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## Elucidate gene actions, GCV, PCV, and regression coefficient for grain yield in barley (*Hordeum vulgare* L.)

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### Abstract

This study involved 10 parents and their 45 F<sub>1</sub>s for the estimation of Gene actions for yield contributing traits in barley during the *rabi* season 2021- 22. The significant value of additive (D) and dominance (H<sub>1</sub>) variance for all characters except number of effective tillers per plant, spike length, grains weight per spike and protein content, indicated these traits are controlled by both additive and dominance gene action. The ratio of average degree of dominance ( $\bar{H}_1/D$ ) reflects the presence of overdominance for all the attributes in both generations except for no of grain per spike in F<sub>2</sub>. The ratio of dominant and recessive genes  $[(4\bar{D}\bar{H}_1)^{0.5}+F/(4\bar{D}\bar{H}_1)^{0.5}-F]$  observed more than unity for almost all the characters except for 1000 grain weight, indicated distribution of dominant genes for concern traits. The regression coefficient 'b' deviated significantly from unity indicating non-allelic gene action for all the characters in both the generations except no. of spikelets per spike and grain weight per spike. High value of PCV (%) were observed for the characters of number of spikelets per spike, flag leaf area, biological yield per plant (g), harvest index (%) and grain yield per plant (g). Moderate value of GCV (%) were observed for the characters of days to maturity and number of spikelets per spike in F<sub>1</sub> generation. The above findings will be useful in the implementation of breeding programs to improve barley.

**Keywords:** Gene action, regression coefficient, GCV, PCV and Barley

### Introduction

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops globally, with significant importance in India due to its adaptability to diverse agro-climatic conditions. In India, barley is cultivated primarily in the northern states, including Uttar Pradesh, Rajasthan, Haryana, and Punjab. Uttar Pradesh, being one of the leading states in barley production, contributes significantly to the national output. The crop is valued for its versatile applications, including its use as food, feed, and in the malting and brewing industries. Furthermore, barley's resilience to abiotic stresses, such as drought and salinity, makes it a suitable crop for marginal and semi-arid regions of Uttar Pradesh.

Despite its adaptability, the productivity of barley in India and Uttar Pradesh remains below the global average. This gap necessitates a deeper understanding of the genetic factors influencing yield and related traits Choudhary and Singh (2020) [2]. The analysis of gene action and genetic components plays a crucial role in identifying traits that can be targeted for improvement through breeding programs. Parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and regression coefficients provide insights into the genetic variability and heritability of important traits, guiding the development of high-yielding and stress-tolerant barley varieties Kumar and Yadav (2019) [6].

Genetic variability, expressed through GCV and PCV, is critical for selecting superior genotypes. A higher magnitude of these coefficients indicates greater potential for genetic improvement. The regression coefficient further aids in understanding the relationship between yield and other agronomic traits, facilitating the selection of desirable genotypes.

Studies conducted in Uttar Pradesh have highlighted the presence of considerable genetic variability among barley genotypes, underscoring the scope for genetic enhancement.

The future of barley production in India and Uttar Pradesh hinges on the development of climate-resilient and high-yielding varieties. With the increasing demand for barley in the malting and brewing industries, coupled with its potential as a health food, there is a pressing need to focus on genetic improvement Sharma and Gupta (2021) [9]. Advances in molecular breeding and biotechnological tools can accelerate the development of varieties with enhanced productivity and stress tolerance Singh and Verma (2022) [12].

This article aims to provide an overview of the genetic components influencing barley productivity in Uttar Pradesh, with a focus on gene action, GCV, PCV, and regression coefficients. The findings will contribute to formulating effective breeding strategies for improving barley production and productivity in the region Uttar Pradesh Agricultural Statistics (2023).

### Materials and Methods

The study took place at the Agriculture Research Farm of B.R.D. P.G. College, Deoria, Uttar Pradesh, during the Rabi season of 2021-2022. We developed 45 F<sub>1</sub> hybrids by crossing 10 selected barley genotypes: NDB-302, NDW-1173, UB-307, DWRB-137, NDW-1459, RD-2804, NDB-1609, NDB-1490, HUB-240, and RD-2772. Selfed seeds from these hybrids were used to create F<sub>2</sub> populations. Our experiment included 100 treatments: 45 F<sub>1</sub> hybrids, 45 F<sub>2</sub> populations, and 10 parent varieties, including a check variety. These were arranged in a randomized block design with three replications, using double rows of 4 meters, spaced 22.5 cm apart between rows and 5 cm between plants for optimal growth.

### Statistical analysis

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967). The significance of difference among treatment means was tested by 'F' test. To test the hypothesis H<sub>0</sub>: t<sub>1</sub> = t<sub>2</sub> = ----- = t<sub>v</sub>, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y<sub>ij</sub> = Yield of i<sup>th</sup> entry in the j<sup>th</sup> replication

μ = Generation mean/over-all mean

t<sub>i</sub> = Effect of the i<sup>th</sup> entry (i = 1, 2, -----, v.)

b<sub>j</sub> = Effect of the j<sup>th</sup> replication (j = 1, 2, -----, r.)

e<sub>ij</sub> = Environmental Effect

### Gene action

The value of the Gene action and regression coefficient was computed as per the formula and methods explained by Jinks, 1956; Hayman 1958; Mather and Jinks, 1971.

The components of variance in diallel cross were computed in F<sub>1</sub> by the use of equation given by Hayman (1954a).

Expectation for F<sub>1</sub> diallel crosses is as follows:

$$V_p = \widehat{D} + \widehat{E}$$

$$V_r = (1/4)\widehat{D} + (1/4)\widehat{H}_1 - (1/4)\widehat{F} + [(n+1)/2n]\widehat{E}$$

$$W_r = (1/2)\widehat{D} - (1/4)\widehat{F} + (1/n)\widehat{E}$$

$$V_m = (1/4)\widehat{D} + (1/4)\widehat{H}_1 - (1/4)\widehat{H}_2 - (1/4)\widehat{F} + (1/2n)\widehat{E}$$

Jinks (1956) and Hayman (1958) gave expectations for F<sub>2</sub> diallel crosses. The expected statistics for F<sub>2</sub> generation are the same of that of F<sub>1</sub> except the contribution of h which is halved by one generation of inbreeding. Hence, the coefficient of H<sub>1</sub> and H<sub>2</sub> are (1/4) of those F<sub>1</sub> statistics while the coefficient of F is halved being second- and first-degree statistics h<sup>2</sup>, respectively. These expectations are as follows:

$$V_p = \widehat{D} + \widehat{E}$$

$$V_r = (1/4)\widehat{D} + (1/16)\widehat{H}_1 - (1/8)\widehat{F} + [(n+1)/2n]\widehat{E}$$

$$W_r = (1/2)\widehat{D} - (1/8)\widehat{F} + (1/n)\widehat{E}$$

$$V_m = (1/4)\widehat{D} + (1/16)\widehat{H}_1 - (1/16)\widehat{H}_2 - (1/8)\widehat{F} + (1/2n)\widehat{E}$$

Where,

$\widehat{D}$  = Components of variation due to additive effects of genes.

$$= V_0L_0 - \widehat{E}$$

$\widehat{H}_1$  = Components of variation due to dominance effects of genes.

$$= V_0L_0 - 4W_0L_{01} + 4V_1L_1 - (3n-2)\widehat{E}/n$$

$$\widehat{H}_2 = \widehat{H}_1 [1-(u-v)^2] = 4V_1L_1 - 4V_0\widehat{L}_1 - 2E$$

Where,

U = Proportion of positive genes in the parents.

V = Proportion of negative genes in the parents

$\widehat{F}$  = The mean of F<sub>r</sub> over the arrays

$$F_r = 2(V_0L_0 - 4W_0L_{01} + V_1L_1 - W_r - V_r) - 2(n-2)\widehat{E}/n$$

$\widehat{H}^2$  = Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses)

$$= 4(M_{L1} - M_{L0})^2 - 4(n-1)\widehat{E}/n^2$$

$\widehat{E}$  = The expected environmental component of variation (Error SS + Replication SS/d.f.)/number of replications.

### Regression coefficient

$$b = \frac{\text{Cov}(W_r, V_r)}{\text{Var}(V_r)}$$

Where,

$$\text{Cov.}(W_r, V_r) = [\sum V_r W_r - \frac{\sum V_r \sum W_r}{n}] / (n-1) \text{ and}$$

$$\text{Var}(V_r) = [\sum V_r^2 - \frac{(\sum V_r)^2}{n}] / (n-1)$$

The standard error of regression coefficient (b) was calculated as:

$$SE(b) = [(\text{Var } W_r - b \text{ Cov. } W_r - V_r) / \text{Var } V_r (n-2)]^{0.5}$$

Where,

N = Number of parents

Now the significance of differences 'b' from zero and unity was tested by using 't' value of (b-0)/SE (b) and (1-b)/SE (b) with (n-2) degree of freedom

Genotypic (GCV), Phenotypic (PCV) and Environment (ECV) coefficients of variation (%): estimated according to the procedure outlined by Johnson *et al.*, (1955):

$$GCV(\%) = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

$$PCV(\%) = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

$$ECV(\%) = \frac{\sqrt{\sigma^2_{gl}}}{\bar{X}} \times 100$$

Where,

$\sigma^2_g$  = Genotypic variance

$\sigma^2_p$  = Phenotypic variance

$\sigma^2_{gl}$  = Genotypic by environment interaction variance

$\bar{X}$  = Mean of the character concerned

The range of GCV, PCV and ECV suggested by Subramanian & Menon (1973): GCV, PCV & ECV variability categorized into three classes :-

Low = <10 %,

Moderate = 10-20%

High = > 20 %.

## Results and Discussion

### Regression coefficient

The regression coefficient of 'b' deviated significantly from unity for almost all the characters in both the generations except no. of spikelets per spike and grain weight per spike, indicating non-allelic gene action in these traits. (Table 1). Nurminiemi, M., & Rognli, O. A. (1996) [7] also observed non allelic interaction in barley. Non-significant values of 't<sup>2</sup>' for all characters in both the generations revealed the validity of hypothesis except for days to 50% flowering days to maturity, flag leaf area in both the generations, which might be due to sampling error. Similar finding was also reported by Kole, *et al.*, (2006) [4].

### Gene actions

The component of variance analysis revealed presence of both additive ( $\hat{D}$ ) as well as dominance ( $\hat{H}_1$  and  $\hat{H}_2$ ) genetic components for all the characters in both the F<sub>1</sub> and F<sub>2</sub> generations. The highly significant value of additive genetic component ( $\hat{D}$ ) were observed for all characters except the number of effective tillers per plant, spike length, grains weight per spike and protein content in both generations, indicating additive gene action for the expression of these characters. Prakash, *et al.*, (2006) [8] also reported additive as well as dominance genetic variances for yield contributing and quality traits in barley. The values of  $\hat{E}$  components were found significant for Days to 50% flowering in F<sub>2</sub> generation, while Plant height in F<sub>1</sub> generations, no of grain per spike and peduncle length in both generations showed considerable involvement of environmental effect in the expression of these attributes. The values of average degree of dominance ( $(\hat{H}_1/\hat{D})^{0.5}$ ) were recorded more than unity for almost all the characters in both the generations, revealed over dominance. Prakash, *et al.*, (2006) [8] also reported over dominance both F<sub>1</sub> and F<sub>2</sub> generations and Sharma, Y., & Sharma, S. (2008) [10] partial dominant in F<sub>1</sub> generations. The proportion of genes with positive and negative effects ( $\hat{H}_2/4\hat{H}_1$ ) was less than the theoretical value (0.25) for all the traits in both the generations. It revealed asymmetrical distribution of positive and negative alleles among the parent. The ratio of dominant and recessive genes  $[(4\hat{D}\hat{H}_1)^{0.5} + F / (4\hat{D}\hat{H}_1)^{0.5} - F]$  in the parents study was observed more than unity for almost all characters, indicating greater role of dominant genes for all these traits. Kakani, *et al.*,

(2010) [3] and Verma, *et al.*, (2007) [14]. The positive values of coefficient of correlation (r) between parental order of dominance and parental measurement indicated that positive genes were mostly dominant in almost all characters (Table 2).

### Genotypic and Phenotypic Coefficient of variance

Genotypic variation is the heritable portion of phenotypic or total variation. GCV and PCV were categorized into three classes, viz., low (less than 10 %), moderate (10-20%) and high (more than 20%) Table 3. Moderate value of GCV (%) were observed for the characters of days to maturity and number of spikelets per spike in F<sub>1</sub> generation. Low GCV (%) were observed for days to 50% flowering, plant height (cm), number of effective tillers per plant, spike length (cm), number of grains per spike, 1000-grain weight (g), flag leaf area, peduncle length, grain weight per spike, grain yield per plant (g), biological yield per plant (g), harvest index (%), and protein content (%) in F<sub>1</sub> generation. Similar finding observed by Verma, I., & Verma, S. R. (2011) [15]. High value of PCV (%) were observed for the characters of number of spikelets per spike, flag leaf area, biological yield per plant (g), harvest index (%) and grain yield per plant (g). Moderate value of PCV (%) were observed for the characters of number of effective tillers per plant, spike length (cm), 1000-grain weight (g), peduncle length, grain weight per spike in F<sub>1</sub> generation. Addisu, F., & Shumet, T. (2015) [1]. Low PCV (%) were observed for Days to 50% flowering, days to maturity, plant height (cm), number of grains per spike and protein content in F<sub>1</sub> generation (Table 3). Similar result were also reported by Kumar *et al.*, (2013) [5] and Shrimali, *et al.*, (2017) [11].

**Table 1:** Regression coefficient analysis followed by 10x10 diallele mating design

S. No.	Characters		b	Se ± b	T test		
					IFB=0	IF B=1	T^2
1	Days to 50% flowering	F <sub>1</sub>	0.21	0.08	2.51	9.71	30.50
		F <sub>2</sub>	0.04	0.07	0.63	14.34	51.89
2	Days to maturity	F <sub>1</sub>	0.44	0.12	3.75	4.78	8.82
		F <sub>2</sub>	0.44	0.15	2.97	3.82	4.65
3	Plant Height (cm)	F <sub>1</sub>	0.14	0.18	0.75	4.69	3.74
		F <sub>2</sub>	0.07	0.20	0.36	4.69	2.96
4	Productive tillers /plants	F <sub>1</sub>	-0.34	0.33	-1.03	4.05	0.00
		F <sub>2</sub>	0.76	0.17	4.40	1.39	0.29
5	Spike length(cm)	F <sub>1</sub>	0.20	0.13	1.49	6.10	9.75
		F <sub>2</sub>	0.25	0.18	1.40	4.22	3.71
6	No. of spikelets/spike	F <sub>1</sub>	0.99	0.02	44.32	0.62	0.28
		F <sub>2</sub>	0.99	0.03	34.29	0.51	0.15
7	No. of grain/spike	F <sub>1</sub>	0.82	0.19	4.32	0.96	0.01
		F <sub>2</sub>	0.84	0.12	6.76	1.31	0.50
8	1000-grain weight (g)	F <sub>1</sub>	0.29	0.12	2.29	5.74	10.20
		F <sub>2</sub>	0.42	0.12	3.55	4.89	9.00
10	Flag leaf Area (cm) <sup>2</sup>	F <sub>1</sub>	0.76	0.04	19.61	6.12	27.40
		F <sub>2</sub>	0.79	0.04	17.83	4.69	16.19
11	Peduncle length(cm)	F <sub>1</sub>	0.47	0.19	2.47	2.73	1.55
		F <sub>2</sub>	0.52	0.22	2.38	2.20	0.64
12	Grain weight per spike(g)	F <sub>1</sub>	0.84	0.25	3.39	0.62	0.18
		F <sub>2</sub>	0.87	0.12	7.21	1.08	0.28
13	Protein content (%)	F <sub>1</sub>	-0.21	0.24	-0.88	5.02	1.02
		F <sub>2</sub>	-0.24	0.31	-0.78	4.02	0.09
14	Biological yield/plant (g)	F <sub>1</sub>	1.10	0.11	9.97	-0.92	2.00
		F <sub>2</sub>	1.07	0.13	7.99	-0.52	1.15
15	Harvest Index (%)	F <sub>1</sub>	0.69	0.10	6.62	3.03	4.56
		F <sub>2</sub>	0.66	0.11	5.84	2.98	4.08

**Table 2:** Components analysis in barley followed by 10x10 diallele mating design

Components		Days to 50% flowering	Days to maturity	Plant Height (cm)	Productive tillers /plants	Spike length(cm)	No. of spikelets/spike	No. of grain/spike	1000-grain weight (g)	Flag leaf Area (cm)2	Peduncle length(cm)	Grain weight per spike(g)	Protein content (%)	Biological yield/plant (g)	Harvest Index (%)	Grain yield/plant (g)
D	F <sub>1</sub>	3.32	9.05	15.77	0.156	0.473	187.48	18.38	5.52	38.95	22.33	0.081	0.089	94.19	50.94	9.48
	SE	5.19	3.61	6.86	0.123	0.235	2.75	1.93	3.44	2.47	5.34	0.020	0.035	2.30	4.00	0.81
D	F <sub>2</sub>	3.00	8.99	16.43	0.17	0.52	199.33	18.57	5.51	38.78	20.87	0.075	0.082	94.24	50.97	9.49
	Se	3.71	3.60	6.60	0.07	0.25	4.05	1.67	3.00	2.17	6.09	0.013	0.036	2.72	3.72	0.77
F	F <sub>1</sub>	4.01	11.30	38.96	0.318	0.714	288.83	10.09	-0.14	57.38	34.71	0.048	0.159	137.28	73.41	14.03
	SE	11.98	8.33	15.82	0.284	0.541	6.35	4.45	7.94	5.70	12.33	0.045	0.081	5.31	9.24	1.87
F	F <sub>2</sub>	5.41	10.89	39.44	0.25	0.88	327.47	9.44	-1.01	57.39	35.46	0.034	0.130	138.35	77.51	14.11
	Se	8.55	8.31	15.24	0.16	0.58	9.34	3.85	6.91	5.00	14.06	0.030	0.082	6.27	8.59	1.77
H <sub>1</sub>	F <sub>1</sub>	58.95	86.39	90.32	1.298	2.655	177.58	31.64	51.37	53.96	77.00	0.198	0.311	79.56	84.19	16.63
	SE	11.06	7.68	14.60	0.262	0.499	5.86	4.10	7.33	5.26	11.37	0.042	0.074	4.90	8.52	1.73
H <sub>1</sub>	F <sub>2</sub>	31.24	79.99	92.70	1.65	3.99	215.09	33.92	46.73	50.97	81.52	0.264	0.305	79.88	81.96	15.18
	Se	7.89	7.67	14.06	0.14	0.53	8.62	3.55	6.38	4.61	12.97	0.027	0.076	5.78	7.93	1.63
H <sup>2</sup>	F <sub>1</sub>	48.87	73.45	48.31	1.038	2.228	65.30	14.83	29.01	32.50	57.20	0.180	0.220	29.23	47.25	9.94
	SE	9.40	6.53	12.41	0.223	0.424	4.98	3.49	6.23	4.47	9.67	0.035	0.063	4.16	7.24	1.47
H <sub>2</sub>	F <sub>2</sub>	25.61	67.04	49.46	1.32	3.53	80.06	23.33	27.24	29.50	60.44	0.241	0.240	28.85	41.95	8.35
	Se	6.70	6.52	11.95	0.12	0.45	7.33	3.02	5.42	3.92	11.03	0.023	0.064	4.91	6.74	1.39
h <sub>2</sub>	F <sub>1</sub>	120.73	484.63	83.01	2.349	14.666	71.53	34.10	15.16	172.58	77.02	0.337	0.168	8.27	141.05	42.99
	SE	6.29	4.37	8.31	0.149	0.284	3.33	2.33	4.17	2.99	6.47	0.024	0.042	2.79	4.85	0.98
h <sub>2</sub>	F <sub>2</sub>	41.26	406.96	63.74	5.30	17.47	87.47	123.29	2.35	146.91	145.31	0.777	-0.006	5.36	87.61	28.21
	Se	4.49	4.36	8.00	0.08	0.30	4.90	2.02	3.63	2.62	7.38	0.016	0.043	3.29	4.51	0.93
E	F <sub>1</sub>	0.74	0.71	1.71	0.114	0.184	0.92	4.01	0.52	0.08	2.63	0.021	0.034	0.28	0.49	0.08
	SE	1.57	1.09	2.07	0.037	0.071	0.83	0.58	1.04	0.75	1.61	0.006	0.011	0.69	1.21	0.24
E	F <sub>2</sub>	1.06	0.77	1.05	0.10	0.14	0.73	3.82	0.53	0.26	4.09	0.027	0.041	0.23	0.47	0.07
	Se	1.12	1.09	1.99	0.02	0.08	1.22	0.50	0.90	0.65	1.84	0.004	0.011	0.82	1.12	0.23
sqrt(h1/d)	F <sub>1</sub>	4.216	3.090	2.393	2.884	2.368	0.973	1.312	3.051	1.177	1.857	1.562	1.872	0.919	1.286	1.324
	F <sub>2</sub>	3.228	2.983	2.375	3.117	2.765	1.039	1.352	2.913	1.146	1.976	1.874	1.926	0.921	1.268	1.264
H2/4h1	F <sub>1</sub>	0.207	0.213	0.134	0.200	0.210	0.092	0.117	0.141	0.151	0.186	0.227	0.176	0.092	0.140	0.149
	F <sub>2</sub>	0.205	0.210	0.133	0.200	0.221	0.093	0.172	0.146	0.145	0.185	0.229	0.197	0.090	0.128	0.138
((4DH1) <sup>5</sup> +F)/((4DH1) <sup>5</sup> -F)	F <sub>1</sub>	1.335	1.506	3.133	2.091	1.934	8.591	1.529	0.992	4.344	2.440	1.466	2.834	8.658	3.550	3.529
	F <sub>2</sub>	1.775	1.510	3.043	1.612	1.877	8.559	1.463	0.939	4.640	2.508	1.272	2.396	8.865	3.995	3.852
h <sup>2</sup> /H2	F <sub>1</sub>	2.471	6.598	1.718	2.263	6.582	1.095	2.300	0.522	5.310	1.347	1.872	0.765	0.283	2.985	4.324
	F <sub>2</sub>	1.611	6.071	1.289	4.013	4.954	1.093	5.284	0.086	4.979	2.404	3.221	-0.024	0.186	2.089	3.378
h2	F <sub>1</sub>	15.52	7.90	25.32	29.28	17.10	4.84	9.97	8.19	12.99	14.93	15.09	24.38	24.38	24.38	24.38
	F <sub>2</sub>	17.75	23.96	42.99	22.75	5.06	14.23	50.51	63.92	15.79	14.46	26.89	7.75	31.75	38.09	33.88
r	F <sub>1</sub>	0.641	0.132	0.856	0.088	-0.753	0.725	-0.187	0.358	0.255	-0.777	-0.060	-0.683	-0.683	-0.683	-0.683
	F <sub>2</sub>	-0.547	0.881	0.493	-0.512	-0.861	0.992	0.811	-0.678	0.966	-0.497	-0.916	-0.836	-0.360	-0.894	-0.490

**Table 3:** Genotypic and Phenotypic Coefficient of variance in barley followed by 10x10 diallele mating design

Genotypes	Mean	Min	Max	GCV (%)	PCV (%)
Days to 50% flowering	81.13	79	85.33	7.90	9.18
Days to maturity	128.83	124	132.67	10.98	9.24
Plant Height (cm)	94.19	87	100.03	8.32	9.24
No.of Productive tillers /plants	5.63	5	6.67	0.73	11.48
Spike length(cm)	8.99	8	10.67	1.60	14.95
No. of spikelets/spike	26.96	20	65.67	11.79	51.01
No. of grain/spike	59.40	53.33	67.67	5.67	10.00
1000-grain weight (g)	42.30	38.33	46.33	8.45	19.18
Flag leaf Area (cm) <sup>2</sup>	21.29	15.86	34.45	7.88	51.45
Peduncle length(cm)	34.34	27.67	43.83	7.14	18.63
Grain weight per spike(gm)	2.53	2.17	2.97	0.39	13.83
Protein content (%)	12.27	11.85	12.81	0.27	2.14
Biological yield/plant (g)	39.24	22.33	55.33	8.30	20.46
Harvest Index (%)	35.57	25.58	43.96	9.55	23.31
Grain yield/plant (g)	13.57	9.40	20.17	4.33	26.15

### Conclusion

In conclusion, the analysis of genetic variance in the studied characters reveals the significant presence of both additive and dominance gene actions, with a notable prevalence of dominant alleles influencing traits such as days to maturity and spikelet count. The findings underscore the complexity of inheritance patterns, including the effects of environmental variance on trait expression.

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