



Genetic gain and morpho-physiological characterisation of BILs (Backcross inbred lines) under different moisture regimes in wheat (*Triticum aestivum* L.)

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Abstract

Drought stress is one of the major yield limiting factors in realising the full genetic potential of wheat. In the present study, backcross inbred line population derived from GW322*2/HI1500 was characterized for different morpho-physiological traits and grain yield under rainfed and irrigated conditions. Principal component analysis revealed that first five components explained over 66.35 per cent of variation. Grain yield showed significant correlation with biomass and physiological traits viz., NDVI2, NDVI3, NDVI5, CT2, CT3 and CT4. The analysis of variance on grain yield data showed that mean squares of environments, genotypes and GEI were highly significant ($p < 0.01$). To determine effects of GEI on grain yield, data were subjected to AMMI and GGE biplot analysis, which identified BILs G20, G2, G254, G214, G44 and G64 as the most stable and high yielding. Based on Smith selection index expected genetic gain for grain yield at 5% was 131.01gm/plot. Hence, selecting genotypes based on morpho-physiological traits will be rewarding under moisture depleting environment.

Key words: Genetic gain, NDVI, CT, PCA, AMMI, GGE

Introduction

Wheat is a crop of global importance and is a major staple food of India and the rest of the world. Various biotic and abiotic stresses affect the wheat crop leading to significant yield penalty in annual wheat production; drought and heat stress are the major yield limiting factors in realizing the yield potential. In India erratic and skewed distribution of rainfall and receding ground

water tables (Rodell et al. 2009) have adversely affected wheat production in some areas. 80% of the wheat crop is cultivated under irrigated conditions (Reynolds et al. 1999); about ~66% of the crop receives only partial irrigation (Collins et al. 2008; Kang et al. 2009) subjecting the wheat crop to water stress, and resulting in reduced grain yield (Joshi et al. 2007). Therefore, there is an immediate need for breeding wheat varieties with higher grain yield potential that require partial irrigation.

With the ever-increasing population and little scope for expansion in wheat area in the country, increasing the productivity is the only option; therefore, breeding for drought and heat tolerance is of most importance (Liu et al. 2019). Drought tolerance is not a simple response, but is mostly conditioned by many component responses, which interact and may vary in different crops, in relation to types, intensity and duration of water deficit (Dashti et al. 2007; Rai et al. 2018). Dissecting component traits like canopy temperature (CT) and Normalized difference vegetative index (NDVI) which are associated with yield under stress will help in large scale screening and gene discovery (Lopes et al. 2012).

Drought susceptible genotypes showed warmer canopies than stress tolerant cultivars (Reynolds et al. 2001). The potential of CT for screening wheat

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genotypes under moisture-stress conditions is based on its significant correlations with grain yield (Reynolds et al. 2001). CT has a strong and reliable association with yield under drought and heat stress and is used in wheat breeding to select for yield (Pierre et al. 2010; Raina et al. 2019).

Normalized difference vegetative index (NDVI) is an integrated measure of both ground cover (leaf area) and the nitrogen content of the canopy. Both NDVI and chlorophyll values provide an indirect estimation of leaf health for photosynthesis associated with leaf nitrogen content and early senescence (Araus et al. 2008). CT can be combined with the NDVI for rapid and efficient screening of drought tolerance in wheat (Reynolds et al. 2007). Integrating breeding for physiological traits with the yield parameters, supplemented with genetics and genomic approaches will help in enhancing stress tolerance in wheat (Jain et al. 2014).

With the above objectives in the background, the present investigation was aimed at characterisation of Backcross inbred line (BILs) population, derived from parental cross GW322*2/HI1500 for morpho-physiological traits under moisture stress as well as to identify wheat genotypes with high and stable yield under rainfed (RF; one pre-sowing irrigation) and irrigation condition (IR; six irrigation).

Materials and methods

Plant material

The plant material in the present study comprised of 280 Backcross inbred line (BILs), and two parents. The BILs are derived from parents GW322 (GW173/GW196) and HI1500 (selection in HW2002*2//STREMPALLI/PNC5). Both parents possess several unique morphological and physiological differences in addition to yield and yield components. GW322 is susceptible to drought stress and causes substantial yield losses in field under limited irrigation, whereas HI1500 is highly tolerant to drought stress and ideally accepted for water limited conditions (www.iiwbr.org/).

Field experiment and observations recorded

The field trial was evaluated in two different moisture regimes viz., timely sown irrigation (DIR, six irrigation) (E1), and timely sown rainfed (DRF, one pre-sowing irrigation) (E2), during rabi season of 2015-2016 and 2016-2017 at the Wheat Research Farm of Division of Genetics, Indian Agricultural Research Institute (IARI),

New Delhi, India. Evaluation of the selected lines included DIR_2015, DRF_2015 and DIR_2016, DRF_2016 (IR; irrigated, RF;rainfed). The lines were evaluated at two other stations: IARI Regional station Indore, Madhya Pradesh (INDRF) (E3) and Powarkheda in ZARS Hoshangabad, Madhya Pradesh (PKWDRF) (E4) under timely sown rainfed condition (2016-17).

The experiment was laid out in alpha-lattice design with two replications in one-meter rows three lines each, and phenotyping was carried out for morpho-physiological traits. The standard cultivation practices prescribed for wheat were followed precisely. The data were recorded for all the genotypes in each replication for various morpho-physiological traits. The recording of observation for morphological traits viz., days to heading (DH), plant height (PHT), grain weight per ten spike (GWP), biomass, grain yield per plot (GY); and physiological traits viz., canopy temperature (CT) and Normalized Difference Vegetative Index (NDVI) were carried out following standard trait dictionary of CIMMYT (Pask et al. 2012). The NDVI were recorded at different stages of plant growth viz., NDVI1 (vegetative stage), NDVI2 (booting stage), NDVI3 (heading stage), NDVI4 (grain filling stage), NDVI5 (double-dough stage). CT was also recorded at different plant growth stages viz., CT1 (vegetative stage), CT2 (heading stage), CT3 (grain filling stage) and CT4 (double-dough stage). CT was measured using hand-held infrared meter (Ayeneh et al. 2002). NDVI was measured with the help of hand held Greenseeker.

Statistical analysis

The collected data were subjected to statistical analysis by using Pearson coefficients of correlation among the fifteen morpho-physiological quantitative traits both under irrigated and rainfed conditions using the OPSTAT software (<http://www.202.141.47.5/opstat/index.asp>). Principal component analysis (PCA) was used to detect underlying sources of morphological variability, and to investigate patterns of genetic diversity (Mohammadi and Prasanna 2003).

To determine the effects of GEI on grain yield, the yield data recorded from all four environments DIR, DRF, INDRF and PKWDRF (E1, E2, E3 and E4, respectively) were subjected to AMMI and GGE biplot analysis using Gen Stat 16th edition (VSN International, Ltd, Hemel Hempstead, UK) and R software 3.3.0 respectively. Then GGE biplot were used to graphically

show the genotypes and environments (Yan 2001). Angles between environment vectors were used to judge correlations (similarities/ dissimilarities) between pairs of environments (Yan and Kang 2003). Smith selection index was followed to find out the values of the traits for selected individuals and the value of the smith selection, means and gains for 5% using RIndSel (Selection Index with R for Windows version 1.0, 2016-11-30); morpho-physiological traits viz., PHT, GWP, mean NDVI and GY were used to calculate Smith index.

Selection indices were constructed using the matrix of the data for PHT (cm), GWP (g), mean NDVI and, GY (g/m^2). The equation was as $I = \Sigma b_i p_i$, where b_i is the vector of coefficients for trait based on p_i which is the phenotypic value of each trait (Falconer and McKay 1996). The Smith-Hazel index (SHI) was constructed using an equation as below (Smith 1936; Hazel 1943)

$$b = P^{-1}Ga$$

where, P^{-1} is the inverse of phenotypic variance-covariance matrix, G is the genotypic variance-covariance matrix and a is the vector of economic weight (a was + 1 for all traits except PH with $a = -1$).

Results and discussion

PCA analysis

Principal component analysis is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components (or sometimes, principal modes of variation). PCA of morpho-physiological traits revealed that first five PCs explained 66.35% variation among 280 wheat BILs, and these results were supported by the findings of Siahbidi et al. (2013), Mishra et al. (2015) and Harikrishna et al. (2016), (Table 1). The first principal component (PC1) accounted for 24.43% of total variance, and characters that contribute more positively to this component were DH, NDVI2, NDVI3, NDVI4 and NDVI5. The second principal component (PC2), accounted for an additional 14.24% of the total variation and is primarily contributed by PHT, biomass, GY and GWP. Finally, third, fourth and fifth principal component (PC3, PC4, and PC5) contributed around 12.93, 7.68 and 7.07%, respectively of the variability present among the accessions for the traits used in the present study. The PC3 explained the patterns of variation in DH and, for PC4 the variation

Table 1. Principal components analysis of BILs under rainfed condition

Principal component analysis (axes)	PC1	PC2	PC3	PC4	PC5
Eigen Values	3.665	2.135	1.940	1.153	1.061
Proportion of variance	24.43	14.24	12.93	7.68	7.07
Cumulative proportion	24.43	38.67	51.60	59.28	66.36
Traits	Eigenvectors				
DH	0.40	-0.19	0.03	-0.04	0.15
PHT	0.10	0.25	-0.38	-0.02	0.18
GWP	-0.03	0.31	0.24	-0.09	0.17
NDVI1	0.16	0.05	-0.38	0.18	-0.45
NDVI2	0.41	-0.09	-0.16	0.07	-0.15
NDVI3	0.44	-0.06	-0.07	0.04	-0.13
NDVI4	0.42	-0.03	0.08	0.03	0.13
NDVI5	0.44	0.00	0.11	0.07	0.10
CT1	-0.14	-0.03	-0.35	0.46	0.39
CT2	-0.06	-0.22	0.07	0.68	-0.02
CT3	-0.12	-0.02	-0.36	0.14	0.23
CT4	-0.19	-0.17	-0.05	0.06	-0.64
Biomass	0.04	0.44	-0.39	-0.17	-0.09
HI	0.05	0.36	0.42	0.41	-0.08
GY	0.07	0.62	0.06	0.21	-0.14

DH= Days to heading, PHT= Plant height, GWP= Grain weight per ten spikes, NDVI1= NDVI at vegetative stage, NDVI2 at booting stage, NDVI3 at heading stage, NDVI4 at grain filling stage, NDVI5 at dough stage, CT1= Canopy temperature at vegetative stage, CT2 at heading stage, CT3 at grain filling stage, CT4 at dough stage, HI= Harvest index and GY = Grain yield per plot

was contributed by CT1, CT2 and CT4. Lastly, the variability of PC5 was mainly contributed by CT3.

Correlation among traits

Phenotypic correlation coefficients among the fifteen morpho-physiological traits of the wheat genotypes under drought and irrigated condition are given in Table 2. Under drought, significant positive correlations were observed for traits like biomass, NDVI2, NDVI3, and NDVI5 with grain yield under stress, similar to that observed by El-Hendawy et al. (2015), and Harikrishna et al. (2016). CT at both vegetative and reproductive stages viz., CT2, CT3 and CT4 were negatively correlated with PH, GWP and GY. Biomass was found to be positively correlated with PH, NDVI1,

Table 2. Pearson correlation coefficients among the morpho-physiological and yield traits

RF/IR	DH	PHT	GWP	NDVI1	NDVI2	NDVI3	NDVI4	NDVI5	CT1	CT2	CT3	CT4	Biomass	HI	GY
DH	1	0.085*	-0.133**	0.014 ^{NS}	0.498**	0.439**	0.509**	0.600**	-0.175**	-0.127**	-0.140**	-0.126**	-0.021 ^{NS}	-0.151**	-0.200**
PHT	-0.228**	1	0.065 ^{NS}	0.160**	0.024 ^{NS}	-0.038 ^{NS}	0.052 ^{NS}	0.062 ^{NS}	0.054 ^{NS}	0.027 ^{NS}	0.020 ^{NS}	-0.042 ^{NS}	0.093*	0.030 ^{NS}	0.063 ^{NS}
GWP	-0.368**	0.379**	1	-0.172**	-0.192**	-0.213**	-0.167**	-0.135**	0.063 ^{NS}	-0.062 ^{NS}	-0.061 ^{NS}	0.033 ^{NS}	0.071 ^{NS}	0.204**	0.251**
NDVI1	-0.039 ^{NS}	0.262**	0.106*	1	0.213**	0.082 ^{NS}	0.187**	0.130**	0.021 ^{NS}	0.133**	-0.035 ^{NS}	-0.053 ^{NS}	0.132**	-0.012 ^{NS}	-0.223**
NDVI2	0.056 ^{NS}	0.468**	0.228**	0.356**	1	0.624**	0.595**	0.600**	-0.198**	-0.124**	-0.209**	-0.092*	0.251**	0.034 ^{NS}	-0.296**
NDVI3	0.129**	0.327**	0.183**	0.298**	0.650**	1	0.563**	0.589**	-0.139**	-0.174**	-0.218**	-0.029 ^{NS}	0.166**	-0.042 ^{NS}	-0.296**
NDVI4	0.366**	0.048 ^{NS}	0.026 ^{NS}	0.205**	0.372**	0.500**	1	0.652**	-0.194**	-0.154**	-0.222**	-0.078 ^{NS}	0.094*	-0.093*	-0.275**
NDVI5	0.624**	-0.332**	0.332**	0.073 ^{NS}	-0.039 ^{NS}	0.097*	0.412**	1	-0.230**	-0.233**	-0.242**	-0.093*	0.101*	-0.083 ^{NS}	-0.270**
CT1	-0.058 ^{NS}	-0.130*	-0.096*	0.044 ^{NS}	-0.083 ^{NS}	-0.140**	-0.161**	-0.100*	1	0.272**	0.194**	0.008 ^{NS}	-0.070 ^{NS}	-0.038 ^{NS}	0.031 ^{NS}
CT2	0.161**	-0.277**	-0.286**	0.022 ^{NS}	-0.197**	-0.199**	-0.032 ^{NS}	0.269**	0.168**	1	0.208**	-0.019 ^{NS}	-0.163**	-0.115**	0.050 ^{NS}
CT3	0.218**	-0.293**	-0.385**	0.012 ^{NS}	-0.396**	-0.335**	-0.037 ^{NS}	0.263**	0.278**	0.274**	1	-0.056 ^{NS}	-0.204**	-0.113**	0.066 ^{NS}
CT4	0.183**	-0.442**	-0.439**	-0.014 ^{NS}	-0.382**	-0.334**	-0.189**	0.205**	0.100*	0.308**	0.440**	1	0.151**	0.097*	-0.058 ^{NS}
Biomass	-0.376**	0.536**	0.445**	0.159**	0.344**	0.291**	0.005 ^{NS}	0.370**	0.050 ^{NS}	-0.420**	-0.307**	-0.397**	1	0.643**	0.292**
HI	0.260**	-0.421**	-0.301**	-0.066 ^{NS}	-0.331**	-0.226**	0.018 ^{NS}	0.428**	-0.053 ^{NS}	0.236**	0.252**	0.347**	-0.474**	1	0.454**
GY	-0.377**	0.438**	0.488**	0.054 ^{NS}	0.314**	0.287**	0.005 ^{NS}	0.319**	-0.047 ^{NS}	-0.409**	-0.433**	-0.422**	0.699**	0.068 ^{NS}	1

**Significance at $p < 0.01$, *Significance at $p < 0.05$. NS = Non-significant, DH = Days to heading, PHT = Plant height, GWP = Grain weight per ten spikes, NDVI1 = NDVI at vegetative stage, NDVI2 at booting stage, NDVI3 at heading stage, NDVI4 at grain filling stage, NDVI5 at dough, CT1 = Canopy temperature at vegetative stage, CT2 at heading stage, CT3 at grain filling stage, CT4 at dough stage, HI = Harvest index and GY = Grain yield per plot

NDVI2, NDVI3, and NDVI5 which is also reported earlier by Cammarano et al. (2011), Harikrishna et al. (2016). CT at all the four stages was found to be positively correlated with each other and CT at all stages showed negative correlation with NDVI2, NDVI3 and NDVI5 as observed by Ramya et al. (2016). However, GW per ten spikes showed positive and negative correlation with NDVI and CT, respectively. Under drought condition magnitude of association of biomass with the grain yield, and GWP with grain yield was more when compared to irrigated condition. CT showed non-significant association with grain yield. Our result showed agreement with the earlier findings of Rai et al. (2018), in which the positive correlation with yield under drought stress was observed for NDVI at vegetative and grain maturity stages, chlorophyll content at grain filling and grain maturity stage, TKW, Harvest index, biomass, spike length and flag leaf area whereas negative correlation was found with DA, DM, DH, and CT. Hence genetic manipulation of traits like NDVI and CT for selection for grain yield in wheat crop under moisture stress will be rewarding.

AMMI analysis

The combined analysis of variance (ANOVA) for grain yield at three different moisture stress environments showed that mean squares of environments, genotypes and genotype X environment interaction (GEI) were highly significant ($p < 0.001$) which accounted for 85.01, 3.56 and 6.57% of model sum of squares (SS), respectively (Table 3). Similar results were reported by (Kaya et al. 2002; Mehari et al. 2015; Verma et al. 2015; Harikrishna et al. 2016).

The environments explained the large variation for yield and indicate the diverse nature of the environments, with large differences among

Table 3. ANOVA table for AMMI model for grain yield tested at four environments

Source	d.f.	M.S.	Percentage variance
Total	2239	41379**	
Treatments	1119	78778**	95.38
Genotypes	279	11827**	3.56
Environments	3	26253329**	85.01
Block	4	55831**	0.24
Interactions	831	7332**	6.57
IPCA 1	281	9745**	52.76
IPCA 2	279	8787**	47.23
Residuals	271	0.79	
Error	1014	4213	

*p<0.05, **p<0.001

environmental means causing most of the variation in grain yield. The environment yield means (averaged across genotypes) varied from 163.5gm/plot under rainfed condition in Powarkheda to 748.8gm/plot in Delhi under irrigated condition. (Table 4), whereas genotype yield means (averaged across environments) varied from 19.50 gm/plot (G237) to 860 gm/plot (G62). In our study, the magnitude of SS due to GE interaction was 1.84 times greater than that for genotypes, which revealed the significant differences in genotypic response across environments as well as indicates the existence of mega-environment (Yan and Hunt 2002; Mohammadi et al. 2009).

The AMMI analysis partitioned the SS of GEI into two interaction principal components axis (IPCA), and both of these IPCA were significant (Table 3). Results from AMMI model showed that the IPCA1 of

Table 4. Mean yield performance in an environment (Em) and first fourteen AMMI selections per environment

Sl No	DRF		DIR		INDRF		PKWDRF	
	Genotype	GY	Genotype	GY	Genotype	GY	Genotype	GY
1	G244	786	G62	877.7	G135	379.6	G135	205.24
2	G20	740.1	G20	826.3	G172	367.1	G35	174.11
3	G13	721.9	G159	808.5	G165	347.2	G172	173.14
4	G214	709.9	G158	779	G248	346.4	G248	169.79
5	G254	707.9	G114	769.7	G35	337.9	G209	168.69
6	G74	690.4	G77	745.2	G19	334.5	G2	165.87
7	G96	679.6	G270	725.1	G206	332.1	G66	159.46
8	G239	678.9	G183	723.7	G209	332	G254	157.76
9	G156	676.4	G150	721	G154	327.1	G62	156.2
10	G18	672.9	G272	712	G58	326.7	G58	154.35
11	G253	667.6	G244	703.5	G109	324	G12	153.15
12	G2	664.4	G260	701.6	G66	322.6	G212	151.89
13	G197	658.4	G115	696.9	G2	320.6	G206	147.89
14	G35	651.8	G212	693.1	G12	320.2	G109	146.21
Mean of selected individuals(Em)		693.3		748.8		337		163.5
Mean of all individuals		520		554.8		266.9		98.3
Selection Differential		173.3		194.0		70.1		65.2
Mean GY (GW322)		465.8		557		270.00		120
Mean GY (HI1500)		514		530		290.00		160
Per cent increase in mean of selected individuals over better parent		34.88		34.29		16.20		1.87

GY = Grain yield per pbt, DRF = Delhi rainfed conditions, DIR = Delhi irrigated conditions, INDRF = Indore rainfed conditions and PKWDRF = Powarkheda rainfed conditions

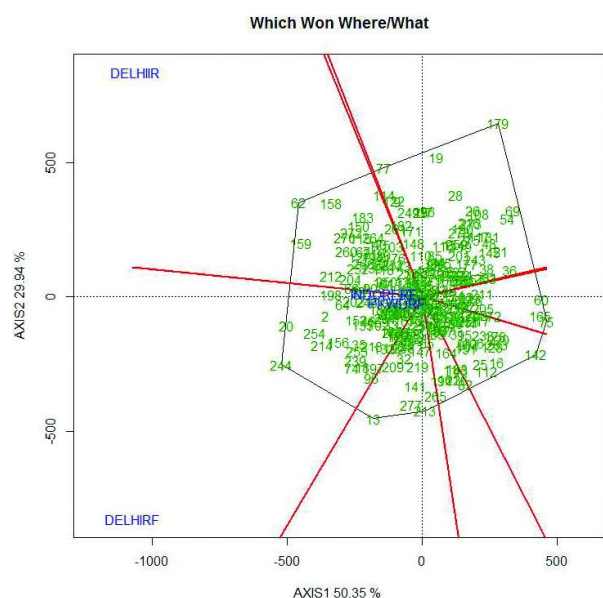


Fig. 1. Polygon of GGE biplot showing “Which Won Where” pattern for genotypes and environment

the interaction captured 52.76% of the interaction sum of squares. Similarly, the second interaction principal component axis (IPCA2) explained a further 47.23% of the genotype-environment interaction sum of squares. At the same time, IPCA1 had sum of squares greater than that of genotypes. The mean squares for both IPCA1 and IPCA2 were significant at $p = 0.001$ level and cumulatively contributed to 99.99% of the total genotype-environment interaction. Based on AMMI analysis, the best fourteen selections in terms of yield performance under moisture stress in each environment were compared (Table 4). Some of the selections were consistently performing in more than one environment under moisture stress.

BIL G20 showed the best and consistent yield performance and was ranked within the best fourteen selections in two out of four environments *viz.*, E1 and E2. According to AMMI analysis and mean performance (grain yield per plot), BIL G244 was the most stable and high yielding genotype in two of the four moisture stress environments followed by BILs G62, G2, G254, G260 and G212. These genotypes showed high yield and consistent performance in all the 4 environments.

GGE biplot analysis

GGE biplot helps in identifying the best performing genotypes in each environment as well as in group of environments. A polygon can be constructed by

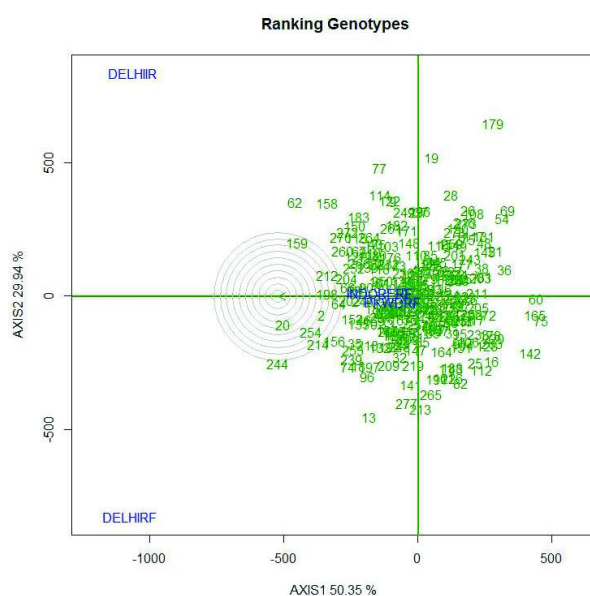


Fig. 2. GGE biplot for genotypes comparison with respect to an ideal genotype

connecting the scores of the genotypes furthest from the origin (Fig. 1), with all remaining genotypes within it, and indicates which genotypes “won where” based on their association with the site scores (Yan et al. 2000). The genotype at the vertex of the polygon performs best in the environment falling within the sectors (Yan 2002; Yan and Tinker 2006). The biplots revealed the existence of GE crossover as well as mega-environment for grain yield. The hexagon has seven BILs *viz.*, G179, G75, G142, G213, G13, G244, and G69 at the vertices. BIL G244 performed best in E1, while G62 being the best in E2 as the winning genotype. Ideal genotype is high performer with high stability across environments (Yan and Tinker 2006). Such an ideal genotype (Fig. 2) is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it. Genotypes are considered to be desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the centre, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype (Yan and Tinker 2006). Hence, in the ranking of genotypes for both mean yield and stability performance across the three environments BIL G20 followed by G2, G254, G214, G244 and G64 were ranked closest to ideal genotype (Fig. 2), indicating them as the most desirable out of 280 BILs. Based on mean performance (grain yield kg/ha) in AMMI and GGE biplot analysis, it is evident that BILs G20, G2,

Table 5. Smith selection Index for genotypes under rainfed condition in Delhi

Entry	PHT	GWP	NDVI	GY mean	Smith index
Entry 34	106.83	14.05	0.34	437.5	2.47
Entry 272	96.5	26.05	0.37	547.5	1.98
Entry 254	103.84	21.42	0.38	705	1.90
Entry 128	90.84	19.23	0.37	477.5	1.84
Entry 40	102.67	19.55	0.38	527.5	1.83
Entry 191	94.5	24.13	0.38	582.5	1.75
Entry 122	97.17	19.15	0.38	455	1.67
Entry 104	123.67	19.8	0.39	517.5	1.67
Entry 274	86.34	13.62	0.38	530	1.55
Entry 27	88.84	23.87	0.39	487.5	1.48
Entry 124	109.84	19.11	0.4	527.5	1.47
Entry 202	98.34	22.03	0.4	625	1.46
Entry 144	98	20.22	0.4	577.5	1.42
Entry 10	94.67	13.53	0.39	472.5	1.39
Mean of selected individuals	99.43	19.69	0.38	533.6	NA
Mean of all individuals	96.52	19.17	0.46	520	NA
Selection Differential	2.91	0.53	-0.08	13.57	NA
Expected genetic gain for 5%	2.76	1.8	-0.01	131.01	NA

PHT = plant height, GWP = grain weight per ten spike, NDVI mean = Mean of NDVI values at vegetative and reproductive stage and GY = grain yield (gm/plot)

G254, G214, G244 and G64 were the highly adapted, most stable and high yielding genotypes in all studied environments. Presence of considerable genotype and GE interactions complicate the selection process and warrant the use of multi-environment trials to evaluate the relative performance of genotypes over the environments and stability analysis like most popular Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot analysis is commonly used to analyse multi-environment trials data (Lal et al. 2019). These wheat genotypes are proven most promising as potential donors in breeding programmes leading to drought tolerant wheat varieties for combating the effects of climate change.

Genetic gain under moisture stress

Genetic gain is the amount of increase in performance that is achieved through genetic improvement

Table 6. Grain yield (q/ha) of selected individuals under different water regimes at Delhi

S.No.	2015		2016	
	DIR	DRF	DIR	DRF
Entry1	63.33	39.67	70.14	47.36
Entry2	50.00	41.00	63.25	48.33
Entry3	48.00	37.00	66.67	55.97
Entry4	60.00	40.07	61.81	57.50
Entry5	60.80	46.33	55.69	53.47
Entry6	45.33	38.73	60.14	47.36
GW322	50.27	30.87	60.83	44.25
HI1500	46.67	38.73	57.78	48.89
CD@5%	2.32	1.52	1.78	2.56
Mean of all individuals	49.33	36.41	NA	NA
Mean of selected individuals	54.73	40.47	62.93	51.66
Per cent increase in mean of selected individuals over better parent	7.88	4.49	3.45	5.66
Per cent increase of best line over the better parent	25.97	19.62	15.30	14.48

DRF = Delhi rainfed conditions and DIR = Delhi irrigated conditions

programs. This is usually used to refer to the increase after one generation has passed. Smith (1936) suggested that better way of exploiting genetic correlation with several traits having high heritability is to construct an index, called selection index which combines information on all characters associated with the dependent variables, like yield. Highest efficiency in grain yield per plot can be accomplished by multi-trait selection approach. The problem of selection for drought tolerance is how to select the best individuals or how to rank them with respect to some related traits (Ajala 2010; Mohammadi et al. 2013). It can be concluded that selection via an index which gives proper weight to each trait is more efficient than selection for individual traits at a time or for several traits with an independent culling level for each trait (Hazel 1943; Mohammadi et al. 2013). In addition, simultaneous selection for multiple traits in wheat genotypes increases the success of drought breeding programs (Cargnin et al. 2007). Smith index values based on four traits viz., plant height, grain weight per 10 spike, mean NDVI and grain yield were calculated for 280 BILs. Heritability for each trait was taken as

weight for constructing smith selection index.

In the present study, the covariance between the Smith selection index and the breeding value obtained was 80.76, the variance of the smith selection index (2.44) and the variance of the breeding value (3362.50) was obtained, among the population Smith selection index ranged from -3.72 (Entry 2) to 2.47 (Entry 34). The mean of selected individuals based on Smith index for GY was 533.08gm/plot, whereas mean of all the individuals was 520.01gm/plot, with a selection differential of 13.57gm/plot. Expected Genetic Gain at 5% for GY was 131.01gm/plot. Smith index among the selected lines ranged from 2.47 (G34) to 1.39 (G10) (Table 5). The mean grain yield, performance of top fourteen selected individuals (Em) in DRF (693.3gm/plot) is 34.82% more than the better parent (HI1500 under RF), performance with selection differential of 173.3 (Table 4). DIR Em (748.8gm/plot) showed an increase to the tune of 34.29% which was more than performance of better parent (GW322 under IR); there was an increase up to 16.2% and 1.87% over better parent (HI1500 under RF) at INDRF (337g) and PKWDRF (163.5gm/plot) location respectively.

The mean of all the individuals under DIR was 49.33q/ha and DRF was 36.41q/ha (Table 6) in 2015. Percent increase in means of the selected individuals over better parent under DIR was 7.88% in 2015, DIR was 3.45% in 2016, DRF was 4.49% in 2015 and DRF was 5.66% in 2016, which indicates percent increment was more in IR condition than RF condition.

Percent increase of entry1 (Highest yield) over better parent (GW322) was highest in DIR in 2015 (25.97%) and 2016 (15.30%) and entry 5 under DRF in 2015 (19.62 %) and entry 4 for DRF in 2016 (14.48%) over better parent HI1500 (Table 6). The results showed that inter relationship between traits, genotypes with higher grain yield may not necessarily be among the top rankings based on the Smith-Hazel model. A practical selection method allows time and cost savings and favours the identification of the best genotypes which is a fundamental step towards development of new cultivars for specific targets such as drought tolerance (Kurek et al. 2001).

The BILs population used in this study revealed considerable segregation and variability for morphological and physiological traits, which can lead to their effective utilization in mapping genomic regions responsible for conferring drought tolerance and their potential utilization in the breeding programmes. The

positive and negative significant correlation of grain yield per plot under rainfed condition with NDVI and CT respectively indicated that the strategy to increase grain yield in wheat crop under moisture stress involves genetic manipulation of morpho-physiological traits. On the basis of grain yield stability BILs G20, G2, G254, G214, G244 and G64 were highly adapted, most stable and high yielding under all three moisture regimes viz., DRF, INDRF and PKWDRF and can be used in convergent wheat breeding programme to develop drought tolerant varieties. The selection indices-based genotype selection based on component traits of drought tolerance will help accelerate selection process thereby increase genetic gain.

Authors' contribution

Conceptualization of research (GPS, KVP, PKS); Designing of the experiments (GPS, PKS, NJ); Contribution of experimental materials (GPS, PKS); Execution of field/lab experiments and data collection (BM, PSK, SB, DC); Execution of field experiment at off season nursery (BM, RP, DA, SVSP, PCM, KKM); Analysis of data and interpretation (BM, HK); Preparation of manuscript (BM, HK, NJ).

Declaration

The authors declare no conflict of interest.

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