

Consolidating the yield gain by exploiting genotype × management interaction in wheat

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Abstract

An experiment was conducted with 42 differentially adapted genotypes of wheat for two subsequent years (2011-13) to quantify the genotype × management interaction using additive main effect and multiplicative interaction (AMMI) and genotype main effect (G) plus genotype by environment interaction (GGE) methods. The material was evaluated in three different environments namely, permanent bed (zero tillage) with full residue retention (CA), freshly prepared raised bed with no residue (CTRB) and conventionally tilled and seeded condition i.e. flat bed (CTFB). Genotypic differences for the traits having relevance in adaptation were found significant. Environment followed by genotype × management interaction were found to be the major source of variation for yield, biomass, harvest index (HI) and number of tillers. AMMI biplot pooled six environments (3 management systems and 2 years) into three groups and grouping was slightly different from the grouping done by GGE. As per AMMI analysis, discriminating ability of CA even during stressed year was equal to that of CTFB during more productive year. GGE identified permanent raised bed with residue as most representative and discriminating environment. GGE identified HD3115, HD3117, CSW2, CSW16, CSW18, CSW23 and CSW25 with specific adaptation for CA and CSW35, CTRB1813, CTRB1816, CTRB1817 and CTFB4566 for CTRB. The results clearly suggest that selection and evaluations of breeding material under CA lead to identification of genotypes broadly adapted to other management practices but no vice-versa. CA is the most representative and informative environment and identification and release of CA specific variety can further consolidate the yield.

Key words: Conservation agriculture, wheat, breeding, genotype × management interaction, AMMI, GGE

Introduction

Food security is increasingly being challenged at global

level due to climate change and natural resources degradation and/or depletion. Wheat (*Triticum aestivum* L.) is the most important food grain crop providing daily sustenance to very large section of world population and thus important component of food security. Dwindling food supply along with increasing population in the developing world is making the issue of food security the most relevant. Declining profit and degrading production environment forced the researchers to think about paradigm shift in the production methods, more particularly in south East Asia including India where rice-wheat (RW) cropping system is predominant [1]. Euphoria generated in India because of record production of wheat (94.8 m tones) attained in 2011-12 melted away very quickly in 2012-13 due to significant dip in wheat production in wheat bowl (Punjab, Haryana and Western UP) of India [2].

Conservation agriculture (CA) based on no tillage farming, residue retention and crop rotation as a healthy agricultural practice to mitigate environmental stresses has gained momentum in recent years. Better productive environment in the form of CA offers an opportunity to select for high yielding genotypes. The observed effect of CA is largely because of change in soil physical properties [3], shift in host weed competition [4], mitigation of green house gases, modulation of soil temperature [5], increased microbiological activities resulting in lesser biotic stress [6], soil moisture availability (especially when sowing deep or under stubble) and change in diseases [7]. There may be a need for genotypes suited to special form of mechanization (e.g. direct sowing into residues) and to agronomic conditions such as

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allelopathy, as well as specific issues relating to problematic soils. Faster emergence and stand establishment under limited moisture and suppression of weeds due to change in crop canopy are some of the important traits which can be selected for identifying the genotypes suited for zero-tillage conditions. The adoption of zero tillage and other resource conservation technologies is now considered of prime importance and breeders are increasingly emphasizing the need to address the new production circumstances. Despite significance of genotype \times management interaction, no systemic efforts have been made to exploit it. CA therefore, offers conditions which are entirely different from those of tilled soils and genotypes selected under conventional conditions could respond differentially under CA.

Multi environment trials conducted across various environments to compare the genotypes usually generate three way data, however, the analysis of these data is only restricted to genotype evaluation based on genotype main effect (G), while GE interactions are treated as noise [8]. Despite of lots of research in understanding GE, in various crops, the major gap remains as how GE is measured and addressed. Researchers studying genotype \times tillage practice interactions have generally reported a lack of interaction in field crops including wheat [9], barley [10], rice [11], sorghum [12] and soybean [13]. These studies failed to detect genotype \times tillage practice interactions largely because of small number of genotypes tested and perhaps the fact that they were bred under conventional tillage conditions [14]. In essence, the identification of the adapted genotypes has been a long standing issue with the plant breeders and many statistical methods like AMMI analysis [15, 16] and GGE biplot analysis [17] have been proposed for the analysis of multi-environment data. Biplot has become a popular tool for cultivar evaluation and mega-environment investigation. The present study was undertaken to test whether selection under different management practices i.e., freshly made raised bed after conventional tillage, permanent bed with no tillage and conventional bed with tillage (flat bed) led to differential adaptation or not.

Materials and methods

The material comprised genotypes selected by wheat breeding programme of Indian Agricultural Research Institute (IARI), New Delhi India, addressing the issues of cropping system and conservation agriculture, by growing early generation and advance lines on

permanent bed (zero tillage) with full residue retention (CA), freshly prepared raised bed with no residue (CTRB) and conventionally tilled and seeded condition i.e., flat bed (CTFB). Thirty nine differentially adapted genotypes along with three recently released varieties viz., HD2967, PBW550 and DBW17 (Table 1) for timely sown, irrigated condition of north western plain zone of India, were grown at IARI in three environments viz., CA, CTRB and CTFB from 2011 to 2013. CA, CTRB and CTFB have been designated as E1, E2, E3 in 2011-2012 and E4, E5, E6 in 2012-2013 respectively.

The environment for CA is being maintained since 2008-2009 by following same cropping system. Each plot under CTFB comprised six rows of 4 meter each with row to row spacing of 23 cm. The plot under CA and CTRB comprised 2 ridges with two rows of 4 m length on each ridge. The distance between two centers of adjacent furrows was 70 cm. Seeding rate was 100 kg/ha for CTFB and 80 kg/ha for CA and CTRB. Under CTFB and CTRB, full dose of phosphatic fertilizer and zinc sulphate along with 50% of urea were broadcasted and mixed in soil with last tillage operation. The remaining urea was broadcasted in two split doses i.e., at crown root initiation (CRI) stage in mid-December after 1st irrigation and after third irrigation. Under CA condition, full dose of phosphatic fertilizer and zinc sulphate along with 50 per cent of urea were broadcasted before seeding. Remaining dose of urea was applied as in case of conventional tillage condition. Under permanent bed condition, glyphosate (Round up) was sprayed evenly on all experimental area, two days before seeding to control all emerged weeds. After emergence, weed control mechanism was similar in all environments. The experiment was laid out in Randomized Block Design (RBD) with two replications in all environments. Under conventional tillage, sowing was done with self-propelled Wintersteiger seed drill. Under permanent bed and freshly raised bed condition, Bhopal seed drill was used to sow seeds in four rows of 4 meter length with row-row spacing of 20 cm on the top of each bed. Standard irrigation schedule and recommended package of practices were followed to raise a good crop.

Statistical analysis

In multi environment trial, two most commonly used statistical methods are additive main effect and multiplicative (AMMI) interaction model proposed and used by Gauch [15] and Zobel [16] and genotype +

Table 1. Parentage of genotypes used in the genotype x management interaction studies

S.No	Genotypes	Genotype codes	Pedigree	Breeding environment
1	HD3115	G1	HW5028/HD2285	CTFB
2	HD3117	G2	HD2733/HD2824//DW127	CA
3	CSW1	G3	HD2329/WR562	CA
4	CSW2	G4	CL1579/HD2329	CTFB
5	CSW3	G5	WL462/VE//KOE1//3/Pastro/MC11	CTFB
6	CSW4	G6	Kauz//Altar84/AOS/3/Milan	CTFB
7	CSW5	G7	PBW502/HW5028//CL1673	CTFB
8	CSW7	G8	CBW38/WR541	CTFB
9	CSW10	G9	HD2377/HD2329	CTFB
10	CSW13	G10	HW1083/CL14820	CTFB
11	CSW15	G11	CL1449/PBW343	CA
12	CSW16	G12	CL1449/PBW343	CA
13	CSW18	G13	PBW343/CL1538	CA
14	CSW21	G14	UP2586/PBW343	CA
15	CSW22	G15	WR567/HD2329	CA
16	CSW23	G16	PBW343/CL1538	CA
17	CSW24	G17	PBW343/HUW567	CTFB
18	CSW25	G18	PBW343/4/CHOIX/Star/3/HEI/3*CNO79//2*SERI	CA
19	CSW26	G19	UP2425/CL1482	CTFB
20	CSW27	G20	HW5055/WR196	CTFB
21	CSW28	G21	HW5015/HD2643	CTFB
22	CSW29	G22	HD2898/MC10	CA
23	CSW30	G23	HD2687/CL1116	CTFB
24	CSW31	G24	CL1449/HUW585	CTFB
25	CSW32	G25	PBW343/HUW567	CA
26	CSW33	G26	HD2687/PBW498	CA
27	CSW34	G27	HW5015/LOK3397	CA
28	CSW35	G28	HW5015/KUNDAN	CA
29	CSW36	G29	PBW343/PH137//MC11	CA
30	CTRB1666	G30	UP2425/CL1461	CTRB
31	CTRB1667	G31	UP2425/UP2626	CTRB
32	CTRB1813	G32	HW5015/HD2643//PBW343	CTRB
33	CTRB1816	G33	UP2586/K9107	CTRB
34	CTRB1817	G34	HD2329/HUW585	CTRB
35	CTFB4550	G35	VL849/NBP1609	CTFB
36	CTFB4565	G36	DW1293/CL1525	CTFB
37	CTFB4566	G37	DW1506/UP2632	CTFB
38	CTFB4567	G38	HD2733/HD2329	CTFB
39	CTFB4639	G39	PBW502/HW5028//CL1673	CTFB
40	DBW17	G40	CMH79A95/3*CNO79//RAJ3777	CTFB
41	PBW550	G41	WH594/RAJ3858//W485	CTFB
42	HD2967	G42	ALD/COC//URES/HD 2160 M// HD2278	CTFB

CA = Zero tillage with full residue retention; CTFB = Conventionally tilled and seeded condition, i.e., flat bed and CTRB = Freshly prepared raised bed with no residue

genotype × environment interaction method (GGE) method [9, 17]. These methods were compared for effectiveness in dealing with multi-environment data [18-20]. Using AMMI and GGE analysis, biplots for yield were constructed, representing different environments generated due to years and management practices. According to Gauch *et al.* [20], AMMI biplot serves equally for breeders and soil scientists by displaying main effects as well as interaction in the same graph, whereas GGE biplot has more utility to breeders as it display only G and GE effects. Statistical analysis has been done by using Genstat Software VSN International Limited, Hemel Hempstead, (UK) Version14.0.

Result and discussion

Efficiency of breeding programme and genetic gain realization are often hampered by genotype-environment (GE) interaction, particularly when ranks of breeding lines change in different environments i.e., presence of cross over interaction [21]. Genetic gains are also limited when breeders overemphasize wide adaptation due to resource limitation. Breeders therefore, often face the dilemma of identifying the ideal environment for carrying out the selection and then on type of yield trials to pick up winning genotypes. More and more researchers are now agreeing to the fact that CA environment is more productive and essential for sustaining production at higher level. Breeders are therefore, are again in dilemma, whether or not to initiate the breeding programme for CA.

Analysis of variance (ANOVA) for seed yield and biomass showed significance of genotype, environment and genotype × environment interaction as a source of variation (Table 2). Similar kind of results has been reported by other workers also [22, 23]. Environment was found to be the most important source of variation accounting for 64 per cent of total variation. Genotype × environment interaction with 23 per cent was the next important source. Genotypes, though significant, accounted for only nine per cent of total variation for seed yield. Like in the most of multi-environment trials, environment typically contributed for more than 60 per cent of yield variation [23] in the present experiment also. The presence of large environmental effect indicates wide difference in ecological potential of different tillage as well configuration systems. Large effect of environment and GE interaction may induce temporal instability in wheat production, if care is not taken while

Table 2. ANOVA for biomass and yield

Source of variation	df	Biomass	Yield
		MSS	MSS
Treatments	251	4.46**	0.592**
Genotypes	41	1.75**	0.312**
Management environments	5	160.56**	19.52**
Block	6	0.22	0.048*
Interactions	205	1.19**	0.186**
IPCA	45	2.32**	0.375**
IPCA	43	1.42**	0.199**
Residuals	117	0.67**	0.109**
Error	246	0.24	0.021

recommending the varieties for production under different environment created by various management practices. Therefore, genotypic evaluation is meaningful, if the mega environment issue is first addressed properly. Simple ANOVA, as in the present case, identifies the presence of genotype × environment interaction and provides no insight into the pattern of environment and genotypes, which results in this interaction.

AMMI analysis for yield

To gain further insight, the data were subject to AMMI analysis [16]. Both AMMI and GGE are helpful in first delineating the mega environments, which are repeatable over years and then picking up the genotypes showing positive interaction with the environment. The results clearly showed that the three environments created by different tillage and configuration practices are highly diverse selecting differentially adapted genotypes. In AMMI analysis, the main effects because of genotype and environment are first identified and residuals (GE) are then partitioned into multiplicative term and deviation from model. To analyze and represent the adaptation pattern effectively in the form of biplot, AMMI model was restricted to two PCA axis. According to AMMI analysis, the first and second PCA accounted for 42.16 and 21.60 per cent of interaction sum of squares, respectively.

The AMMI biplot (figure not shown) with main effects (genotype and environment means) as abscissa and first PCA scores as ordinate, explained 85.6 per cent of sum of squares. Environments E5 and E6 along with three checks viz., DBW17, PBW550

and HD2967 and many other genotypes like CSW28, CSW31, CSW34 and HD31179 are close to axis with PCA score near zero. Their yield data therefore, can easily be explained with additive model. On the other hand, the environments E1, E4 (CA) and E3 CTFB in (2011-12) has high and positive PCA score and interact favorably with genotypes HD3117, CSW2, CSW16, CSW18, CSW23 and CSW25. In both years, CA environment was the most productive, though only marginally better than CTFB but has higher positive PCA score and therefore, can be exploited by deploying specifically adapted genotypes. CTRB (E2 and E5) was the poorest yielding environment in both the years and has very high negative PCA score during the year 2011-12. E2 had positive interaction with genotypes like CSW33, CSW35, CTRB1666, CTRB1667, CTRB1813, CTRB1816 and CTFB4566 etc. E5 (CTRB) and E6 (CTFB) being very close to origin were less informative and least discriminatory. In the year 2012-13, the environment E4 and E6 have only limited difference in the main effect but varying greatly for interaction term. HD3117, CSW2, CSW18 and CSW25 which shows positive and high interaction with CA has high biomass largely because of longer stem and therefore, it is clear from the study that CA favors the genotype with higher biomass. Maximum average yield (6.03 t/ha) was realized under permanent bed condition during 2011-12 (E1) and followed by flatbed (5.95 t/ha) during the same year. The yield realization was least in both years on CTRB. The four entries picked up on the basis of average yield over the environment are HD3117, CSW2, CTRB1813 and CTFB4566.

The winning cultivars identified by AMMI analysis for yield data has been presented in Table 3. The winning cultivars picked by AMMI are slightly different than those picked up by GGE but there seems to some

broad agreement in two analysis, if we extend the analysis for top four genotypes. HD3117 was found winning in E4 and second best in E1 and E4 and similarly CSW2. In south-east Asia, as the most of years are not favorable for higher yield realization, selection under the production environment created by conventional tillage is not an effective strategy. CTRB offers little advantage under Indian condition, where temperature rise in the month of March and April is abrupt with very poor water holding capacity of the soil, in majority of north western plain zone, resulting in terminal heat and moisture stress. However, evaluation under CTRB can be used for culling unstable genotypes for broad adaptation, as multi environment data (MED) analysis in south east Asia favors broadly adapted genotypes at the cost of higher yield of specifically adapted genotype.

GGE biplot for yield

GGE biplots captured 80.40% of the variation for the yield via PC1 (41.61%) and PC2 (38.79%) for 2011-2012 (figure not shown). All the three environments viz., CA (E1), CTRB (E2) and CTFB (E3) were falling in separate sectors and picking up different winning genotypes. However as the angle between E1 and E3 is acute, they are correlated in the response. CTRB represent completely independent environment compared to CA and CTFB, as the angle between the environment CA and CTRB is nearly perpendicular. During the year 2011-12 CA and CTRB were comparatively more discriminative than CTFB, however the two are totally unrelated environments and indicates, the presence of fairly large GE interaction. The genotype HD3115, HD3117, CSW2, CSW4, CSW16, CSW18, CSW23, CSW25, and CTFB4566 are more adapted to both CA and CTFB while

Table 3. Winning cultivars identified by AMMI analysis for yield

Environment	Mean yield (t/ha)	PC score	Rank of genotypes in respective environments			
			1	2	3	4
E4 (CA 2012-13)	4.40	0.5434	HD3117	CSW2	HD3115	CSW16
E1 (CA 2011-12)	6.03	0.4196	CSW18	HD3117	CSW23	CSW34
E3 (CTFB 2011-12)	5.95	0.3441	CSW2	HD3117	<i>HD3115</i>	CSW16
E6 (CTFB 2012-13)	4.34	0.1111	<i>CTFB4550</i>	CSW2	<i>HD3115</i>	<i>CTFB4566</i>
E5 (CTRB 2012-13)	3.95	0.0821	CSW2	<i>CTFB4566</i>	CTRB1813	HD3117
E2 (CTRB 2011-12)	4.33	-1.500	CTRB1817	<i>CTFB4566</i>	CSW33	CTRB1813

The genotypes highlighted in bold : bred through selection in conservation agriculture environment; The genotypes in italics: bred through selection in CTFB (conventional tillage and flat bed); The genotypes in normal font: bred through selection in CTRB (conventional tillage and raised bed)

completely unsuitable for CTRB. CSW33, CTRB1666, CTRB1816, CTRB1817 and CTFB4539 are grouped together for E2.

During the year 2012-13, GGE biplot (figure not shown) accounted for 85.28 per cent of interaction sum of squares with strong correlation between CA (E4) and CTRB (E5) and they were different from CTFB (E6). Angle between E5 and E6 was near 90 degree and therefore, are almost unrelated, whereas E4 was making acute angle with both of them. Therefore, E4 was found, more representative environment for broad adaptation during the year 2012-13. HD3117, CSW1, CSW13, CSW15, CSW16, CSW18, CSW23, CSW25, DBW17 and HD2967 are very close to vector of E4 and E5 and therefore specifically adapted to these environments. CSW21 along with CSW26, CSW30, and PBW550 are close to origin and therefore more stable genotypes.

Combined GGE biplot analysis for yield

Combined biplot for both years accounted comparatively lesser per cent (61.92) of sum of squares (Fig. 1). The CTFB E3 and (E6) was highly repeatable over the years as the angle between them is almost negligible but the ability of this environment to differentiate the genotype is comparatively less as length of its vector is smaller than E1 and E4. CTRB is completely different from all other environment as

its angle with other environment is either near 90 or more than 90. HD3115, CSW2, CSW16, CSW18, CSW23 and CSW25 showed positive interaction with CA and CTFB. Genotypes CSW5, CSW24, CTFB4566 and CTFB4567 are close to origin and therefore more stable. Genotypes CSW33, CTRB1666 and CTRB1817 are more adapted to CTRB.

Which-won-where according to GGE

GGE biplot is constructed by plotting first principal component (PC1) score against second principal component (PC2) score for both genotype and environment (Fig. 2). The “which-won-where” view of the GGE biplot [17] displayed by an irregular polygon and by a perpendicular lines drawn from the biplot origin on each side represent the winner genotypes in that environment. Genotypes farthest from the origin mark the vertices of the polygon and others are contained within the resulting polygon. In the present study, the polygon for yield was constituted by the genotypes HD3115, HD3117, CSW28, CSW33, CTFB4550 and CTFB4566. According to this polygon, the winner genotype for E1, E3, E5 and E6 was HD3117 for E4 was CSW18 and for E2 was CTFB4566 (Fig. 2). Specific interaction of the genotype with environment can be drawn with cosine of angle between their vectors. If the angle is acute, its performance in that environment is better than average and if the angle is obtuse, its performance is poor than average.

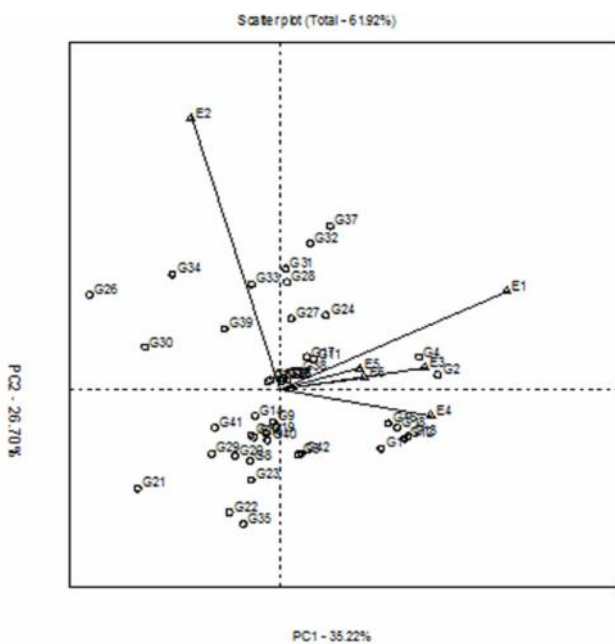


Fig. 1. GGE biplot for yield over genotypes, years and management practices

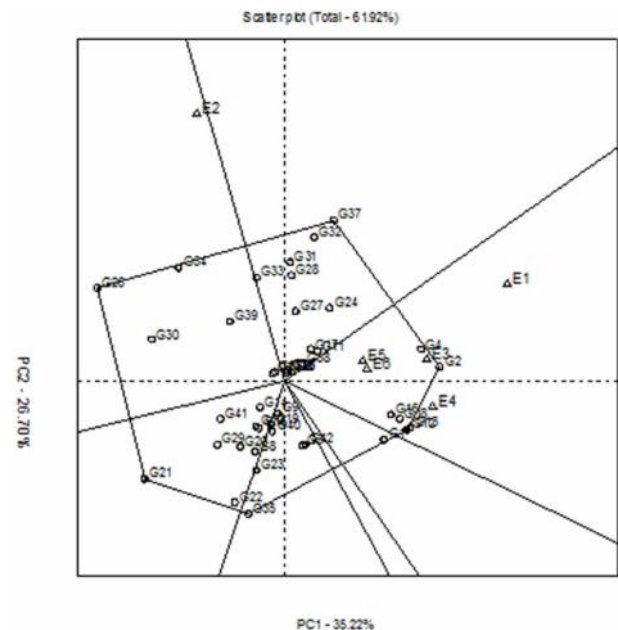


Fig. 2. The which-won-where view of the GGE biplot to show which genotypes performed best in which environments

In another way, the perpendicular lines can be drawn from the origin of biplot to the polygon sides and thus dividing the biplot into number of sectors with each having its own winning cultivar at the vertex. The winning cultivar is positioned usually, but not necessarily, within its winning sector [17]. The pattern suggests that target environment basically comprised three mega environments and different cultivars should be developed and deployed for each mega environment. In the present analysis, HD3117 and CSW2 are showing very good adaptation for E1, E3, E5 and E6, whereas, HD3115 CSW16, CSW18, CSW23 and CSW25 in environment E4 and CSW35, CTB1813, CTB1816, CTB1817 and CTFB4566 in E2. The winning cultivars identified by AMMI through evaluation under CTFB in good year (2011/12-E1) and under CA during heat stressed year (2012/13) were same. It implies that discriminating ability of CA even during bad years is almost equal to CTFB in good years. Through further yield consolidation in good years, CA can identify the winning genotypes different than those identified by CTFB. India receives large number of breeding material in the form of international trial and nurseries from CIMMYT, where predominating form of crop production environment is CTB. These lines are then tested by the Indian breeders under flatbed condition, the environment, which is usually prone to lodging. If the two environments, happen to be strongly different exploring different traits of genotypes as indicated by the present study, chances of strong cross over interaction is imminent. Existence of cross over interaction is also pointed out by the fact that many cultivars after being released from the coordinated trial on the basis of mean are never adopted by the farmers [24], whereas many other cultivars never released for a production environment are strongly adopted by the farmers for e.g. adoption of variety HD 2851 in cotton growing belt of India. Hildebrand and Stroup *et al.* [25, 26] have also argued that breeders usually ignore the presence of G x E interactions of crossover type by selecting the lines on the basis of average over environment largely in search of widely adapted variety for a large scale centralized seed production, discarding the top yielding lines at either extreme. HD3117 and CSW2 can be used for yield enhancement, both under CA as well as CTFB whereas CSW16, CSW18, CSW23, CSW25, HD3115 can be recommended for CA. CTB1813, CTB1817 and CTFB4566 can be recommended for exploiting genotype x environment interaction under CTB.

Ideal environment for identification of generally adapted genotypes

The figure with concentric circle clearly shows that within mega environment represented by E1, E3, E5 and E6, ideal test environment (E1) is the most informative and representative (Fig. 3). Therefore, it is clear from the present experimentation that for selection of generally adapted genotype, CA in a favorable year is better than all other environment. For specific adaptation, E2 and E4 are better than others. E5 and E6 are least discriminatory and therefore provide very little information about the discrimination of the genotypes. Discriminating but non representative environment like E2 are very useful for culling the highly unstable environment if there happens to be only one mega environment.

As yield is considered to be poorly inherited trait and direct selection of it in any of the environments carry little meaning. Biomass is considered comparatively better mean of judging the potential of the lines in any environment particularly under stress condition. For biomass, 71.78 per cent of treatment sum of square was accounted by environment, 21.79 per cent by genotype x environment and only 6.42 per cent by genotype. Highest biomass (15.58 t/ha) was realized in environment E1 (CA of 2011-12), followed by E3 15.0t/ha, (CTFB in 2011-12) and E4 11.81 t/ha (CA in 2012-13). Minimum biomass was accumulated

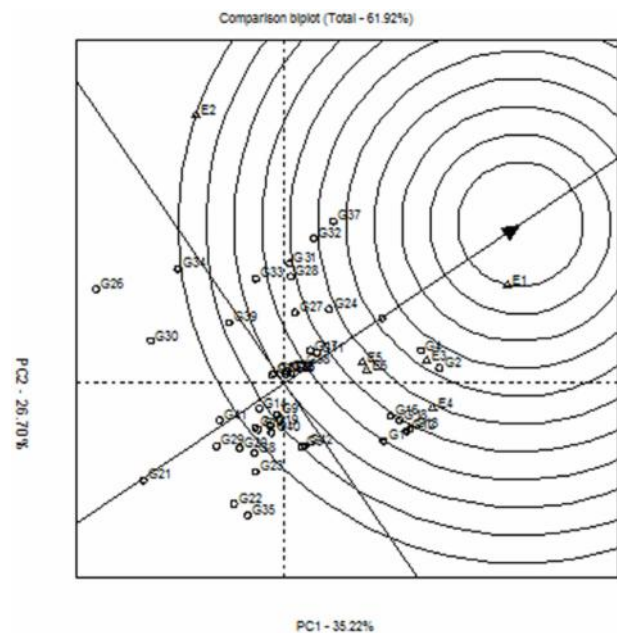


Fig. 3. Ranking of environments based on discriminating ability and representativeness

under CTRB. AMMI analysis showed that first two principal components accounted for 68 per cent of interaction sum of squares and therefore were important for analyzing G × E interaction. Winner genotype were totally different for CTRB and CA, however, there was some overlapping of winner genotype under CA and CTFB. GGE analysis pooled the three environments namely E1, E3 and E5 in one sector, E4 and E6 in another sector and E2 in totally different sectors.

The cosine of angle between vectors in GGE approximate the correlation between them and according to this CTFB and CA seems to have very little correlation with CTRB condition. According to the same biplot, CA and CTFB seems to be repeatable over the years, however same is not true for CTRB. In each year, CA seems to be more discriminative environment. GGE analysis clearly identifies E1 as the ideal environment, which is informative as well as representative. Even, during the bad year, CA was more informative than other largely because, the longer duration varieties with higher biomass, which otherwise get penalized due to terminal heat stress under conventional condition, get better chance of yield realization due to temperature modulation and moisture conservation under CA. It is thus clear from the present study that management practices like zero till, residue retention and bed configuration interact significantly with genotypes, therefore, selection and testing in one environment is not necessarily valid for others.

It is clear that cross over interaction is major hurdle in identifying the genotypes suited for management practices. In both years under testing, cross over interaction was present and examples of cross over interaction can be found in literature for number of crops and range of environments [27] in maize, Jackson *et al.* [28] in barley, Blum and Pnuel [29], Yadav *et al.* [30] in wheat, Virk and Mangat [31] in pearl millet. Selection on the basis of yield is highly unreliable largely because of low inheritance and therefore, the analysis was extended to total biomass. For biomass, CA was able to discriminate the genotypes, more effectively than other environments in both years. It can be clearly inferred from above results that among the three environments, CA is most representative as well as informative and therefore, should be more actively integrated in the breeding programme for development and identification of new high yielding cultivars for specific adaptation as well as broad adaptation.

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