Estimation of Some Genetic Parameters of the Second Generation of Durum Wheat Genotypes

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Abstract

The study was conducted during the winter agricultural season of 2021, in the agricultural fields in the Ba'ashiqah region (city of Mosul). It involved ten parental genetic combinations of durum wheat, which were divided according to the factorial mating design (A.B). Six of these combinations were paternal lines, obtained from the International Center for Agricultural Research in Dry Areas (ICARDA), while four were maternal lines, including three approved varieties. Additionally, a fourth genetic entry that had been previously cultivated under the region's environmental conditions and proven suitable was included. The second-generation seeds were obtained from the first-generation seeds provided by the supervising professor. The parental genetic combinations and their factorial hybrids, totaling twenty-four hybrids, were sown using a completely randomized block design with three replications.

The performance of the male and female parents and hybrids was evaluated, and the mean squares of the parents and high significant hybrids were calculated. All studied traits, except for the weight of a thousand grains (for hybrids), showed significant differences at a 0.05 probability level. The best mean calculated for the female parent (svevo) was followed by the traits of the number of days to flowering, number of grains/ m^2, weight of a thousand grains, biological yield, and grain yield. The male parent (Adnham) excelled in the traits of plant height and grain yield, as well as protein content. The hybrid (Sardar x Gigamor) outperformed in three traits: number of grains/ spike, grain yield, and harvest index. The hybrid (Duma - 1x Gigamor) ranked next in the traits of plant height and leaf area. In a broad sense, the inheritance values were moderate for most of the studied traits and high for the protein content trait. In a narrow sense, the inheritance values were low for most of the studied traits, moderate for leaf area and number of grains/ spike, and protein content. The values of dominance variance were higher than the values of additive variance as an average for all studied traits. Therefore, to improve the studied traits can use hybridization programed in durum wheat genotypes.

Keywords: wheat, hybrids, variance, Heritability

Introduction

Wheat is one of the major cereal crops and holds great importance in terms of production and significance. It belongs to the *Poaceae* family and tops the list of staple food commodities. Wheat is considered the most essential food item for humans due to its balanced composition of proteins and carbohydrates in its grains. Wheat grains are known for being a primary source of protein, with levels ranging from 12% to 17% depending

on the varieties. They also contain starch (75%), fats (1.5%), vitamins (such as B1 and B2), and beneficial minerals like calcium, magnesium, phosphorus, and iron [1]. Wheat is the main food source for people worldwide and serves as a fundamental ingredient used daily for human and animal nutrition [2].

Wheat ranks as a strategic crop that receives significant attention from breeders and farmers in Iraq, as it plays a crucial role in meeting food requirements. The cultivation of durum wheat is concentrated in the rain-fed region of Iraq, particularly in the areas surrounding Nineveh Governorate. This is primarily due to the high dependency of the population in these regions on wheat for food, after undergoing various manufacturing processes. It is used extensively in the production of bulgur, semolina, pasta, spaghetti, and pastries. The gluten in durum wheat stands out for its flexibility and low elasticity, attributed to the absence of the D chromosome group responsible for elasticity [3]. This type of wheat possesses two sets of chromosomes, labeled A and B, with a diploid chromosome number of 28 (2n=28). In 2022, the global cultivated area of wheat reached approximately 222 million hectares, with a grain production of 779 million metric tons (USDA, 2022). The cultivation of durum wheat is prevalent in the rain-fed region of Iraq, particularly in the areas surrounding Nineveh Governorate. Several studies in this field have shown that the expected genetic improvement values, as a percentage of the overall average, were low for traits such as leaf area index, plant height, number of spikes/ plant, number of grains/ spike, 1000-grain weight, individual plant yield, biological yield, and harvest index [4].

Ayoub found that the degree of dominance was greater than one for the traits of plant height in the first hybrid and the number of spikes in the plant in the second hybrid. However, dominance was complete for the traits of the number of spikes in the plant in the first hybrid and plant height in the second hybrid. There was partial dominance for the traits of the number of grains/ spike, weight of 1000 grains, and grain yield in the plant in both hybrids when studying six early generations of wheat [5].

Anis and Al-Mujamai found in their study of ten varieties of wheat, that the broad-sense heritability was high for the traits of the number of days until 50% of the spikes were expelled, leaf area, plant height, number of spikes/ plant, number of grains/ spike, weight of 1000 grains, individual yield, plant lodging, and harvest index. However, narrow-sense heritability was low for all of the above traits except leaf area and harvest index [6].

According to Al-Janabi study, the mean squares of the male and female genotypes, as well as the mean squares of the hybrids, were significantly high for all the studied traits except for protein content (in parental varieties) at a significance level of 0.05 [7].

Bayati concluded that the genetic variance was higher than the environmental variance for all the studied traits in the second generation [8].

Materials and Methods

In the study, ten genetic combinations were used, consisting of six male parents and four female parents, as detailed in Table 1. Seeds of the second generation were obtained from the seeds of the first generation. These seeds, along with their parental genetic combinations, were planted, resulting in twenty-four experimental hybrids. The planting took place in the region of Ba'ashiqah, located at a latitude of 36.451° north and a longitude of 43.352° east.

During the Winter season of 2021-2022, sowing date was on November 26, a complete randomized block design (R.C.B.D) with three replications was used. The experimental unit included two rows, each measuring 2.5m in length, with a spacing of 30 cm between them. Duncan's Multiple Range Test was employed for statistical analysis. The study encompassed

various traits, including the number of days to 50% flowering, plant height, leaf area, spike length, number of grains/ spike, number of spikes, thousand grain weight, biological yield, grain yield, harvest index, and protein content.

Triple Super Phosphate fertilizer (P_2O_5) with a concentration of 46% was applied at a rate of

200 kg/ha during land preparation, and urea with a concentration of 46% was applied in two separate doses: the first during land preparation and the second when the plants reached the flowering stage [9].

Table 1: Numbers, names, and pedigree of the genetic combinations used in the study and their sources of acquisition.

Number	Name (male parent)	Genotype
1	Maggy	Terbol975/Geruftel2/7/Icasyr1//Mrf2/T.dids20123/6/319ADDO/5/D68193A1A//Ruff/Fg/3/Mtl5/4/Lahn
2	Zeina2	IcamorTA0471//IcamorTA0459/Ammar8/4/Stj3//Dra2/Bcr/3/Ter3
3	Joudille	Atlast1/961081//Icasyr1/3/Tilling/ch17
4	Gigamor	IcamorTA459/4/Gdr2//SwAlg/Gdr1-43/3/IcamorTA463/5/Ammar1
5	Icarasha2	Stj3//Bcr/Lks4/3/Ter3
6	Adnham	Adnan1//Mgnl3/Ainzen1
Number	**Name (female parent)**	**Genotype**
7	Svevo	Registered at the National Committee for Registration and Accreditation of Agricultural Varieties under Decision (20) on 8/10/2012 - Seed Inspection and Certification - Ninawa Branch
8	Sardar	Research Station ,Erbil University - Origin: Icarda
9	Grecale	Registered at the National Committee for Registration and Accreditation of Agricultural Varieties under Decision (20) on 8/10/2012 - Seed Inspection and Certification - Ninawa Branch
10	Duma -1	Seed Inspection and Certification - Ninawa Branch

Phenotypic, genetic, and environmental variations were estimated according to Al-Zubaidi and Al-Jubouri [10] and calculated using the following equations:

Dominant variance
$D = Ø_{mf} σ^2$

Phenotypic variance
$E G + σ^2 P = σ^2 σ^2$

Environmental variance
$σ^2 E = Mse$

Additive genetic variance from male parents
$Ø_m = 1/2 σ^2 A$ then $σ^2 A = 2Ø_m$

Genetic variance
$D + σ^2 A σ^2 G = σ^2$

Additive genetic variance from mothers
$Ø_f = 1/2 σ^2 A$ then $σ^2 A = 2Ø_f$

The additive genetic variance is the average of the two values σ^2 A = (2Øm + 2Øf)/

Since:

σ^2E = environmental variance, σ^2G = genetic variance, σ^2P = phenotypic variance

σ^2A = Additive variance, σ^2D = Dominant variance

The significance of the variances was tested from zero by the method reported by Kempthorne [11].

Genetic parameters (heritability, average degree of dominance, and expected genetic improvement)

Heritability degree:

Heritability in the broad sense was calculated according to Al-Zubaidi and Al-Jubouri [10] based on the following equations:

Broad-sense heritability = B.S. $h^2 \frac{\sigma^2_G}{\sigma^2_p}$ X 100

Narrow-sense heritability = N.S. $h^2 \frac{\sigma^2_A}{\sigma^2_p}$ X 100

Genetic variance of the trait: σ^2_G, Phenotypic variance of the trait: σ^2_pp, Environmental variance of the trait: σ^2_E , σ^2A = Additive variance .

The thresholds for broad-sense heritability were adopted according to Ali [12] as follows:

Less than 40%: Low heritability; 40% - 60%: Moderate heritability; More than 60%: High heritability

The thresholds for narrow-sense heritability were adopted according to Al-Adhari [13] as follows:

Less than 20%: Low heritability; 20% - 50%: Moderate heritability; More than 50%: High heritability.

The Average Degree of Dominance is calculated according to the following equation:-

The Average Degree of Dominance = ā $\sqrt{2\sigma^2 D/\sigma^2 A}$

The Average Degree of Dominance for a quantitative trait indicates the average dominance of multiple genes affecting that trait, as described by Hallauer and Miranda [14].

ā = zero: No dominance exists.

0 < ā < 1: Partial dominance exists.

ā = 1: Complete dominance exists.

ā > 1: Over dominance exists.

Expected Genetic Improvement:

The expected genetic improvement, expressed as a percentage, can be calculated using the method outlined by Al-Zubaidi and Al-Jubouri [10] as indicated in the following equations.

$$E.G.A = K.H^2_{N.S}.\sigma_P$$

Where:

E.G.A: represents the expected genetic improvement.

$H^2_{N.S:}$ represents the narrow-sense heritability.

: Standard deviation of the phenotypic variance.

K: represents the selection intensity and is equal to 1.75 when selecting 10% of the plants.

The expected genetic improvement, as a percentage, can be calculated using the following equation:

$$E.G.A\% = \frac{E.G.A}{X^-} \times 100$$

Where:

E.G.A% represents the expected genetic improvement as a percentage of the overall average of the trait.

E.G.A represents the expected genetic improvement.

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X^- : represents the average of the trait.

The thresholds for the expected genetic improvement, as a percentage of the average, were adopted based on the suggestions by Agarwal and Ahmed [15] as follows:

Less than 10%: Low expected genetic improvement; 10% - 30%: Moderate expected genetic improvement; More than 30%: High expected genetic improvement.

Results and Discussion

The arithmetic means of the ten parental genotypes (male and female).

From Table (2), it can be observed that in calculating the means of the ten parental genotypes (male and female), the trait "number of days to flowering at 50%" indicated that parent (7) significantly outperformed the other parental combinations with the fewest number of days, averaging 122.000 days. It did not differ significantly from parents (3), (6), (8), (9), and (10), while parental combination (5) showed the least earliness with an average of 125.000 days and did not differ significantly from parental combinations (1), (2), and (4).

The genetic compositions for the plant height trait showed that genotypes (5) and (6) exhibited the highest height, averaging 86.867 and 86.733 cm, respectively, and did not differ significantly from parents (1), (3), (9), and (10). Parent (4) had the lowest height with an average of 72.667 cm and differed significantly from the other parents.

The leaf area trait, which contributes to carbohydrate transfer to the grains formed in the spike, showed the highest mean for parent (2) with 28.058 cm, which did not differ from parents (6), (7), (8), and (9). Parental combinations (1) and (3) showed the lowest means of 25.070 and 24.968 cm, respectively, and did not differ significantly from each other.

Regarding the spike length trait, parent (5) had the highest mean of 7.095 cm, significantly different from the other parents, while parent (3) had the lowest mean of 5.809 cm. For the number of grains/ spike trait, parent (10) exhibited the highest mean of 41.733 grains/ spike and differed significantly from the other parents except for parent (6), while parent (1) recorded the lowest mean of 34.467 grains/ spike.

The number of spikes/ m^2 trait distinguished genotypes (7) and (9) with the highest means of 312.667 and 320.333 spikes/ m^2, respectively, while parent (8) had the lowest mean of 218.333 spikes/ m^2.

In terms of the weight of 1000 grains trait, genotypes (7) and (4) showed the highest means of 49.667 and 49.333 grams, respectively, and did not differ significantly from each other, while the lowest means were recorded by parents (1), (2), (3), (6), (9), and (10) at 41.667, 41.000, 41.667, 43.333, 41.667, and 42.667 grams, respectively.

The biological yield trait showed that parents (6) and (7) had the highest means of 13,576.443 and 13,487.049 kilograms/ hectare (kg/ha), respectively, while parents (1) and (8) had the lowest means of 7,308.182 and 7,819.116 kg/ha, respectively.

The grain yield trait exhibited the highest mean for parents (6), (7), (9), and (10) at 5,089.267, 5,392.617, 4,977.480, and 5,067.167 kg/ha, respectively, while the lowest mean of 3,239.960 kg/ha was recorded for parent (1).

For the harvest index trait, parent (8) had the highest mean of 47.237%, significantly different from the other parents except for parent (4), while parent (5) had the lowest mean of 35.873%.

In terms of protein content, parents (5), (6), (8), and (10) had the highest means of 10.433%, 10.367%, 10.400%, and 10.467%, respectively, while parent (3) had the lowest mean of 9.833%.

From Table 2, it can be concluded that the female parent (7) excelled in several traits, including the number of days to flowering, the number of spikes/ m^2, weight of a thousand grains, biological yield, and grain yield. It is followed by the male parent (6), which excelled in traits such as plant height and grain yield, followed by the male parent (5), which excelled in traits such as plant height, spike length, and protein content. Similarly, the female parent (3) excelled in traits such as number of grains/ spike, grain yield, and protein content.

The means of hybrid combinations, male parents, female parents, and their interactions according to the factorial mating system.

We observe from Table (3) the analysis of variance according to the factorial mating system for the hybrids, male parents, female parents, and their interactions. The mean squares of hybrids were significant at a 0.01 probability level for all studied traits except for the trait of biological yield (kg/ha), which was significant at a 0.05 probability level. The male parents showed significant differences at a 0.01 probability level for the traits of number of grains/spike, number of spikes/m², and protein percentage, and significant differences at a 0.05 probability level for the traits of plant height (cm) and leaf area (cm²). The remaining traits did not reach statistical significance. As for the female parents, they showed significant differences at a 0.01 probability level for the traits of number of days to 50% flowering, leaf area (cm²), number of grains/ spike, and protein percentage, while they were significant at a 0.05 probability level for the traits of number of spikes/m², thousand-grain weight, grain yield, and harvest index. The remaining traits did not reach statistical significance. The interactions between male and female parents were significant at a 0.01 probability level for all studied traits, except for the traits of number of days to 50% flowering and biological yield (kg/ha), which were significant at a 0.05

probability level. Protein percentage did not reach statistical significance.

Table 2: Arithmetic Means of the Ten Parental Varieties (Male and Female)

Traits Studied		Days to 50% Flowering	Plant Height (cm)	Leaf Area (cm^2)	Spike Length (cm)	Grain count /spike	Spike count/m2	1000 Grain Weight (g)	Biological yield (kg/ha)	Grain yield (kg/ha)	Harvest index (%)	Protein content (%)
Parental Varieties												
1	Male Parents	A-B 124.667	A-C 82.933	D 25.07	B-D 6.323	D 34.467	DH 225.333	B 41.667	D 7308.182	C 3239.96	BC 44.333	AB 10.233
2		A-B 124.667	CD 78.333	A 28.058	B-D 6.143	B-D 36.133	C-H 231.333	B 41	CD 8377.278	BC 3429.627	D 40.94	AB 10.233
3		B-D 123.333	AB 84.4	D 24.968	D 5.809	B-D 37.533	A-C 291.667	B 41.667	A-C 11402.009	AB 4564.417	D 40.032	C 9.833
4		A-C 124	H 72.667	CD 25.452	AB 6.714	B-D 37.933	B-H 244.333	A 49.333	B-D 9951.017	AB 4577.468	AB 46	AB 10.333
5		A 125	A 86.867	B-D 26.038	AB 7.095	BC 38.2	B-H 248.667	AB 46	AB 12176.193	A-C 4367.953	H 35.873	AB 10.433
6		B-D 123.333	A 86.733	A-C 26.813	B-D 6.143	AB 39.333	AB 298.333	B 43.333	A 13576.443	A 5089.267	H 37.486	AB 10.367
7	Female Parents	D 122	DH 75.2	AB 27.723	BC 6.476	CD 34.733	A 312.667	A 49.667	A 13487.049	A 5392.617	D 39.984	A-C 10.133
8		B-D 123.333	B-C 80	A-D 26.365	CD 6.047	B-D 36.867	H 218.333	AB 46	D 7819.116	BC 3693.51	AB 47.237	A 10.4
9		B-D 123.333	AB 84.167	A-C 26.852	B-D 6.093	B-D 37.333	A 320.333	B 41.667	A-C 11238.208	A 4977.48	BC 44.291	BC 10.033
10		CD 123	AB 85.2	B-D 26.14	CD 5.904	A 41.733	A-D 284.333	B 42.667	AB 11712.925	A 5067.167	C 43.261	A 10.467
Male Parent Means		124.167	81.989	26.067	6.371	37.267	256.611	43.833	10465.187	4211.449	40.777	10.239
Female Parent Means		122.917	81.142	26.77	6.13	37.667	283.917	45	11064.324	4782.693	43.693	10.258
Overall Means		123.667	81.65	26.348	6.275	37.427	267.533	44.3	10704.842	4439.946	42	10.247

Table 3: Averages of squares of male and female crosses and parents and their overlap according to the global mating system.

Studied Characteristics / sources of variance	Degrees of Freedom	Number of Days to 50% Flowering	Plant Height (cm)	Leaf Area (cm²)	Spike Length (cm)	Number of Grains/Spike	Number of Spikes/m²	Weight of 1000 Grains (g)	Biological Yield (kg/ha)	Grain Yield (kg/ha)	Harvest Index (%)	Protein Content(%)
Replications	2	0.722	51.215	15.979	0.041	17.224	5766.056	49.389	1333587.471	518133.366	10.264	0.517
Crosses	23	** 1.99	** 48.716	** 10.71	** 0.573	** 14.363	** 3288.115	** 39.998	* 2576729.63	** 1445574.23	** 35.391	** 0.226
Males	3	0.956	* 51.816	* 7.35	0.445	** 16.799	** 4214.981	18.422	962685.734	582183.403	19.114	** 0.158
Females	5	** 4.704	22.639	** 21.66	0.387	** 18.313	* 3564.532	* 54.241	3255053.827	* 1653119.95	* 36.495	** 0.392
M x F	15	* 1.793	** 52.898	** 9.64	** 0.653	** 12.762	** 2923.877	** 44.341	* 2979079.422	** 1691862.02	** 40.595	0.216
Error Experiment	46	0.838	19.134	2.992	0.238	3.696	1023.157	15.432	1341297.067	477615.984	9.075	** 0.082
Total	71											

** Significantly different at the 0.01 level of significance.

*Significantly different at the 0.05 level of significance.

Genetic, environmental and phenotypic variations and coefficient of variance:

The results of Table (4) demonstrate the components of phenotypic variance. It can be observed that the additive variance of the female parents differed significantly from zero for all studied traits except for plant height, spike length, and grain yield. On the other hand, the additive variance of the male parents differed significantly from zero for all traits except for the number of days to 50% flowering, spike length, thousand grain weight, grain yield, and harvest index. The dominance variance, based on the mean basis, differed significantly from zero for all traits except for plant height, spike length, thousand grain weight, and grain yield. The additive variance was found to differ significantly from zero for all studied traits, indicating the importance of using hybridization in improving these traits. These results are consistent with the findings of Hasan [16] and Al-Bayati [8]. When comparing the coefficient of Additive variance with the coefficient of dominance variance, it was found that the coefficient of dominance variance was higher than the coefficient of Additive variance for all traits. This suggests the possibility of obtaining desirable traits in early segregating generations using hybridization, which is in line with the results of Al-Dulaimi [17], Hasan [16], and Al-Janabi [7]. The total genetic variance compared to the environmental variance was high for traits such as leaf area, number of grains/ spike, number of spike/ m^2, grain yield (kg/ha), and harvest index (%), while it was low for other traits. As for the environmental variance, it differed significantly from zero for all studied traits. The phenotypic variance ranged from 0.103 for protein percentage to 1961993.395 for grain yield (kg/ha).

Heritability values, average degree of dominance, and expected genetic improvement as a percentage of the general mean of the trait:

From Table (5), it can be observed that the broad-sense heritability values were moderate for most of the studied traits, except for the number of days to 50% flowering and grain yield, which were low, and protein percentage, which was high. This indicates the importance of genetic variance, which is one of the main components of phenotypic variance for these traits. It suggests the presence of superior genetic composition in terms of phenotypic appearance and the reliance on hybridization in improving these traits. The reason for this is the high value of genetic variance and the low value of environmental variance. These results are consistent with, Al-Dulaimi [17], Hasan [16], and Askander [18]. On the other hand, the narrow-sense heritability values were low for most of the studied traits, except for leaf area (cm²), number of grains/ spike, and protein percentage, which were moderate. This is attributed to the low values of Additive variance. These results align with Shimelis [19] and Ali [20]. The values of the mean degree of dominance were greater than one for all traits, indicating the presence of over dominance. These results are consistent with Al-Dulaimi [17], Al-Janabi [7], and Hasan [16]. The expected genetic gain as a percentage of the average was low for all studied traits, which can be attributed to the low narrow-sense heritability, leading to a decrease in the expected genetic improvement. These results align with Hasan [16] and Al-Hiti [21].

Table 4: Genetic, environmental and phenotypic variances and coefficients of their differences for the studied traits.

Traits Studied Genetic Variance	Flowering Days at 50%	Plant Height (cm)	Leaf Area (cm²)	Spike Length (cm)	/Grain/ Spike	/Spikes m²	1000 Grain Weight (g)	Biological Yield (kg/ha)	Grain Yield (kg/ha)	Harvest Index (%)	Protein Percentage (%)
Additive Variance of Female Parents	0.43 ± 0.331	0.389 ± 1.649	2.074 ± 1.524	0.016 ± 0.028	1.624 ± 1.29	282.375 ± 251.562	4.312 ± 3.828	212639.64 ± 230755.917	130611.551 ± 116673.391	3.047 ± 2.573	0.041 ± 0.028
Additive Variance of Male Parents	0.02 ± 0.09	5.447 ± 4.662	0.726 ± 0.663	0.034 ± 0.04	2.184 ± 1.502	531.971 ± 377.11	0.498 ± 1.723	---------- ± 97146.973	17427.903 ± 54350.755	1.673 ± 1.731	0.022 ± 0.014
Additive Variance as Rate	0.225 ± 0.21	2.918 ± 3.155	1.4 ± 1.093	0.025 ± 0.034	1.904 ± 1.395756	407.173 ± 314.3363	2.405 ± 2.775	74768.876 ± 163951.445	74019.727 ± 85512.0734	2.36 ± 2.151	0.031 ± 0.02
Dominance variance	0.318 ± 0.213	11.254 ± 6.186	2.216 ± 1.121	0.138 ± 0.076	3.022 ± 1.481	633.573 ± 341.466	9.636 ± 5.177	545927.452 ± 352620.213	404748.679 ± 196145.489	10.507 ± 4.682	0.045 ± 0.025
Total Genetic Variance	0.543	14.173	3.616	0.164	4.926	1040.746	12.041	620696.327	478768.407	12.866	0.076
Environmental Variance	0.838 ± 0.171	19.134 ± 3.906	2.992 ± 0.611	0.238 ± 0.049	3.696 ± 0.755	1023.157 ± 208.851	15.432 ± 3.15	1341297.067 ± 273791.117	477615.984 ± 97492.954	9.075 ± 1.853	0.082 ± 0.006
Phenotypic Variance	1.381	33.307	6.608	0.402	8.622	2063.903	27.474	1961993.395	956384.391	21.942	0.103

Negative variances resulting from sampling error are considered zero.

Table 5: values of heritability, average degree of dominance and expected genetic improvement as a percentage of the general average of the trait for the eleven studied traits.

Traits Genetic Features	Days to 50% flowering	Plant height (cm)	Leaf area (cm²)	Spike length (cm)	Number of grains/spike	Number of spikes/m²	Weight of 100 grains (g)	Biological yield)kg/ha(	Grain yield)kg/ha (	Harvest index (%)	Protein content (%)
Broad-sense heritability(%) H²B.S	39.3	42.551	54.728	40.714	57.129	50.426	43.829	31.636	50.06	58.639	73.355
Narrow-sense heritability(%) H²N.S	16.261	8.761	21.191	6.326	22.082	19.728	8.754	3.811	7.74	10.755	30.175
Coefficient of dominance a⁻	1.683	2.777	1.779	3.297	1.782	1.764	2.831	3.821	3.307	2.984	1.692
Expected Genetic Advance EGA	0.334	0.885	0.953	0.07	1.135	15.685	0.803	93.414	132.455	0.882	0.17
Expected Genetic Advance as a percentage of the overall mean EGA%	0.271	1.051	3.517	1.107	3.067	5.836	1.799	0.866	2.988	2.164	1.642

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