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Research Note

Genetic variability for yield contributing traits in bread wheat under irrigated condition of Chhattisgarh Plains

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Abstract
The present study evaluated thirty-six bread wheat (*Triticum aestivum* L.) genotypes, including four standard checks, under timely sown irrigated conditions during *Rabi* 2024–25 to assess genetic variability and identify key yield-contributing traits. The experiment was conducted in a 6 × 6 simple lattice design, and observations were recorded for fourteen agronomic and physiological traits. Analysis of variance revealed highly significant differences among genotypes for all characters, indicating substantial genetic variability. Narrow differences between GCV and PCV for most traits suggested limited environmental influence on trait expression. High heritability (72.78 %) coupled with high genetic advance as % of mean (21.67) for grain yield per plot indicated the predominance of additive gene action and the effectiveness of direct selection. Grain yield showed strong positive correlations with productive tillers per plant (0.705**), biological yield (0.633**), harvest index (0.621**), spike length (0.400**), and flag leaf length (0.396**). Path coefficient analysis identified biological yield (0.395), harvest index (0.333) and productive tillers (0.319), as the most influential traits due to their high positive direct effects on grain yield. Genotypes PBW975, GW575, GW576, AKAW5347, and MP3620 outperformed the standard checks, highlighting their potential for breeding programmes. Overall, selection based on productive tillers, biological yield, and harvest index would be most effective for improving wheat yield under irrigated conditions.

Keywords: Bread wheat, GCV,PCV, heritability, GA,GAM, correlation, path analysis

Wheat (*Triticum aestivum* L.) is one of the most widely cultivated cereal crops and serves as a major source of calories, protein, and essential nutrients for a large proportion of the global population. Owing to its wide adaptability, the crop has expanded from its centre of origin in the Near East to diverse agro-ecosystems across temperate, subtropical, and high-altitude regions. Bread wheat, a hexaploid species (2n = 6x = 42; AABBDD), is preferred globally because of its high productivity, superior grain quality, and versatility in food processing. Rising population pressure, climate variability, and increasing nutritional demands further highlight the importance of improving the productivity and stability of wheat.

Global wheat production for 2024–25 is estimated at 799.9 million metric tonnes (USDA 2025), while India has recorded all-time high production of 115.43 million metric tonnes (Ministry of Agriculture, GOI 2025). The crop contributes nearly 21 % of global caloric intake and about 20 % of dietary protein, thereby playing a key role in global food and nutritional security. In India, wheat is the second most important cereal crop after rice, with its acreage concentrated in the northern, western, and central zones. In Chhattisgarh, wheat is cultivated mainly under irrigated conditions during the *rabi* season and serves as an important component for diversifying the rice-dominated cropping system. Enhancing wheat

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productivity in such non-traditional areas is essential for stabilizing food supplies and improving farmer incomes.

Genetic enhancement of wheat depends on the availability and exploitation of sufficient genetic variability for grain yield and its component traits. Grain yield is a complex, polygenic trait governed by numerous morphological and physiological factors, and its improvement requires a clear understanding of the magnitude of variability and the extent to which these traits are heritable. Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance provide valuable information for designing suitable breeding strategies. High heritability coupled with high genetic advance indicates the predominance of additive gene action, which favours effective selection in early generations.

Correlation and path coefficient analyses are important tools in plant breeding as they help quantify the contribution of component traits toward grain yield. While correlation measures the degree of association between traits, path analysis partitions these correlations into direct and indirect effects, enabling the identification of key traits for simultaneous improvement. Although several studies have evaluated variability and trait associations in wheat, information specific to timely sown, irrigated conditions of Chhattisgarh remains limited. Such data are crucial for identifying adaptable and high-yielding genotypes suited to the agro-ecological conditions of the region.

Therefore, the present investigation was undertaken to assess genetic variability, heritability, associations, and path coefficients for grain yield and related traits in thirty-six bread wheat genotypes. The outcomes will aid in identifying promising genotypes and selecting important traits for wheat improvement programmes under irrigated ecosystems.

The present investigation was carried out during *Rabi* 2024–25 at the Research Farm of Barrister Thakur Chhedilal College of Agriculture and Research Station, Bilaspur, under Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh. The experimental site falls under the Chhattisgarh Plains agro-climatic zone, characterized by a subtropical climate with cool winters and assured irrigation facilities

A total of thirty-six bread wheat genotypes **(Table 1),** including four standard checks—GW322, DBW187, HI1650, and MACS6222—were evaluated in a 6 × 6 Simple Lattice Design with two replications. Each genotype was sown in a plot measuring 6.0 m × 1.20 m (7.20 m²) with recommended row spacing. The crop was grown following standard agronomic practices, including timely irrigation, weed control, and plant protection measures. A fertilizer dose of 120:60:40 kg N, P_2O_5, and K_2O/ha was applied, with nitrogen split-applied at sowing, tillering, and booting stages.

Observations were recorded on fourteen yield and yield-related traits. Five competitive plants were randomly selected from each plot for plant-based traits such as plant height, spike length and grain number per spike. Plot-based traits including biological yield, grain yield, and harvest index were recorded from the entire plot. The mean values were used for statistical analyses.

Variability among genotypes was assessed through analysis of variance (ANOVA) as described by Singh and Chaudhary (1985). Genotypic and phenotypic variances were estimated following Johnson *et al.* (1955). Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed using the procedure of Burton (1952) and categorized according to Sivasubramanian and Madhava Menon (1973). Heritability (broad sense) was calculated following Allard (1999), whereas genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated as per Johnson *et al.* (1955).

Correlation coefficients were computed according to Miller *et al*. (1958) to determine the degree of association among traits. To assess the contribution of component traits toward grain yield, path coefficient analysis was performed using the method of Dewey and Lu (1959), partitioning correlations into direct and indirect effects.

Analysis of variance: The analysis of variance for thirty-six wheat genotypes evaluated for fourteen quantitative traits is presented in **Table 2**. The ANOVA showed highly significant differences among genotypes for all traits, indicating the presence of substantial genetic variability in the experimental material. Considerable variability was observed in traits such as grain yield per plot, number of productive tillers per plant, spike length, flag leaf length, and 1000-grain weight, suggesting that the evaluated genotypes were diverse in origin. Such divergence provides a strong basis for effective selection and future genetic improvement of wheat under irrigated conditions.

Genetic parameters of variation:The phenotypic coefficient of variation (PCV) exceeded genotypic coefficient of variation (GCV) for all the traits, though the differences were small, indicating minimal environmental influence and a strong genetic control over trait expression (**Table 3**). Moderate PCV and GCV values recorded for grain yield per plot (16.94, 14.45 %) and flag leaf length (10.70, 10.20 %) reflect considerable inherent genetic variability.

High heritability (72.78 %) coupled with high genetic advance as percent of mean (GAM) (21.67) was obtained for grain yield per plot, indicates the predominance of additive gene action, which favours direct selection. followed by flag leaf length (heritability 90.95 %, GAM 19.12 %), peduncle length (heritability 90.19 %, GAM 17.45 %), number of grains on the main spike (heritability 86.08 %, GAM 17.28), spike length (heritability 79.78%, GAM 15.91 %), number of spikelets per spike (heritability

Table 1. List of 36 wheat genotypes used in the experiment

S. No.	Name of genotype	Source of genotype
1	GW569	SDAU, Vijapur
2	UAS3035	UAS, Dharwad
3	MACS6874	ARI, Pune
4	MACS6872	ARI, Pune
5	MACS6887	ARI, Pune
6	PWU50	MPUAT, Udaipur
7	NIAW4761	ARS, Niphad
8	HI1706	ICAR–IARI, Delhi
9	HI1704	ICAR–IARI, Delhi
10	MP3610	JNKVV, Jabalpur
11	DBW488	ICAR–IIWBR, Karnal
12	GW570	SDAU, Vijapur
13	MP1407	JNKVV, Powarkheda
14	HI1703	ICAR–IARI, Delhi
15	DBW489	ICAR–IIWBR, Karnal
16	WH1350	HAU, Hisar
17	CG1053	IGKV, RS Bilaspur
18	LOK84	LOK BHARTI, Sanosara
19	HI1705	ICAR–IARI, Delhi
20	RAJ4596	RARI, Durgapura
21	GW571	SDAU, Vijapur
22	MP1408	JNKVV, Powarkheda
23	PWU49	MPUAT, Udaipur
24	GW575	JAU, Junagadh
25	UAS3036	UAS, Dharwad
26	GW576	JAU, Junagadh
27	MP3620	JNKVV, Jabalpur
28	JWS1501	JNKVV, RS Sagar
29	PBW975	PAU, Ludhiana
30	NIAW4728	ARS, Niphad
31	DBW490	ICAR–IIWBR, Karnal
32	AKAW5347	PDKV, Akola
33	GW322 (Check)	RARS, Vijapur
34	DBW187 (Check)	ICAR–IIWBR, Karnal
35	HI1650 (Check)	ICAR–IARI, Delhi
36	MACS6222 (Check)	ARI, Pune

81.19 %, GAM 15.68 %), and grain filling period (heritability 82.97 %, GAM 15.08 %).These traits therefore offer strong potential for selection-based improvement and represent important contributors to yield enhancement. Some traits displayed high to moderately high heritability combined with moderate GAM, reflecting the influence of both additive and non-additive gene effects. Examples include thousand-grain weight (heritability 71.95 %, GAM 11.34 %), harvest index (heritability 63.87 %, GAM 10.59 %), and plant height (heritability 74.18 %, GAM 10.43 %). These traits may still respond to selection, but the expected improvement per cycle would be comparatively moderate.

On the other hand, biological yield per plot (heritability 51.30 %, GAM 9.99 %) and days to 50% flowering (heritability 50.85 %, GAM 5.08 %) exhibited moderate heritability but low GAM, indicating a greater influence of the environment and limited expected progress through direct selection. Finally, days to maturity, although possessing moderately high heritability (69.68 %), showed very low GAM (2.83 %), suggesting the predominance

Table 2. Analysis of variance for yield and yield attributing traits in wheat genotypes

S.No.	Traits	Mean sum of square (MSS)			
		Replication	Genotype	Block within replication	Error
	Degree of freedom (df)	1	35	10	25
1	Days to 50% flowering (DAS)	26.056	36.170**	17.597	9.461
2	Grain filling period	6.742	35.528**	2.423	3.662
3	Days to maturity (DAS)	0.008	13.100**	2.854	2.136
4	Plant height	0.07	63.507**	13.034	7.965
5	Peduncle length	3.984	21.679**	0.826	1.235
6	Number of tillers per plant	0.049	0.654**	0.06	0.055
7	Spike length	0.02	4.902**	0.934	0.398
8	Number of spikelets/spike	0.101	4.425**	0.72	0.355
9	Number of grain/main spike	3.248	50.071**	4.534	3.431
10	Flag leaf length	0.021	5.007**	0.159	0.268
11	1000 grain weight	0.221	26.221**	3.405	4.627
12	Biological yield per plot	0.073	1.886**	0.679	0.579
13	Harvest index	1.917	28.015**	5.735	6.354
14	Grain yield/plot	0.09	0.597**	0.097	0.093

** significant at 1% probability level,

Table 3. Genetic parameters of 14 quantitative traits

Trait	Mean	Minimum	Maximum	PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GAM (%)
Plant height (cm)	76.19	64.36	89.11	7.93	6.83	74.18	7.95	10.43
Flag leaf length	15.13	11.51	17.73	10.70	10.20	90.95	2.89	19.12
Spike length (cm)	15.24	12.02	17.61	10.84	9.68	79.78	2.42	15.91
Number of spikelets/spike	15.02	12.60	18.90	10.40	9.37	81.19	2.36	15.68
Peduncle length(cm)	34.14	26.14	40.04	9.89	9.39	90.19	5.96	17.45
Numbers of productive tillers/plant	7.02	6.40	8.40	8.49	7.78	84.17	0.95	13.50
Number of grain per main spike	49.40	41.80	62.90	10.50	9.74	86.08	8.53	17.28
Days to 50% flowering	72.03	65.50	83.50	6.80	4.85	50.85	3.66	5.08
Days to maturity	117.51	111.00	121.00	2.36	1.97	69.68	3.33	2.83
Grain filling period (days)	45.49	37.00	53.00	9.69	8.82	82.97	6.86	15.08
1000 grain weight	43.28	36.02	50.70	9.02	7.65	71.95	4.91	11.34
Grain yield /plot (kg)	3.47	2.16	4.54	16.94	14.45	72.78	0.75	21.67
Biological yield per plot (kg)	8.46	6.12	10.30	13.20	9.45	51.30	0.85	9.99
Harvest index (%)	41.06	31.08	47.08	10.07	8.05	63.87	4.35	10.59

of non-additive genetic effects and implying that simple selection would not be efficient for improving this trait. These findings align with earlier reports by Khinchi *et al*. (2022), and Mohan *et al.* (2022), who also reported high heritability and GAM for yield-related traits in wheat. Overall, grain yield, biological yield, number of productive tillers, and harvest index emerged as key traits for genetic improvement.

Correlation coefficient analysis: Genotypic and phenotypic correlation coefficients (**Table 4**) revealed that grain yield per plot had a highly significant and positive association with number of productive tillers per plant (0.705**), biological yield (0.633**), harvest index (0.621**), spike length (0.400**), and flag leaf length (0.396**). Positive and significant correlations were also observed with 1000-grain weight (0.271*), number of spikelet's per spike (0.235*), and number of grains per main spike (0.223*), indicating their strong contribution toward yield formation. These results agree for bread wheat with the findings of Karla *et al*. (2024) for spike length, grains per spike, and 1000-grain weight; Kumar *et al*. (2023) for number of productive tillers, biological yield, and harvest index; Gebremariam *et al*. (2022) and Kumar *et al*. (2022) for

Table 4. Genotypic and phenotypic correlation matrix (Above diagonal Phenotypic and below diagonal Genotypic value)

Trait	DFF	GFP	DM	PH	PDL	NTPP	SL	NS	NGMS	FLL	TGW	BYPP	HI	GYPP
DFF	**1.000**	-0.692**	0.241*	-0.024	0.032	-0.265*	-0.256*	0.216	0.12	-0.116	-0.203	0.059	-0.252*	-0.116
GFP	-0.694**	**1.000**	0.240*	-0.009	0.112	0.004	0.143	-0.274*	-0.158	0.049	0.113	-0.289*	0.166	-0.104
DM	0.239*	0.240*	**1.000**	0.045	0.203	-0.467**	-0.194	-0.053	-0.032	-0.137	-0.197	-0.359**	-0.185	-0.384**
PH	-0.024	-0.009	0.045	**1.000**	0.328**	-0.024	-0.035	0.302**	0.251*	-0.118	0.027	-0.162	-0.112	-0.227
PDL	0.023	0.117	0.203	0.327**	**1.000**	-0.142	-0.09	-0.161	-0.21	-0.108	0.014	-0.252*	-0.179	-0.268*
NTPP	-0.268*	0.007	-0.467**	-0.024	-0.139	**1.000**	0.633**	0.15	0.235*	0.614**	0.344**	0.445**	0.569**	0.704**
SL	-0.255*	0.143	-0.194	-0.035	-0.089	0.633**	**1.000**	0.075	0.269*	0.865**	0.018	0.212	0.334**	0.400**
NS	0.217	-0.275*	-0.053	0.303**	-0.163	0.148	0.075	**1.000**	0.734**	0.031	-0.151	0.175	0.236*	0.236*
NGMS	0.124	-0.16	-0.032	0.251*	-0.212	0.233*	0.269*	0.734**	**1.000**	0.196	-0.009	0.234*	0.223	0.226
FLL	-0.116	0.05	-0.137	-0.118	-0.107	0.614**	0.865**	0.031	0.195	**1.000**	-0.009	0.268*	0.272*	0.396**
TGW	-0.2	0.112	-0.197	0.027	0.013	0.343**	0.017	-0.15	-0.009	-0.009	**1.000**	0.173	0.261*	0.272*
BYPP	0.062	-0.290*	-0.359**	-0.162	-0.253*	0.443**	0.212	0.176	0.235*	0.268*	0.173	**1.000**	0.169	0.636**
HI	-0.245*	0.162	-0.185	-0.112	-0.181	0.566**	0.333**	0.237*	0.224	0.272*	0.261*	0.169	**1.000**	0.625**
GYPP	-0.123	-0.099	-0.383**	-0.227	-0.263*	0.705**	0.400**	0.235*	0.223	0.396**	0.271*	0.633**	0.621**	**1.000**

* Significant at 5% probability level, ** Significant at 1% probability level

NOTE - DFF = Days to 50% flowering, GFP = grain filling period , DM = Days to maturity, PH = Plant height , PDL = Peduncle length, NTPP = Numbers of productive tillers/plant, SL = Spike length , NS = Number of spikelets/spike, NGMS = Number of grain per main spike, FLL = Flag leaf length, TGW = 1000 grain weight, BYPP = Biological yield per plot , HI = Harvest index , GYPP = Grain yield /plot

spike-related traits and grain weight. The importance of flag leaf length, 1000-grain weight, and grains per spike have also been emphasized by Ayer *et al*. (2017), and Vaghela *et al*. (2021).

Path coefficient analysis: Correlation analysis only indicates association; therefore, path coefficient analysis was performed to partition correlations into direct and indirect effects (**Table 5**). The path analysis revealed that productive tillers per plant (0.319, 0.305), biological yield per plot (0.395, 0.399), and harvest index (0.333, 0.343) exerted strong and positive direct effects on grain yield at both genotypic and phenotypic levels. These traits also showed strong positive correlations with grain yield, confirming their reliability as primary yield-determining traits. Similar findings in bread wheat were reported by Kumar *et al*. (2023).

Spike length, number of spikelet's per spike, and grains per main spike influenced grain yield mainly through favourable indirect effects, particularly *via* biological yield, productive tillers, harvest index, and flag leaf length. Although their direct effects were modest, their substantial cumulative indirect contributions highlight their value as secondary selection traits, consistent with observations by Karla *et al*. (2024), and Gebremariam *et al*. (2022). Thousand-grain weight also exhibited a positive direct effect alongside consistently positive correlations with grain yield, as reported by Devesh *et al*. (2021). In contrast, flag leaf length showed a negative direct effect but maintained an overall positive association through strong indirect effects mediated by biological yield, spike length, and harvest index. Similar trends were noted in bread wheat by Ayer *et al*. (2017) and Vaghela *et al*. (2021).Overall, the results clearly indicate that productive tillers per plant, biological yield, harvest index , and thousand-grain weight are the most dependable traits for direct selection to enhance grain yield in wheat, while spike length , spikelet's per spike, grains per spike, and flag leaf length function as supportive traits owing to their substantial indirect contributions.

The study revealed substantial genetic variability among thirty-six bread wheat genotypes, indicating strong potential for improvement under timely sown irrigated conditions. Narrow differences between phenotypic and genotypic coefficients of variation suggested limited environmental influence. High heritability with moderate to high GAM for flag leaf length, peduncle length, spike length, grain filling period, productive tillers per plant, thousand-grain weight, and grain yield indicated additive gene action, favouring direct selection. In contrast, days to 50% flowering and days to maturity showed low GAM, implying non-additive effects. Productive tillers, spike length, biological yield, and harvest index strongly influenced yield. Genotypes PBW975, GW575, GW576, AKAW5347, and MP3620 were most promising.

Table 5. Phenotypic and genotypic path coefficient values for 13 quantitative characters
(Off diagonal Phenotypic value on top, Off Genotypic value below; Direct Effects In Bold diagonal values)

Traits	DFF	GFP	DM	PH	PDL	NTPP	SL	NS	NGMS	FLL	TGW	BYPP	HI	Correlation for GYPP
DFF	**0.001** **0.015**	-0.001 0.011	0.000- 0.004	0.000 0.000	0.000 0.000	0.000 0.004	0.000 0.004	0.000- 0.003	0.000- 0.002	0.000 0.002	0.000 0.003	0.000- 0.001	0.000 0.004	-0.116 -0.123
GFP	0.022 0.026	**-0.032** **-0.037**	-0.008 -0.009	0.000 0.000	-0.004 -0.004	0.000 0.000	-0.005 -0.005	0.009 0.010	0.005 0.006	-0.002 -0.002	-0.004 -0.004	0.009 0.011	-0.005 -0.006	-0.104 -0.099
DM	0.000 0.002	0.000 0.002	**-0.001** **0.006**	0.000 0.000	0.000 0.001	0.000- 0.003	0.000- 0.001	0.000 0.000	0.000 0.000	0.000- 0.001	0.000- 0.001	0.000 -0.002	0.000 -0.001	-0.384 -0.383
PH	0.003 0.003	0.001 0.001	-0.006 -0.006	**-0.135** **-0.140**	-0.044 -0.046	0.003 0.003	0.005 0.005	-0.041 -0.042	-0.034 -0.035	0.016 0.017	-0.004 -0.004	0.022 0.023	0.015 0.016	-0.227 -0.227
PDL	0.000 0.000	-0.002 -0.001	-0.003 -0.002	-0.004 -0.002	**-0.013** **-0.007**	0.002 0.001	0.001 0.001	0.002 0.001	0.003 0.002	0.001 0.001	0.000 0.000	0.003 0.002	0.002 0.001	-0.268 -0.263
NTPP	-0.081 -0.085	0.001 0.002	-0.142 -0.149	-0.007 -0.008	-0.043 -0.044	**0.305** **0.319**	0.193 0.202	0.046 0.047	0.072 0.074	0.187 0.196	0.105 0.109	0.136 0.141	0.173 0.181	0.704** 0.705**
SL	-0.016 -0.014	0.009 0.008	-0.012 -0.011	-0.002 -0.002	-0.006 -0.005	0.039 0.035	**0.061** **0.054**	0.005 0.004	0.016 0.015	0.053 0.047	0.001 0.001	0.013 0.012	0.020 0.018	0.400** 0.400**
NS	0.033 0.034	-0.041 -0.043	-0.008 -0.008	0.046 0.047	-0.024 -0.025	0.023 0.023	0.011 0.012	**0.151** **0.156**	0.111 0.115	0.005 0.005	-0.023 -0.024	0.026 0.027	0.036 0.037	0.236* 0.235*
NGMS	-0.013 -0.014	0.017 0.018	0.003 0.004	-0.027 -0.027	0.023 0.023	-0.025 -0.026	-0.029 -0.029	-0.079 -0.080	**-0.108** **-0.109**	-0.021 -0.021	0.001 0.001	-0.025 -0.026	-0.024 -0.025	0.226 0.223
FLL	0.005 0.005	-0.002 -0.002	0.006 0.006	0.005 0.005	0.005 0.005	-0.027 -0.026	-0.038 -0.037	-0.001 -0.001	-0.009 -0.008	**-0.043** **-0.043**	0.000 0.000	-0.012 -0.011	-0.012 -0.012	0.396** 0.396**
TGW	-0.008 -0.007	0.004 0.004	-0.007 -0.007	0.001 0.001	0.001 0.000	0.013 0.012	0.001 0.001	-0.006 -0.005	0.000 0.000	0.000 0.000	**0.037** **0.033**	0.006 0.006	0.010 0.009	0.272* 0.271*
BYPP	0.024 0.025	-0.116 -0.115	-0.143 -0.142	-0.065 -0.064	-0.100 -0.100	0.178 0.175	0.085 0.084	0.070 0.070	0.094 0.093	0.107 0.106	0.069 0.068	**0.399** **0.395**	0.067 0.067	0.636** 0.633**
HI	-0.087 -0.082	0.057 0.054	-0.064 -0.062	-0.038 -0.037	-0.061 -0.060	0.195 0.188	0.114 0.111	0.081 0.079	0.076 0.075	0.093 0.090	0.090 0.087	0.058 0.056	**0.343** **0.333**	**0.625**** **0.621****

Residual effect Phenotypic path = 0.201
*Significant at 5% probability level, ** Significant at 1% probability level
Residual effect Genotypic path = 0.215

NOTE: DFF = Days to 50% flowering, GFP = grain filling period , DM = Days to maturity, PH = Plant height , PDL = Peduncle length, NTPP = Numbers of productive tillers/plant, SL = Spike length , NS = Number of spikelets/spike, NGMS = Number of grain per main spike, FLL = Flag leaf length, TGW = 1000 grain weight, BYPP = Biological yield per plot , HI = Harvest index , GYPP = Grain yield /plot

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