passed on from parents to their offspring (Falconer, 1981).

According to (Zecevic *et al.*, 2001; Shukla *et al.*, 2004; Clarke *et al.*, 2010), heritability and genetic advance are frequently employed in wheat to assess the degree of diversity in breeding material, choose the best selection methods, and forecast the breeding advance in improving key traits.

The results of the investigation show that applying nitrogen at the right level considerably boosted wheat production (Gwal *et al.*, 1999; Ali *et al.*, 2000). Nitrogen is the most crucial nutrient for vegetative crop growth, plant productivity, and grain quality among all the necessary nutrients sprayed in the field (Mariotti, 1997).

The main objective of the present study is to estimate the simple correlation among characters and determined some variability genotypic coefficient variance (Gcv), phenotypic coefficient variance (Pcv), heritability in broad sense (h2.b.s), genetic advance (GA) percent of mean.

MATERIALS & METHODS

Twelve varieties of bread wheat (Adana-99, Adana, APST-33, APST-36, APST-26, IPA-95, Jihan-99, Criso, APST-6, BABAGA-3, APST-35, TAWA-HI-3), genotypes with source showed in table (1), with four level of nitrogen(0, 75, 150, 225 Kg N h^{-1}), Which are sown in growing season, in farmer field which located in summel/batel (hazaz villiage) in (2021), At maturity, ten plant from each genotype were taken at random for recording observation, the characters are days to 75% flowering, plant height(cm), grain filling, grain yield, number of spikes/plant, spike length(cm), grain weight11000 g., flag leaf area(cm), biomes g., harvest index and protein percent. Al-zubaidy, Kh. M. D. and Kh. K. A. Al- Jubory (2016) Analysis were done to according Al-zubaidy, Kh. M. D. and Al-Juboury, the simple correlation among traits was estimated using the following formula:

$$r = \frac{\sum XY - \frac{(\sum X)(\sum Y}{n}}{\sqrt{\sum X^2 - \frac{(\sum X^2)}{n}} \; X \sqrt{\sum Y^2 - \frac{(\sum Y^2)}{n}}}$$

Where:
n = number of the treatments (observations).
r = correlation coefficient value,
the correlation coefficients between grain yield (y) and each of grain filling (X1), number of spike (X2), spike length (X3), grain weight 1000 (X4), leaf area (X5), biomass (X6), harvest index (X7), the method outlined by (Al-Rawi, 1987).:

Genetic advance
(Allard 1960)
GA= I x h^2.b.s σ p
K. slection indensity 10% = 1.76
σp = phenotypic standard deviation.
GA as percent
GA y.. = GA/y^ - X 100 (Kempthorne 1969)

Genetic advance
Low less than 10%
Medium 10 – 30 %
High more than 30% (Agarwal and Ahmed (1982).
Estimation Gcv and Pcv (according to Dudlx and Moll 1969), (Burton (1952),

$$Gcv = \frac{\sqrt{\sigma^2 g}}{Y^-} X\ 100$$

$$Pcv = \frac{\sqrt{\sigma^2 P}}{Y^-} X\ 100$$

y- = general mean

And the Broad sense heritability measured high when it is more than 60%, it is medium between 40% - 60% and low when it is less than 40%, (Ali, 1999),

$$h2.b.s = \frac{\sigma^2 G}{\sigma^2 P}$$

Where:
h^2.b.s = broad sense heritability
σ^2 G = standard variance of genotypic
σ^2 P = standard variance of phenotypic

Table(1):- Genotypes used in the study and their sources

#	Genotype	Source
1	Adana	Kurdistan region / certified
2	Adana-99	Kurdistan region / certified
3	APSTA-33-85577	Italy / not certified
4	APSTA-36-85576	Italy / not certified
5	APSTA-26-85579	Italy / not certified
6	IPA-95	Baghdad / certified
7	Jihan-99	Kurdistan region / certified
8	Creiso	Kurdistan region / certified
9	APSTA-6-85576	Italy / not certified
10	BABAGA-3	ICARDA
11	APSTA-35-85574	Italy / not certified
12	TAWA-HI-3	ICARDA

RESULT AND DISCUSSION

Table (2) Analysis of variance of wheat genotypes and nitrogen levels on studied traits showed for genotype highly significant at 1% for traits (number of spike/plant, flag leaf area, biomes and harvest index). And significant at 5% for as (days of 75% flowering and plant height, while not significant for the other traits. And for the nitrogen showed highly significant at 1% for (plant height, grain yield, number of spike/plant, spike length, flag leaf area, protein and significant at 5% for (grain weight, biomes harvest index), and not significant for the other traits, for the interaction between nitrogen and genotype showed the highly significant at 1% for traits (spike length, flag leaf area, biomes and harvest index), and significant at 5% for the (grain yield .g and number of spike/plant), and there is not significant for the other traits. Similar findings were also reported by Navin et al. (2014); Dabi et al. (2019).

Table (2):- Analysis of variance of wheat genotypes and nitrogen levels on studied traits.

Source Of variance	characters DF	Treatments MS										
		Days of 75% Flowering	Plant height (cm)	Grain filling	Grain yield g.	Number of spike/plant	Spike length(cm)	Grain weight (1000) g.	Flag leaf area (cm)	Biomes g.	Protein %	Harvest index
Replication	2	4.00	30.11*	17.27*	8.71*	43.38	0.06	19.58*	64.80	96.60	0.48	5.07
Nitrogen (n)	3	15.52	270.46**	8.60	39.18**	511.19**	1.73**	69.37*	422.79**	121.23*	12.71**	15.53*
Replication nitrogen	6	3.21	14.34	13.90*	7.25*	34.88	0.36	17.47	60.47*	85.30	3.39*	9.25*
Genotypes (g)	11	24.78*	34.28*	10.58	3.47	209.63**	0.30	18.83	184.85**	389.70**	2.12	12.63**
N X G	33	11.35	16.02	9.15	5.44*	73.12*	0.54**	22.10	68.58**	137.42**	1.78	9.74**
Error	88	11.91	11.70	6.87	3.22	41.65	0.23	18.47	32.73	55.74	1.72	4.69
Total	143											

*and ** significant different at level 0.05 and 0.01 respectively

The mean value of effected of interaction between bread wheat genotype and nitrogen level on study tried presented in table (3) presented that for days of 75% flowering there are significant differences among all the genotype with their interaction with nitrogen level which are latest in flowering which are ranged between (135.66 - 136.33 - 137.00) days 75% of flowering accept the genotype (N0V1- N0V10- N1V5- N1V7- N1V9- N1V1- N2V2- N2V3- N2V4- N2V9- N3V1- N3V8), regarding number plant height (N3V12) recorded the maximum value with (71.43), and minimum value for (N0V2- N1V6) the value (57.36- 57.66), and regarding the grain filling (N2V6- N3V6) the maximum value range (56.33 – 56.00) and minimum value for (N0V2)(44.33), and the grain yield g. (N3V7- N3V12) the maximum value with (83.00- 82.00),and minimum value for (N1V2- N2V2- N3V5) is (59.00), and the result of number of spike/plant (N0V4) the maximum value is (8.86) and minimum value for (N2V3) (7.00), the result showed of the spike length(cm) (N1V2) recorded the maximum value with(49.20) and minimum value for (N3V7) the range is (37.86), the result of 1000 grain weight indicated (N1V4- N1V12) the highest weight (70.56- 69.16), while (N3V5) showed the lowest value (44.83), flag leaf area (cm) the (N1V12) recorded the maximum value with (132.60 cm) and minimum value for (N0V9) (98.21), and the result of the biomass .g the (N0V8) recorded the maximum value (25.83) and minimum value for (N0V5) is (15.54), protein have a maximum value (N2V3- N2V7) its (12.32- 12.30) and minimum value for (N3V5) with (9.16), and the result of harvest index indicated (N0V8) the maximum value (26.00) and the minimum value for (N0V5) is (17.63), Similar findings were also reported by (Ortiz- Monasterio et al,. 1997), and (Moll, R. H. Kamprath and Jackson W.A. (1982).

Table(3):- Effect of interaction between wheat genotypes and nitrogen levels on studied traits.

Treatments

Character	Days of 75% flowering	Plant height (cm)	Grain filling	Grain yield g.	Number of spike	Spike length (cm)	Grain weight (1000).g	Flag leaf area(cm)	Biomes g.	Protein %	Harvest index
N0V1	136.33 A	58.56 jk	52.66 ab	60.33 gh	8.13 a-i	42.63 abcd	58.96 a-m	107.50 e-l	19.23 b-i	10.26 Abcd	20.56 b-j
N0V2	131.33 Ab	57.66 k	44.33 C	71.00 a-h	8.73 Ab	44.40 abcd	57.13 b-m	105.03 e-l	18.49 c-l	9.72 a bcd	19.36 Hij
N0V3	134.33 ab	65.26 a-j	54.66 ab	66.00 c-h	7.93 a-j	46.56 abcd	64.56 a-h	112.40 b-l	19.71 b-i	11.56 a bcd	22.03 b-l
N0V4	133.00 Ab	68.13 abcd	54.00 Ab	73.33 a-g	8.86 A	47.36 abc	55.03 f-n	104.34 f-l	19.62 b-i	11.30 a bcd	20.53 b-j
N0V5	128.00 B	61.60 d-k	54.33 ab	63.66 efgh	8.13 a-i	41.30 abcd	56.86 c-m	113.46 b-l	15.54 l	10.93 a bcd	17.63 j
N0V6	132.00 Ab	65.50 a-j	55.00 ab	68.66 b-h	7.13 Jk	45.90 abcd	65.56 a-g	110.40 d-l	17.97 d-i	10.62 abcd	19.86 d-j
N0V7	134.33 Ab	64.16 b-k	54.00 ab	80.00 ab	7.63 d-k	41.76 abcd	56.60 c-m	105.00 e-l	19.77 b-i	10.30 abcd	20.73 b-j
N0V8	132.00 Ab	68.40 abcd	54.33 ab	72.00 a-h	8.40 a-f	44.93 abcd	65.43 a-g	100.87 h-l	25.83 a	11.66 abcd	26.00 a
N0V9	131.33 Ab	58.63 jk	53.66 Ab	64.00 efgh	8.60 abcd	43.53 abcd	51.03 j-n	98.21 l	20.97 b-g	9.96 abcd	20.56 b-j
N0V10	135.66 A	59.90 g-k	54.00 ab	64.33 efgh	8.06 a- j	42.33 abcd	61.06 a-k	101.70 g-l	19.42 b-i	11.06 abcd	19.73 e-j
N0V11	135.00 Ab	63.06 d-k	54.00 ab	62.33 fgh	7.26 Hijk	48.43 Ab	66.23 a-g	106.83 e-l	19.68 b-i	10.18 abcd	20.96 b-j
N0V12	134.00 ab	63.90 c-k	53.66 ab	78.66 abc	8.40 a-f	47.70 ab	63.03 a-i	104.07 f-l	19.16 b-i	11.96 abc	19.90 c-j
N1V1	133.66 Ab	59.50 hijk	54.00 ab	62.66 fgh	7.16 Ijk	38.86 Cd	48.63 lmn	101.00 g-l	20.76 b-g	9.86 abcd	20.90 b-j
N1V2	134.33 Ab	59.23 ijk	52.00 ab	59.00 h	7.66 c-k	49.20 A	56.26 d-m	111.60 c-l	18.62 c-i	9.47 Cd	20.60 b-j
N1V3	132.00 Ab	63.90 c-k	52.33 ab	63.66 efgh	8.43 a-f	43.46 abcd	54.80 g-m	100.34 ijkl	23.56 ab	12.13 abc	23.56 abc
N1V4	132.66 Ab	64.10 b-k	53.66 ab	68.00 b-h	8.63 Abc	47.43 abc	70.56 A	103.50 f-l	18.80 c-i	11.46 abcd	19.43 f-j
N1V5	137.00 A	60.56 f-k	52.66 ab	62.33 fgh	7.73 c-k	45.36 abcd	61.96 a-k	106.93 e-l	18.19 d-i	9.84 abcd	19.40 ghij
N1V6	135.00 Ab	57.36 k	52.00 ab	63.66 efgh	8.10 a-j	44.73 abcd	68.56 Ab	117.43 b-e	17.67 e-i	11.51 abcd	20.73 b-j
N1V7	137.00 A	65.63 a-i	53.00 ab	78.66 abc	7.93 a-k	47.13 abc	68.00 abc	126.80 ab	16.90 ghi	11.77 abcd	21.43 b-l
N1V8	135.00	64.70 a-k	53.33 ab	65.00 d-h	8.33	47.06 abc	64.90	101.13	20.82 b-g	10.31 abcd	21.06 b-j

	Ab				a-f		a-g	g-l			
N1V9	135.66 A	63.33 d-k	53.33 ab	67.66 b-h	7.60 e-k	44.63 abcd	56.26 d-m	126.00 ab	15.68 hi	10.52 abcd	19.63 e-j
N1V10	133.33 Ab	63.33 d-k	50.33 B	70.66 a-h	7.33 g-k	43.83 abcd	67.26 a-e	122.60 abcd	17.38 fghi	9.55 bcd	21.13 b-j
N1V11	134.00 Ab	62.16 d-k	53.66 ab	79.00 abc	8.10 a-j	47.30 abc	62.50 a-j	116.13 b-g	19.60 b-i	10.67 abcd	22.70 a-I
N1V12	133.33 Ab	64.76 a-k	54.00 ab	70.66 a-h	8.43 a-f	43.20 abcd	69.16 A	132.60 a	16.84 ghi	10.16 abcd	22.16 b-I
N2V1	137.66 A	60.63 e-k	52.00 ab	61.66 fgh	8.46 a-e	46.76 abc	56.53 c-m	103.23 f-l	20.23 b-g	9.75 abcd	20.86 b-j
N2V2	135.66 A	62.10 e-k	51.33 ab	59.00 h	7.86 b-k	41.90 abcd	64.00 a-i	108.16 d-l	18.80 d-i	12.13 abc	20.20 b-j
N2V3	135.66 A	63.96 c-k	53.33 ab	67.33 b-h	7.00 K	42.60 abcd	66.80 a-e	114.17 b-k	19.70 b-i	12.32 a	22.33 b-I
N2V4	135.66 A	63.33 d-k	54.00 ab	72.33 a-g	8.36 a-f	47.60 abc	65.03 a-g	106.93 e-l	22.20 abcd	10.84 abcd	23.66 ab
N2V5	133.33 ab	67.43 a-f	53.00 ab	74.33 a-f	8.00 a-j	40.90 abcd	60.66 a-k	115.43 b-i	18.07 d-i	12.20 ab	20.90 b-j
N2V6	133.00 Ab	59.43 ijk	56.00 A	79.00 abc	8.23 a-h	40.73 abcd	53.26 h-n	100.11 jkl	21.97 a-e	11.28 abcd	22.03 b-I
N2V7	132.00 Ab	66.56 a-g	53.66 ab	77.66 abcd	8.40 a-f	48.20 Ab	64.53 a-h	103.07 f-l	22.78 abc	12.30 a	23.10 a-f
N2V8	133.66 ab	70.86 ab	54.66 ab	76.00 a-e	8.10 a-j	48.66 ab	67.70 abcd	102.73 f-l	22.01 a-e	10.90 abcd	22.60 a-I
N2V9	135.66 A	59.73 g-k	53.33 ab	63.00 Efgh	7.46 f-k	40.90 abcd	66.60 a-f	102.87 f-l	20.08 b-h	10.18 abcd	20.63 b-j
N2V10	131.00 Ab	63.93 c-k	55.33 Ab	68.33 b-h	8.26 a-g	41.23 abcd	59.00 a-m	107.56 e-l	20.67 b-g	10.56 abcd	22.16 b-I
N2V11	133.33 Ab	70.30 abc	55.66 ab	72.33 a-f	8.06 a-j	41.43 abcd	61.36 a-k	107.43 e-l	17.61 e-I	11.86 abc	19.06 hij
N2V12	134.00 Ab	67.46 a-f	53.66 ab	74.00 a-f	8.40 a-f	47.13 abc	63.40 a-I	119.70 a-e	19.47 b-i	12.16 abc	23.03 a-h
N3V1	136.33 A	61.90 d-k	53.00 ab	70.33 a-h	7.90 a-k	40.30 bcd	52.56 i-n	101.60 g-l	19.35 b-i	9.57 bcd	19.66 e-j
N3V2	131.00 Ab	59.66 g-k	54.66 ab	70.00 a-h	8.20 a-h	43.90 abcd	60.63 a-k	99.80 kl	20.27 b-g	11.53 abcd	20.23 b-j
N3V3	128.00 B	67.60 a-e	55.00 ab	70.00 a-h	8.33 a-f	41.96 abcd	65.90 a-g	103.07 f-l	20.61 b-g	11.96 abc	21.26 b-j
N3V4	132.00 Ab	66.43 a-h	53.66 ab	78.66 abc	7.93 a-k	42.23 abcd	65.16 a-g	115.66 b-h	19.93 b-I	12.18 ab	23.06 a-g
N3V5	132.66 Ab	60.26 g-k	54.00 ab	59.00 h	7.66 c-k	46.86 abc	44.83 N	99.91 jkl	20.11 b-g	9.16 d	20.10 b-j
N3V6	128.00 B	64.10 b-k	56.33 A	68.00 b-h	8.30 a-g	42.86 abcd	60.30 a-k	100.60 h-l	19.92 b-i	9.64 abcd	20.06 b-j
N3V7	132.66	67.56 a-e	53.66 ab	82.00	8.40	37.86	55.76	115.13	19.19 b-I	10.94 abcd	21.86 b-I

	Ab			a	a-f	D	e-m	b-j			
N3V8	135.66 A	62.80 d-k	52.66 ab	73.33 a-g	8.16 a-h	43.36 abcd	51.10 j-n	112.03 c-l	20.98 b-g	11.56 abcd	23.43 abcd
N3V9	134.44 Ab	63.63 c-k	53.66 ab	80.00 ab	8.03 a-j	41.16 abcd	50.56 klmn	100.60 h-l	20.11 b-g	9.66 abcd	20.23 b-j
N3V10	132.66 Ab	62.50 d-k	53.00 ab	73.66 a-f	7.66 c-k	46.66 abc	47.73 Mn	100.63 h-l	20.77 b-g	10.93 abcd	20.96 b-j
N3V11	132.00 Ab	67.23 a-f	55.00 ab	71.00 a-h	8.26 a-g	45.46 abcd	55.63 e-n	108.26 d-l	21.59 b-f	11.93 abc	23.23 a-e
N3V12	132.66 Ab	71.43 a	52.33 ab	83.00 a	8.60 abcd	46.80 abc	59.56 a-l	115.43 b-i	19.80 b-l	11.37 abcd	22.83 a-h

Values followed by the same latter for each trait are not significantly different.
Where: levels of nitrogen (N0= 0, N1=75, N2=150, N3= 225 kg N ha^{-1}).
V= genotype (V1= APST-6, V2= APST-36, V3= BABAGA-3, V4=APST-35, V5= Adana-99, V6= IPA-95, V7= Crezo, V8= APSTA-26, V9= Jihan-99, V10= Adana, V11=APSTA-33, V12=TAWA)

Table (4) revealed simple correlations coefficients between all studied characters in bread wheat. Highly significant and positive correlation was shown between days of 75% flowering and biomes yield g. While significant and positive correlation was found between days of 75% flowering, grain weight 1000 g. and flag leaf area, While negative highly significant harvest index and grain filling. And negative significant with number of spike/plant, while not significant with other trait. Highly significant and positive correlation was showed between plant height (cm) and number of spike/plant. While significant and positive correlation was found between plant heights (cm), spike length (cm) and grain yield .g, and not significant with other traits. In grain filling showed highly significant and positive correlation in the number of spike/plant, grain weight 1000 g. and protein, while significant and positive correlation was found between grain filling, spike length (cm) and biomes g. while not significant for other traits. While Significant and positive correlation was showed between numbers of spike/plant and spike length (cm). While not significant for all other traits. Highly significant and positive correlation was showed between spike length (cm) and grain weight 1000g.while negative highly significant flag leaf area (cm) and grain yield g. while not significant for other traits. Highly significant and positive correlation was showed between grain weight 1000 g, flag leaf area (cm), harvest index, protein% and grain yield g. while not significant for all other traits. Highly significant and positive correlation was showed between flag leaf area (cm) and biomes g. and while negative highly significant in harvest index. And all other traits were not significant. Highly significant and negative correlation was showed between biomes g. and harvest index. And negative significant form protein%. While not significant for other traits. Highly significant and positive correlation was showed between harvest index and grain yield g. and significant positive from protein%. And other traits not significant. While highly significant and positive correlation was showed between protein% and grain yield g. and other traits not significant. Similar results have been reported by other researcher (Ahmad and Al-Taweal, 2007).

Table(4):- phenotypic correlation for studies traits.

Phenotypic correltion												
Characters		days of 75 % Flowering	Plant height (cm)	Grain filling	Number of spike	Spike length (cm)	Grain weight 1000g.	Flagleaf area (cm)	Biomes g.	Harvist index	Protein %	Grain yield g.
Days 75% flowering	1	1	-0.0860	-0.5302**	-0.2096*	0.0979	0.2342*	0.2481*	0.2719**	-0.3471**	0.0344	-0.0718
Plant height(cm)	2		1	0.0550	0.6959**	0.2377*	0.0821	-0.1464	0.0928	0.0112	0.1551	0.2531*
Grain filling	3			1	0.2981**	-0.2362*	0.2942**	-0.0678	-0.2611*	0.1974	0.3363**	0.1682
Number of spike	4				1	0.2169*	-0.0918	-0.2068	0.0667	0.0436	0.1293	0.1902
Spike length(cm)	5					1	2.2355**	-0.3574**	-0.2051	0.0576	-0.1055	-1.2425**
Grain weight(cm)	6						1	0.4193**	0.0149	0.4531**	0.7007**	0.6348**
Flag leaf area(cm)	7							1	0.3247	-0.361**	0.0709	-0.1271

			7		
Biomes g.	8	1	-0.6949	* -0.2102	0.1158
Harvest index	9		1	* 0.2245	** 0.8428
Proein%	10			1	** 0.4645
Grain yield g.	11				1

*and ** significant difference at level 0.05% (r= 0.207) and 0.01 (r= 0.269) respectively.

Estimation of variance component for twelve genotypes with eleven traits is presented table (5), the phenotypic and genotypic coefficient of variation reveled that for all studied traits had greater than phenotypic coefficients of variation more than influenced by the environmental. Similar result were also found by (Adhiena, M., and Taddesse, D., 2016).

According (Ali, 1999), heritability estimation showed low values of all studied traits indicated that the characters are influenced by environment. For the genetic advance as percent according (Al-Rawi 1987) were height for days of 75% flowering, grain filling, number of spike/plant, flag leaf area (cm), biomes g. and protein percent.in which value of heritability indicating that these traits are not governed by additive gene action and could be equally improve through hybridization program. While moderate genetic advance found for (plant height, spike length (cm) and harvest index, while low for other traits. Similar result was also found by (Delta M, and Zerga, 2020). And (Muhder, N., and Sorsa, Z., 2020).

Table (5):- component analysis and genotypic parameters for studies traits.

Treatments	$\sigma^2 g$	$\sigma^2 p$	Gcv	Pcv	h^2.b.s	GA	GA%
Days of 75% flowering	1.072	12.99	0.775	2.699	8.257	0.523	39.232
Plant height (cm)	1.881	15.026	2.155	6.091	12.519	0.854	13.422
Grain filling	0.308	7.947	1.039	5.2733	3.883	0.192	36.044
Number of spike	13.998	66.140	5.346	11.620	21.164	3.029	43.286
Spike length (cm)	0.005	0.343	0.936	7.268	1.659	0.017	21.224
Grain weight 1000 g.	0.029	19.716	0.387	10.022	0.149	0.011	2.633
Flag leaf area (cm)	12.676	57.362	5.915	12.583	22.098	2.945	48.940
Biomes g.	27.829	110.801	4.869	9.716	25.116	4.653	42.951
Harvest index	0.661	7.036	4.125	13.452	9.406	0.439	22.270
Protein %	0.033	1.779	1.680	12.208	1.893	0.044	40.689
Grain yield	0.020	3.986	0.675	9.411	0.515	0.018	8.534

Where: σ^2p = phenotypic variance, σ^2g = genotypic variance, Gcv= genotypic coefficient of variation, Pcv= phenotypic coefficient of variance, h^2.b.s= broad sense heritability, GA= genetic advance, GA%= genetic advance percent.

CONCLUSION

According to the results obtained the following can be concluded:

The correlation study revealed that yield and strong positive association with, this correlation studies indicated that grain yield of wheat can be improved by selecting genotypes having higher performance for the above characters.

Path-coefficient analysis revealed that the maximum positive direct effect exhibited by biomess yield followed by harvest index, path-coefficient analysis suggest that biomess and harvest index may serve as effective selection attribute, during breeding program for yield improve and in wheat.

For breeding program attention should be paid to traits with moderate to high variability and genetic advance like days to 75% flowering, grain yield, number of spike, flag leaf area, biomess yield and protein. In order to produce and effective responses to yield enhancement, the genotype exanimated under the level (225 kg N ha-1) was more effective on the yield and it component for all studied genotype.

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پوخته

دوازده جورین گه نمێ نانی دگه ل چار رێژه یێن په یننێ نایتروجینی (٢٢٥،١٥٠،٧٥،٠)كغم/هيكتار. هاتیه چاندن ب رێیا پارچه یێن ژێكڤه كری ب سێ جاركی ل سالا ٢٠٢١. هه ڤبه ست و هوكارێن ژێک جودا یێن بوماوه یی و شێوه ی. بوماوه دگه ل باشكرنا بوماوه یێ گومان لیكری هاتنه هژمارتن بو سالوخه تێن هژمارا روژێن گولی دانێ ٧٥٪ و بلندیا رووه كی و تژی بونا دندكێ و به رێ دندكێ و فره هیا به لگێ و به رێ بایلوژی/بنا رووه كی و ریژین پروتینی. دگه ل ریبه رێ دروینی هاتیه دیتن كو هه ڤبه ستا پوزه تیف یا بلند یا به رچاڤ دناڤبه را به رێ دروینێ و سه نگا ١٠٠٠ دندكا. ریبه رێ دروینێ و ریژا پروتینی یا پوزه تیف یا به رچاف ل ده ڤ ریژا ٥٪ دگه ل سالوخه تێن بلندیا رووه كی. بوماوه یێ ب رامانا فره هـ یا كیم بو بو هه مم سالوخه تان. سه باره ت نافه راستا كشتی دناڤبه را بهایێ نافه راست بو یین نزم بو وان سالوخه تین هاتینه خاندن.

الخلاصة

اثنتا عشر تركيب وراثي مع أربعة مستويات من سماد نيتروجين (٢٢٥،١٥٠،٧٥،٠)كغم/هكتار. تم زراعتها وفق تصميم القطاعات المنشقة بثلاث مكررات في الموسم الزراعي (٢٠٢١). الأرتباط و معامل الأختلاف الوراثي والمظهري، التوريث مع التحسين الوراثي المتوقع تم تقديرها لكل من ٧٥ % يوم التزهير، ارتفاع النبات (سم)، أمتلاء الحبة، حاصل الحبوب غم، مسافة ورقة العلم (سم)، الحاصل البيولوجي غم، نسبة البروتين المعنوية مع دليل الحصاد وجدت أرتباط موجب عالي المعنوية بين صنفة الحاصل مع وزن ١٠٠٠ حبة غرام، دليل الحصاد و نسبة البروتين مئوية بينما كانت معنويا و موجبا عنده 5% مع صفة ارتفاع النبات سم. التوريث المفهوم الواسع كانت منخفضا لكل الصفات رافقتها التحسين التورثي المتوقع نسبتا الى المتوسط العام بين قيم متواسط الى منخفضة للصفات المدروسة.

الكلمات الدالة: حنطة الخبز, التوريث, الارتباط مع التحسين الوراثي المتوقع