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Gene Effect Analysis for Grain Yield, Yield Components and Physiological Characters in Bread Wheat Under Water Limited Conditions of Bundelkhand Region

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ABSTRACT

The present study was conducted during *rabi*, 2019–20 and 2020–21 with 08 bread wheat diverse parents and their 28 F_1s (half diallel, excluding reciprocals) to study gene effects and heterosis for grain yield, yield attributes and physiological traits. Days to heading and days to maturity had general mean values of 89.8 days and 130.4 days, respectively. The parent GW 322 showed early heading in 88 days, while the genotype DBW 110 exhibited early maturity in 128 days. The hybrid NW 5054×PBW 723 (13.45 cm) had the highest spike length, followed by HD 3086×NW 5054 (13.40 cm) and PBW 723×NIAW 34 (13.25 cm). The grain yield plant^{-1} ranged from 17.37 g to 21.85 g in parents and 14.99 g to 23.41 g among hybrids. The cross HD 3086×K 1006 (23.41 g) and the parent HD 3086 (21.85 g) depicted the highest grain yield per plant. The parent NIAW 34 and the hybrid HD 3086×NIAW 34 showed the highest chlorophyll fluorescence. All three key physiological traits showed significant and positive associations with grain yield and harvest index. All the seventeen characters showed high GCA effects than SCA effects and indicated for preponderance of additive gene effects for yield, its components and physiological traits. An appraisal of GCA effects found that HD 3086 was a good general combiner for the majority of characters, while the crosses, HI 1544×NIAW 34, HI 1544×GW 322 and NW5054×PBW723 with significant SCA effects were found promising under water limited conditions of Bundelkhand region.

KEYWORDS: Chlorophyll fluorescence, gene effects, heterosis, LAI, wheat

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1. INTRODUCTION

Wheat is one of the most important staple food crops, which contributed nearly 34% of the total food grains production in India during *rabi*, 2022–23 (Anonymous, 2023). Globally, wheat provides about 20% of the required dietary calories and above 40% population is chiefly dependent on it for food purposes (Shiferaw et al., 2013; Maryami et al., 2020; Vikas et al., 2022). With the burgeoning population wheat production needs to be increased, however the climate change poses a serious threat for enhanced wheat production (Ejaz et al., 2023; Zahra et al., 2023). Wheat demand is expected to increase by 50% by 2050 compared to where it is now. Meanwhile, the crop is threatened by new and more aggressive pests and diseases, dwindling water supplies, a scarcity of usable land, and unpredictable weather, notably heat (IIWBR Vision, 2050). To develop high yielding wheat genotypes coupled with desirable gene effect and manifestation of heterosis are useful being wheat a self-pollinated crop. In cross pollinated crops the exploitation of heterotic effects is of great success for hybrid development and it is highly directional for pure line development in wheat. (Garcia et al., 2008; Li et al., 2008; Song et al., 2010; Gupta et al., 2019). The prospective heterosis is anticipated to significantly contribute to addressing future population growth despite the hybrid wheat area being less than 0.2% of the global total due to the yield increase of 3.5–15% (Longin et al., 2012; Ni et al., 2017).

By developing new cultivars with increased genetic diversity and improved performance in a range of agroclimatic conditions, wheat productivity can be raised. Researchers developed methods for analyzing genotypes for all feasible cross-combinations (Griffing, 1956; Hayman, 1954; Mather and Jinks, 1982). When choosing suitable parents for hybridization, recognizing quantitative trait inheritance, and spotting potential crossovers for later use in breeding programs, knowledge of combining ability is essential. Over the past ten years, the public and private sectors have developed a greater interest in hybrid wheat breeding (Boeven and Longin, 2019). It is necessary to identify wheat genotypes and overall combiners that perform better in terms of grain production and component traits. To begin a niche-specific breeding program, an outstanding cross-combination with high GCA effects is essential.

The breeding strategy to be utilized can be determined by the type of gene action associated with the inheritance of various traits, which is crucial information that is provided by combining ability analysis. Because of the numerous types of gene action, their magnitude and their impacts, the essence of gene action may help in forecasting selection efficacy. It outlines the intent behind different gene behavior and their range to weed out ineffective crossings in the initial generations. The main objectives of the proposed investigation were to estimate the degree of heterosis and delineation of gene effects in the parents and developed wheat hybrids for grain yield and physiological traits in bread wheat.

2. MATERIALS AND METHODS

2.1. *Experimental materials site and experimental design*

Eight elite diverse bread wheat varieties - HD3086 (P1), HI544 (P2), DBW110 (P3), K1006 (P5), NW5054 (P6), PBW723 (P7) and NIAW34 (P8) were taken into consideration for the study (Table 1). The NIAW34 has a drought tolerance, which is much needed in the region, whereas the PBW723 is an enhanced variant of the dominant wheat variety PBW343.

The Griffing (1956) method 2 and Model I mating design was used to make half diallel crosses between the eight elite wheat genotypes (excluding reciprocals) during *rabi*, 2019–20. The 08 parents and 28 F_1s were planted during *rabi*, 2020–21, in paired rows of 2 m length and 30 cm between rows using a randomized complete block design with two replications at the Research Farm, Rani Lakshmi Bai Central Agricultural University Jhansi (UP).

2.2. *Observations*

From each parent and F_1 progeny, five plants were randomly

Table 1: Details of eight wheat varieties used in the study

Sl. No.	Parent	Symbol	Developed at	Parentage
1.	HD 3086	P1	ICAR-IARI, New Delhi	DBW14/HD2733//HUW468
2.	HI 1544	P2	ICAR-IARI, Indore	HINDI62/BOBWHITE/CPAN 2099
3.	DBW 110	P3	ICAR-IIWBR, Karnal	KIRITAT/4/2*SERI*2/3/KAUZ*2/BOW//KAUZ
4.	GW 322	P4	RARS, Vijapur, Gujarat	GW 173/GW 196
5.	K 1006	P5	CSAUA&T, Kanpur	PBW343/HP1731
6.	NW 5054	P6	NDUA&T, Faizabad	THELIN//2*ATTILA*2PASTOR
7.	PBW 723	P7	PAU, Ludhiana	Unnat PBW343
8.	NIAW 34	P8	MPKV, Niphad	CNO 79/PRL "S"

selected, and the following quantitative characteristics were recorded. Fourteen quantitative traits, including days to heading (DH), days to maturity (DM), flag leaf length (FLL), flag leaf width (FLW), spike length (SL), peduncle length (PL), awn length (AL), number of tillers meter^{-1} (TPM), plant height (PH), number of grains spike^{-1} (GPS), 1000 grain weight (TGW), grain yield plant^{-1} (GY), biological yield plant^{-1} (BY) and harvest index (HI) and for three physiological traits *viz*., leaf area index (LAI), chlorophyll fluorescence (CF), and chlorophyll content (CC) were evaluated on plot basis during *rabi*, 2020–2021. The Sun scan canopy analyzer was utilized to estimate the leaf area index for each row between 11:00 AM and 2:00 PM using par measurements above and below the canopy. The Fv/Fm ratio were observed using handheld chlorophyll Fluorometer and SPAD meter was used to measure the total chlorophyll content of the plants that were chosen randomly.

2.3. *Statistical analysis*

The analysis of variance (ANOVA) for the Randomized Block Design (RBD) was conducted individually for each of the characteristics following standard procedures. The average mean of each hybrid over two replications was used to compute the heterosis for each attribute. The effects of relative heterosis and heterobeltiosis/better parent heterosis were assessed using the Singh and Chaudhary (1977) and Fonseca and Patterson (1968) in MS Excel.

3. RESULTS AND DISCUSSION

3.1. *Analysis of variance*

The analysis of variance indicated substantial variations for all of the traits, showing that the genotypes had enough genetic variation for all the characters. Further partitioning of mean squares due to treatments was also significant. It revealed that adequate of variation was present between parents and F_1s. The mean and range values of the parents and their crosses are presented in Table 2. Days to heading and maturity had general mean values of 89.8 days and 130.4 days, respectively and ranged from 88.0 days to 93.5 days and 128.5 days to 133.5 days in parents and 85.5 days to 92.5 days and 127.0 days to 134.5 days in hybrids, respectively. The parent GW 322 showed early heading in 88 days and the genotype DBW 110 exhibited early maturity with 128.5 days. Flag leaf length and width in hybrids ranged from 19.65 cm to 25.90 cm and 1.69 cm to 2.18 cm, respectively. The parent K 1006 showed maximum flag leaf length (23.80 cm), while the maximum flag leaf width was observed in the parent NW 5054 (2.07 cm). General mean for peduncle length was 31.62 cm. The parental and hybrid means were 29.06 cm and 32.35 cm, respectively. The parent NW 5054 (34.35 cm) and the cross DBW 110×K1006 (36.65 cm) had the highest mean values for the trait. The parent HD 3086 showed the highest number of grains per spike

Table 2: Grand mean, mean±SE (m) and range in parents and F_1s in bread wheat

Characters	GM	Parents		F_1s	
		Mean±SE(m)	Range	Mean±SE(m)	Range
Days to heading	89.85	90.50±0.97	88–93.50	89.66±0.97	85.50–92.50
Days to maturity	130.40	131.19±1.03	128.50–133.50	130.17±1.03	127.0–134.5
Flag leaf length (cm)	22.37	22.21± 0.76	19.90– 23.80	22.42±0.76	19.65–25.90
Flag leaf width (cm)	1.96	1.96±0.05	1.77–2.07	1.95±0.05	1.69–2.18
Spike length (cm)	12.38	11.92±0.30	10.90–13.30	12.51±0.30	10.78–13.45
Peduncle length (cm)	31.62	29.06±0.79	25.15–34.35	32.35±0.79	28.60–36.65
Awn length (cm)	6.61	6.47±0.28	5.54–7.00	6.65±0.28	5.85–7.88
Number of tillers m^{-1}	136.83	132.81±6.86	117.50–177	137.98±6.86	103.00–191.50
Plant height (cm)	90.29	87.31±1.11	80.90–96.30	91.14±1.11	81.65–100.20
No. of grains spike^{-1}	66.65	64.4±1.80	59.00–69.00	67.3±1.80	57.0–77.0
1000 grain weight (g)	43.31	40.96±1.14	40.00–42.50	43.99±1.14	39.85–46.80
Grain yield plant^{-1} (g)	20.56	19.95±0.81	17.37–21.85	20.73±0.81	14.99–23.41
Biological yield plant^{-1} (g)	49.73	50.12±2.09	45.15–54.78	49.61±2.09	36.37–58.48
Harvest index (%)	0.41	0.40±0.01	0.39–0.41	0.42±0.01	0.38–0.44
Leaf area index	1.85	1.71±0.08	1.28–2.18	1.89±0.08	1.18–2.30
Chlorophyll fluorescence	0.74	0.73±0.01	0.72–0.75	0.75±0.01	0.71–0.78
Chlorophyll content	40.03	39.53±0.96	38.18–42.28	40.18±0.96	31.68– 45.31

(69). The highest estimates were observed in the cross HD 3086×GW 322 (77), followed by HD 3086×HI 1544 (76), HI 1544×NIAW 34 (73), HD 3086×NW 5054 (72.5) and HI 1544×GW 322 (72), respectively. The parent GW 322 (42.5 g) and the cross HD 3086×NW 5054 (46.8 g) depicted maximum 1000 grain weight, followed by HD 3086×HI 1544 (46.50 g), HD 3086×K 1006 (46.3 g) and HI 1544×NW 5054 (46.1 g), respectively. The grain yield per plant ranged from 17.37 g to 21.85 g in parents and 14.99 g to 23.41 g among hybrids. The cross HD 3086×K 1006 (23.41 g) and the parent HD 3086 (21.85 g) depicted the highest grain yield per plant. The hybrids NW 5054×PBW 723 (23.3 g), HI 1544×NIAW 34 (23.14 g), K 1006×PBW 723 (22.91 g) and HD 3086×NW 5054 (22.80 g) were the top identified crosses for grain yield per plant, respectively. The average leaf area index (LAI) was 1.85 and the parent, K 1006 revealed the highest LAI of 2.18 among the parental genotypes. The mean chlorophyll fluorescence in the parents and F_1s was 0.73 and 0.75, respectively. The parent NIAW 34 (0.75) showed the highest mean value, while the cross HD 3086×NIAW 34 depicted the highest fluorescence, followed by NW 5054×PBW 723 (0.77). The highest total chlorophyll content was observed in the cross combination PBW 723×NIAW 34 (45.31), followed by HD 3086×K 1006 (45.05), HD 3086×NIAW 34 (44.81) and NW 5054×NIAW 34 (44.72), respectively.

3.2. Heterosis and heterobeltiosis

Heterosis for days to heading varied from -5.0% (HI 1544×NW 5054) to 2.81% (GW 322×NW 5054) (Table 3). Eight crosses showed significant heterobeltiosis for early heading, ranging from -5.46% (GW 322×K 1006) to -3.24% (HD 3086×DBW 110). Six crosses showed significant heterobeltiosis for days to maturity, ranging from -3.76% (HD 3086×NW 5054 and HI 1544×NW 5054) to -3.28% (DBW 110×NW 5054 and K 1006×NW 5054). In fourteen crosses flag leaf length heterosis and in thirteen crosses flag leaf width heterosis was significant. The hybrid HD 3086×HI 1544 (15.88%) depicted the most significant positive heterosis for flag leaf length, followed by cross K 1006×PBW 723 (10.98%), GW 322×PBW 723 (10.59%), DBW 110×PBW 723(8.15%) and NW 5054×PBW 723 (8.01%), respectively. Significant heterosis for peduncle length was exhibited in twenty-six crosses and ranged from 4.59% (HD 3086×NIAW 34) to 24.38% (DBW 110×K 1006). The highest positive heterosis was exhibited by the hybrid DBW 110×K 1006 (24.38%), followed by DBW 110×GW 322 (19.56%), HI 1544×NIAW 34 (19.37%), PBW 723×NIAW 34 (18.53%) and HI 1544×PBW 723 (16.84%), respectively. For 1000 grain wt., the highest estimates of positive heterobeltiosis were exhibited by the hybrid HD 3086×NW 5054 (13.73%), followed by HD 3086×HI 1544 (13.0%), HI 1544×NW 5054 (12.71%), HD 3086×K 1006 (11.57%) and HI 1544×NIAW 34, respectively.

Table 3: Mean (%) and range of heterosis and heterobeltiosis for yield and yield components in bread wheat

Characters	Heterosis		Heterobeltiosis	
	Mean	Range	Mean	Range
Days to heading	-0.92	-5.00–2.81	-2.14	-5.46–1.67
Days to maturity	-0.77	-3.21–1.72	-1.48	-3.76–1.14
Flag leaf length	1.04	-12.37–15.88	-2.42	-14.12–13.35
Flag leaf width	-0.60	-10.95–9.02	-2.95	-12.56–5.46
Spike length	5.05	-6.51–16.26	0.81	-11.32–13.97
Peduncle length	11.53	-4.96–24.38	5.10	-9.75–20.16
Awn length	2.83	-10.86–24.51	-0.98	-12.50–15.81
No. of effective tillers m^{-1}	4.34	-23.70–29.61	-2.23	-35.03–22.78
Plant height	4.45	-5.74–15.78	1.17	-7.85–12.31
No. of grains $spike^{-1}$	4.57	-10.94–14.96	1.53	-17.39–11.59
1000 grain weight	7.39	-0.75–14.78	6.00	-1.12–13.73
Grain yield $plant^{-1}$	3.75	-26.19–18.41	0.15	-27.26–15.21
Biological yield $plant^{-1}$	-1.07	-28.61–8.18	-4.00	-28.31–7.79
Harvest index	4.86	-3.80–10.13	3.78	-6.17–10.13
Leaf area index	9.89	-24.80–30.58	0.51	-36.49–18.92
Chlorophyll fluorescence	1.87	-3.40–5.88	1.12	-4.05–5.52
Chlorophyll content	1.64	-18.84–17.30	-0.45	-20.22–16.60

Heterobeltiosis for grain yield per plant ranged from -27.26 (HI 1544×NW 5054) to 15.21% (HI 1544×NIAW 34). The hybrid HI 1544×NIAW 34 (15.21%) had the highest positive heterobeltiosis, followed by HI 1544×GW 322 (13.92%), NW 5054×PBW 723 (12.70%), GW 322×K 1006 (12.10%) and K 1006×PBW 723 (11.48%), respectively. The extent of heterosis for leaf area index ranged from -24.80% (DBW 110×GW 322) to 30.58% (HD 3086×DBW 110). Significant heterobeltiosis for chlorophyll fluorescence was exhibited in nineteen crosses and ranged from 0.67% (PBW 723×NIAW 34) to 5.52% (NW 5054×PBW 723). The highest significant positive heterosis was observed in the cross HD 3086×K 1006 (17.30%), followed by cross NW 5054×PBW 723 (14.79%), PBW 723×NIAW 34 (11.57%), HD 3086×NIAW 34 (10.76%) and NW 5054×NIAW 34 (11.71%), respectively. For grain yield and yield-contributing traits in bread wheat, significant heterosis and heterobeltiosis have been reported by Singh et al. (2004); Kumar et al. (2011); Jain and Sastry (2012); Lal et al. (2013); Mehta (2013); Noorka et al. (2013); Kumar et al. (2014); Baloch (2016); Hei et al. (2016); Murugan and Kannan (2017) and Askander et al. (2021).

3.3. Combining ability

The *per se* performance due to GCA and SCA were significant for all the traits. GCA effects for day to heading, days to maturity, flag leaf length, flag leaf width, spike length, awn length, number of effective tillers meter^{-1}, plant height, number of grains spike^{-1}, thousand grains weight, grain yield plant^{-1}, biological yield plant^{-1}, harvest index, leaf area index and chlorophyll fluorescence were estimated to be higher than SCA effects, showing that additive gene effects were predominant for these traits. Many researchers have noted variations in wheat for a wide range of yields and its component traits, including Akram et al. (2011); Raj and Kandalkar (2013); Ammar et al. (2014); Saeed and Khalil (2017); Ingle et al. (2018); Sharma et al. (2019) and Srivastava et al. (2020).

Two parents NIAW 34(-0.86) and GW 322 (-0.7) depicted negative significant GCA effects for days to heading, whereas, the parents NIAW 3034 (-1.01), DBW 110 (-1.01) and HI 1544 (-0.713) exhibited significant negative GCA effects for days to maturity (Table 4). Significant positive GCA effects for spike length were exhibited by the parents NW 5054 (0.49) and PBW 723 (0.37). The hybrids HD 3086×HI 1544 (1.12), GW 322×NIAW 34 (0.88) and HD 3086×DBW 110 (0.80) depicted positive significant SCA effect for spike length. The parent GW 322 (17.5) and K 1006 (5.55) exhibited significant positive GCA effects for effective tillers per meter, thus could be known as good general combiners for this character. The crosses GW 322×K 1006 (31.62), DBW 110×K 1006 (29.07), HD 3086×NIAW 34 (25.97), HD 3086×HI 1544(22.82), HI 1544×NW 5054 (20.02) and DBW 110×NW 5054 (15.17) had significant positive SCA effects for tillers m^{-1}.

Table 4: Estimation of GCA effects for some quantitative traits in bread wheat

Genotype	DH	DM	FLL	FLW	SL	PL	AL	GPS	TKW	GY	LAI	CL
HD 3086	0.79*	0.14	0.42	-0.13	0.10	0.34	0.23**	2.31**	0.92**	1.48**	0.08**	1.54**
HI 1544	-0.51	-0.71*	0.02	0.00	-0.54	-0.34	-0.23	2.11**	0.50	-0.70	-0.01	-0.80
DBW 110	-0.16	-1.01**	-1.06	-0.02	-0.22	0.27	-0.07	-2.19	-1.22	-2.30	-0.39	-1.07
GW 322	0.71*	0.24	0.40	0.06**	-0.27	-0.14	0.16	1.86**	0.69*	0.257	0.04	0.05
K 1006	-0.41	0.44	0.49*	0.01	0.01	1.38**	-0.45	-1.69	0.13	0.20	0.22**	-1.74
NW 5054	-0.06	-0.01	0.16	0.05**	0.49**	1.92**	0.24**	-0.84	0.03	0.08	-0.05	-1.23
PBW 723	1.94**	1.94**	-0.25	0.04**	0.37**	-2.06	0.01	0.01	-0.19	1.10**	-0.01	1.0**
NIAW 34	-0.86**	-1.01**	-0.17	0.00	0.07	-1.38	0.10	-1.59	-0.87	-0.12	0.10**	2.22**
SE (gi)	0.29	0.30	0.22	0.01	0.09	0.23	0.08	0.53	0.34	0.24	0.02	0.28

*: Significant at (p=0.05) per cent level; **: Significant at (p=0.01) per cent level

For the number of grains spike^{-1} three parents exhibited significant GCA effects. The cross HD 3086×GW 322 (6.17) depicted the highest significant positive SCA effects, followed by HI 1544×NIAW 34 (5.82), HD 3086×HI 1544 (4.92) and HD 3086×DBW 110 (4.72), respectively. GCA effects computed for 1000 grain weight exhibited that parents HD 3086 (0.92) and GW 322 (0.69) exhibited positive significant GCA effects. The hybrid HD 3086×NW 5054 (2.54) had the highest specific combining ability for this trait, followed by HI 1544×NW 5054 (2.26) and HD 3086×DBW 110 (2.13). The parents HD 3086 (1.48) and PBW 723 (1.10) exhibited significant positive GCA effects for grain yield per plant hence appeared as the superior combiners. The cross HI 1544×NIAW 34 (3.39) showed the maximum SCA effect, followed by HI 1544×GW 322 (2.76), and HD 3086×DBW 110 (2.26) and NW 505×PBW 723 (1.56). The parents K1006 (0.22), NIAW 34 (0.105) and HD 3086 (0.08) showed positive significant GCA effect for leaf area index, whereas the parent HD 3086 (0.008) and NIAW 34 (.006) exhibited positive significant GCA effect for chlorophyll fluorescence. The highest significant positive SCA effects were showed by HD 3086×NIAW 34 (0.02) and NW 5054×PBW 723 9(0.02). Significant positive GCA effects for chlorophyll content was depicted by the parents

NIAW 34 (2.22), HD 3086 (1.54) and NW 5054 (1.0). The highest significant positive SCA effects were exhibited by the cross HD 3086×K 1006 (5.22), followed by NW 5054×PBW 723 (4.64), NW 5054×NIAW 34 (3.69) and DBW 110×PBW 723 (2.80), respectively.

3.4. Correlation

Days to heading showed positive significant correlations with days to maturity (0.59**), grain yield per pant (0.39*) and biological yield plant^{-1} (0.43**) (Table 5). Flag leaf length was positively correlated with flag leaf width (0.34*), spike length

Table 5: Simple correlations for seventeen yield, yield components and physiological characters in bread wheat

Traits	DH	DM	FLL	FLW	AL	PL	TPM	PH
DM	0.59**							
FLL	0.17^{NS}	0.20^{NS}						
FLW	0.14^{NS}	0.23^{NS}	0.34*					
AL	0.17^{NS}	0.01^{NS}	0.25^{NS}	0.021^{NS}				
PL	-0.34*	-0.15^{NS}	-0.00^{NS}	-0.131^{NS}	0.02^{NS}			
TPM	-0.25^{NS}	-0.06^{NS}	0.10^{NS}	0.131^{NS}	-0.30^{NS}	0.36*		
PH	-0.23^{NS}	-0.18^{NS}	0.06^{NS}	-0.016^{NS}	0.10^{NS}	0.55**	0.28^{NS}	
GY	0.39*	0.30^{NS}	0.71**	0.254^{NS}	0.33^{NS}	-0.10^{NS}	-0.07^{NS}	0.11^{NS}
BY	0.44**	0.34*	0.70**	0.301^{NS}	0.35*	-0.21^{NS}	-0.08^{NS}	0.06^{NS}
HI	0.15^{NS}	0.05^{NS}	0.47**	0.005^{NS}	0.14^{NS}	0.17^{NS}	-0.05^{NS}	0.17^{NS}
GPS	0.25^{NS}	0.04^{NS}	0.58**	0.226^{NS}	0.24^{NS}	-0.01^{NS}	-0.21^{NS}	0.06^{NS}
TGW	-0.10^{NS}	-0.11^{NS}	0.43**	-0.100^{NS}	0.21^{NS}	0.34*	-0.00^{NS}	0.20^{NS}
SL	0.23^{NS}	0.15^{NS}	0.35*	0.213^{NS}	0.40*	0.13^{NS}	0.00^{NS}	0.30^{NS}
LAI	-0.07^{NS}	0.03^{NS}	0.52**	0.067^{NS}	0.06^{NS}	0.07^{NS}	-0.05^{NS}	0.10^{NS}
CF	0.06^{NS}	-0.07^{NS}	0.15^{NS}	-0.153^{NS}	0.18^{NS}	0.01^{NS}	-0.16^{NS}	0.00^{NS}
CC	0.30^{NS}	0.12^{NS}	0.28^{NS}	0.078^{NS}	0.28^{NS}	-0.37*	-0.38*	-0.19^{NS}

Table 5: Continue...

Traits	GY	BY	HI	GPS	TGW	SL	LAI	CF
DM								
FLL								
FLW								
AL								
PL								
TPM								
PH								
GY								
BY	0.96**							
HI	0.71**	0.50**						
GPS	0.56**	0.50**	0.50**					
TGW	0.39*	0.21^{NS}	0.67**	0.58**				
SL	0.49**	0.45**	0.39*	0.34*	0.30^{NS}			
LAI	0.64**	0.51**	0.70**	0.36*	0.54**	0.32^{NS}		
CF	0.40*	0.28^{NS}	0.60**	0.25^{NS}	0.41*	0.19^{NS}	0.44**	
CC	0.55**	0.56**	0.34*	0.37*	0.09^{NS}	0.26^{NS}	0.19^{NS}	0.56**

*: Significant at (p=0.05) per cent level; **: Significant at (p=0.01) per cent level

(0.35*), grain yield plant^{-1} (0.71**), biological yield plant^{-1} (0.700**), grains spike^{-1} (0.58**), 1000 grain weight (0.43**), harvest index (0.47**) and leaf area index (0.52**). 1000 grain weight was positively significantly correlated with flag leaf length (0.43**), number of grains spike^{-1} (0.58**), peduncle length (0.34*), grain yield plant^{-1} (0.39*), harvest index (0.67**), leaf area index (0.54**), chlorophyll fluorescence (0.41*). Grain yield was found significantly correlated with days to heading (0.39*), flag leaf length (0.71*), spike length (0.48**), biological yield plant^{-1} (0.96**), grains spike^{-1} (0.56**), 1000 grain weight (0.39*), harvest index (0.71**), leaf area index (0.64**), chlorophyll fluorescence (0.40*) and chlorophyll content (0.55**). Leaf area index had significant positive associations with flag leaf length (0.52**), grains spike^{-1} (0.36*), 1000 grain weight (0.54**), grain yield plant^{-1} (0.64**), biological yield plant^{-1} (0.51**), harvest index (0.70**), chlorophyll fluorescence (0.44**).

Chlorophyll fluorescence was significant positively correlated with grain yield per plant (0.40*), harvest index (0.60**), 1000 grain weight (0.41*), leaf area index (0.44**) and chlorophyll content (-0.38*).

Sokoto et al. (2012); Kumar et al. (2014); Ayer et al. (2017); Zare et al. (2017); Ojha et al. (2018); Upadhyay (2020) and Kiran and Singh (2020) were also reported significant positive correlation for grain yield and its attributing traits.

4. CONCLUSION

Grain yield, yield components and three key physiological traits were found under additive gene effects and showed degree of dominance less than unity. The parental genotypes HD3086, GW322, NIAW34 and HI1544 were found better suited for Bundelkhand region. The hybrid combinations, HI1544×NIAW34, HI1544×GW322, HD3086×NIAW34, NW5054×PBW723, HD3086×K1006, HI1544×GW322 can be further fruitfully utilized for developing climate resilient breeding populations.

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