

SCREENING BREAD WHEAT ENTRIES FOR FERTILE TILLERS UNDER PHOSPHORUS FERTILIZATION AND EVALUATING OF YIELD AND ITS COMPONENT FOR SUPERIOR UNDER TWO SEEDING RATES

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ABSTRACT

The objective of this study was to know the effect of screening for the No. of fertile tillers m^{-2} is effective on yield in next generations. The research was conducted at field of College of Agriculture - University of Baghdad during two winter seasons, 2015-2016 and 2016-2017. Fifteen entries of wheat were introduced from CIMMYT with local variety (Abugraib3) were screened under three phosphorous rates (0, 75 and 150 $kg\ ha^{-1}$). Superior entries in No. of fertile tillers m^{-2} were selected in addition to entries that gave the lowest means in this trait. In both experiments, randomized complete block design (RCBD) in split plots arrangement with three replicates was used where phosphate rates in 1st exp. and seeding rates in 2nd exp. were assigned for main plots while genotypes were in subplots. Results showed that abugraib3, G11 and G5 gave the highest means in fertile tillers m^{-2} (322.1, 310 and 293.3), respectively. While G14 and G13 gave the lowest means (147 and 198.4), respectively. Phosphate rate 75 $kg\ ha^{-1}$ gave higher mean in fertile tillers per m^2 than phosphate rate at 150 $kg\ ha^{-1}$. Comparison trial results showed G13 and G11 were significantly superior in grain yield which reached 11.104 and 10.555 $t\ ha^{-1}$, respectively. G13 and G11 gave the highest means in fertile tillers m^{-2} and biological yield were 759.2 and 825.8 spikes m^{-2} and 25.48 and 27.52 $t\ ha^{-1}$, respectively. All genotypes planted under 160 $kg\ seed\ ha^{-1}$ were decreased in spikelets spike⁻¹ while fertile tillers m^{-2} , grain yield, biological yield and harvest index were increased. Genotypic variance was higher than environmental variance indicating high genetic components controlling on the traits inheritance. Fertile tillers m^{-2} was the highest in phenotypic and genotypic variances were 2639.2 and 2610, respectively. This reflects high heritability value in broad sense was 98%. It can be concluded that screening genotypes according to No. of fertile tillers under phosphate fertilizer rates led to high potential of fertile tillers as a result of best gene expression. The best genotypes in No. of fertile tillers m^{-2} might be not the best in grain yield but this is related a lot with optimum seeding rate of cultivar.

Key words: entries, heritability, phenotypic variance, fertile tillers, screening

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غريبة مدخلات من حنطة الخبز للأشطاء الخصبة تحت التسميد الفوسفاتي وتقييم الحاصل ومكوناته للمتفوقة تحت معدلين من البذار

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المستخلص

الهدف من هذه الدراسة لمعرفة تأثير الغريبة لعدد الأشطاء الخصبة م⁻² على الحاصل في الاجيال اللاحقة. نفذ البحث في حقول كلية الزراعة جامعة بغداد خلال الموسمين الشتويين 2015-2016 و 2016-2017. غربت خمسة عشر مدخلاً وراثياً من الحنطة مدخلة من CIMMYT مع الصنف المحلي (أبو غريب3) تحت ثلاثة مستويات من الفسفور (0 و 75 و 150 كغم ه⁻¹). انتخب المدخلات المتفوقة في عدد الأشطاء الخصبة م⁻² فضلاً عن المدخلات التي أعطت أقل المتوسطات في هذه الصفة. في كلا التجريبتين، استخدم تصميم القطاعات الكاملة المعشاة بترتيب الواح منشقة بثلاثة مكررات إذ وضعت مستويات الفسفور في التجربة الأولى ومدلات البذار في التجربة الثانية في الالواح الرئيسية في حين خصصت الالواح الثانوية للتراكيب الوراثية. أظهرت النتائج إن الصنف أبو غريب3 والسلالتين G11 و G5 قد أعطت أعلى المتوسطات في الأشطاء الخصبة م⁻² بلغ 322.1 و 310 و 293.3 بالتتابع في حين أعطى G14 و G13 أقل المتوسطات بلغ 147 و 198.4 بالتتابع. حقق مستوى الفسفور 75 كغم ه⁻¹ متوسطاً أعلى في عدد الأشطاء الخصبة م⁻² من المستوى 150 كغم ه⁻¹. أظهرت نتائج تجربة المقارنة تفوق G11 و G13 في حاصل الحبوب الذي بلغ 11.104 و 10.555 طن ه⁻¹ بالتتابع. أعطى G13 و G11 أعلى المتوسطات في الأشطاء الخصبة م⁻² والحاصل الحيوي بلغ 759.2 و 825.8 سنبله م⁻² و 25.48 و 27.52 طن ه⁻¹ بالتتابع. كل التراكيب الوراثية المزروعة تحت 160 كغم بذور ه⁻¹ قل فيها عدد السنبيلات بالسنبلة في حين ازداد متوسطات عدد الأشطاء م⁻² وحاصل الحبوب ودليل الحصاد. كان التغيرات الوراثي أعلى من التغيرات البيئي مؤشراً بوجود مكون وراثي عال مسيطراً على توريث هذه الصفات. حقق أعلى تباين مظهري ووراثي في صفة الأشطاء م⁻² بلغ 2639.2 و 2610 بالتتابع. انعكس ذلك في إعطاء قيمة درجة توريث عالية بالمعنى الواسع بلغت 98%. يمكن الاستنتاج إن غريبة المدخلات الوراثية إتماداً على عدد الأشطاء الخصبة تحت مستويات التسميد الفوسفاتي أدى إلى اظهار القابلية القصوى لتكوين الأشطاء نتيجة للتعبير الجيني العالي. إن أفضل المدخلات في الأشطاء الخصبة م⁻² قد لا يكون هو الأفضل في حاصل الحبوب ولكن ذلك مرتبط بقوة مع معدل البذار الأمثل للصنف.

الكلمات المفتاحية: المدخلات، التوريث، التغيرات المظهري، الأشطاء الخصبة، الغريبة
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INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an essential cereal crop that used for nutrition by numerous of human. To face risk of famine as a result of increasing world population, efforts should be concerted to find out genotypes superior in their yield. This is considered the biggest challenge that plant breeders have been worked to improve. Screening entries usually base on yield or one of yield components. Evaluating the performance in next generations will give a best understanding about its success in increasing yield instead of discarding many entries in early generations. Therefore, in this study, the entries were screened depend on fertile tillers per m² under various phosphorous rates to show their genetic variability and potentiality. Fertile tillers per m² is affected by other yield components, according to compensation principle. Mirabella et al, (22) found out that fertile tillers per m² had high heritability with additive gene action. However, that needs special attention to determine the benefit of this trait as a selection criterion in breeding program to increase yield. Tillers appearance, growth and their survival are critical factor because fertile tiller is a yield component (30). Tillers may effect negatively or positively in wheat grain yield depending on availability of many factors such as water, light and nutrients (14). Tillers formation starts after appearance of three leaves on main stem (15). Wheat cultivars with high ability to absorb phosphor show high efficiency of root system, tillers appearance percentage and accumulate phosphor in grains (32). Fioreze et al (17) stated that high phosphor rates increased tillers appearance and their survival, particularly the secondary tillers. This was reflected positively on grain yield. Valle and Calderini (31) reported that phosphor availability had a main role in differentiating, leaves expansion and tillers formation. Tillering characteristic is distinguished property of wheat. Tillers formation begin after appearance of three leaves on main stem and then new tiller emerges after every additional leaf appearance (4). Tillers formation is considered a critical factor for wheat productivity because of grain yield is associated with number of plant per unit area and fertile tillers per plant. Main

stems contribute about 30-50% in grain yield while 50-70% comes from fertile tillers under normal conditions (26). Ozturk et al, (23) stated that increasing in seeding rate to 525 seeds m² led to increase tillers per m². The core of this study was to determine if the screening of fertile tillers per m² will effect on yield in next generations especially when the evaluation will performed at various seeding rates.

MATERIALS AND METHODS

This trail was conducted at field of College of Agriculture, University of Baghdad Al-Jadriya during the winter season of 2015-2016 and 2016-2017. Initial chemical characteristics of the soil were show in Table 1. Fifteen bread wheat entries were introduced from CIMMYT and local variety (Abugraib3) was planted under different phosphorous rates (0, 75 and 150 kg ha⁻¹). Selecting was performed on entries that gave the highest number of fertile tillers per m² and evaluating them under two seeding rates. In the first season trail, RCBD with split plots arrangement with three replicates was used where P rates were assigned for main plots while sub plots were occupied by entries. In the second season trail, the superior entries in fertile tillers per m² from the past season trail were G16, G5 and G11 have been planted under 75 kg phosphor ha⁻¹, as well as two entries that yielded the lowest fertile tillers per m² were G14 planted under 150 kg phosphor ha⁻¹ and G13 planted under control were used to determine the behavior of this trait after screening under different seeding rates. RCBD with split plots arrangement with three replicates were used. Seeding rates (100 and 160 kg ha⁻¹) were occupied in main plots while selected entries were assigned for sub plots. Soil and crop managements were done as recommended. Traits studied were ratio of fertile tillers per m²/total tillers per m², yield and its components which were number of fertile tillers per m², number of spikelets per spike, number of grains per spike, 1000 grains weight as well as biological yield and harvest index. Data was analyzed by GenStat program (edition14) and means were tested by LSD values at 0.05 probability.

Estimation of phenotypic and genotypic variances: The expected mean squares for each of source of variation according to Federer and King (16) are:

$$MS_{rep} = \sigma_e^2 + g\sigma_{dr}^2 + dg\sigma_r^2$$

$$MS_d = \sigma_e^2 + r\sigma_{dg}^2 + g\sigma_{dr}^2 + rg\sigma_d^2$$

$$MSe(a) = \sigma_e^2 + g\sigma_{dr}^2$$

$$MS_g = \sigma_e^2 + r\sigma_{dg}^2 + rd\sigma_g^2 \dots\dots\dots (1)$$

$$MS_{dg} = \sigma_e^2 + r\sigma_{dg}^2 \dots\dots\dots(2)$$

$$MSe(b) = \sigma_e^2$$

Genetic variance can be calculated by abstracting equation 2 from equation known:

$$\sigma_g^2 = \frac{MS_g - MS_{dg}}{rd}$$

As known: $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where: σ_e^2 is environmental variance that is equal to error(b).

MS_{rep} = mean square of replication , MS_d = mean square of seeding rates,

$MSe(a)$ = mean square of error(A), MS_g = mean square of genotypes MS_{dg} = mean square of interaction between seeding rates and genotypes and, $MSe(b)$ = mean square of error(B).

PCV% and GCV% and h_{bs}^2 were estimated according to Sing and Chaudhary (24).

$$PCV\% = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$GCV\% = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where: PCV% is phenotypic coefficient variance and GCV% is genotypic coefficient variance.

$$h_{bs}^2\% = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where: h_{bs}^2 is heritability in broad sense

Table 1. Chemical properties of the soil

Test Unit	EC Dsm ⁻¹	PH	Ca MegL ⁻¹	Mg MegL ⁻¹	Na MegL ⁻¹	N %	P ppm	K ppm	Cl MegL ⁻¹	HCO ₃ ⁻ MegL ⁻¹
value	1.7	7.4	5.61	3.11	7.66	0.015	15.7	33.9	5.2	1.5
Soil particles and texture										
Sand	%	65.2								
Silt	%	22.0								
Clay	%	12.8								
Texture: sandy loam										

RESULTS AND DISCUSSION

Effects of genotypes and P rates on number of fertile tillers per m²

Results showed significant differences between genotypes, seeding rates and their interactions (Table 2). Variety abugraib3 gave the highest mean of No. spike m⁻² amounted to 322.1, while G14 gave the lowest No. of spike m⁻² amounted to 147. The variation among genotypes in this trait probably due to the difference in their ability in tillers formation and utilized from growth factors. Genotypes with high potentiality to produce fertile tillers will give high number of spikes per unit area compared with genotypes with low fertile tillers potential. Also, increasing plant height is considered as a factor that stimulates substantial tillers that they did not survive and most of them will die later, Consequently, the grain yield will decrease (18). 75 kg P ha⁻¹ gave the highest mean of spikes per m² was

262. Phosphorus levels resulted in increasing tillers formation especially secondary tillers. Fioreze et al (17) found the same of this result. For interaction, abugraib3, G3 and G5 gave the highest response when planted at 75 kg P ha⁻¹ while G14 and G15 gave the lowest response. Screening of genotypes depends on tillers per m⁻² as a selection criterion can diagnose superior genotypes in grain yield. Mirabella et al, (22) used this trait to screen genotypes superior in yield in early generations. Removal of unfertile tillers is considered one of approaches to increase yield. Tillers contribute in grain yield as a source of sugars and excess assimilates materials from main stem. Tillers ensure decreasing the loss of yield at minimum range especially in regions that exposure to stress by insects, diseases and other environmental factors.

Table 2. Effects of genotypes and P rates on number of fertile tillers m⁻² in the first season

Genotypes	P rates (kg ha ⁻¹)			Mean
	0	75	150	
G1	208.7	307.7	224.0	246.8
G2	258.7	190.0	201.3	216.7
G3	198.0	280.0	233.3	237.1
G4	226.0	312.7	268.3	269.0
G5	264.7	338.7	278.7	293.8
G6	206.0	209.3	264.3	226.6
G7	256.3	232.7	230.0	239.7
G8	264.0	288.0	253.3	268.4
G9	218.7	263.3	229.3	237.1
G10	246.3	266.7	178.3	230.4
G11	298.7	310.0	321.3	310.0
G12	232.7	262.3	234.7	243.2
G13	167.0	211.0	217.3	198.4
G14	145.3	152.7	143.0	147.0
G15	227.3	215.0	220.0	220.8
Abugraib3	278.0	358.7	329.7	322.1
LSD 0.05		29.8		17.5
Mean	231.0	262.4	239.2	244.2
LSD 0.05		7.7		

Effects of genotypes and seeding rates on yield and its component

Number of fertile tillers per m²

Results showed that No. of fertile tillers per m² were significantly influenced by genotypes, seeding rates, and their interaction (Table 3). G11 produced the highest number of tillers per m² amounted to 825.83 while G14 gave the lowest tillers amounted to 663.33. Also, G11 gave the highest mean in this trait in the first season trail. This refers there is a high genetic component of its heritability. Dwarf genes led to reduce plant height and spike length and then increasing fertile tillers survival. G11 gave the lowest plant height and spike length (data is not published). The compensation principle between yield components had a big role, where G11 gave the highest mean in spikes per m², grain weight and lowest mean in spikelets per spike and number of grains per spike. G14 gave the lowest mean in spikes per m², grains per spike, high mean in spikelets per spike and 1000 grain weight. The difference among entries was attributed to their potential to produce tillers and their survival (10, 13, 21). Spikes per m² increased under 160 kg seed ha⁻¹ that gave higher mean amounted to 766.22 spike m⁻² than 100 kg seed ha⁻¹ that gave 698.39. Spikes per m² was affected by fertile tillers formation that decreased at high seeding rate as a result of competition among plants and within plant itself. This result agreed with finding of

Tolmay, (27) and Abdulkerim et al, (1) who found by increasing seeding rate at certain quantity led to increase spikes per unit area. Interaction was significant where G11 gave the highest mean at both seeding rates but its response was not more than abugraib3 sel, G5 and G13. This refers that G11 had high stability in this trait at different seeding rates.

Table 3. Effect of genotypes and seeding rates on fertile tillers per m² for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	659.67	754.67	707.17
G11	815.00	836.67	825.83
G13	720.67	797.67	759.17
G14	653.33	673.33	663.33
abugraib3 sel.	666.67	785.00	725.83
abugraib3 org.	675.00	762.00	718.50
L.S.D. 5%		10.19	6.49
Mean	698.39	768.22	733.31
L.S.D. 5%		11.12	

Ratio of fertile tillers/total tillers

Result showed that there was only significant difference among genotypes while, it was not significant for seeding rates and interaction (Table 4). G14 gave the highest mean was 0.88 but it was not significant difference with G11 and G5. Abugraib3 org. gave the lowest mean was 0.77. This trait increased by increasing fertile tillers but it was not the only decisive factor that determine the superior genotypes. G14 that recorded the lowest spikes per m² gave the highest ratio, this was, it had low unfertile tillers while G11 gave the highest

mean of spikes per m² (Table 3) but its mean was not higher than G14. Ishaq and Taha (19) found nitrogen fertilizer led to increase this ratio. In addition, increasing the flag leaf area caused shadowing, therefore, tillers buds growth will cease.

Table 4. Effect of genotypes and seeding rates on ratio of fertile tillers/total tillers for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	0.85	0.85	0.85
G11	0.91	0.84	0.87
G13	0.84	0.76	0.80
G14	0.89	0.88	0.88
abugraib3 sel.	0.82	0.747	0.78
abugraib3 org.	0.77	0.78	0.77
L.S.D. 5%		n.s	0.05
Mean	0.84	0.81	0.85
L.S.D. 5%		n.s	

Spikelets per spike

There were significant differences among genotypes, seeding rates and their interaction (Table 5). Abugraib3 org. gave the highest mean was 19.55 but it was not significant with G14, abugraib3 sel. and G5 that recorded 19.30, 18.97 and 18.87, respectively. While genotypes with low fertile tillers per m² such as abugraib3 org. led to increase distributing assimilates to form spikelets primordia. This will lead to increase spikelets per spike. Controversy, G11 and G13 that had high tillers formation gave the highest spikes per m². Therefore, competition increased and then spikelets per spike decreased. Genotypes differ in spikelets per spike because of variation in their genetic makeup (5, 6). Increasing seeding rates to 160kg ha⁻¹ lead to decrease spikelets per spike. Increasing plants per unit area and spikes per m² resulted in high competition on growth factors and assimilates between and within plants. This reduced spikelets per spike. This finding agreed with results of other researches that stated increasing seeding rates lead to decrease spikelets per spike (6, 7) but it disagreed with results of Baktash and Hassan, (5). There was significant interaction between the two factors, this probably due to different responses of genotypes to seeding rates. Since, Abugarib3 sel. and abugraib3 org. decreased significantly by increasing seeding rates. Abugraib3 sel. at 100 kg seed ha⁻¹ gave the highest mean was

20.6 while G11 recorded the lowest mean at 160 kg seed ha⁻¹ was 16.6.

Table 5. Effect of genotypes and seeding rates on spikelets per spike for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	19.10	18.63	18.87
G11	16.83	16.60	16.72
G13	17.30	17.03	17.17
G14	19.73	18.87	19.30
abugraib3 sel.	19.93	18.00	18.97
abugraib3 org.	20.60	18.50	19.55
L.S.D. 5%		0.98	0.74
Mean	18.92	17.94	18.43
L.S.D. 5%		0.47	

Grains per spike

There were significant differences between genotypes in this trait (Table 6). Abugraib3 sel. gave the highest mean of grains per spike amounted to 64.08 as a result of recording the highest mean in spikelets per spike while G11 gave the lowest mean was 49.15 because it had low mean in spikelets per spike. Genetic factor caused increasing grains per spike by increasing spikes per m² and spikelets per spike according to compensation principle (Table 3 and 5). These results agreed with the results of (6, 7). Interaction was significant because of different responses and behaviors of genotypes to various seeding rates. All genotypes were decreased when raising seeding rate to 160 kg ha⁻¹. The lowest decrease was for abugraib3 sel. and G13.

Table 6. Effect of genotypes and seeding rates on grains per spike for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	58.87	57.07	57.97
G11	52.27	46.03	49.15
G13	53.17	50.77	51.97
G14	53.20	51.80	52.50
abugraib3 sel.	67.57	60.60	64.08
abugraib3 org.	61.63	59.70	60.67
L.S.D. 5%		3.93	1.15
Mean	57.78	54.33	56.06
L.S.D. 5%		n.s	

1000 grain weight

There were significant differences among genotypes and the interaction (Table 7). G11 recorded the highest mean in this trait amounted to 44.69g, while abugraib3 org. gave the lowest mean mounted to 30.21g. Increasing grains per spike led to reduce grain weight. Therefore, G11 was superior in this trait because it was the lowest in spikelets per spike and grains per spike (Table 5 and 6).

Valerio et al (30) found that genotypes with high potential in tillering had high mean in 1000 grain weight. Increasing the ratio of fertile tillers/total tillers led to increase this trait. G14, G11 and G5 that superior in the ratio of fertile tillers/total tillers gave the highest mean in 1000 grain weight (Table 4 and 7). Interaction was significant because of magnitude and direction of response. Mean of this trait increased by high seeding rates for abugraib3 org, G14 and G5 while it had low mean in G16, G13 and G11. G11 planted under 100kg seed ha⁻¹ gave the highest mean was 46.77 while the lowest was 29.30 came from abugraib3 org that planted under 100kg seed ha⁻¹. Abdulkerim et al (1) found that genotypes planted under high plant density caused increasing spikes per m², in addition to, there were high competition leading to reduce photosynthesis efficiency and then lowered grain weight.

Table 7. Effect of genotypes and seeding rates on 1000 grain weight for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	39.87	41.60	40.73
G11	46.77	42.60	44.69
G13	40.90	40.17	40.53
G14	38.87	43.30	41.08
abugraib3 sel.	32.10	29.73	30.92
abugraib3 org.	29.30	31.12	30.21
L.S.D. 5%	3.47		2.47
Mean	37.97	38.09	38.03
L.S.D. 5%		n.s	

Grain yield

Results in table 8 showed G13 gave the highest mean was 11.104 t ha⁻¹ while abugraib3 sel. gave the lowest mean was 8.479 t ha⁻¹. By increasing fertile tillers, grain yield could increase. Therefore, G13 and G11 that achieved highest means in fertile tillers gave the highest grain yield. This agreed with the results of Abdulkerim et al (1) they found that genotypes differed in grain yield because of variation in yield components. Genotypes with high potential in fertile tillers gave the highest grain yield. This agreed with the results of Xie et al (28) who found that high potential of tillers formation had an essential role in grain yield. Seeding rates effects were significant in grain yield. 160 kg seed ha⁻¹ was higher than 100 kg seed ha⁻¹ in grain yield. Increasing seeding rate to optimum led to increase plants in unit area, spikes per m² and biological yield (Table 3 and 9). This agreed with the results of

others (1, 8, 29). Al-Hassan (3) found that by increasing seeding rate to a certain range, grain yield will increase as a results of increasing spikes per m² and biological yield. Interaction was significant, this indicated that there were different responses of genotypes under various seeding rates. G13 planted under 160 kg seed ha⁻¹ gave the highest grain yield was 12.728 t ha⁻¹ while the lowest mean was 7.392 t ha⁻¹ recorded by abugraib3 org. planted under 100 kg seed ha⁻¹.

Table 8. Effect of genotypes and seeding rates on grain yield for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	8.804	11.919	10.361
G11	9.557	11.553	10.555
G13	9.479	12.728	11.104
G14	8.338	9.931	9.134
abugraib3 sel.	7.661	9.296	8.479
abugraib3 org.	7.392	10.685	9.039
L.S.D. 5%		1.857	0.610
Mean	8.538	11.019	9.779
L.S.D. 5%		2.418	

Biological yield

Significant differences were found between genotypes and seeding rates (Table 9). G11 gave the highest mean was 27.52 t ha⁻¹ while G16 gave the lowest mean was 23 t ha⁻¹. Dwarf genes had a big role in producing high number of tillers per m² and grain weight and then biological yield. G11 had the highest spikes per m² and 1000 grain weight (Table 3 and 7) in addition to it increased by prolonging the duration of reproductive growth. This agreed with finding of Brancourt-Hulmel et al (11) and disagreed with Bhatta et al (9) who stated that there are no significant differences between genotypes in biological yield. Seeding rate at 160 kg ha⁻¹ gave higher mean than seeding rate at 100 kg ha⁻¹. Increasing seeding rate to an optimum rate led to increase plants per unit area, spikes and plant height, therefore, biological yield will increase. This result agreed with finding of Abdulkerim et al (1).

Table 9. Effect of genotypes and seeding rates on biological yield for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	20.88	26.78	23.83
G11	24.69	30.35	27.52
G13	23.57	27.39	25.48
G14	20.31	27.69	24.00
abugraib3 sel.	21.29	25.05	23.17
abugraib3 org.	21.67	25.94	23.80
L.S.D. 5%		n.s	1.39
Mean	22.07	27.20	24.63
L.S.D. 5%		3.82	

Harvest index

Results indicated G5 gave the highest mean was 42.3% while abugraib3 sel. gave the lowest mean amounted to 36.21% (Table 10). The differences among genotypes in harvest index were attributed to variation of assimilation partitioning efficiency to grain yield. G5 gave the highest mean in spikelets per spike, grains per spike, 1000 grain weight and grain yield. The difference was significant between seeding rates in this trait. 160 kg seed ha⁻¹ gave the highest mean in harvest index was 41.06% while under 100 kg seed ha⁻¹ it amounted to 37.18%. At high seeding rates, number of plants per unit area and spikes will increase. This result agreed with finding of Bhatta (8). Interaction was significant where G5 planted at 160 kg seed ha⁻¹ gave the highest mean was 45.61%. in addition to, G5 and G14 achieved the highest responses in this trait when changing the seeding rate from 100 to 160kg ha⁻¹. while Abugraib3 org. at 100 kg seed ha⁻¹ gave the lowest mean amounted to 34.11%.

Table 10. Effect of genotypes and seeding rates on harvest index for second season 2016-2017

Genotypes	Seeding rates (kg ha ⁻¹)		Mean
	100	160	
G5	38.98	45.61	42.30
G11	38.07	39.96	39.01
G13	38.81	44.52	41.67
G14	38.36	38.17	38.27
abugraib3 sel.	34.77	37.66	36.21
abugraib3 org.	34.11	40.43	37.27
L.S.D. 5%	2.59		0.93
Mean	37.18	41.06	39.12
L.S.D. 5%	3.40		

Phenotypic and genotypic variances and heritability in broad sense

Table 11. Phenotypic and genetic variance components and heritability in broad sense

traits	σ^2_g	σ^2_e	σ^2_p	% PCV	% GCV	h^2_{bs} %	Mean
*Ratio ft/tt	0.0028	0.0024	0.0042	7.826	5.099	42.5	0.8305
Spikes per m ²	2610	29.1	2639.2	7.00	6.96	98.8	733.31
Spikelets per spike	1.23	0.38	1.61	6.88	6.08	76.3	18.43
Grains per spike	31.76	0.90	32.66	10.19	10.05	97.2	56.06
1000 grain weight	33.32	4.22	37.54	16.11	15.1	88.7	38.03
Grain yield	0.90	0.25	1.15	10.96	9.70	78.2	9.779
Biological yield	2.07	1.33	3.40	7.48	5.84	60.8	24.63
Harvest index	3.92	0.59	4.51	5.42	5.06	86.9	39.12

*Ratio of fertile tillers/ total tillers

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Genetic variance is considered as a main source of genes that improve yield quantity and quality. Results in table 11 revealed that most of traits studied had high genetic variance compared to environmental variance. This refers there is a high genetic component controlling on the traits. High genetic variance reflected on high heritability in broad sense in most traits studied, particularly, in fertile tillers per m² and grains per spike that were 98.8 and 97.2%, respectively. Therefore, screening genotypes depended on fertile tillers could be more effective. Most values of phenotypic and genotypic coefficient variances were low according to Sivasubramanian and Menon (25) who stated that when value of variance coefficient lower than 10, this is considered low, while if it ranges from 10 to 20, this will be high, but if it is more than 20, this is high value. 1000 grain weight recorded the highest values of PCV% and GCV% were 16.11 and 15.1, respectively. For each trait, the PCV% value was close to GCV% indicating there was a little of environmental effects. These results were in coincidence with finding of others who found that genetic variance was higher than environmental variance (2, 12, 20). It can be concluded from the results above the screening depending on the number of fertile tillers per m² is not valid for each cultivar but It should be taken in our consideration the optimum seeding rates when designing selection program.

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