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Heterosis and Diallel Analysis for Grain Yield, Yield Attributes and Physiological Traits in Barley (*Hordeum vulgare* L.)

Supriya Patel[1], Vishnu Kumar[1,2], Manoj Kumar Saini[1], Anshuman Singh[1], Sultan Singh[3], K. K. Singh[3], Aavula Naveen[4], Vemula Anjula Krishna[1] and S. K. Chaturvedi[1]

[1]Dept. of GPB, Rani Lakshmi Bai Central Agricultural University, Jhansi, Uttar Pradesh (284 003), India
[2]ICAR-National Bureau of Plant Genetic Resources, New Delhi (110 012), India
[3]ICAR-Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh (284 003), India
[4]ICAR-Indian Agricultural Research Institute, New Delhi (110 012), India

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Corresponding vishnupbg@gmail.com

0000-0002-9259-3012

ABSTRACT

The present study was carried out during November–April, 2019–2020 and 2020–21 with eight diverse barley genotypes and their developed 28 F_1s (half diallel, excluding reciprocals) to ascertain gene effects, hetrosis and correlations for grain yield, yield attributes and physiological traits under water limited conditions of Bundelkhand region. Days to heading and days to maturity exhibited general mean values of 86 days and 127 days, respectively. The parental genotypes, DWRB180, RD2794 and RD2899 showed early spike emergence and maturity. The cross combinations, namely DWRB160 /DWRB180, DWRB180/RD2907 and BH946/RD2552 were promising for flag leaf length and width. The GCA effects were significant and prevalent for all the characters, except days to heading, plant height and tillers count. The parents, DWRB160 (5.29^{**}) and BH902 (1.59^{**}) depicted high GCA effects for 1000 grain weight. The parents, DWRB180, RD2552, and BH946 exhibited significant positive GCA effects for leaf area index and chlorophyll fluorescence, whereas the genotypes, RD2907, BH946 and RD2899 showed higher GCA effects for chlorophyll content. Grain yield exhibited significant positive correlations with flag leaf width (0.60^{**}), tillers per meter (0.35^{*}), grains per spike (0.39^{*}), harvest index (0.53^{**}), chlorophyll content (0.69^{**}), leaf area index (0.49^{**}) and chlorophyll fluorescence (0.68^{**}). The parents, BH946, DWRB180 and RD2907 and the hybrids, RD2552/DWRB180, BH902/RD2794, DWRB160/DWRB180 and BH946/RD2907 were found promising for yield and yield attributes in the dry agro-ecology of Bundelkhand region. The crosses, DWRB160/BH902 and DWRB160/BH946 can be explored for developing superior segregants for malt barley breeding.

KEYWORDS: Barley, Bundelkhand region, correlations, gene effects, heterosis

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1. INTRODUCTION

Barley (*Hordeum vulgare* L.) is an autogamous ancient coarse cereal crop domesticated in the "*Fertile Crescent*" region of the world (Newton et al., 2011, Kumar et al., 2018, Haas et al., 2019). It belongs to the family Poaceae, tribe triticeae and genus *Hordeum* having almost 350 species (Kumar et al., 2014). The genus *Hordeum* comprises about 32 species, including cultivated and wild ones for versatile uses (Visioni et al., 2023). The crop was mainly utilized for feed and food purposes but with shifting towards urbanization and adoption of western culture has led its utilization more for industrial purposes (Meints and Hayes, 2019, Kumar et al., 2023, Patial et al., 2023). Barley is also known as poor man's crop with low input requirement, well buffering capacity under harsh environmental conditions, salinity tolerance and with many positive health effects (Verma et al., 2016, Meng et al., 2023). It has high nutritive value coupled with high soluble fiber concentration of β-glucan, helpful in lowering risk of cardio-vascular diseases, hyperlipidaemia and blood cholesterol as compared to other cereal grain crops (De Paula et al., 2017, Kumar et al., 2018a). Worldwide during 2021, barley ranked fourth in terms of production with 145.62 m t from 48.94 mha after maize (1210 m t), rice (787.29 mt) and wheat (770.87 mt) (Anonymous, 2023). The production of 1.68 m t barley grains has been estimated in India during 2022–23 from an acreage of about 6.2 lakh ha (Anonymous, 2023). Rajasthan, Uttar Pradesh, Madhya Pradesh and Haryana are major barley producing states in India. Due to the inherent tolerant capability of barley for drought, salinity, heat, early maturity and low water conditions the crop is one of the favoured traditional crops of MP and UP Bundelkhand region (Elakhdar et al., 2023, Panwar and Sharma, 2019).

Bundelkhand region of Uttar Pradesh and Madhya Pradesh is one of the drought and terminal heat prone areas, which receives erratic rainfall. The crop productivity is comparatively very low than national average for most of the crops. Barley has low water and fertilizer requirements and has inherent potential to tolerate drought, heat and other abiotic stresses. It is one of the predominant crops in this region, however the cultivating varieties are low yielding, tall and disease susceptible, particularly for spot blotch. Slafer and Savin (2023) also substantiated that barley is most preferred cereal than wheat in the stress prone areas due to its better yielding potential, genetic architecture, plasticity, physiological adaptations and climate resilience (Cossani et al., 2011, Cossani et al., 2012, Dawson et al., 2015, Ryan et al., 2008). Lack of high yielding varieties and scanty information on the kind of gene effects in different germplasm and cultivars for grain yield are the major drawbacks for lower yields of this crop in the Bundelkhand region. A sound understanding of the nature and extent of gene effects and heterosis for grain yield, yield components and key physiological characters is essential for initiating successful barley improvement in the region (Liaqat et al., 2023, Machado et al., 2023, Zhang et al., 2015). The knowledge of favourable gene effects and gene constellations will be helpful in accumulating desirable alleles contributing towards attainable high yield levels. Further, the incorporation for lodging tolerance, high foliage and spot blotch resistance will enrich genetic diversity of barley in the region. The identified desirable segregants can be evaluated under varying soil types and water regimes of Bundelkhand region for developing suitable high yielding and disease resistant genotype of barley. This combined studies for heterosis and gene effects with positive trait associations will lead to the production and productivity enhancement in the region.

In this direction, the present investigation was carried out to estimate gene effects, heterosis and trait association in barley for developing promising segregants for grain yield, yield attributes and key physiological traits in particular for harsh weather conditions of Bundelkhand region.

2. MATERIALS AND METHODS

The present study was carried out during November–April, 2019–2020 and 2020–21 with eight diverse barley genotypes, namely BH902, BH946, DWRB160, DWRB180, RD2552, RD2794, RD2899 and RD2907 were crossed in half diallel (Excluding reciprocals) mating design (Griffing 1956, method II, Model I). The salient attributes of these parental genotypes are presented in Table 1. During November–April, 2020–21, 28 obtained F_1s were grown in 2 replications in randomized complete block design in 2 m row length and 30 cm spacing. The parents were grown in paired rows of same row length and spacing.

The observations were recorded on five randomly selected plants for fourteen quantitative traits, namely 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 per meter (TPM), plant height (PH), number of grains per spike (GPS), 1000 grain weight (TGW), grain yield per plant (GY), biological yield per plant (BY) and harvest index (HI). Three major physiological traits *viz.*, leaf area index (LAI), chlorophyll fluorescence (CF) and chlorophyll content (CC) were also recorded during November–April, 2020–2021. The Fv/Fm ratio was recorded adopting chlorophyll Fluorometer and SPAD meter was utilized for chlorophyll content. Sun scan canopy analyser was used to find out the leaf area index using par measurements during bright sun shine hours. Analysis of variance (ANOVA) for all the traits was carried out individually following standard procedures as described in Singh and Chaudhary (1977).

Table 1: Details of diverse barley genotypes selected for half diallel mating

Sl. No.	Genotype	Parentage	Trait
1.	BH946	BHMS22A/BH959//RD 2552	Six row high yielding and promising for agronomic traits
2.	DWRB160	DWRB62/DWRB73	Two-rowed malt barley having high 1000 grain wt
3.	BH902	BH495/RD2552	Six row high yielding and promising for agronomic traits
4.	RD2552	RD2035/DL472	Six row high yielding and climate resilient
5.	RD2794	RD2035/RD2683	Good agronomic base with salinity tolerance
6.	RD2899	RD2592/RD2035//RD2715	Six row high yielding and climate resilient
7.	DWRB180	P.STO/3/LBIRAN/UNA8/LIGNEE640/4/ BLLU/5/PETUNIA 1/6/M111	Six row and spot blotch resistance
8.	RD2907	RD103/RD2518//RD 2592	Good agronomic base with salinity tolerance

The mean heterosis and heterobeltiosis over better parent were computed following standard procedures in MS Excel.

3. RESULTS AND DISCUSSION

3.1. *ANOVA and per se performance*

The analysis of variance revealed significant differences for all the characters indicating the presence of adequate genetic variation among the treatments. The mean squares of treatments for all the seventeen characters are presented in the Table 2**.** The significant difference for different quantitative traits have been also reported by Singh et al. (2007), Aty et al. (2011), Amer et al. (2012), Singh et al. (2013), Madic et al. (2014), Kren et al. (2015), Mohtashami (2015), Pesaraklu et al. (2016), Hailu et al. (2016), Madakemohekar et al. (2018); Medimagh and Fellah (2019).

Days to heading and days to maturity exhibited a general mean value of 86 days and 127 days, respectively (Table 3). DWRB180, RD2794 and RD2899 showed early spike emergence and maturity. The general mean for spike length and awn length was 9.61cm and 10.39 cm, respectively. Parents DWRB160 (10.91cm) and DWRB180 (10.60

Table 2: Analysis of variance (ANOVA) for grain yield and physiological traits

Characters	Replication	Treatment	Error
	(1)	(35)	(35)
Days to heading	1.39	11.44**	2.05
Days to maturity	3.13	9.17**	2.33
Flag leaf length	5.64	4.18**	0.83
Flag leaf width	0.01	0.04**	0.01
Peduncle length	2.09	9.14**	1.07
Spike length	0.11	2.74**	0.13
Awn length	0.76	2.11**	0.34
No of tillers/m	28.13	153.89**	7.93
Plant height	2.47	27.21**	2.39
No of grains spike^{-1}	2.90	434.57**	3.90
1000 grain weight	0.001	40.09**	1.17
Grain yield plant^{-1}	0.08	4.21**	1.02
Biological yield plant^{-1}	0.07	19.27**	7.21
Harvest index	0.0001	0.0003**	0.0002
Leaf area index	0.005	0.09**	0.004
Chlorophyll fluorescence	0.0001	0.0009**	0.0001
Chlorophyll content	0.03	14.30**	1.04

**Significant at (p=0.01) per cent and * (p=0.05) levels

Table 3: Grand mean, mean±SE(m) and range for grain yield and physiological traits

Characters	GM	Parents		F_1s	
		Mean±SE(m)	Range	Mean±SE(m)	Range
Days to heading	86.0	87.19±2.10	85.5–88.5	85.26±2.11	79.0–90.5
Days to maturity	127.0	128.5±1.07	126–132.5	127.12±1.0	123.0–132.0
Flag leaf length (cm)	17.22	15.72±0.64	13.75–17.1	17.65±0.64	14.90–19.85
Flag leaf width (cm)	1.75	1.61±0.07	1.34–1.80	1.79±0.079	1.56–1.99
Peduncle length (cm)	21.28	19.34±0.73	18.06–20.43	21.83±0.73	18.83–26.7
Spike length (cm)	9.61	8.8±0.25	8.05–10.91	9.84±0.25	8.52–12.37
Awn length (cm)	10.39	9.15±0.41	7.85–10.6	10.75±0.41	9.35–12.09
No. of tillers m^{-1}	128.30	116.5±1.99	106.5–126	131.69±1.99	118.0–145.0
Plant height (cm)	91.28	95.06±1.09	92.08–98.30	90.20±1.09	87.06–100.24
No. of grains $spike^{-1}$	58.0	56.02±1.39	29.0–62.0	58.12±1.39	28.0–71.5
1000 grain weight (g)	46.12	41.87±0.76	39.48–51.10	47.33±0.77	42.98–59.15
Grain yield $plant^{-1}$ (g)	17.77	16.43±0.71	14.75–18.09	18.16±0.71	15.2–20.09
Biological $plant^{-1}$ (g)	43.68	41.08±1.89	36.86–44.49	44.43±1.89	38.87–51.83
Harvest index (%)	0.40	0.40±0.01	0.39–0.41	0.40±0.01	0.38–0.43
Leaf area index	1.70	1.57±0.04	1.32–1.87	1.74±0.04	1.21–2.02
Chlorophyll fluorescence	0.75	0.73±0.008	0.71–0.75	0.76±0.008	0.72–0.79
Chlorophyll content	39.37	35.86±0.72	30.95–39.28	40.37±0.72	36.85–42.05

cm) showed higher mean values for spike and awn length, respectively. Average grains $spike^{-1}$ were recorded as 58, where the parent BH946 (62) and F_1 hybrid BH902/RD2907 (71), BH946/RD2907 (71) and BH902/DWRB180 (70) showed maximum grains $spike^{-1}$. The mean values for 1000 grain wt. were for parents and F_1 hybrid were 41.87 g and 47.33 g, respectively. Among the parental genotypes and crosses, the higher mean values for 1000 grain weight were revealed by DWRB160 (51.11 g) and DWRB160/BH902 (59.15 g), BH946/DWRB160 (57.22 g) and DWRB160/RD2552 (51.86 g). The highest grain yield $plant^{-1}$ was observed in the genotype RD2907 (18.09 g), followed by RD2899 (17.09 g) and BH946 (16.96 g). The crosses *viz*., DWRB180/RD2907 (20.10 g), followed by BH946/RD2907 (20.0 g), RD2899/RD2907 (19.63 g), BH946/RD2552 (19.24 g), BH946 /DWRB180 (19.15 g) and RD2899/DWRB180 (19.13 g) were found promising for grain yield per plant. Parental genotype RD2899 (0.42) and crosses BH946/RD2907 (0.44) followed by RD2794/RD2907 (0.44), DWRB160/DWRB180 (0.43), BH946/BH902 (0.43), RD2552/RD2899 (0.43) and DWRB180/RD2907 (0.43) recorded higher harvest index. Leaf area index (LAI) showed general mean of 1.70. Leaf area index was recorded in the range of 1.21 to 2.02 for hybrid.

Chlorophyll fluorescence general mean value was 0.75 (Table 3). Parental genotypes RD2794 (0.75) and DWRB160 (0.75) and cross combinations *viz*., DWRB180/RD2907 (0.79), RD2899/RD2907 (0.79), RD2794/RD2899 (0.79), RD2552/DWRB180 (0.79), RD2552/ RD2907 (0.79) and BH946/RD2907 (0.79) showed high mean values for chlorophyll fluorescence, respectively. The parental genotype RD2907 (39.28) and crosses viz., RD2899 / RD2907 (42.06), BH946/RD2907 (41.73) and RD2794/DWRB180 (41.57) were promising for chlorophyll content.

3.2. Heterosis and heterobeltiosis

Heterosis for days to heading ranged from -9.19 (RD2794/RD2899) to 3.13 (RD2794/RD2907) (Table 4). It was significant in ten crosses, out of which all crosses depicted negative heterosis. The negative heterobeltiosis was recorded in the cross combinations BH946/RD2899 (-7.17), followed by RD2552/RD2794 (-4.21), BH946/RD 2552 (-4.15), BH946/BH902 (-3.77) and BH946/RD2794 (-3.77). For flag leaf width the higher positive heterobeltiosis was recorded in the crosses, RD2552/RD2899 (17.21) and BH902/RD 2899 (16.67). The cross combinations, namely DWRB160/RD2899 (31.10), followed by BH946/RD2899 (24.82), RD2552/RD 2907 (22.58) and DWRB160/RD2552 (20.97) showed high heterobeltiosis for awn length. Heterosis for grains $spike^{-1}$ ranged from -36.65 (DWRB 160/RD2794) to 24.18 (BH946/DWRB160). Twenty-four crosses were observed with significant heterobeltiosis for 1000 grain weight. It ranged from -5.30

Table 4: Mean (%) and range of heterosis and heterobeltiosis (%) for grain yield and physiological traits in barley

Characters	Mid parent (MP)		Better parent (BP)	
Days to heading	-2.20	-9.19-3.13	-2.84	-10.23–2.84
Days to maturity	-1.06	-4.84-2.16	-2.12	-7.16–1.98
Flag leaf length	12.37	-2.35-24.78	7.53	-6.99–18.51
Flag leaf width	11.25	-0.95-25.91	5.15	-7.14–17.22
Spike length	11.43	-1.50-28.84	6.06	-4.80–15.06
Peduncle length	12.97	-1.57-40.48	9.92	-5.38–38.44
Awn length	17.60	2.61–33.96	11.23	-5.19–31.10
No. of tillers m^{-1}	13.16	1.51–21.31	9.45	-6.34–25.57
Plant height	-5.11	-8.84–4.54	-6.29	-10.06–3.40
No. of grains $spike^{-1}$	1.99	-36.65–24.18	-4.37	-52.06–17.21
1000 grain weight	12.10	4.0–26.1	8.67	-5.30–15.74
Grain yield $plant^{-1}$	10.52	-3.71–18.61	6.6	-7.40–17.55
Biological $plant^{-1}$	8.17	-2.24–20.93	4.52	-5.09–16.50
Harvest index	2.24	-7.3–9.55	1.08	-8.4–8.86
Leaf area index	11.20	-20.0–33.33	3.66	-27.76–31.85
Chlorophyll fluorescence	4.17	-2.01–9.72	3.14	-3.36–8.38
Chlorophyll content	12.81	2.55–26.22	7.307	1.57–20.34

(DWRB160/RD2899) to 15.74 (DWRB160/BH902) (Table 4). The highest significant positive heterosis was depicted in the cross DWRB160/BH902 (26.01), followed by BH946/DWRB160 (24.18) and BH902/RD2907 (18.33). Average heterosis and heterobeltiosis ranged from -3.71 (DWRB160/ RD2899) to 18.61 (RD2552/DWRB180) and -7.40 (DWRB160/RD2899) to 17.55 (RD2552/DWRB 180), respectively for grain yield per plant. The high estimates of significant positive heterobeltiosis were noticed in the cross combinations *viz.*, RD2552/DWRB180 (17.55), DWRB160/DWRB180 (17.15), DWRB160/RD2552 (13.43), BH946/RD2552 (13.41) and BH946/DWRB180 (12.91). Average heterosis and heterobeltiosis for harvest index ranged from -7.3 (DWRB160/RD2794) to 9.5 (DWRB160/DWRB180) and -8.4 (DWRB160/RD2794) to 8.86 (DWRB160/DWRB180), respectively. For chlorophyll fluorescence, twenty-four crosses were found significant and the highest significant positive heterobeltiosis was exhibited in the crosse BH946/RD2907 (9.72), followed by DWRB180/RD2907 (7.59) and BH946 /DWRB180 (7.52).

Positive significant heterosis for grain yield and other attributes in barley was also reported by Ram et al. (2009), Amer et al. (2012); Shouny et al. (2015), Tofiq et al. (2015), Ram and Shekawat (2017), Lal et al. (2018), Madakemohekar et al. (2018), Patial et al. (2018), Panwar and Sharma (2019), Bouchetat et al. (2020) and Katiyar et al. (2021).

3.3. Gene effect analysis

In the present investigation, the mean squares due to GCA and SCA effects were significant for all the characters, except the GCA effect of harvest index. In general, the GCA effects were higher than the SCA effects, however the higher SCA effects were observed for days to heading, plant height and tillers m^{-1}, indicating preponderance of dominance gene effects for the above three traits. Singh et al. (2007); Singh et al. (2013), Madic et al. (2014); Ram and Shekhawat (2017) also reported importance of additive gene effects for quantitative characters in barley.

GCA effects computed for days to heading revealed that the genotype RD2899 exhibited negative significant GCA effects ((-1.52**), whereas, the parents RD2899 (-1.34**) and DWRB180 (-1.04**), were found with significant negative GCA effects for days to maturity (Table 5). GCA effects showed that three parents *viz.*, BH946, DWRB160 and DWRB180 were good general combiners for flag leaf length, whereas the genotype DWRB180 was also promising for flag leaf width. The crosses, namely BH902/RD2899, BH946/RD2552 for flag leaf length and DWRB160/RD 2907 for flag leaf width exhibited higher SCA effects, respectively. For tillers per meter the positive significant GCA effects (4.76**) were depicted in the parent DWRB160, where the cross BH946/RD2907, followed by BH946/DWRB180, DWRB 160/RD2907, DWRB160/BH902 and DWRB160/DWRB180 showed the highest significant SCA effects. Significant positive GCA effects were exhibited by seven parents *viz.*, BH946, DWRB 180, RD2899, BH902, RD2794 and RD2552 for grains $spike^{-1}$.

The parents DWRB160 (5.29**) and BH902 (1.59**) depicted high GCA effects for 1000 grain weight and eleven crosses showed positively significant SCA effects. GCA effects revealed that parents RD2907 (0.90**), DWRB180 (0.49*) and BH946 (0.46*) showed high significant positive

Table 5: Estimation of GCA effects for grain yield and yield components in barley

Genotype	DH	DM	FLL	SL	PL	T/M	PH	TGW	GY/P	CF	CC
BH 946	0.77^{*}	1.31^{**}	0.80^{**}	-0.23	0.97^{**}	-3.39	-0.28	0.12	0.46^{*}	-0.01	1.04^{**}
DWRB 160	0.22	0.46	0.42^{*}	1.64^{**}	-0.70	4.76^{**}	0.57	5.29^{**}	-0.86	-0.01	-0.33
BH 902	0.42	0.06	-0.58	-0.43	-0.97	-0.09	1.29^{**}	1.59^{**}	-1.01	-0.005	-0.65
RD 2552	0.22	0.36	-0.57	-0.33	-0.31	0.26	-1.15^{**}	-1.12	-0.30	0.001	-1.39
RD 2794	-0.07	-0.39	-0.06	-0.47	-0.51	-1.59	0.73*	-1.68	0.20	0.003	-0.71
RD 2899	-1.52^{**}	-1.34^{**}	-0.69	-0.38	0.53^{*}	0.01	-0.83**	-2.20	0.12	0.004	0.94^{**}
DWRB 180	-0.57	-1.04^{**}	0.76^{**}	0.24^{**}	0.48^{*}	-0.34	-0.90**	-0.68	0.49^{*}	0.009^{**}	-0.16
RD 2907	0.53	0.56	-0.07	-0.04	0.53^{*}	0.36	0.57	-1.33	0.90^{**}	0.01^{**}	1.27^{**}

effects for grain yield per plant. Only two crosses, BH902/RD 2794 (1.8^{**}) and DWRB160/DWRB180 (1.4^{*}) showed significant SCA effects for grain yield. The parental genotypes, namely DWRB180 (0.18^{**}), RD2552 (0.12^{**}) and BH946 (0.03^{*}) revealed significant positive GCA effects for leaf area index. Among the parents, DWRB180, RD2552 and BH946 showed significant positive GCA effects for Chlorophyll fluorescence, while RD2907 (1.27^{**}), BH946(1.04^{**}) and RD2899 (0.94^{**}) were found with high GCA effects for chlorophyll content.

3.4. Correlations

It is important to understand the association between two traits regarding the trait affecting another in a positive or negative mode. Grain yield is the final product of its component, which influence yield either directly or indirectly. Days to heading showed positive significant correlation with days to maturity (0.42^{*}) and plant height (0.45^{**}), however it was negatively associated with chlorophyll fluorescence (-0.40^{*}). Flag leaf length showed positive correlation with flag leaf width (0.44^{**}), spike length (0.49^{**}), awn length (0.42^{*}), peduncle length (0.41^{*}), tillers per meter (0.46^{**}), 1000 grain weight (0.35^{*}), grain yield (0.44^{**}), harvest index (0.38^{*}) and chlorophyll content (0.41^{**}). Grain yield exhibited positive significant correlations with flag leaf width (0.60^{**}), flag leaf length (0.44^{**}), awn length (0.49^{**}), peduncle length (0.71^{**}), tillers meter^{-1} (0.35^{*}), grains spike^{-1} (0.39^{*}), biological yield plant^{-1} (0.91^{**}), harvest index (0.53^{**}), chlorophyll content (0.69^{**}), leaf area index (0.49^{**}) and chlorophyll fluorescence (0.68^{**}). Chlorophyll content showed significant positive associations with flag leaf length, flag leaf width, grain yield, biological yield and chlorophyll fluorescence. Grain yield had highly significant positive correlations with component traits reported in the findings of Tofiq et al. (2015).

4. CONCLUSION

Genetic analysis suggested that the parents BH946, DWRB180 and RD2907 were found promising for grain yield and yield components under water limited conditions of Bundelkhand region. The parental genotype DWRB160 was promising and good general combiner for high 1000 grain weight and tillers/meter required to breed malt barley genotypes in the region.

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