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EVALUATING TRAIT ASSOCIATIONS AND CAUSAL RELATIONSHIPS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) FOR BREEDING SUCCESS

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ABSTRACT

The present investigation was carried out to study "Evaluating Trait Associations and Causal Relationships in Bread Wheat (*Triticum aestivum* L.) for Breeding Success'' in a randomised block design with four replications at Agriculture Research Station, S. D. Agricultural University, Ladol, Gujarat during *rabi* 2020-21 to evaluate for genetic variability, heritability and genetic advance of thirty-eight accessions. Based on average of four replication data, total yield ranged from 341.85 gm to 817.85 gm per plot and maximum observed in Raj-3777 (817.85 gm). The analysis of variance revealed that mean sum of squares due to genotypes was found significant for all the traits under studied. This indicated the presence of adequate amount of variability in the experimental material and the accession under study showed genetically diverse. Traits with high heritability couple with high genetic advance as a percent of mean was reported for number of effective tillers per meter, 1000 grain weight and grain yield per plot indicates the high responsiveness to selection and presence of additive effects. The close affinity between PCV and GCV was observed for the traits viz., days to heading, days to maturity, plant height, spike length, number of grain per spike, 1000 grain weight, protein content and sedimentation value suggesting the environmental influence was narrow for the expression of these traits. Based on the mean performance of grain yield per plot, accession viz., Raj-3777, 17th HTWYT-38, VA 2016-22 and HI-1634 were categorised as high yielding genotypes. So, for the improvement of yield and their components traits more emphasis could be given to these genotypes and with planning of research for more number of seasons and locations to get more precise results.

***Keywords* :** Bread wheat; variability; genetic advance; accession and heritability.

Introduction

Since the Neolithic period 10,000 years B.C., bread wheat (*Triticum aestivum* L.), one of the world's most significant cereal crops, is thought to have been one of the earliest grains domesticated by humans. It is the most nutrient-dense of all food crops, ranks first in area coverage and second in global production only to maize (FAOSTAT, 2019). The most frequently farmed food crop in the world is wheat. More than a billion people throughout the world consume it in various forms. Following rice, it is the second most significant staple food crop in India. Hexaploid species include bread wheat (2n = 6x = 42 = AABBDD). It has an interesting history and serves as an illustration of how naturally occurring crossovers between closely related species and genera can result in polyploidy. Hexaploid wheat was proven by cytogenetic data to be the result of the fusion of three separate ancestral gene pools. The species of the genus *Triticum* that modern bread wheat varieties belong to and their close relatives can be divided into diploid, tetraploid, and hexaploid species, with chromosome numbers 2n = 14 = AA, 2n = 14 = BB, 2n = 28 = AABB, and 2n = 42 = AABBDD and basic chromosome number = (x) = 7, respectively. A wild diploid *Triticum urartu*, rather than *Triticum monococcum*, was shown to be the donor of the A genome (Dvorak *et al*., 1993), while a wild diploid *Aegilops speltoides* was found to be a potential donor of the B genome (Feldman *et al*., 2015).

Wheat is grown on 222.11 million hectares worldwide, producing 778.6 million metric tons, with a productivity of 3.51 t/ha (OECD/FAO 2021-22). In practically all of India's states, wheat is grown, although only in Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, Rajasthan, Bihar, and Gujarat is it grown extensively. According to the Directorate of Economics and Statistics' DAC and FW 2021-22 report, wheat is grown on 31.13 million hectares of irrigated land in India, with an annual production of 109.59 million tonnes. While in Gujarat, wheat is grown on 1.3 million hectares, producing 4.3 million tonnes and yielding 3156.29 Kg/ha (Directorate of Agriculture, Gujarat State, 2020-21). Wheat is grown in both rainfed and irrigated environments. In the last fifty years, the production of wheat has increased eight-fold, from 10.40 million tonnes in 1965–1966 to 109.59 million tonnes in 2021-22 (Directorate of Economics and Statistics, DAC and FW 2021-22)

Genetic variability is essential for natural selection and adaptation, allowing populations to respond to environmental changes. Heritability indicates the genetic influence on traits, helping breeders target specific characteristics for improvement. Genetic advance, on the other hand, quantifies the expected progress in a trait after selective breeding, aiding in the efficient development of desired traits in plant and animal breeding programs.

Material and Method

The experiment was conducted on "Evaluating Trait Associations and Causal Relationships in Bread Wheat (*Triticum aestivum* L.) for Breeding Success" in *rabi* 2020-21 at Agricultural Research Station, Sardarkrushinagar Dantiwada Agricultural University, Ladol, Gujarat. The centre is located between latitudes 230 38' and 230 41' N and longitudes 720 41' and 720 44' E. *Triticum aestivum* L. (bread wheat) genotypes representing 38 different genetic origins (Table 4.) used as the experimental material for this study. These taken from the Wheat Research Station, S.D.A.U., Vijapur, Gujarat. Four replications of the current experiment were done using a Randomized Block Design (RBD). Each genotype has a double row that is 3.0 meters long and spaced 22.5 cm (plant to plant spacing) apart. Twelve different traits, including days to heading (N), days to maturity (N), plant height (cm), effective tillers per meter, number of grains per spike, spike length (cm), grain yield per plot (g), biological yield per plot (g), harvest index (%), 1000 grain weight (g), protein content (%) and sedimentation value (ml), were observed for this investigation. Except for the traits of days to heading (N), days to maturity (N), number of effective tillers per meter, grain yield per plot (g), biological yield per plot (g), harvest index (%), 1000 grain weight (g), protein content (%) and sedimentation value (ml), observations were made on five randomly chosen plants from each replication. According to the methods outlined by Panse and Sukhatme, an analysis of variance was performed to determine the importance for each character.

Result and Discussion

Analysis of variance

The analysis of variance was carried out for all twelve characters considered for the study. The analysis of variance depicting the mean sum of squares for different characters studied are presented in Table 1. The result revealed highly significant differences among the tested genotypes for all the traits *viz.,* days to heading, days to maturity, plant height, number of effective tiller per meter, spike length, number of grain per spike, biological yield per plot, harvest index, 1000 grain weight, protein content, sedimentation value and grain yield per plot. This indicated the presence of considerable genetic variability among the genotypes for various characters.

Table 1: Analysis of variance (ANOVA) for different characters of bread wheat genotypes/accessions

Sr.No	Character	Mean sum of square		
		Replications	**Genotypes**	**Error**
	Degree of freedom	**3**	**37**	**111**
1	Days to heading (N)	3.18	115.89**	1.46
2	Days to maturity (N)	4.89	75.66**	1.92
3	Plant height (cm)	86.68	186.10**	22.07
4	Number of effective tillers per meter	153.91	710.19**	73.00
5	Spike length (cm)	0.08	1.34**	0.22
6	Number of grain per spike	9.81	67.19**	8.60
7	Biological yield per plot (g)	156388.13	236368.87**	40157.56
8	Harvest index (%)	3.67	111.27**	18.73
9	1000 grain weight (g)	6.88	61.43**	1.75
10	Protein content (%)	0.48	1.30**	0.23
11	Sedimentation value (ml)	4.61	37.99**	5.27
12	Grain yield per plot (g)	9963.63	42503.53**	3708.72

** Significant at 0.01 level of probability

Variance components and variability parameters

Analysis of variance (ANOVA) may not reveal the absolute variability and this could be accessed through standardizing the phenotypic and genotypic variances by obtaining coefficient of variability. The genetics of metric characters are centered on the study of its variation. The amount of variation is measured and expressed as the variance

Heritability in broad sense and genetic advance as per cent of mean are direct selection parameters that provide an index of transmissibility of traits which indicates the effectiveness of selection in improving the characters. The estimation of Genotypic and phenotypic Variances of each character as well as other genetic components *viz.,* genetic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability in broad sense (h^2b) and genetic advance as per cent of mean (GA% of mean) are narrated in Table 2.

Mean performance

The mean value of grain yield per plot was 548.64 and it ranged from 341.85 to 817.85 g. Genotype Raj-3777 (817.85 g) had the highest grain yield per plot followed by 17th HTWYT-38 (718.60 g) and VA 2016-22 (708.85 g) while, the genotype Raj-3065 (341.85 g), VA 2019-04 (356.85 g) and VA 2019-05 (398.85 g) were recorded the least grain yield per plot.

Based on the data given in table 3, it can be estimated that more emphasis should be given to number of grain per spike, spike length, grain yield per plot, biological yield per plot, number of effective tiller per meter, 1000 grain weight and plant height while doing selection for genetic improvement in bread wheat. Based on the mean performance of grain yield per plot, genotypes *viz.,* Raj-3777, 17th HTWYT-38, VA-2016-22 and HI-1634 were categorized as high yielding genotypes. So, for the improvement of yield and their components traits more emphasis could be given to these genotypes and with planning of research for more number of seasons and locations to get more precise results.

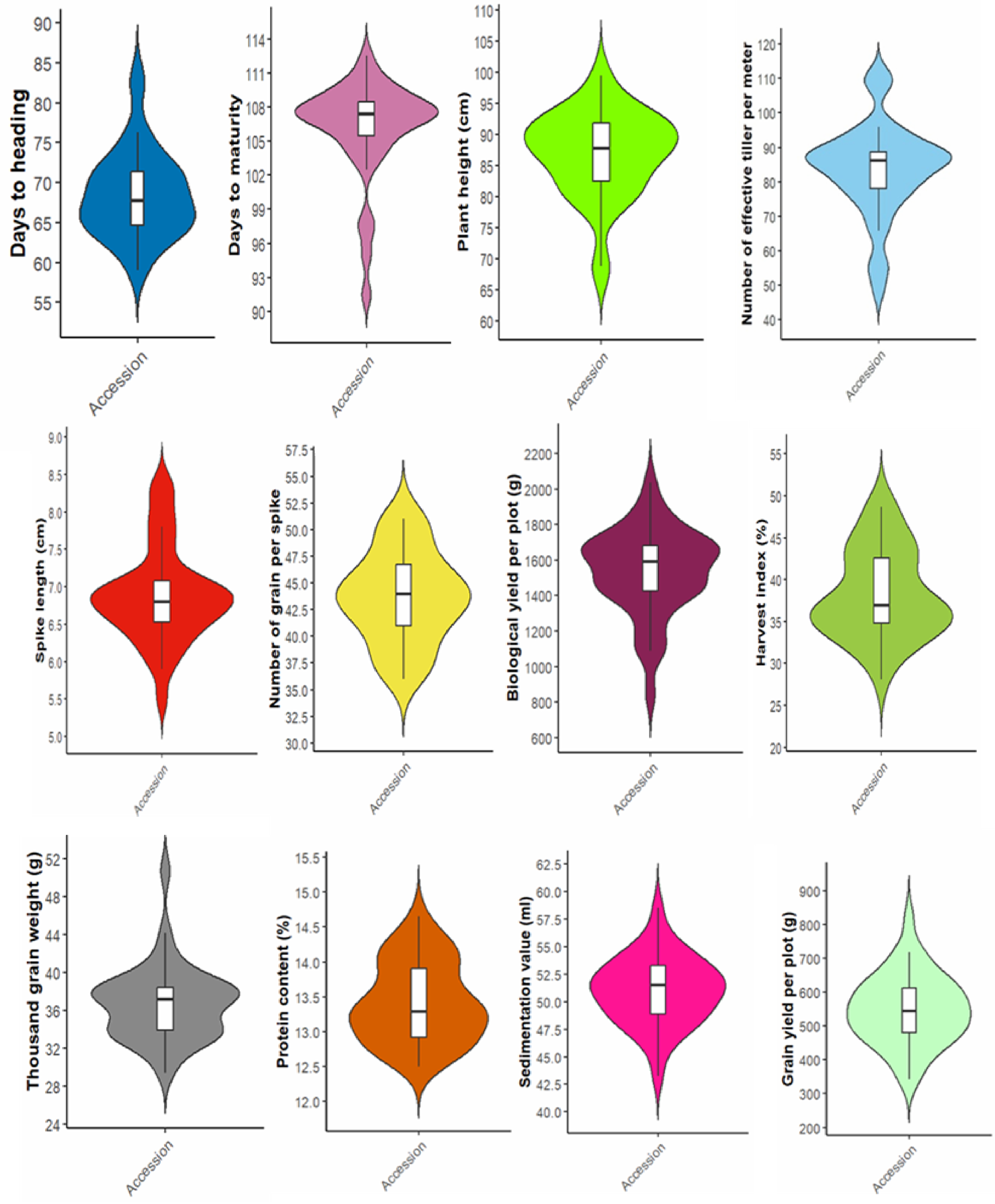

Fig. 1 : Violin graph representing the mean performance of genotypes for yield and yield contributing characters in bread wheat

Variance components

The estimation of phenotypic and genotypic components of variance was obtained for different characters (Table 2). A wide range of variation was observed for all the characters. The highest genotypic variance was recorded for biological yield per plot (49052.83) and it was followed by grain yield per plot (9698.70). The highest phenotypic variance was recorded for biological yield per plot (89210.39) followed by grain yield per plot (13407.42).

Table 2: Genetic parameter of variation for grain yield and its contribution character in bread wheat.

Sr.No	**Characters**	**σ^2g**	**σ^2p**	**GCV (%)**	**PCV (%)**	**h^2(b.s) %**	**GA**	**GA (% of Mean)**
1	Days to heading (N)	28.61	30.07	7.81	8.01	95.15	10.75	15.70
2	Days to maturity (N)	18.43	20.36	4.04	4.25	90.56	8.42	7.92
3	Plant height (cm)	41.01	63.08	7.36	9.13	65.01	10.64	12.23
4	Number of effective tillers per meter	159.30	232.30	15.09	18.22	68.57	21.53	25.74
5	Spike length (cm)	0.28	0.50	7.68	10.29	55.60	0.81	11.79
6	Number of grain per spike	14.65	23.24	8.85	11.14	63.02	6.26	14.47
7	Biological yield per plot (g)	49052.83	89210.39	14.39	19.41	54.99	338.32	21.98
8	Harvest index (%)	22.09	44.99	12.29	17.53	49.10	6.78	17.73
9	1000 grain weight (g)	14.92	16.67	10.53	11.13	89.52	7.53	20.53
10	Protein content (%)	0.27	0.50	3.85	5.28	53.24	0.78	5.79
11	Sedimentation value (ml)	8.18	13.45	5.61	7.19	60.83	4.60	9.01
12	Grain yield per plot (g)	9698.70	13407.42	17.95	21.10	72.34	172.55	31.45

Genotypic and Phenotypic Coefficient of Variance

Even though the differences were slight, the values of PCV were found to be greater than the GCV (Table 2) for all the traits studied, showing the influence of environment on the expression of these qualities. When traits like days to heading, days to maturity, plant height, spike length, number of grains per spike, 1000 grain weight, protein content and sedimentation value were observed, it was found that PCV and GCV had a strong affinity for each other, indicating that the environment had a limited impact on how these traits were expressed. Low estimates of both PCV and GCV were shown by the attributes, including days to heading, days to maturity, plant height, protein content, and sedimentation value, suggesting a lower chance that the traits will be improved through direct selection. The same conclusion was reached, according to Semun (2010), Dutamo *et al.* (2015) and Dabi *et al.* (2019).

Estimation of heritability, genetic advance and genetic advance expressed as percentage of mean

We reported (Table 2) high broad sense heritability for all the traits excluding spike length, biological yield per plot, harvest index and protein content which had moderate value of broad sense heritability. The expected genetic advance as a percentage of the mean was ranged from 5.79 per cent for protein content to 31.45 per cent for grain yield per plot. Furthermore, low genetic advance as a percent of mean was reported for days to maturity, protein content and sedimentation value and high genetic advance per cent of mean was reported for number of effective tiller per meter, biological yield per plot, 1000 grain weight and grain yield per plot. Characters with high genetic advance as a percent of mean allow the improvement of the characters through selection.

Number of effective tillers per meter, 1000 grain weight and grain yield per plot were reported to have traits with high heritability and high genetic advance as a percent of mean, which shows the presence of additive effects and high responsiveness to selection. Kalimullah *et al.* (2009), Kumar *et al.* (2013) and Barman *et al.* (2020) all reported similar findings. Days to heading, plant height, spike length, number of grains per spike and harvest index were character traits with high to moderate heritability and moderate genetic advance that showed both additive and non-additive gene action as a percentage of mean. Therefore, mass selection and progeny testing-based breeding could be used to improve these qualities. It is also important to mention that high to moderate heritability coupled with lower genetic advance as per cent of mean was recorded for days to maturity, protein content and sedimentation value which indicated the non-additive gene effects which were responsible for the expression of this trait therefore, selection for such trait may not be rewarding.

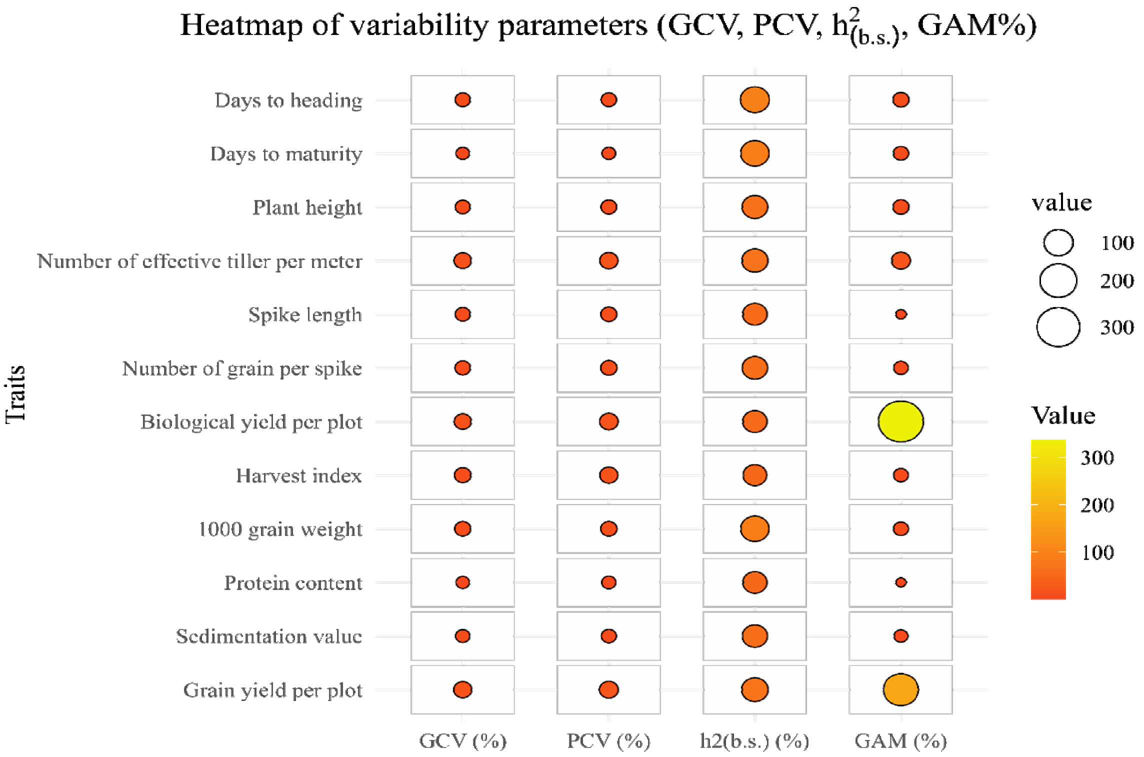

Fig. 2 : Heatmap of variability parameters for genetic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability in broad sense (h^2b) and genetic advance as per cent of mean (GA% of mean) for yield and yield contributing characters in bread wheat

Conclusion

According to the analysis of variance, all of the tested traits mean sums of squares due to genotypes were determined to be significant. This demonstrated that the experimental material included an acceptable quantity of diversity and that the genotypes under investigation were genetically diverse. Based on the mean performance of grain yield per plot, genotypes *viz.,* Raj-3777, 17th HTWYT-38, VA 2016-22 and HI-1634 were categorized as high yielding genotypes. So, for the improvement of yield and their components traits more emphasis could be given to these genotypes and with planning of research for more number of seasons and locations to get more precise results. Number of effective tillers per meter, 1000 grain weight and grain yield per plot were traits with strong heritability coupled with high genetic advance as a percent of mean. Which was attributed to the predominance of additive gene action, which is fixable for governing the character and obtained high selectivity value; as a result, selection pressure could be put successfully on certain traits for their judicious enhancement by adhering to various breeding techniques.

Table 3 : Mean performance of thirty-eight genotypes for yield and yield contributing characters in bread Wheat

No	GENOTYPE	DH	DM	PH	TIL/M	SL	NGS	BYP	HI	TGW	PC	SV	GYP(g)
1	ABV 2019-23	60	92	90.9	86	7.0	39	1647.54	44.79	40.84	12.80	48.4	593.10
2	ABV 2019-39	64	108	87.8	66	6.7	50	1362.04	33.20	37.54	13.27	48.2	483.35
3	ABV 2019-48	72	110	86.3	96	6.6	47	1675.04	41.77	30.65	13.29	51.5	566.60
4	ABV 2019-50	65	108	90.8	82	6.5	43	1529.54	39.80	36.16	13.49	52.2	478.85
5	ABV 2019-68	69	113	99.5	92	6.9	40	1711.54	35.58	38.57	13.09	49.3	546.60
6	VA 2016-22	64	95	82.5	88	7.2	45	1800.29	48.40	37.66	13.35	48.5	708.85
7	VA 2019-04	66	97	86.8	68	7.1	46	1115.30	45.51	33.62	14.04	52.0	356.85
8	VA 2019-05	63	109	86.3	74	5.9	37	1419.29	43.26	38.27	13.99	51.6	398.85
9	VA 2019-06	64	108	80.3	77	6.8	44	1422.29	36.66	37.50	12.61	43.3	530.35
10	VA 2019-16	59	108	87.3	83	6.2	51	1679.04	34.91	38.29	12.74	47.4	634.10
11	VA 2019-18	65	105	77.5	109	7.2	37	1681.04	45.03	40.24	13.07	48.2	592.10
12	HI-1633	66	107	80.8	55	6.8	47	1117.05	33.08	37.82	12.85	45.6	453.10

13	HI-1634	62	98	81.8	72	7.0	50	1671.79	48.70	38.44	13.27	48.8	705.10
14	Raj-3065	64	106	87.5	49	5.5	43	846.30	42.68	35.25	12.78	49.7	341.85
15	Raj-3777	63	108	90.0	110	7.6	42	2037.54	34.36	41.90	13.07	50.4	817.85
16	Raj-4079	68	108	79.3	88	6.6	38	1259.79	37.05	38.60	12.50	47.4	513.35
17	Raj-4083	65	108	80.5	88	6.8	44	1537.54	42.27	37.11	12.87	49.7	635.85
18	17th HTWYT-38	67	108	92.5	85	6.6	47	1897.04	37.40	38.57	13.77	53.7	718.60
19	17th HTWYT-49	72	108	92.0	94	7.5	44	1413.04	34.34	33.93	13.23	51.7	449.35
20	36th SAWSN-3002	76	110	85.8	80	7.0	38	1269.54	35.37	32.95	13.62	51.6	417.85
21	36th SAWSN-3047	71	109	93.3	95	6.9	45	1583.54	32.34	34.10	13.46	53.4	544.10
22	36th SAWSN-3048	67	104	94.0	89	7.0	49	1692.29	35.08	50.73	13.22	51.5	646.35
23	36th SAWSN-3073	75	103	88.3	87	6.3	41	1695.29	32.11	33.99	14.65	56.1	604.35
24	36th SAWSN-3129	72	110	91.3	81	8.4	41	1619.79	34.79	32.84	13.31	52.2	603.60
25	36th SAWSN-3261	71	107	68.8	86	6.6	44	1597.29	40.74	37.72	14.15	53.6	561.10
26	29th HRWSN-2040	69	106	87.8	89	6.5	41	1662.54	36.30	32.57	14.22	53.9	613.85
27	29th HRWSN-2054	76	107	89.5	86	6.3	43	1466.79	30.31	33.77	13.95	50.3	465.60
28	29th HRWSN-2129	70	107	89.3	87	6.8	45	1606.79	36.99	34.04	14.15	53.5	560.10
29	DBW-187	71	109	93.8	75	6.5	51	1758.04	37.15	37.23	14.12	54.3	651.10
30	DBW-222	70	105	90.0	94	6.9	51	1789.04	43.56	35.98	13.57	52.8	635.10
31	MP-1203	83	111	68.3	78	6.9	43	1457.04	43.85	29.39	14.37	58.5	498.35
32	MP-1338	66	104	85.8	81	6.8	41	1443.79	48.67	34.05	13.22	51.6	567.85
33	RWP 2018-29	82	111	93.0	89	7.8	47	1468.79	36.29	32.02	13.79	54.5	476.10
34	CG-1029	67	109	93.5	88	6.2	44	1879.54	38.08	36.36	12.67	46.4	513.85
35	WH-730	72	106	98.3	57	6.0	43	1089.55	28.11	44.18	14.37	55.8	431.60
36	LOK 1	68	107	92.0	110	8.1	37	1659.29	32.54	39.33	13.29	49.6	520.10
37	GW 322	72	107	82.5	89	8.3	45	1473.29	36.88	33.45	12.83	51.1	530.85
38	GW 451	68	104	81.3	81	7.9	36	1450.54	35.80	38.31	12.83	50.5	481.85
	MEAN	68	106	87.02	84	6.9	44	1539.10	38.26	36.68	13.42	51.0	548.64
	RANGE	59-83	92 - 113	68.3 - 99.5	49 - 110	5.5 - 8.4	36 - 51	846.30-2037.54	28.11 - 48.70	29.39 - 50.73	12.50 - 14.65	43.3 - 58.5	341.85-817.85
	S.Em ±	0.60	0.69	2.35	4.27	0.24	1.47	100.20	2.39	0.66	0.24	1.15	30.45
	C.D. @ 5 %	1.69	1.94	6.58	11.97	0.68	4.11	280.79	6.71	1.85	0.68	3.22	85.33
	C.V.%	1.76	1.31	5.40	10.21	7.02	6.78	13.02	12.51	3.60	3.61	4.50	11.10

Where **DH** = days to heading (N), **DM** = days to maturity (N), **PH** = plant height (cm), **TIL/M** = number of effective tiller per meter, **SL** = spike length (cm), **NGS** = number of grain per spike, **BYP** = biological yield per plot (g), **HI** = harvest index (%), **TGW** = 1000 grain weight (g), **PC** = protein content (%), **SV** = sedimentation value (ml) and **GYP** = grain yield per plot (g).

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