phenotypic correlations with the other studied traits. Plant height and spike length showed insignificant positive or negative genotypic and phenotypic correlations with the other studied traits. Biological yield showed high significant positive genotypic and phenotypic correlations with grain yield per row, number of spikes per row and 100 grain weight. Significant ($p < 0.05$ or 0.01) positive genotypic and phenotypic correlations were found among grain yield per row, number of spikes per row and 100 grain weight. These results were in harmony with those reported by Ali *et al.* (2024) and Kumar *et al.* (2024).

On the other hand, path analysis was used to divide the genotypic or phenotypic correlation into direct and indirect effects. Therefore, based on genotypic level, the highest direct effect on the grain yield/row was the biological yield per row (1.953), followed by the no. of spikes/row (0.363) and the plant height (0.130) (Table 10). While, based on phenotypic level, the highest direct effect on the grain yield/ row was 'the biological yield per row (1.027), followed by days to heading and 100 grain weight (0.076) then plant height (0.063). Similar results were obtained by Fouad (2018).

The results of path coefficient analysis (Table 10 and Fig. 1) exhibited high positive direct effect of (the biological yield per row and number of spikes per row) and (the biological yield per row and 100 grain weight) on the grain yield per row on genotypic and phenotypic levels, respectively. These results were in agreement with Ali *et al.* (2024). Moreover, its indirect effects were negative via other intervening traits such as the days to heading, plant height, spike length, number of spikes per row and the 100-grain weight by (0.055 and -0.052), (-0.001 and 0.001), (0.001 and 0.001), (0.323 and -0.127) and (-1.343 and 0.064) on genotypic and phenotypic levels, respectively, (Table 9). Similar results reported by Choudhary *et al.* (2025).

The genotypic and phenotypic path analysis exhibited the residual effect of 0.158 and 0.383, indicating that 84.20 and 61.73%, respectively of the variability in grain yield per row was contributed by traits included in path analysis study and the remaining 15.8 and 38.30 % was the contribution of other traits which were not included in the path analysis. Similar results obtained by Chumamo (2025).

Molecular evaluation

To evaluate the genetic diversity among twelve bread wheat (*Triticum aestivum* L.) genotypes, ten Start Codon Targeted (SCoT) primers were employed, generating a range of amplified DNA fragments with sizes varying between 340 and 2940 base pairs (bp) as shown in

Table (11) and Fig. (2). The total number of bands generated across all primers was 67, of which 59 were polymorphic, 10 were unique, and only 8 were monomorphic. These results confirm the high efficiency of the SCoT marker system in revealing genetic variability, with an average polymorphism percentage of $89.12\% \pm 3.65$, indicating substantial genomic differences among the genotypes tested. High levels of polymorphism observed in this study are consistent with earlier reports that have demonstrated the effectiveness of SCoT markers in evaluating genetic diversity in wheat and other crop species (Hamidi *et al.* 2014; Abouseada *et al.* 2023 and Altaf *et al.* 2024).

Among the primers, SCoT-4 (512–2750 bp) exhibited the highest genetic informativeness, producing 13 bands in total 1 monomorphic, 4 unique, and 8 polymorphic, yielding a polymorphism percentage of 92.3% (Table 11). This suggests that SCoT-4 is highly effective in detecting both common and genotype-specific loci. SCoT-3 (525–1490 bp). Also demonstrated high discriminative power, generating 10 bands, with 1 monomorphic, 1 unique, and 8 polymorphic bands, resulting in a polymorphism level of 90%. The presence of unique bands in these primers may indicate rare alleles or potential markers linked to agronomical important traits (Shaban *et al.*, 2022).

Three primers SCoT-2 (578–1745 bp), SCoT-5 (340–1200 bp), and SCoT-9

(2500–2940 bp) achieved 100% polymorphism, despite producing fewer bands (5, 4, and 3, respectively), and had no monomorphic or unique bands. The complete absence of monomorphic bands in these primers underscores their effectiveness in revealing genetic differences among the genotypes, even if they cover a narrower fragment size range. Similar findings were reported by Yalinkilic *et al.* (2024), where certain SCoT primers revealed high informativeness despite producing fewer bands.

Another primer worth noting is SCoT-10 (1200–2670 bp), which, although generating only 5 bands, contributed 3 unique bands, indicating its potential for identifying rare or genotype-specific alleles. This primer also recorded 100% polymorphism, reinforcing its utility in genotype discrimination and diversity studies.

In contrast, SCoT-1 (393–707 bp) exhibited the lowest polymorphism percentage (71.4%), producing 7 bands, of which 2 were monomorphic and 5 polymorphic, with no unique bands. This suggests that SCoT-1 targets more conserved genomic regions, limiting its ability to detect variability. Similarly, SCoT-6 and SCoT-7 also showed relatively low polymorphism percentages (75% each), possibly due to higher proportions of monomorphic bands (1 and 2, respectively).

The overall mean number of monomorphic bands per primer was $0.8 \pm$

0.25, unique bands 1.0 ± 0.47 , and polymorphic bands 4.9 ± 0.67 , while the total mean number of bands per primer was 6.7 ± 0.99 . These averages indicate a consistent amplification pattern across the primers, with high reproducibility and diversity detection. Similar values have been observed in other studies assessing genetic diversity in wheat using SCoT and ISSR markers (Fouad *et al.*, 2024a and Abouseada *et al.*, 2023).

Collectively, these findings confirm the efficacy of SCoT markers as a robust molecular tool for genetic diversity studies in wheat. The high level of polymorphism, presence of unique alleles, and the diversity of banding patterns observed across primers suggest that this marker system can provide valuable information for wheat germplasm characterization, conservation, and molecular breeding programs aimed at crop improvement under diverse environmental conditions (Ray *et al.*, 2012 and Shaygan *et al.*, 2021).

Dice's similarity coefficients among the twelve bread wheat genotypes revealed varying degrees of genetic relatedness. According to data in Table (12), Line 1 showed the highest similarity with line 13 (0.844), followed by line 2 (0.825), while its lowest similarity was observed with line 38 (0.507). Line 2 was most similar to line 1 (0.825), and closely related to lines 13 (0.814), 23 (0.810), and 21 (0.805). Line 13 showed a high similarity with line 21 (0.907), and also had relatively high coefficients with line

23 (0.831) and 1 (0.844). Line 21 displayed a strong relationship with line 13 (0.907), followed by line 23 (0.889) and 27 (0.854).

Line 23 exhibited high similarity with line 21 and 2 (both 0.889), as well as line 13 (0.831). Line 27 was most similar to line 23 (0.889), followed by line 21 (0.854) and line 37 (0.795). Line 32 shared moderate similarity with line 35 (0.829), Sids 4 (0.761), and line 27 (0.827). Line 35 was most similar to line 32 (0.829), followed by line 37 (0.824) and Sids 4 (0.761). Line 37 showed strong similarity with line 35 (0.824), line 27 (0.795), and line 23 (0.784). Line 38 had its highest similarity with Sids 4 (0.841), then with Giza 164 (0.767) and line 37 (0.727), although it was generally less similar to the other genotypes. Sids 4 showed the greatest similarity with Giza 164 (0.842), followed closely by line 38 (0.841) and lines 32 and 35 (both 0.761). Finally, Giza 164 had the highest similarity with Sids 4 (0.842), then line 23 (0.741), line 27 (0.700), and line 35 (0.747).

Cluster analysis based upon start codon targeted (SCoT) markers (Fig. 3) was performed on twelve bread wheat genotypes and showed distinct relationships for the genotypes, establishing two primary clusters based upon degree of similarity. The first cluster contained Lines 1, 2, 13, 21, 23, and 27 indicating that these genotypes are genetically closely related to each other. Within this first cluster, Lines 1 and 2

exhibited high genetic similarity. In addition, Lines 23 and 27 comprise a closely related sub-cluster also suggesting that they share similar genetic backgrounds or descent. Cluster two comprised Lines 32, 35, 37, and 38 and included commercial cultivars Sids 4 and Giza 164 representing moderate to high levels of genetic similarity. Lines 35 and 37 were also highly associated with each other, whereas commercial cultivar Sids 4 clustered with commercial cultivar Giza 164, which confirmed the genetic relationship between the two. The cluster patterns obtained from the clustered analysis are consistent with the phenotypic measurements observed through the agronomic traits measured for the twelve lines therefore providing evidence for the reliability of SCoT markers in differentiating between wheat genotypes. Collectively, the dendrogram indicates substantial sources of genetic diversity among the twelve genotypes evaluated and demonstrates distinct groups that could be utilized for enhancing the genetic bases and developing yield-enhancing traits through breeding programs for wheat.

Overall, the dendrogram reveals clear genetic groupings among the wheat genotypes, supporting the results of the similarity matrix. These groupings suggest potential shared ancestry or similar evolutionary paths, which could be valuable for breeding and conservation programs. In conclusion, both agronomic evaluation and efficient utilization of SCoT markers, genetic distance and

phenotypic variation are expected to be of substantial benefit in improving wheat.

SUMMARY

Analysis of variance (ANOVA) indicated that all of the traits evaluated showed significant ($P \leq 0.05$ and 0.01) differences in the different environments, genotypes, and the interaction of genotype $\times$ environment; consequently, there was considerable variability in the genetic make-up and differential response to environmental conditions of the activities of these twelve genotypic types of bread wheat grown. For the third environment tested, the heading date was the earliest; however, in the first and second environments, these two locations showed a superior performance in plant height, biological yield, grain yield, spike length, number of spikes/row, and 100 grain weight than the third location. Six genotypes, specifically lines (1, 2, 13, 35, 37, and 38), yielded higher grain yield than Giza 164, the commercial standard variety; thus demonstrating the potential to improve the overall genetic quality of the wheat crop. The use of 10 SCoT primers to carry out molecular analysis produced 67 Amplifications with 89.12% Polymorphism, demonstrating to be very efficient markers for the genetic difference. The genetic distance values corresponded with a high correlation with a high degree of phenotypic variation. In conclusion, both agronomic evaluation and efficient utilization of SCoT markers, genetic distance, and phenotypic variation

are expected to be of substantial benefit in improving wheat.

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Table (1). Name and pedigree of the two Egyptian bread wheat cultivars.

Name	Pedigree
L1, L2, L13, L21, L23, L27, L32, L35, L37 and L38	Sids 4/ Giza 164
Sids 4 Giza 164	Maya (S) /Man (S) //CMH 74A-592/3/Giza 157*2 Kvz / Buha “ S ” // kal / Bb.

Table (2). Layout of the three environments used in this study.

Environment	E1	E2	E3
Season	2021/2022	2022/2023	2023/2024
Location	Assiut	Minia	Minia

Table (3). Means of maximum, minimum air temperature (°C) and relative humidity (%) during the three environments.

Weather Month	Max. Temp.			Min. Temp.			Humidity%		
	E1	E2	E3	E1	E2	E3	E1	E2	E3
November	29	35	34	10	9	10	53	52	53
December	28	28	24	6	8	2	59	61	57
January	30	26	22	6	5	2	s	54	60
Febreuary	30	28	27	4	4	5	53	48	53
March	37	34	34	8	9	5	35	39	42
April	39	41	42	8	12	9	27	35	33
May	40	43	44	14	15	17	27	27	31

*The data were scored from the website: <http://www.timeanddate.com/weather>, E1, E2 and E3 refers to the different cultivation environments.

Table (4). Base sequences of used ten SCoT primers.

No.	Primers Name	Sequence (5'-3')
1	SCoT-1	5' -CAACAATGGCTACCACCA-3'
2	SCoT-2	5' -CAACAATGGCTACCACCC-3'
3	SCoT-3	5' -CAACAATGGCTACCACCG-3'
4	SCoT-4	5' -CAACAATGGCTACCACCT-3'
5	SCoT-5	5' -CAACAATGGCTACCACGA-3'
6	ScoT-6	5' -ACGACATGGCGACCATCG-3'
7	ScoT-7	5' -AACCATGGCTACCACCAC-3'
8	ScoT-8	5' -CACCATGGCTACCACCAT-3'
9	ScoT-9	5' -ACCATGGCTACCACCGTC-3'
10	ScoT-10	5' -ACCATGGCTACCACCGTG-3'

Table (5). The form of analysis of variance and mean square expectations.

S.O.V.	d.f.	Mean square expectations
Replication	r-1	
Environments	e -1	
Replication x Environment	e (r-1)	
Genotypes	g-1	$\sigma^2 e + r \sigma^2 ge + re \sigma^2 g$
Genotypes x Environments	(g-1) (e-1)	$\sigma^2 e + r \sigma^2 ge$
Error	e (r-1) (g-1)	$\sigma^2 e$

Table (6). Mean squares of the studied traits for the genotypes under the three environments.

S.O.V.	d.f.	DH	PH	SL	BY/Row	NS/Row	GY/Row	100G W
Rep.	2	7.95	411.84	0.18	1393.00	80.30	544.00	0.01
Environments	2	92.90**	5733.51* *	14.10*	2808.00	327.58	8227.70**	0.60
Rep x Envi.	4	2.11	66.68	1.03	1311.00	53.40	159.80	0.60
Genotypes	11	375.59* *	184.21**	21.64* *	122905.00* *	3270.62* *	14673.50* *	3.65**
Genot. X Envi.	22	3.91*	57.41**	3.98**	15458.00**	621.34**	2129.70**	0.89**
Error	66	1.88	10.20	0.76	1064.00	38.08	153.20	0.15

*, **significance at 5% and 1% probability of levels.

Table (7). Mean performance of the genotypes for days to heading, plant height and spike length under the three environments.

Trait	DH				PH; cm				SL; cm				BY/Row; gm				NS/Row			
Genot.\Envi.	E1	E2	E3	Average	E1	E2	E3	Average	E1	E2	E3	Average	E1	E2	E3	Average	E1	E2	E3	Average
1	72.00	70.67	71.33	71.33	107.33	83.67	94.67	95.22	10.00	15.33	12.00	12.44	685.00	798.33	845.67	776.33	116.67	115.00	94.33	108.67
2	72.67	71.00	71.67	71.78	112.00	88.67	93.33	98.00	11.67	14.67	12.33	12.89	678.33	645.33	598.67	640.78	115.00	114.33	93.33	107.56
13	89.33	85.33	82.00	85.56	116.33	98.67	102.00	105.67	11.67	12.67	12.67	12.33	306.67	306.50	353.33	322.17	39.67	47.83	49.33	45.61
21	79.00	77.67	76.67	77.78	105.00	87.00	95.67	95.89	10.67	12.33	12.33	11.78	520.00	514.17	490.00	508.06	88.00	85.33	85.17	86.17
23	86.33	85.00	83.33	84.89	110.00	88.33	96.00	98.11	16.33	16.00	15.00	15.78	480.00	469.00	509.67	486.22	63.33	83.67	72.33	73.11
27	88.00	85.33	83.33	85.56	115.00	94.00	97.67	102.22	13.67	14.67	14.00	14.11	400.00	439.00	481.67	440.22	61.67	51.17	59.00	57.28
32	88.33	84.67	82.00	85.00	108.33	84.67	90.33	94.44	15.00	14.00	14.33	14.44	336.67	349.50	441.67	375.94	45.00	50.83	54.67	50.17
35	73.67	72.00	73.00	72.89	113.33	82.00	84.33	93.22	10.33	12.33	11.83	11.50	650.00	589.00	539.33	592.78	113.33	107.00	91.83	104.06
37	82.67	81.00	81.33	81.67	115.00	99.00	101.67	105.22	14.33	12.67	12.67	13.22	520.00	480.67	506.67	502.44	67.67	85.17	78.67	77.17
38	73.67	72.00	71.00	72.22	116.67	86.33	89.67	97.56	12.67	13.33	12.33	12.78	590.00	586.67	577.67	584.78	89.00	92.50	85.67	89.06
Sids 4	75.67	72.00	72.33	73.33	108.33	87.00	89.33	94.89	10.67	13.67	15.00	13.11	420.00	373.33	389.33	394.22	85.00	72.33	89.00	82.11
Giza 164	89.33	87.00	85.33	87.22	116.67	79.00	79.33	91.67	9.33	9.67	10.00	9.67	470.00	430.33	457.33	452.56	95.33	93.50	75.33	88.06
Average	80.89	78.64	77.78	79.10	112.00	88.19	92.83	97.68	12.19	13.44	12.88	12.84	504.72	498.49	515.92	499.64	81.64	83.22	77.39	80.75
RLSD5%	2.14	1.79	2.30	1.31	6.39	2.44	6.46	3.16	1.20	1.55	1.43	0.86	25.56	55.98	54.99	31.21	6.46	7.93	13.49	5.91
RLSD e 5%	0.92				2.15				0.59				21.91				4.15			
RLSDg.e5%	3.16				5.45				1.49				50.87				9.62			

***DH:** Days to 50% heading, **PH:** Plant height; **SL.:** Spike length; **BY/Row:** Biological yield per row; **NS/Row:** Number spikes per row; **cm** : centimeter; **gm:** gram;
E1, E2 and E3 : the three ifferent environments

Table (8). Mean performance of the genotypes for grain yield per row and 100 grain weight under the three environments.

Trait	GY/Row; gm				100GW; gm			
Genot.\Envi.	E1	E2	E3	Average	E1	E2	E3	Average
1	222.67	226.67	206.00	218.44	5.60	6.69	6.27	6.19
2	245.33	190.17	209.33	214.94	4.60	7.19	6.76	6.19
13	185.95	156.67	184.67	175.76	6.21	5.48	5.27	5.65
21	195.67	97.33	139.33	144.11	6.04	5.36	5.64	5.68
23	183.00	142.33	163.67	163.00	6.25	6.04	6.01	6.10
27	120.33	160.50	160.00	146.94	6.55	7.43	6.85	6.95
32	120.00	115.97	116.72	117.56	5.39	5.18	5.31	5.29
35	220.00	167.83	182.67	190.17	5.07	4.31	4.69	4.69
37	196.00	150.67	175.67	174.11	5.24	4.92	5.10	5.09
38	235.67	189.33	321.67	248.89	4.28	5.50	5.47	5.08
Sids 4	115.00	104.00	133.33	117.44	5.38	5.36	5.27	5.34
Giza 164	151.00	157.83	160.00	156.28	5.07	5.22	5.17	5.16
Average	182.55	154.94	179.42	172.30	5.47	5.72	5.65	5.62
RLSD5%	9.04	17.66	26.84	11.84	0.87	0.45	0.56	0.38
RLSD e 5%		8.31				0.26		
RLSD g.e 5%		19.30				0.66		

*GY/Row: grain yield per row; 100 GW: weight of 100 grain.

Table (9). Genotypic (above diagonal) and phenotypic correlation coefficients (below diagonal) among the studied traits over three environments.

rp\rg	DH	PH	SL	BY/Row	NS/Row	100GW	GY/Row
DH	-	-0.164	-0.129	-0.729**	-0.799**	-0.849**	-0.642*
PH	-0.085	-	0.428	-0.008	-0.050	0.076	-0.008
SL	-0.085	0.193	-	-0.045	-0.087	-0.050	-0.016
BY/Row	-0.684*	0.008	-0.011	-	0.890**	0.980**	0.988**
NS/Row	-0.729**	-0.019	-0.082	0.768**	-	0.942**	0.866**
100GW	-0.751**	0.031	0.018	0.836**	0.775**	-	0.961**
GY/Row	-0.564	0.061	-0.038	0.913**	0.630*	0.751**	-

*, **significance at 5% and 1% probability of levels.

Table (10). Direct effects (diagonal) and indirect effects of the studied traits on grain yield / row over three environments on genotypic and phenotypic level.

Traits	Genotypic level.							Phenotypic level						
	DH	PH	SL	BY/Row	NS/Row	100GW	rg	DH	PH	SL	BY/Row	NS/Row	100GW	rp
DH	-0.075	-0.021	0.004	-1.423	-0.290	1.164	-0.642	0.076	-0.005	0.004	-0.702	0.121	-0.057	-0.564
PH	0.012	0.130	-0.013	-0.016	-0.018	-0.104	-0.008	-0.006	0.063	-0.009	0.008	0.003	0.002	0.061
SL	0.012	0.056	-0.030	-0.088	-0.031	0.068	-0.013	-0.006	0.012	-0.047	-0.011	0.014	0.001	-0.038
BY/Row	0.055	-0.001	0.001	1.953	0.323	-1.343	0.988	-0.052	0.001	0.001	1.027	-0.127	0.064	0.913
NS/Row	0.060	-0.006	0.003	1.739	0.363	-1.292	0.866	-0.055	-0.001	0.004	0.789	-0.166	0.059	0.630
100GW	0.064	0.010	0.001	1.914	0.342	-1.370	0.961	-0.057	0.002	-0.001	0.859	-0.128	0.076	0.751
Residual	0.158							0.383						

Table (11): Analysis of monomorphic, polymorphic, and unique bands using ten scot primers in twelve bread wheat lines used in this study.

Primers	Fragment size (bp)	Monomorphic bands	Polymorphic bands			Total number of bands	Polymorphism (%)
			Unique bands	Polymorphic without Unique	Polymorphic with Unique		
SCoT-1	393-707	2	0	5	5	7	71.4
SCoT-2	578-1745	0	0	5	5	5	100
SCoT-3	525-1490	1	1	8	9	10	90
SCoT-4	512-2750	1	4	8	12	13	92.3
SCoT-5	340-1200	0	0	4	4	4	100
SCoT-6	520-1324	1	0	3	3	4	75
SCoT-7	462-2839	2	2	4	6	8	75
SCoT-8	465-1135	1	0	7	7	8	87.5
SCoT-9	2500-2940	0	0	3	3	3	100
SCoT-10	1200-2670	0	3	2	5	5	100
Total		8	10	49	59	10	89.12± 3.65
Mean ± SE		0.8±0.25	1±0.47	4.9±0.67	5.9±0.89	6.7±0.99	

Table (12). Dice's similarity coefficient matrix (1945) among twelve bread wheat genotypes based on polymorphic band patterns generated by SCoT (Start Codon Targeted) primers.

Lines	1	2	13	21	23	27	32	35	37	38	S4	G164
1	-											
2	.825	-										
13	.844	.814	-									
21	.791	.805	.907	-								
23	.771	.810	.831	.889	-							
27	.732	.744	.773	.854	.889	-						
32	.623	.685	.699	.786	.789	.827	-					
35	.571	.603	.627	.714	.789	.773	.829	-				
37	.667	.648	.667	.707	.784	.795	.735	.824	-			
38	.507	.535	.593	.683	.676	.685	.676	.706	.727	-		
Sids4	.538	.622	.643	.706	.701	.684	.761	.761	.696	.841	-	
G164	.537	.590	.636	.719	.741	.700	.720	.747		.767	.842	-

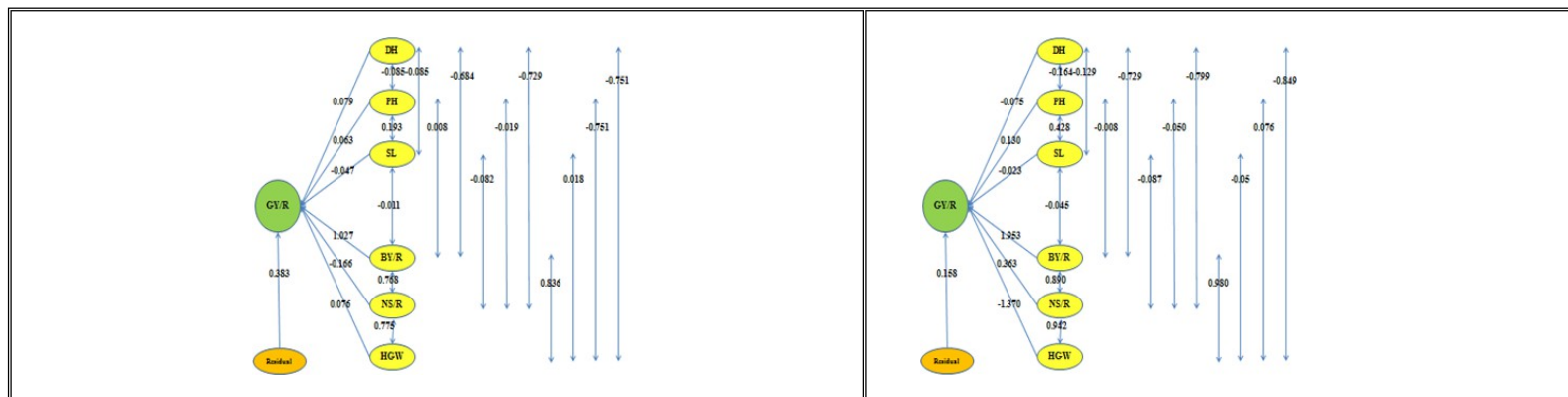


Fig. (1). Path coefficient diagram of the grain yield per row indicating direct effects (single headed arrows) and correlation (double headed arrows) under on genotypic level (left) and phenotypic level (right). Where: GY/R: grain yield/row, PH: Plant height, SL: Spike length, BY/R: Biological yield/row, NS/R: Number of spikes/row, HGW:100 grain weight and Residual: Residual effect.

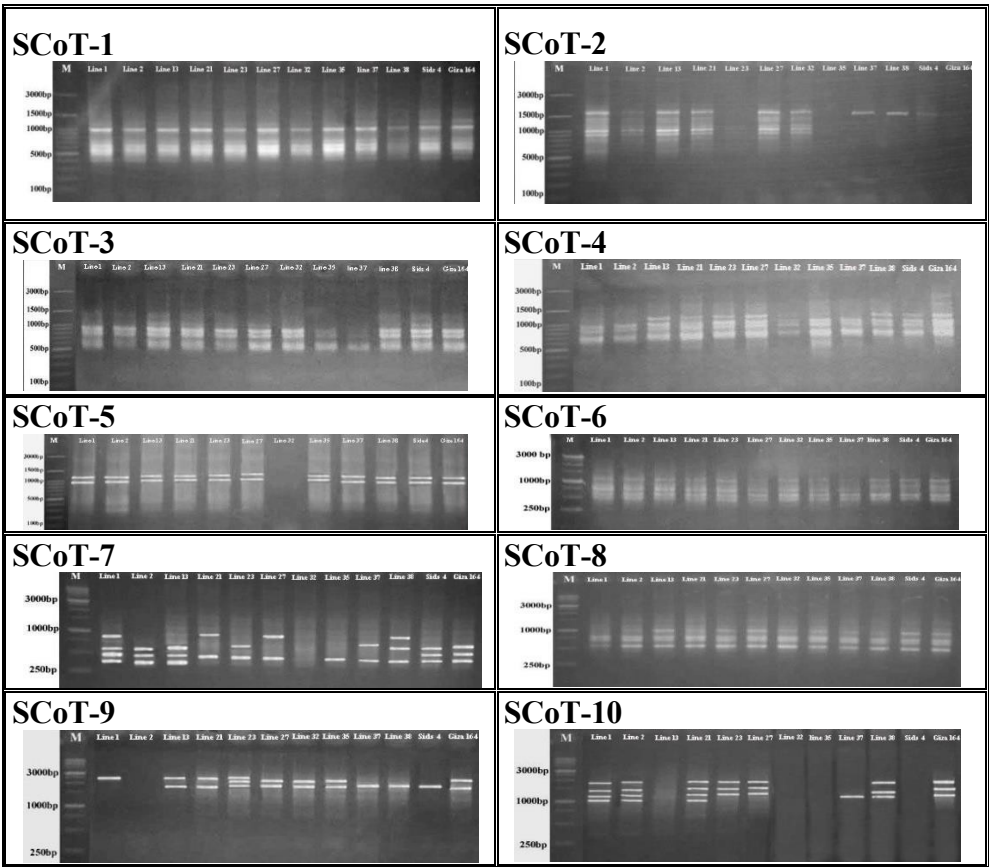


Fig. (2). Electrophoretic gel profiles of SCoT amplification products generated by ten primers (SCoT1–SCoT10) across twelve Egyptian bread wheat genotypes.

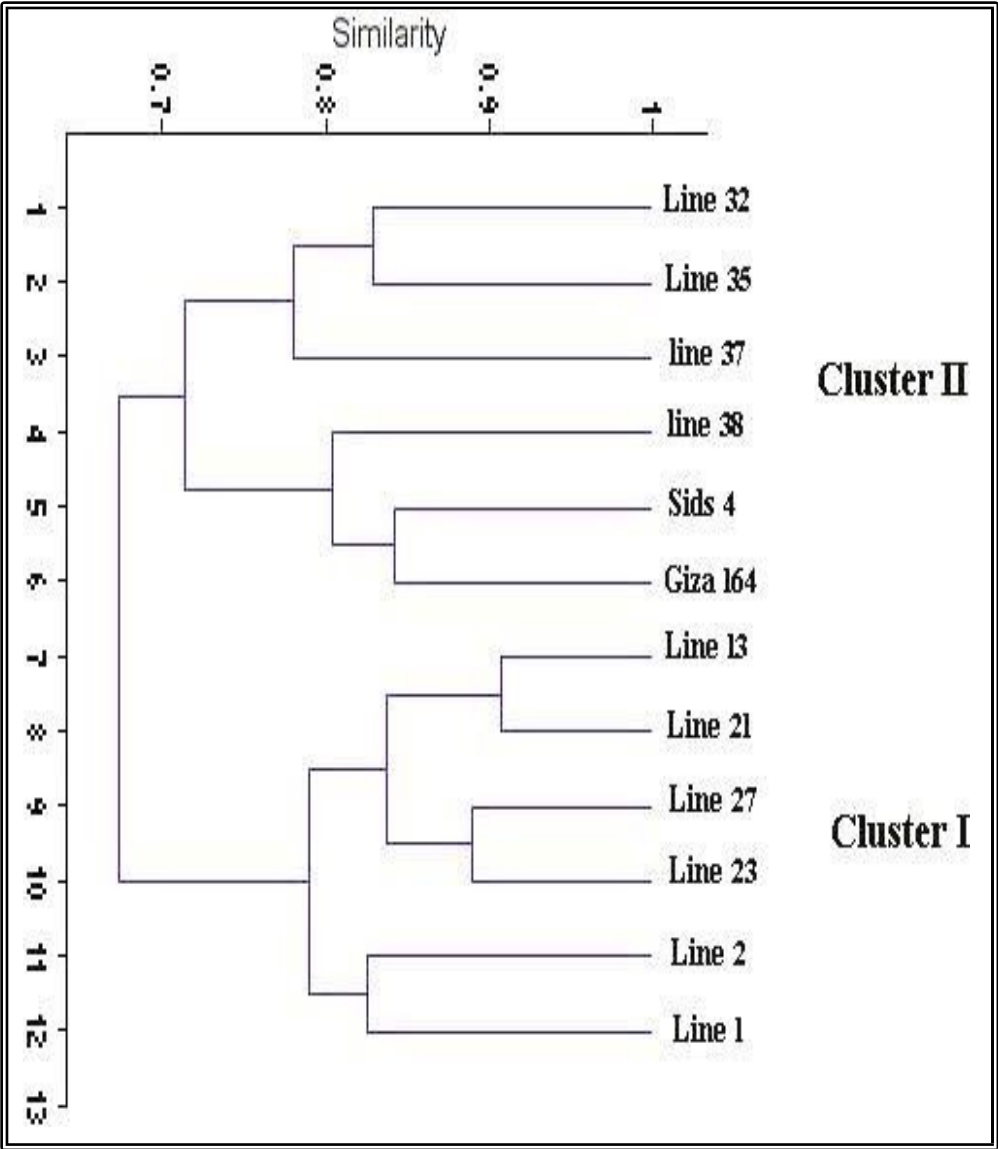


Fig. (3). Dendrogram illustrating the genetic relationships among twelve bread wheat genotypes based on SCoT (Start Codon Targeted) marker analysis.