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Line by Tester Analysis for Estimates Combining Ability in Bread Wheat Under Different Levels of Nitrogen Fertilizer

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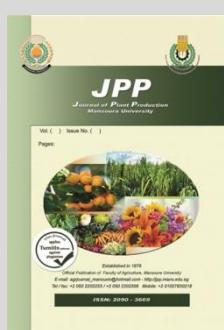
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Cross Mark



ABSTRACT

Ten genotypes of bread wheat were crossed in a line x tester mating design. The twenty-one F_1 's and their parents (seven lines and three testers) were estimated under three levels of nitrogen fertilizer; low (25 kg N/fed), mid (50 kg N/fed) and normal (75 kg N/fed) in three experiments. Each experiments in a randomized complete block design with three replications at the Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt during 2019/2020. The results cleared that nitrogen fertilizer levels mean squares were significant for all studied traits. A significant difference was found among lines, testers, line x testers and their interaction with nitrogen levels for all studied traits. Analysis of genetic revealed that GCA and SCA variances were significant for all studied traits under different levels of nitrogen fertilizer, indicating the importance of both additive and non-additive components in the inheritance of these traits. However, the hybrids L1 x T1, L2 x T1, L2 x T3, L3 x T2, L4 x T2, L5 x T2, L6 x T2, L7 x T1 and L7 x T3 were excellent harmonious combiners for specific combining ability effects for grain yield per plant and most of its components under different nitrogen fertilizer levels. The parental lines 1, 4, 6 and 7 proved to have better general combiners for grain yield per plant and most of its components under different levels of nitrogen. Therefore, these genotypes must be taken care of when breeding to tolerate low levels of nitrogen fertilization.

Keywords: Wheat, Nitrogen fertilizer levels, Line x tester analysis, General and Specific combining ability.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop in world and Egypt. The area of wheat cultivated in Egypt amounted to about 3.16 million fedden during the 2018/2019 season, it produced 9.30 million tons of grains, with an average of 2.94 tons/ fed (19.6 ard/fed) (FAO, 2019). Wheat crop is known to have high nitrogen requirement, and the applied nitrogen fertilization level significantly affect the grain yield produced. In Egypt, the optimum nitrogen fertilization level for wheat crop differs widely depending on characteristics and soils fertility level. Selection of different wheat genotype under environmental stress conditions is one of the main tasks of crop breeders for exploiting the genetic variations to improve the stress-tolerant wheat cultivars (Gebrel *et al.*, 2014; Khan and Mohammad, 2016; Al-Naggar *et al.*, 2017). Information of general and specific combining abilities influencing yield and its components has become increasingly important for plant breeders to select appropriate parents while developing hybrids (Rasheda *et al.*, 2014). Line x tester analysis is one of the most important tools for predicting the general combining ability (GSA) of parental lines and choosing the appropriate parents and their subsequent F_1 hybrids with high specific combining ability (SCA) (Abd-El-Nour *et al.*, 2011; El-Gammaal and Morad 2018; Kutlu and Sirel 2019). The objective of the present study was to identify the good

general combining lines, testers and specific combining of crosses for several traits under different levels of nitrogen.

MATERIALS AND METHODS

Experimental procedures

This study was carried out at the Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt during successive seasons 2018/2019 and 2019/2020. In the first season (2018-19), seven parental lines (female) and three parental testers (male) were intercrossed (by hand emasculation and pollination techniques) to produce twenty-one F_1 crosses. The name and pedigree of these genotypes are presented in Table 1.

In the second season (2019-2020), twenty-one hybrids and their parents (seven lines and three testers) were sown in 20th November under three different levels of nitrogen fertilizer. Nitrogen as ammonium nitrogen (33.5% N) was applied at three levels; low (25 kg N/fed) (L), mid (50 kg N/fed) (M) and normal (75 kg N/fed) (N) in two doses 1/3 during sowing and 2/3 at tillering stage. Each experiment was laid in a randomized complete blocks design with three replications in rows with 3m long and 20 cm between rows and 10 cm between plants within rows. Soil characterization of the experimental site during 2019/2020 season are listed in Table 2.

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Table 1. Name and pedigree of the parental wheat genotypes used in the study.

Genotypes	code	pedigree
Lines		
Line 1	L1	KITAI/WBLL1 CGM230099Y-099M-18WGY-0B-0GM
Line 2	L2	QAF2AH-18.CMSS93YOO6215-4AP-1AP-3AP-O.APS-OAP
Line 3	L3	SOLEO7/ QUM8Y, 123B-TOPY- 6GY-0BGY
Sakha 94	L4	OPATA/RAYON//KAUZ.CMBW90Y3180-0TOM-3Y-010M-010Y-10M-015Y-0Y-0AP-0S.
Misr 3	L5	CGSS 05 BOO123T-099T-0PY-099M-099NJ-6WGY-0B-0BGY-0GZ.
Sids 12	L6	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX. SD7096-4SD-1SD-1SD-0SD.
Shandawee 1	L7	SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC. CMSS93B00567S-72Y-010M-010Y-010M-0HTY-0SH.
Testers		
Giza 171	T1	Sakha 93/ Gemmeiza 9 Gz 2003-101-1Gz- 4Gz-1Gz-2Gz-0Gz
Misr 1	T2	OASIS/SKAUZ//4*BCN/3/2*PASTOR.
Gemmeiza 10	T3	CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y--0EGY

Table 2. Soil status at the experimental farm of Faculty of Agriculture, Menoufia University at Shebin El-Kom season 2019/2020.

Characteristics	Analysis	
	Chemical analysis	Mechanical analysis
EC ds/m	3.0	
pH	8.3	
N ppm	266	
P ppm	8.64	
K ppm	35.75	
		Mechanical analysis
Find sand%	59.7	
Silt %	10.2	
Clay %	29.33	
Soil texture	Clay	

Measurements

Ten competitive plants were taken randomly for the parental genotypes and their F₁'s from each plot for recording observations on different traits i.e. plant height (cm), number of spikes per plant, spike length (cm), grain yield per spike (g), 1000-grain weight (g) and grain yield per plant (g).

Table 3. Mean squares for all traits at line x tester crosses under low nitrogen (L), mid nitrogen (M), normal nitrogen (N) and their combined analysis.

S.O.V	d.f			Plant height (cm)			No. of spikes per plant			
	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
N		2				2544.34**				837.37**
Rep / N	2	6	5.59*	2.85	5.47*	4.63**	0.34	0.23	0.66*	0.41**
Genotypes	30	30	79.71**	91.47**	78.72**	231.22**	4.14**	5.62**	9.82**	15.35**
parents	9	9	93.66**	94.34**	79.73**	232.60**	6.24**	8.29**	20.20**	25.54**
Crosses	20	20	73.52**	92.51**	76.96**	231.08**	3.40**	4.30**	5.58**	11.49**
P vs C	1	1	78.00**	44.93**	104.96**	221.53**	0.00	7.87**	1.30**	0.87*
Lines	6	6	161.11**	210.49**	149.96**	506.88**	3.06**	4.13**	2.28**	8.23**
Testers	2	2	193.79**	206.38**	235.78**	627.52**	4.45**	9.31**	6.30**	18.84**
Line X Tester	12	12	9.67**	14.54**	13.98**	27.11**	3.40**	3.56**	7.11**	11.89**
Genotype x N		60				9.34**				2.11**
Crosses X N		40				5.95**				0.90**
Lines X N		12				7.34**				0.62**
Testers X N		4				4.22*				0.61**
Line X Tester X N		24				5.54**				1.08**
Parents X N		18				17.56**				4.60**
P vs C X N		2				6.36*				8.31**
Error	60	180	1.33	1.19	1.50	1.34	0.20	0.14	0.15	0.16
σ^2 GCA			1.66	2.03	1.64	36.01	0.00	0.02	-0.04	0.11
σ^2 SCA			2.78	4.45	4.16	2.86	1.06	1.14	2.32	1.30
GCA/SCA			0.60	0.46	0.39	12.57	0.00	0.02	-0.02	0.08
σ^2 GCA x N						0.02				-0.03
σ^2 SCA x N						1.40				0.31

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

Statistical analysis

Data for each trait depicting significant difference were further analyzed for line x tester according by Kempthorne (1957). Analysis of variance of RCB was performed as outlined by Gomez and Gomez (1984).

RESULTS AND DISCUSSION**Analysis of variance**

Mean squares of line by tester analysis for all studied traits under three levels of nitrogen fertilization and their combined analysis are presented in Table 3.

Mean squares for nitrogen fertilizer levels were significant for all studied traits, indicating differences between the three levels of nitrogen with the traits. The mean squares due to genotypes and their interaction with nitrogen levels were significant for all studied traits, indicating the wide diversity between the parental material and nitrogen levels. These results are in line with these of Gebrel *et al.* (2014) and Al-Naggar *et al.* (2017).

Table 3. Cont.

S.O.V	d.f					Spike length (cm)				Grain yield per spike (g)			
	N	Comb.	L	M	N	Comb.	L	M	N	Comb.			
N	2					216.44**							16.17**
Rep / N	2	6	0.03	0.19	0.08	0.10	0.01	0.13*	0.00	0.05*			
Genotypes	30	30	12.91**	15.51**	21.01**	46.53**	0.66**	1.08**	1.30**	2.74**			
parents	9	9	12.04**	14.03**	27.78**	50.89**	0.27**	0.52**	0.54**	1.23**			
Crosses	20	20	13.30**	14.97**	15.43**	41.28**	0.35**	0.78**	1.04**	1.76**			
P vs C	1	1	13.00**	39.47**	71.59**	112.23**	10.32**	12.19**	13.42**	35.84**			
Lines	6	6	37.25**	41.60**	43.69**	116.43**	0.19**	0.28**	0.43**	0.53**			
Testers	2	2	13.71**	17.69**	19.22**	49.55**	0.52**	3.41**	3.45**	6.32**			
Line X Tester	12	12	1.25**	1.21**	0.67**	2.32**	0.40**	0.60**	0.95**	1.61**			
Genotype x N	60					1.45**							0.15**
Crosses X N	40					1.21**							0.21**
Lines X N	12					3.06**							0.18**
Testers X N	4					0.54*							0.53**
Line X Tester X N	24					0.40**							0.17**
Parents X N	18					1.48**							0.05*
P vs C X N	2					11.83**							0.10*
Error	60	180	0.14	0.21	0.16	0.17	0.02	0.03	0.02	0.02			
σ^2 GCA			0.31	0.36	0.38	5.38	0.00	0.00	0.00	0.12			
σ^2 SCA			0.37	0.33	0.17	0.24	0.13	0.19	0.31	0.18			
GCA/SCA			0.84	1.07	2.23	22.45	0.00	0.03	0.01	0.26			
σ^2 GCA x N						0.09				0.01			
σ^2 SCA x N						0.08				0.05			

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 3. Cont.

S.O.V	d.f					1000-grain weight (g)				Grain yield per plant (g)			
	N	Comb.	L	M	N	Comb.	L	M	N	Comb.			
N	2					2031.49**							6489.52**
Rep / N	2	6	0.25	2.87	1.56	1.56	1.33	4.54	0.82	2.23			
Genotypes	30	30	165.70**	181.54**	209.32**	530.88**	32.05**	96.84**	172.88**	230.36**			
parents	9	9	82.70**	69.58**	64.64**	212.98**	35.49**	84.22**	56.21**	159.08**			
Crosses	20	20	161.89**	221.62**	273.91**	627.96**	24.86**	106.51**	232.96**	271.74**			
P vs C	1	1	988.84**	387.84**	219.67**	1450.27**	144.81**	16.90**	21.29**	44.32**			
Lines	6	6	412.47**	549.52**	711.23**	1616.97**	11.86**	60.23**	145.08**	142.75**			
Testers	2	2	244.23**	417.11**	432.23**	1074.60**	29.46**	388.20**	712.79**	860.77**			
Line X Tester	12	12	22.87**	25.08**	28.85**	59.02**	30.59**	82.70**	196.93**	238.06**			
Genotype x N	60					12.84**							35.70**
Crosses X N	40					14.73**							46.29**
Lines X N	12					28.13**							37.21**
Testers X N	4					9.48*							134.84**
Line X Tester X N	24					8.90**							36.08**
Parents X N	18					1.97							8.42**
P vs C X N	2					146.08**							138.68**
Error	60	180	2.43	2.68	3.40	2.84	1.01	1.73	1.72	1.49			
σ^2 GCA			3.62	5.12	6.38	85.78	-0.14	0.62	0.94	17.58			
σ^2 SCA			6.81	7.47	8.48	6.24	9.86	26.89	65.07	26.29			
GCA/SCA			0.53	0.69	0.75	13.74	-0.01	0.02	0.01	0.67			
σ^2 GCA x N						0.66				3.33			
σ^2 SCA x N						2.02				11.53			

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

The mean square due to crosses was significant for all traits. Mean squares due to the interactions between crosses and nitrogen fertilizer levels were highly significant for all studied traits. The mean squares due to lines, testers and line x testers were highly significant for all studied traits, indicating that both lines and testers were different from one to another in top crosses. Mean squares due to the interaction between lines, testers and line x tester with nitrogen fertilizer levels were highly significant for all studied traits. These results were coincident with those obtained by Abd El-Nour *et al.* (2011); Kumar and Prasad (2017) and Ranjitha *et al.* (2018).

Mean performance

The genotype mean performance under low, mid, normal nitrogen fertilizer levels and their combined are

presented in Table 4. The results showed that the mean values at normal nitrogen level (75 kg N/ fed) was higher than those at low nitrogen level (25 kg N/ fed) and mid nitrogen level (50 kg N/ fed) for all studied traits. For plant height, the parental L5 and L6 gave the lowest values under all treatments and their combined. For number of spikes per plant, the parental L4 gave the highest value under all levels of nitrogen and their combined. For spike length, the parental L5, L6 and L7 gave the highest values under all treatments and their combined. For grain yield per spike, L4 and L6 gave the highest values under all levels of nitrogen and their combined. The parental L3 and L6 gave the highest values for 1000-grain weight under all treatments and their combined.

Table 4. Genotype mean performance at low nitrogen (L), mid nitrogen (M), normal nitrogen (N) and their combined for all studied traits.

Genotype	Plant height (cm)				No. of spikes per plant			
	L	M	N	Comb.	L	M	N	Comb.
L1	103.88	108.27	110.07	107.41	9.16	11.06	13.32	11.18
L2	102.18	108.28	110.96	107.14	6.28	9.05	10.84	8.72
L3	95.65	104.72	112.29	104.22	9.42	11.39	14.60	11.80
L4	97.66	105.80	112.50	105.32	9.26	12.88	19.63	13.92
L5	93.96	97.89	105.34	99.06	6.22	8.22	15.62	10.02
L6	92.20	93.75	96.22	94.06	6.37	7.85	10.53	8.25
L7	109.15	111.83	113.88	111.62	8.47	9.89	14.43	10.93
T1	103.71	108.76	111.57	108.01	8.80	11.10	13.14	11.01
T2	96.15	107.09	110.27	104.50	9.51	12.22	15.68	12.47
T3	93.57	100.60	107.41	100.53	6.63	9.94	13.92	10.17
L1 x T1	106.04	109.11	114.09	109.75	8.18	10.73	12.66	10.52
L1 x T2	98.87	109.44	112.06	106.79	7.64	9.88	13.61	10.38
L1 x T3	103.58	111.07	113.45	109.37	7.09	10.65	13.68	10.47
L2 x T1	106.02	109.95	114.86	110.27	6.65	9.46	11.64	9.25
L2 x T2	97.87	105.99	108.90	104.25	6.90	10.10	14.24	10.42
L2 x T3	99.43	103.58	110.87	104.63	8.05	11.02	14.72	11.26
L3 x T1	101.45	106.59	114.90	107.65	8.35	11.69	15.00	11.68
L3 x T2	96.87	99.48	103.57	99.97	7.80	9.87	12.26	9.98
L3 x T3	93.99	97.86	106.52	99.46	6.71	9.10	13.04	9.62
L4 x T1	105.73	114.51	120.57	113.60	8.28	11.58	15.15	11.67
L4 x T2	100.60	108.27	113.57	107.48	8.60	12.11	15.85	12.19
L4 x T3	102.46	108.44	112.81	107.91	7.48	10.16	12.78	10.14
L5 x T1	99.88	106.60	110.67	105.72	7.83	12.43	14.72	11.66
L5 x T2	94.38	99.46	105.56	99.80	8.97	12.80	15.35	12.37
L5 x T3	97.82	101.99	109.37	103.06	7.24	9.85	11.88	9.66
L6 x T1	99.73	105.94	111.19	105.62	9.17	12.43	15.74	12.45
L6 x T2	94.78	98.50	103.47	98.92	7.85	11.15	13.85	10.95
L6 x T3	92.94	96.24	101.83	97.00	8.33	10.79	12.80	10.64
L7 x T1	111.04	115.68	119.95	115.55	11.24	13.62	16.15	13.67
L7 x T2	108.28	112.78	116.40	112.49	6.69	10.08	12.66	9.81
L7 x T3	104.43	108.42	113.21	108.69	8.94	11.17	14.51	11.54
Average crosses	100.77	106.19	111.33	106.09	8.00	10.98	13.92	10.97
Average lines	98.81	104.70	109.05	104.19	8.01	10.36	14.17	10.85
Average testers	100.14	105.71	110.59	105.48	8.00	10.78	14.00	10.93
LSD5%	1.88	1.78	2.00	1.20	0.74	0.61	0.62	0.43
LSD1%	2.50	2.37	2.66	1.60	0.98	0.81	0.83	0.57

Table 4. Cont.

Genotype	Spike length (cm)				Grain yield/ spike (g)			
	L	M	N	Comb.	L	M	N	Comb.
L1	10.50	12.24	13.07	11.94	1.79	2.07	2.83	2.23
L2	10.94	13.01	13.67	12.54	1.55	2.05	2.58	2.06
L3	10.69	12.89	14.00	12.53	1.88	2.56	2.64	2.36
L4	12.18	13.39	14.95	13.51	2.11	2.70	3.05	2.62
L5	13.67	16.17	17.34	15.73	1.75	1.93	2.32	2.00
L6	14.71	15.52	17.65	15.96	2.17	2.56	3.16	2.63
L7	12.77	13.73	16.13	14.21	1.46	1.75	2.17	1.80
T1	16.30	18.39	21.92	18.87	2.33	2.90	3.49	2.91
T2	14.22	16.58	19.87	16.89	2.18	2.68	3.14	2.66
T3	14.98	17.51	20.16	17.55	1.59	1.84	2.44	1.96
L1 x T1	10.79	12.06	13.27	12.04	1.91	1.87	2.43	2.07
L1 x T2	11.18	11.88	12.42	11.83	1.57	1.79	1.72	1.69
L1 x T3	9.91	10.08	12.13	10.71	0.94	1.55	1.92	1.47
L2 x T1	12.04	13.20	13.61	12.95	1.50	1.64	1.75	1.63
L2 x T2	10.76	12.00	12.37	11.71	1.04	1.29	1.64	1.32
L2 x T3	9.44	10.62	12.13	10.73	0.96	1.07	1.47	1.17
L3 x T1	13.15	13.97	14.73	13.95	0.72	0.92	0.99	0.88
L3 x T2	11.89	12.18	12.39	12.15	1.60	2.59	2.89	2.36
L3 x T3	10.84	11.59	13.16	11.86	0.82	0.84	1.34	1.00
L4 x T1	14.22	15.61	17.33	15.72	0.74	0.92	1.19	0.95
L4 x T2	12.20	13.32	15.23	13.58	1.65	2.50	2.93	2.36
L4 x T3	11.25	13.13	14.58	12.98	1.10	1.23	2.46	1.60
L5 x T1	10.97	12.96	16.39	13.44	0.91	1.52	2.08	1.51
L5 x T2	10.29	11.62	14.91	12.27	1.34	2.22	2.98	2.18
L5 x T3	9.83	12.00	14.18	12.00	1.10	1.35	1.56	1.34
L6 x T1	16.17	17.81	19.04	17.67	0.90	0.99	1.49	1.13
L6 x T2	15.58	16.41	18.15	16.71	1.32	1.92	2.86	2.03
L6 x T3	16.04	17.21	17.66	16.97	0.93	0.97	1.78	1.23
L7 x T1	14.87	16.60	18.34	16.60	1.06	1.89	1.79	1.58
L7 x T2	13.01	14.57	15.87	14.48	0.91	1.58	2.00	1.50
L7 x T3	13.78	15.73	17.05	15.52	1.52	1.46	2.07	1.68
Average crosses	12.30	13.55	15.00	13.61	1.17	1.53	1.97	1.56
Average lines	13.10	14.94	16.87	14.97	1.88	2.30	2.78	2.32
Average testers	12.55	14.00	15.60	14.05	1.40	1.78	2.23	1.80
LSD5%	0.61	0.74	0.65	0.39	0.21	0.29	0.26	0.16
LSD1%	0.81	0.99	0.86	0.52	0.28	0.39	0.34	0.21

Table 4. Cont.

Genotype	1000-grain weight (g)				Grain yield/ plant (g)			
	L	M	N	Comb.	L	M	N	Comb.
L1	40.85	43.88	46.44	43.72	14.88	18.41	27.23	20.17
L2	36.00	40.48	45.67	40.72	7.85	13.80	21.16	14.27
L3	45.56	48.27	50.94	48.26	13.48	23.20	31.39	22.69
L4	41.71	46.31	48.85	45.62	16.41	26.75	33.95	25.70
L5	28.35	32.69	36.35	32.46	8.69	11.38	20.75	13.61
L6	43.48	47.55	51.47	47.50	10.24	14.30	26.25	16.93
L7	39.39	44.10	46.59	43.36	10.11	12.69	23.00	15.27
T1	46.91	49.39	53.14	49.81	15.91	21.73	29.24	22.29
T2	41.84	44.61	47.79	44.75	16.23	20.50	26.74	21.16
T3	40.56	42.32	45.65	42.84	8.95	12.78	23.77	15.17
L1 x T1	31.05	39.84	44.29	38.39	15.45	20.41	30.83	22.23
L1 x T2	25.14	29.74	31.02	28.63	12.35	17.64	23.00	17.66
L1 x T3	23.49	25.99	27.62	25.70	6.85	16.81	26.42	16.69
L2 x T1	31.45	37.05	43.73	37.41	9.77	15.57	20.52	15.29
L2 x T2	28.74	34.17	36.36	33.09	6.72	12.48	23.29	14.16
L2 x T3	27.23	35.64	41.64	34.83	8.54	11.55	21.60	13.90
L3 x T1	44.43	50.21	57.55	50.73	6.61	10.47	15.12	10.73
L3 x T2	46.65	53.80	58.54	53.00	12.67	24.47	35.52	24.22
L3 x T3	34.05	44.24	49.22	42.50	5.74	7.49	17.05	10.09
L4 x T1	46.19	52.81	58.41	52.47	6.30	10.32	18.46	11.69
L4 x T2	43.38	49.22	53.37	48.66	14.18	29.07	46.51	29.92
L4 x T3	41.03	44.72	48.58	44.78	8.44	12.17	31.43	17.35
L5 x T1	32.97	35.90	38.51	35.80	7.65	17.97	30.26	18.63
L5 x T2	25.42	28.05	30.33	27.93	12.28	27.41	46.18	28.62
L5 x T3	25.56	25.82	28.04	26.48	8.20	13.78	18.17	13.38
L6 x T1	36.25	48.04	51.92	45.40	9.73	12.18	24.02	15.31
L6 x T2	33.27	43.19	48.48	41.65	10.58	20.84	39.07	23.50
L6 x T3	34.79	38.02	44.65	39.15	8.06	11.41	22.38	13.95
L7 x T1	37.19	45.46	47.95	43.53	11.44	24.50	29.33	21.76
L7 x T2	29.12	36.93	43.84	36.63	6.90	16.89	25.12	16.30
L7 x T3	25.87	32.58	39.97	32.81	13.26	16.04	30.53	19.94
Average crosses	33.49	39.59	44.00	39.03	9.61	16.64	27.37	17.87
Average lines	40.47	43.96	47.29	43.90	12.28	17.55	26.35	18.73
Average testers	35.74	41.00	45.06	40.60	10.47	16.94	27.04	18.15
LSD5%	2.55	2.67	3.01	1.79	1.64	2.15	2.14	1.15
LSD1%	3.39	3.55	4.01	2.38	2.18	2.86	2.85	1.53

For grain yield per plant, the parental L1, L3 and L4 gave the highest value under all nitrogen levels and their combined. On the other hand, the parental T1 gave high value in spike length, grain yield per spike, 1000-grain weight and grain yield per plant, the parental T2 gave high value in number of spikes per plant and grain yield per plant, the parental T3 gave low value for plant height under all levels of nitrogen and their combined.

For plant height, four crosses (L3 x T3), (L5 x T2), (L6 x T2) and (L6 x T3) gave the lowest values under nitrogen levels and their combined. Ten crosses showed the highest number of spikes per plant under all nitrogen treatments and their combined. The crosses L6 x T1 and L6 x T3 gave the highest value for spike length under all levels of nitrogen and their combined. For grain yield per spike, the crosses (L1 x T1), (L3 x T2), (L5 x T2) and (L3 x T2 and L4 x T2) gave the highest values under low, mid, normal nitrogen and the combined data, respectively. Eight crosses gave the highest values for 1000-grain weight under all levels of nitrogen and their combined. Seven, four, nine and two crosses gave the highest values for grain yield per plant under low, mid, normal nitrogen and the combined data, respectively. These findings are in accordance with the results of Gebrel *et al.* (2014); Al-Naggar *et al.* (2017) and El-Gammaal and Morad (2018).

Combining ability

a- General combining ability effects (GCA)

General combining ability estimation for parents (line and testers) under three nitrogen levels and their combined analysis for all traits are presented in Table 5.

Inbred lines

The results cleared that three parental lines; L3, L5 and L6 were a good general combiner for shortness as they showed highly significant negative GCA, while the parental L1, L4 and L7 were a good general combiner for tallness as they showed highly significant positive GCA effects. For this trait, tall plants are preferred for straw purpose while short plants are more lodging resistance thus preference depends upon the breeding objective. For the number of spikes per plant, the parental lines; L4 showed significant GCA effects under mid, normal nitrogen and the combined analysis, L5 under mid nitrogen and the combined analysis, L6 under low, mid nitrogen and the combined analysis and L7 under all nitrogen levels and their combined. For spike length, the parental lines; L4, L6 and L7 showed highly significant GCA effects under the levels of nitrogen fertilizer and their combined. For 1000-grain weight, the parental lines; L3, L4 and L6 showed highly significant for GCA effects under all treatments and their combined.

Table 5. Estimates of general combining ability (GCA) effects for parents (lines and testers) in low nitrogen (L), mid nitrogen (M), normal nitrogen (N) and their combined for all studied traits.

Parents	Plant height (cm)				No. of spikes per plant				Spike length (cm)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
L1	2.06**	3.69**	1.87**	2.54**	-0.36*	-0.57**	-0.60	-0.51	-1.67**	-2.21**	-2.39	-2.09
L2	0.34	0.32	0.22	0.29	-0.80**	-0.79**	-0.39	-0.66	-1.55**	-1.61**	-2.29	-1.82
L3	-3.34**	-4.87**	-2.99	-3.73	-0.38*	-0.76**	-0.48	-0.54	-0.33**	-0.97**	-1.57	-0.96
L4	2.16**	4.22**	4.33**	3.57**	0.12	0.30*	0.67**	0.37**	0.26*	0.47**	0.71**	0.48**
L5	-3.41**	-3.50**	-2.79	-3.23	0.01	0.71**	0.06	0.26**	-1.93**	-1.36**	0.16	-1.04
L6	-4.95**	-5.96**	-5.83	-5.58	0.45**	0.47**	0.21	0.38**	3.63**	3.59**	3.28**	3.50**
L7	7.15**	6.11**	5.20**	6.15**	0.95**	0.64**	0.52**	0.70**	1.59**	2.08**	2.09**	1.92**
LSD 5%	0.77	0.73	0.82	0.49	0.30	0.25	0.26	0.17	0.25	0.30	0.26	0.16
LSD 1%	1.02	0.97	1.09	0.65	0.40	0.33	0.34	0.23	0.33	0.40	0.35	0.21
T1	3.50**	3.58**	3.85**	3.64**	0.53**	0.72**	0.52**	0.59**	0.88**	1.05**	1.10**	1.01**
T2	-1.96**	-1.34**	-2.25	-1.85	-0.22*	-0.13	0.06	-0.10	-0.17*	-0.41**	-0.52	-0.37
T3	-1.54**	-2.24**	-1.60	-1.79	-0.31**	-0.59**	-0.57	-0.49	-0.71**	-0.64**	-0.58	-0.65
LSD 5%	0.50	0.48	0.53	0.32	0.20	0.16	0.17	0.11	0.16	0.20	0.17	0.10
LSD 1%	0.67	0.63	0.71	0.43	0.26	0.22	0.22	0.15	0.22	0.26	0.23	0.14

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 5. Cont.

Parents	Grain yield per spike (g)				1000-grain weight (g)				Grain yield per plant (g)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
L1	0.30**	0.21**	0.05	0.19**	-6.93**	-7.73**	-9.69	-8.12	1.94**	1.65**	-0.62	0.99**
L2	0.00	-0.20**	-0.35	-0.18	-4.35**	-3.97**	-3.43	-3.92	-1.26**	-3.44**	-5.57	-3.42
L3	-0.12**	-0.08	-0.23	-0.14	8.22**	9.83**	11.10**	9.72**	-1.27**	-2.50**	-4.81	-2.86
L4	0.00	0.02	0.22**	0.08*	10.04**	9.32**	9.45**	9.61**	0.04	0.55	4.76**	1.78**
L5	-0.05	0.17**	0.24**	0.12**	-5.51**	-9.67**	-11.70	-8.96	-0.23	3.08**	4.17**	2.34**
L6	-0.12**	-0.23**	0.08	-0.09	1.28*	3.49**	4.35**	3.04**	-0.15	-1.83**	1.12*	-0.29
L7	-0.01	0.11	-0.02	0.03	-2.76**	-1.27*	-0.08	-1.37	0.93**	2.50**	0.96*	1.46**
LSD 5%	0.09	0.12	0.10	0.07	1.04	1.09	1.23	0.73	0.67	0.88	0.88	0.47
LSD 1%	0.11	0.16	0.14	0.09	1.38	1.45	1.64	0.97	0.89	1.17	1.16	0.62
T1	-0.06*	-0.14**	-0.29	-0.16	3.59**	4.60**	4.91**	4.36**	-0.04	-0.72*	-3.29	-1.35
T2	0.18**	0.45**	0.46**	0.37**	-0.39	-0.29	-0.87	-0.52	1.20**	4.62**	6.73**	4.18**
T3	-0.12**	-0.32**	-0.17	-0.20	-3.20**	-4.30**	-4.04	-3.85	-1.16**	-3.89**	-3.43	-2.83
LSD 5%	0.06	0.08	0.07	0.04	0.68	0.71	0.81	0.48	0.44	0.57	0.57	0.31
LSD 1%	0.07	0.10	0.09	0.06	0.91	0.95	1.07	0.64	0.58	0.76	0.76	0.41

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

For grain yield per spike and grain yield per plant, the parental lines; L1 showed highly significant GCA effects under low, mid nitrogen and the combined analysis, L4 under normal nitrogen and the combined analysis, L5 under all treatments except low nitrogen. The parental lines L6 showed significant GCA effects under normal nitrogen only and the parental line L7 under all nitrogen levels for grain yield per plant only.

Testers

Results in Table 5 indicated that the parental tester T1 showed highly significant GCA effects for number of spikes per plant, spike length and 1000-grain weight under all levels of nitrogen and their combined. The parental tester T2 showed negative significant GCA effects for plant height under low and mid nitrogen, while showed positive significant GCA effects for grain yield per spike and grain yield per plant. The parental tester T3 showed negative significant GCA effects for plant height under low and mid nitrogen. These results are in line with those reported by Rasheda *et al.* (2014); Kumar and Prasad (2017) and Ranjitha *et al.* (2018) and Kizilgeci (2020).

b- Specific combining ability SCA effects

Estimations of specific combining ability SCA effects for all F1 crosses under the three nitrogen levels and their combined are listed in Table 6.

For plant height, the crosses L1 x T2, L3 x T3, L6 x T3 and L7 x T3 under low nitrogen and L1 x T1, L5 x T2,

L6 x T3 and L7 x T3 under mid nitrogen showed negative significant SCA effects. For number of spikes per plant, the crosses L1 x T3 and L3 x T1 under low, normal nitrogen and the combined analysis, the cross L2 x T2 under normal nitrogen, the crosses L2 x T3, L4 x T2, L5 x T2 and L7 x T1 under all conditions and the crosses L6 x T1 and L7 x T3 under normal nitrogen and the combined analysis showed positive significant SCA effects. The crosses L1 x T2 and L6 x T3 under low, mid nitrogen and the combined analysis, the crosses L2 x T2 and L3 x T1 under combined and the crosses L4 x T1 and L7 x T3 under all conditions, showed positive significant for spike length.

For grain yield per spike, four crosses under all treatments, three crosses under normal nitrogen and the combined analysis and only one cross under low, normal nitrogen and the combined showed positive significant SAC effects. For 1000-grain yield weight, the crosses L1 x T1 and L2 x T3 under mid, normal nitrogen and combined analysis, the crosses L3 x T2 and L5 x T1 under all treatments and their combined, the cross L6 x T3 under low nitrogen and L7 x T1 under low, mid nitrogen and combined analysis showed positive significant SCA effects. For grain yield per plant, six crosses under all treatments and their combined, the cross L1 x T3 under mid and normal nitrogen, the crosses L4 x T3 and L5 x T1 under normal nitrogen, the cross L6 x T2 under normal nitrogen and combined analysis, the cross L7 x T1 under mid, normal nitrogen and combined analysis

and the cross L7 x T3 under low, normal nitrogen and combined analysis showed significant SCA effects. These results are in agreement with Gebrel *et al.* (2014); Kumar

and Prasad (2017), Ranjitha *et al.* (2018) and Kizilgeci (2020) to determine the combining abilities of wheat genotypes for yield and its components.

Table 6. Estimates of specific combining ability (SCA) effects for 21 F₁'s in low nitrogen (L), mid nitrogen (M), normal nitrogen (N) and their combined for all studied traits.

crosses	Plant height (cm)				No. of spikes per plant				Spike length (cm)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
L1 x T1	-0.29	-4.35**	-2.96	-2.53	0.01	-0.41	-1.17	-0.52	-0.71**	-0.33	-0.45	-0.50
L1 x T2	-1.99**	0.91	1.11	0.01	0.22	-0.41	0.24	0.02	0.72**	0.95**	0.34	0.67**
L1 x T3	2.28**	3.44**	1.85*	2.52**	-0.24	0.82**	0.94**	0.51**	-0.01	-0.62*	0.11	-0.17
L2 x T1	1.41*	-0.14	-0.54	0.25	-1.08**	-1.45**	-2.41	-1.65	0.42	0.21	-0.20	0.14
L2 x T2	-1.28	0.82	-0.39	-0.28	-0.08	0.04	0.65**	0.21	0.18	0.47	0.19	0.28*
L2 x T3	-0.14	-0.68	0.93	0.04	1.16**	1.41**	1.76**	1.44**	-0.60**	-0.68*	0.01	-0.42
L3 x T1	0.51	1.70**	2.72**	1.64**	0.21	0.75**	1.05**	0.67**	0.31	0.34	0.20	0.28*
L3 x T2	1.40*	-0.49	-2.51	-0.54	0.40	-0.22	-1.23	-0.35	0.10	0.01	-0.52	-0.14
L3 x T3	-1.91**	-1.21	-0.21	-1.11	-0.60*	-0.53*	0.18	-0.32	-0.41	-0.35	0.32	-0.15
L4 x T1	-0.70	0.52	1.07	0.30	-0.37	-0.43	0.04	-0.25	0.79**	0.54*	0.51*	0.61**
L4 x T2	-0.36	-0.80	0.17	-0.33	0.70**	0.96**	1.20**	0.95**	-0.19	-0.29	0.04	-0.15
L4 x T3	1.07	0.28	-1.24	0.04	-0.33	-0.53*	-1.24	-0.70	-0.59**	-0.25	-0.55	-0.47
L5 x T1	-0.98	0.34	-1.72	-0.78	-0.71**	0.01	0.22	-0.16	-0.27	-0.28	0.13	-0.14
L5 x T2	-1.02	-1.89**	-0.72	-1.21	1.18**	1.23**	1.31**	1.24**	0.09	-0.16	0.27	0.07
L5 x T3	1.99**	1.55*	2.44**	1.99**	-0.47	-1.25**	-1.53	-1.08	0.18	0.45	-0.39	0.08
L6 x T1	0.41	2.13**	1.84*	1.46**	0.19	0.25	1.09**	0.51**	-0.64**	-0.38	-0.35	-0.46
L6 x T2	0.93	-0.38	0.22	0.25	-0.38	-0.18	-0.34	-0.30	-0.19	-0.33	0.39	-0.04
L6 x T3	-1.34*	-1.75**	-2.06	-1.72	0.19	-0.07	-0.75	-0.21	0.83**	0.71**	-0.04	0.50**
L7 x T1	-0.38	-0.20	-0.43	-0.33	1.75**	1.28**	1.19**	1.41**	0.11	-0.09	0.15	0.06
L7 x T2	2.33**	1.83**	2.13**	2.09**	-2.04**	-1.42**	-1.83	-1.77	-0.71**	-0.65*	-0.69	-0.69
L7 x T3	-1.95**	-1.63*	-1.71	-1.76	0.29	0.14	0.64**	0.36*	0.61**	0.74**	0.54*	0.63**
L.S.D. (Sij) 5%	1.33	1.26	1.42	0.85	0.52	0.43	0.44	0.30	0.43	0.52	0.46	0.28
L.S.D. (Sij) 1%	1.77	1.68	1.13	1.13	0.70	0.57	0.40	0.40	0.57	0.70	0.37	0.37
L.S.D. S(jk-ki) 5%	1.09	1.03	0.69	0.69	0.43	0.35	0.25	0.25	0.35	0.43	0.22	0.22
L.S.D. S(jk-ki) 1%	0.71	0.67	0.45	0.45	0.28	0.23	0.16	0.16	0.23	0.28	0.15	0.15

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 6. Cont.

crosses	Grain yield per spike (g)				1000-grain weight (g)				Grain yield per plant (g)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
L1 x T1	0.50**	0.27*	0.70**	0.49**	0.91	3.39**	5.07**	3.12**	3.94**	2.85**	7.38**	4.72**
L1 x T2	-0.08	-0.40**	-0.76	-0.42	-1.03	-1.83	-2.42	-1.76	-0.41	-5.27**	-10.48	-5.38
L1 x T3	-0.42**	0.13	0.06	-0.07	0.13	-1.56	-2.65	-1.36	-3.54**	2.42**	3.10**	0.66
L2 x T1	0.39**	0.44**	0.42**	0.42**	-1.28	-3.16**	-1.75	-2.06	1.47*	3.09**	2.01*	2.19**
L2 x T2	-0.30**	-0.50**	-0.44	-0.41	-0.01	-1.16	-3.35	-1.51	-2.83**	-5.33**	-5.24	-4.47
L2 x T3	-0.09	0.06	0.02	-0.01	1.29	4.32**	5.10**	3.57**	1.36*	2.24**	3.23**	2.28**
L3 x T1	-0.26**	-0.39**	-0.46	-0.37	-0.87	-3.80**	-2.46	-2.38	-1.69**	-2.95**	-4.15	-2.93
L3 x T2	0.38**	0.69**	0.69**	0.58**	5.33**	4.68**	4.30**	4.77**	3.13**	5.71**	6.23**	5.02**
L3 x T3	-0.11	-0.29**	-0.23	-0.21	-4.46**	-0.87	-1.84	-2.39	-1.44*	-2.76**	-2.08	-2.09
L4 x T1	-0.36**	-0.50**	-0.71	-0.52	-0.93	-0.70	0.05	-0.53	-3.30**	-6.14**	-10.38	-6.61
L4 x T2	0.31**	0.50**	0.27**	0.36**	0.23	0.60	0.78	0.54	3.34**	7.27**	7.65**	6.09**
L4 x T3	0.06	0.00	0.44**	0.16**	0.70	0.11	-0.83	-0.01	-0.04	-1.12	2.73**	0.52
L5 x T1	-0.14	-0.04	0.17	0.00	1.40	1.38	1.31	1.36*	-1.69**	-1.02	2.02*	-0.23
L5 x T2	0.04	0.07	0.31**	0.14*	-2.18*	-1.58	-1.10	-1.62	1.70**	3.07**	7.92**	4.23**
L5 x T3	0.10	-0.03	-0.48	-0.14	0.78	0.20	-0.21	0.26	-0.01	-2.05*	-9.93	-4.00
L6 x T1	-0.09	-0.17	-0.26	-0.17	-2.11*	0.36	-1.34	-1.03	0.31	-1.90*	-1.17	-0.92
L6 x T2	0.09	0.17	0.35**	0.20**	-1.12	0.40	1.00	0.09	-0.08	1.42	3.86**	1.73**
L6 x T3	0.00	0.00	-0.10	-0.03	3.22**	-0.76	0.34	0.93	-0.23	0.49	-2.68	-0.81
L7 x T1	-0.04	0.38**	0.13	0.16**	2.88**	2.54**	-0.88	1.51*	0.95	6.08**	4.30**	3.78**
L7 x T2	-0.43**	-0.52**	-0.42	-0.46	-1.22	-1.10	0.79	-0.51	-4.84**	-6.87**	-9.93	-7.22
L7 x T3	0.47**	0.14	0.28**	0.30**	-1.66	-1.44	0.09	-1.00	3.89**	0.79	5.64**	3.44**
L.S.D. (Sij) 5%	0.15	0.21	0.18	0.11	1.80	1.89	2.13	1.27	1.16	1.52	1.52	0.81
L.S.D. (Sij) 1%	0.20	0.28	0.15	0.15	2.39	2.51	1.68	1.68	1.54	2.02	1.08	1.08
L.S.D. S(jk-ki) 5%	0.12	0.17	0.09	0.09	1.47	1.54	1.03	1.03	0.95	1.24	0.65	0.66
L.S.D. S(jk-ki) 1%	0.08	0.11	0.06	0.06	0.96	1.01	0.68	0.68	0.62	0.81	0.42	0.43

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

Genetic components:

Estimation of variance due to GCA, SCA and their interactions with nitrogen levels (Table 3) cleared that SCA effects played the major role in controlling the inheritance

of all traits under nitrogen fertilizer levels except spike length, revealing that non-additive gene effects was controlling these traits.

The ratio GCA/SCA mean square was less than unity for all traits under nitrogen levels except spike length under mid, normal nitrogen and the combined analysis, indicating that non-additive was larger in magnitude and more important than additive gene effects in controlling the inheritance of most traits under nitrogen levels. On the other hand Abd El-Aty and Hamand (2006) showed that the ratio GCA/SCA mean square was more than unity, indicating that additive was larger in magnitude and more important than non-additive gene effects in controlling the inheritance of all the studied traits under different levels of nitrogen fertilizer.

The mean square due to SCA x N was higher in magnitude than those due to GCA x N for all studied traits except spike length, suggesting that SCA is more affected by nitrogen fertilizer than GCA for most traits. Similar results were showed by Ranjitha *et al.* (2018) and Kutlu and Sirel (2019). The results of heritability in broad and narrow sense under different levels of nitrogen are showed in Table 7. Heritability values in broad sense were larger than the corresponding values of narrow sense for all traits under this investigation. Values were obtained for the average degree

of dominance (a) mean that the presence of over dominance (greater than unity) for all traits under the three levels of nitrogen but showed partial dominance for spike length in mid, normal nitrogen and the combined date. Additive variance ($\sigma^2 A$) was greater than dominance variance ($\sigma^2 D$) in plant height under low nitrogen, spike length and 1000-grain weight under all nitrogen levels. In the remaining traits a dominance variance was greater than additive variance, indicating that the importance of both additive and non-additive gene action in the inheritance of these traits under different levels of nitrogen fertilization. These results are in line with those of Al-Naggar *et al.* (2017); El-Gammaal and Morad (2018) and Kutlu and Sirel (2019). The proportional contribution of lines (females), testers (males) and their interactions (crosses) to total variance for different traits in F1 hybrid revealed that maximum contribution to total variance of most traits were made by female lines under the different levels of nitrogen. Similar results were obtained by Abd El-Nour *et al.* (2011) and El-Gammaal and Morad (2018).

Table 7. Genetic components and proportional contribution for all traits in low nitrogen (L), mid nitrogen (M), normal nitrogen (N) and their combined.

Source	Plant height (CM)				No. of spikes per plant				Spike length (cm)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
H2 (broad sense)	82.15	87.73	83.21	98.24	83.86	89.41	93.87	90.30	87.73	83.61	85.68	98.50
H2 (narrow sense)	44.74	41.87	36.68	94.49	0.02	2.95	-3.34	12.99	55.19	57.05	70.00	96.35
82 A	3.33	4.06	3.28	72.01	0.00	0.04	-0.08	0.22	0.63	0.72	0.77	10.76
82 D	2.78	4.45	4.16	2.86	1.06	1.14	2.32	1.30	0.37	0.33	0.17	0.24
Average degree of dominance (\bar{a})	1.29	1.48	1.59	0.28	84.34	7.65	7.63	3.45	1.09	0.97	0.67	0.21
Proportional contribution to the total variation												
Due to lines	65.75	68.26	58.46	65.81	27.02	28.77	12.24	21.49	84.05	83.35	84.93	84.62
Due to testers	26.36	22.31	30.64	27.16	13.09	21.64	11.29	16.40	10.32	11.81	12.45	12.00
Due to lines x testers	7.89	9.43	10.90	7.04	59.90	49.59	76.46	62.11	5.64	4.84	2.62	3.38

Table 7. Cont.

Source	Grain yield per spike (g)				1000-grain weight (g)				Grain yield per plant (g)			
	L	M	N	Comb.	L	M	N	Comb.	L	M	N	Comb.
H2 (broad sense)	88.41	86.09	92.72	94.51	85.25	86.86	86.19	98.43	90.48	94.21	97.49	97.64
H2 (narrow sense)	-1.89	4.13	1.49	54.71	43.92	50.22	51.78	94.97	-2.82	4.11	2.73	55.87
82 A	0.00	0.01	0.01	0.24	7.24	10.24	12.76	171.57	-0.30	1.24	1.88	35.16
82 D	0.13	0.19	0.31	0.18	6.81	7.47	8.48	6.24	9.86	26.99	65.07	26.29
Average degree of dominance (\bar{a})	9.79	6.30	11.06	1.21	1.37	1.21	1.15	0.27	8.11	6.60	8.33	1.22
Proportional contribution to the total variation												
Due to lines	16.08	10.57	12.44	9.10	76.44	74.39	77.90	77.25	14.32	16.97	18.68	15.76
Due to testers	15.10	43.47	33.11	35.95	15.09	18.82	15.78	17.11	11.85	36.45	30.60	31.68
Due to lines x testers	68.82	45.97	54.45	54.95	8.48	6.79	6.32	5.64	73.83	46.59	50.72	52.56

CONCLUSION

Nitrogen is the most limiting nutrient for wheat production that affects the rapid plant growth and improves grain yield. The mean values under the low level of fertilization (25 kg N/fed) were the lowest for all traits. The parental lines L3, L5 and L6 were a good combiners for shortness, line L7 for number of spikes per plant, spike length and grain yield per plant under low level of fertilization. The parental tester T1 and T2 were a good combiners for most traits under low level of fertilization. Seven hybrids were excellent combiners for specific combining ability for grain yield per plant under low level of fertilization. These genotypes are recommended for use

in wheat breeding programs to tolerate low levels of nitrogen fertilization.

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تحليل سلالة في كشاف لتقدير القدرة على التاليف في قمح الخبز تحت مستويات مختلفة من السماد الأذوتى

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أجرى هذا البحث بهدف دراسة القدرة على التاليف في عشرة تراكيب وراثية من قمح الخبز من خلال تحليل سلالة في كشاف ، حيث تم تهجين بين سبعه تراكيب وراثية (أمهات) مع ثلاث كشافات (أباء) وذلك في موسم ٢٠١٩/٢٠١٨ . في موسم ٢٠٢٠/٢٠١٩ تم تقييم واحد وعشرون هجين مع الأباء تحت ثلاث مستويات من التسميد الأذوتى هي ٤٥ ، ٥٠ كجم أذوت / فدان (معدل متخصص) ، ٧٥ كجم أذوت / فدان (معدل عالي) وذلك في ثلاث تجارب منفصلة. كل تجربة تم تنفيذها في قطاعات كاملة العشوائية في ثلاثة مكررات في المزرعة لكلية الزراعة - جامعة المنوفية - مصر، وكانت الصفات المدروسة هي ؛ طول النبات (سم) ، عدد السنابل / نبات ، طول السنبلة (سم) ، مصروف حبوب السنبلة (جم) ، وزن أحادي (جم) ، بمصروف النبات الفردي (جم). وفيما يلي أهم النتائج المتحصل عليها: أدى استخدام المسمى المتخصص (٤٥ كجم أذوت / فدان) إلى انخفاض متطلبات التراكيب الوراثية المختلفة لكل الصفات المدروسة. التباين الرابع إلى مستويات التسميد الأذوتى كان على المعنوية لكل الصفات المدروسة. التباين الرابع إلى السلالات الأبوية ، الكشافات ، السلالة x كشاف كان معنوياً لكل الصفات المدروسة وذلك تحت كل مستويات التسميد الأذوتى والتحليل المشترك لهم. تقديرات القدرة العامة والقدرة الخاصة على التاليف كانت عالية المعنوية لمجموع الصفات المدروسة تحت مستويات التسميد الأذوتى المختلفة والتحليل المشترك لهم، مما يوضح أهمية كلاً من الفعل الجيني المضييف وغير المضييف في وراثة هذه الصفات. التباين غير المضييف في وراثة هذه الصفات، وذلك تحت مستويات التسميد الأذوتى والتحليل المشترك لهم. كانت صفة طول السنبلة حيث كان الفعل الجيني المضييف هو الأكثر أهمية لدراسة هذه الصفة، وذلك تحت مستويات التسميد الأذوتى والتحليل المشترك لهم. كانت التراكيب الوراثية (سلالة ١ ، سخا ٩٤ ، سس ١٢ ، شندول ١) أفضل الأباء للقدرة العامة على التاليف لصفة المصروف تحت مستويات التسميد الأذوتى والتحليل المشترك لهم، كما كان الكشافان (جيزة ١٧١ ، مصر ١) أفضل للقدرة العامة لصفة المصروف تحت مستويات التسميد الأذوتى والتحليل المشترك لهم. قيم درجة التوريث بالمعنى الواسع كانت أعلى من قيم درجة التوريث بالمعنى الضيق لكل الصفات المدروسة تحت مستويات التسميد الأذوتى والتحليل المشترك لهم. المساهمة النسبية للسلالات في التباين الكلي كانت هي الأعلى ل معظم الصفات المدروسة تحت مستويات التسميد الأذوتى والتحليل المشترك لهم. يجب الاهتمام بالسلالات الأبوية L3 ، L4 ، L5 ، L6 ، L7 في برامج التربية عند التربة لتحمل مستويات منخفضة من التسميد الأذوتى.