

Multi-environment analysis of grain yield in a diverse set of bread wheat genotypes

Charan Singh*, Arun Gupta, Pradeep Kumar, Sendhil Ramdas, Gopalareddy Krishanappa, Vikas Gupta, Sanjay Kumar Singh, Amit Kumar Sharma, Bhudeva Singh Tyagi, Gyanendra Singh, Ravish Chatrath and Gyanendra Pratap Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal, India - 132001

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*Corresponding author

Email: n_charansingh@hotmail.com

Abstract

A diverse set of 50 bread wheat genotypes was evaluated at 16 different locations belonging to four major wheat growing zones of India during 2016-17. The yield data was analyzed using Eberhart and Russel (1966), AMMI and GGE biplot stability models. Genotypes G14 and G26 were identified as the most stable genotypes based on Eberhart and Russel (1966) model, whereas genotypes G10, G14, G18, G23, G26, G30, and G47 were identified stable as per AMMI model whereas five genotypes G26, G23, G10, G43 and G14 were found stable as per GGE biplot analysis. Genotypes G14 and G26 were turned out to be the most stable genotypes based on these three stability models. The G48 ranked best for (Durgapura and Pantnagar); G29 (Powarkheda) and G35 (Hisar, Delhi and Ludhiana) based on grain yield performance. The GGE bi-plot indicated Durgapura to be an ideal environment followed by Hisar, Ludhiana, Delhi, Pantnagar, and Powarkheda that could be recommended for the future wheat breeding programmes aiming towards yield enhancement.

Keywords: AMMI, GGE, genotype × environment interaction, grain yield stability, wheat

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1. Introduction

Wheat is a staple food crop of many countries across the globe including India, which plays an important role in nutritional as well as food security. India is one of the prime producer and consumer of wheat. In India, wheat was cultivated over 29.55 million hectares with a production of 101.20 million tons during 2018-19 (3rd estimates, Anonymous, 2019). India is divided into five mega agro-climatic zones for wheat cultivation i.e., Northern Hill Zone, North Western Plains Zone, North Eastern Plains Zone, Central Zone and Peninsular Zone. Climate change and increasing human population around the globe are the most critical challenges to meet the ever increasing demand of food grain production for the growing population. Recently, major wheat growing regions are experiencing extreme and unpredictable weather conditions due to climate change. Therefore, the development of high yielding climate resilient wheat genotypes is of paramount importance to meet the global demand of wheat production. Due to these challenges,

wheat production needs to be sustainably increased by 2-3% annually. Gene expression is subjected to modification by the environment; therefore, genotypic expression of the phenotypes is environmentally dependent (Kang, 1998). The performance of genotypes is greatly affected by genotype-environment interaction (GEI) (Becker and Leon, 1988). The major focus of plant breeding community across the globe is to develop genotypes either with general adaptability and/or specific adaptability (Ebdon and Gauch, 2002a). The complexity of GEI makes selection procedure cumbersome to identify the best performing and most stable genotypes (Yau, 1995). The adaptability of a variety over diverse environments is usually tested by the degree of its interaction with different environmental factors under which it is grown. Stability, or genotype (G) × environment (E) interactions, is necessary for researcher's to develop a genotype that respond optimally and consistently across environments (Blanchi *et al.* 2008). A variety or genotype is considered to be more adaptive or stable one, if it has a high mean yield but low degree of fluctuation in yielding ability,

when grown over diverse environments. GE interactions exist when the responses of two genotypes to different levels of environmental stress are crossovers (Allard and Bradshaw, 1964). Numerous tools have been developed to measure the response of genotypes to changes in environment (Eberhart and Russell, 1966; Shukla, 1972; Gauch, 1988; Lin and Binns, 1988). Eberhart and Russell (1966) (ER) regression model describes a stable variety which should have around unit regression coefficient over environments ($b_i=1$) and minimum deviation from the regression ($S^2di=0$) in addition to higher grain yield than population mean. The other popular stability models additive main effect and multiplicative interaction (AMMI) and genotype plus genotype-by-environment (GGE) overcomes the limitations of univariate models and also are more informative compared to other methods (Shukla, 1972; Gauch, 1988; Zobel *et al.* 1988). However, GGE biplot offers breeders a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents both mean performance and stability (Yan, 2001). Widespread acceptance of GGE biplot for its ability to evaluate mean performance and stability and to identify mega-environments has created a need for research to compare GGE Biplot to other “traditional” stability analysis tools.

AMMI and GGE are the two commonly used bi-plots techniques to visualize G×E interactions (Yan *et al.* 2000). The GGE biplot is an effective method based on principal component analysis (PCA) to fully explore multi-environmental data (Rao *et al.* 2011; Singh *et al.* 2019). It has always been challenging to define how new genotypes would respond under different climatic conditions, without graphically presenting the data, when many cultivars are evaluated across many sites, seasons and years (Yan *et al.*

2001). The researchers usually focus on G×E interaction to select the genotypes for general adaptation and crossover G×E interaction for the specific adaptation (Matus-Cadiz *et al.* 2003).

Development of high buffering genotypes which adapts to diverse agro-climatic conditions is both economical and sustainable strategy to sustain the wheat production in changing climatic conditions. In this study, genotypes received from CIMMYT as a Semi-Arid Wheat Yield Trial (SAWYT) were evaluated for grain yield across different environments to identify stable genotypes for general and specific adaptation. Therefore, the present study was aimed (i) to identify mega-environments in major wheat growing regions of India (ii) to identify high yielding and stable performing genotypes.

2. Materials and methods

A set of 50 advanced generation bread wheat genotypes of 24th Semi-Arid Wheat Yield Trial (24th SAWYT) of CIMMYT were grown at 16 locations in India during *rabi*, 2016-17 (Table 1 and 2). The genotypes were planted in an randomised complete block design with two replications per genotype in a six row plot of 6 m length with a plant-to-plant distance and row to row distance of 10cm and 25cm, respectively. Grain yield from 4 middle rows with a net plot size of 4.8 m² was converted into q ha⁻¹ at 10% standard grain moisture and utilized for further statistical analysis. Standard agronomic practices were followed for raising a healthy crop. The data of 50 genotypes were subjected to pooled analysis of variance using SAS statistical package. A principal component analysis (PCA) was performed to construct a GGE and AMMI biplot using IRRI-STAT software (ver. 5.0). The stability parameters for grain yield were worked out as

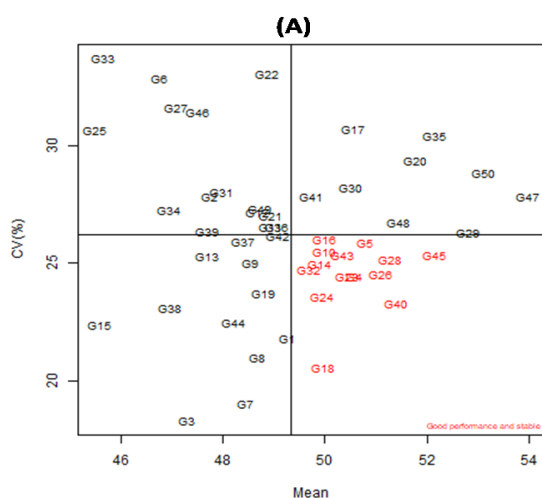


Fig 1 Bi plot of CV for grain yield

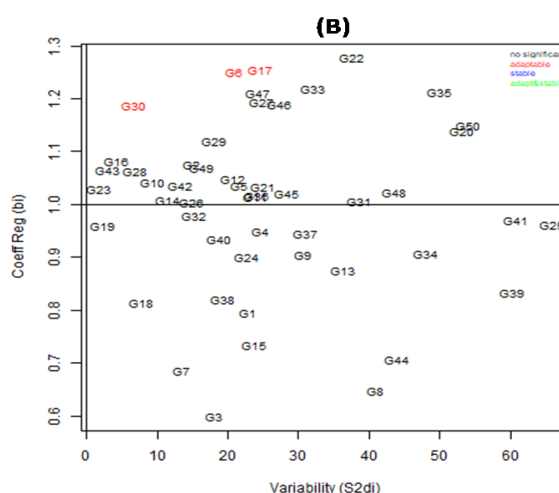
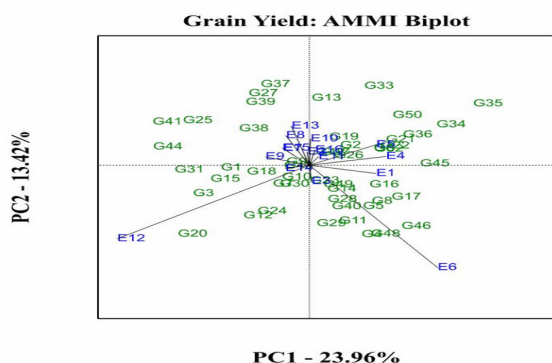


Fig 2 Bi plot of stability parameters for grain yield

Table 1. Details of 16 locations (environments) used for conduction of experiments.

| Env. code | Location | Latitude | Longitude | Mean sea level (m) | Mean grain yield (qha ⁻¹) |
|-----------|------------|----------|-----------|--------------------|---------------------------------------|
| E1 | Delhi | 28°39'N | 77°13'E | 227.0 | 46.51 |
| E2 | Karnal | 29°41'N | 76°59'E | 253.0 | 71.93 |
| E3 | Pantnagar | 29°30'N | 79°31'E | 243.8 | 60.14 |
| E4 | Hisar | 29°10'N | 75°46'E | 215.2 | 55.07 |
| E5 | Ludhiana | 30°54'N | 75°51'E | 252.0 | 60.37 |
| E6 | Durgapura | 26°55'N | 75°46'E | 432.0 | 57.96 |
| E7 | Faizabad | 26°46'N | 82°8'E | 104.0 | 38.36 |
| E8 | Kota | 25°10'N | 75°50'E | 267.0 | 65.81 |
| E9 | Powarkheda | 21°50'N | 76°43'E | 229.0 | 74.08 |
| E10 | Vijapur | 21°11'N | 72°49'E | 20.0 | 36.76 |
| E11 | Junagadh | 21°52'N | 70°46'E | 97.0 | 54.42 |
| E12 | Jabalpur | 23°10'N | 79°57'E | 416.0 | 39.00 |
| E13 | Pune | 18°31'N | 73°51'E | 562.0 | 60.10 |
| E14 | Indore | 22°43'N | 75°51'E | 550.0 | 48.89 |
| E15 | Bilaspur | 22°4'N | 82°9'E | 264.0 | 33.67 |
| E16 | Dharwad | 15°27'N | 75°0'E | 724.0 | 35.09 |

per procedure (Eberhart and Russell 1966; Singh and Chaudhary, 1985).

**Fig 3** Bi plot depicting the relationship among test environments by AMMI

3. Results and discussion

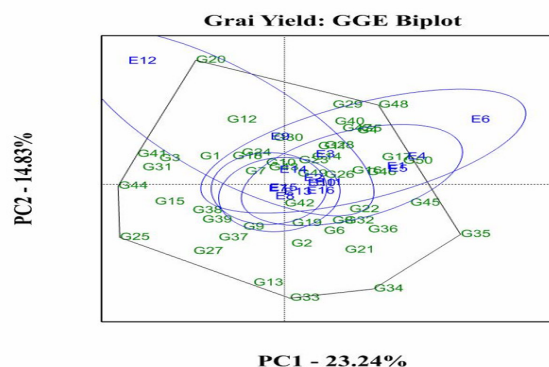
3.1 Genetic variability

The genotypes under study showed a wide spectrum of variability with respect to their mean value of grain yield at different locations (Table 1). The location wise mean yield ranges from 33.67q/ha (Bilaspur) to 74.08 q/ha (Powarkheda). The highest yielding genotypes at individual test locations are G5 (63.82q/ha) at Delhi, G47 (55.25q/ha) at Karnal, G11 (50.25q/ha) at Pantnagar, G50 (78.96q/ha) at Hisar, G50 (70.67q/ha) at Ludhiana, G48

(73.44q/ha) at Durgapura, G44 (47.40q/ha) at Faizabad, G21 (76.98q/ha) at Kota, G20 (86.30q/ha) at Powarkheda, G47 (52.92q/ha) at Vijapur, G29 (68.87q/ha) at Junagadh, G20 (63.37q/ha) at Jabalpur, G26 (68.47q/ha) at Pune, G10 (48.60q/ha) at Indore, G18 (39.10)q/ha at Bilaspur and G39 (49.35q/ha) at Dharwad. Out of 50 genotypes, only two genotypes (G50 and G47) ranked first at two locations each. Genotype G50 was the top yielder at Hisar and Ludhiana whereas G47 at Karnal and Vijapur locations. The differential ranking of genotypes showed their crossover type of GEI effects. This differential expression of genotypes with respect to gain yield is due to greater magnitude of environmental effects in their complete expression. The coefficient of variation (CV) of the genotypes ranged from 18.31% (G3) to 33.69% (G33). The genotypes with high mean values with comparatively low CV are G5, G10, G14, G16, G18, G24, G26, G28, G32, G43, G45 and G46 are considered to be desirable (Table 4 and Fig.1).

3.2. Stability analysis by Eberhart and Russell model

The genotype-environment interaction component (GEI) was further elaborated by using the joint regression model of stability analysis (Eberhart and Russell, 1966). Stable genotypes were identified based on stability parameters *viz.*, linear response ($b_i=1$), minimum deviation from linearity ($S^2di=0$), and higher trait mean. The genotypes

**Fig 4** Bi plot depicting the relationship among environments by GGE

viz., G5, G10, G16, G17, G20, G23, G28, G29, G30, G35, G43, G45, G47, G48 and G50 were specifically suited to high productive/favorable environments due to their higher mean values than population mean, regression coefficient (b_i) more than unity with non-significant deviations from their respective regression. Similarly, the genotypes G4, G18, G24, G32, G41, G40, G125 and G126 are better suited to low productive/unfavorable environments due to their higher mean values than populations mean coupled with regression coefficient

Table 2. Pedigree details of 50 genotypes used in the present study

| Code | Pedigree details |
|------|--|
| G1 | LOCAL CHECK |
| G2 | PBW65/2*PASTOR |
| G3 | KA/NAC//TRCH/3/DANPHE #1 |
| G4 | FITIS |
| G5 | FRANCOLIN #1//WBLL1*2/BRAMBLING |
| G6 | FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC |
| G7 | BECARD #1/3/PBW343*2/KUKUNA//PBW343*2/KUKUNA |
| G8 | SUP152/3/TRCH/SRTU//KACHU |
| G9 | WAXWING/7/TNMU/6/CEP80111/CEP81165/5/IAC5/4/YKT406/3/AG/ASN//ATR/8/ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92 |
| G10 | KACHU/SAUAL/3/TRCH/SRTU//KACHU |
| G11 | ROLF07/4/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI/5/SAUAL/MUTUS |
| G12 | WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/6/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/KACHU #1 |
| G13 | PBW343*2/KUKUNA//PBW343*2/KUKUNA*2/8/SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA |
| G14 | PRL/2*PASTOR*2/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 |
| G15 | KACHU*2/6/YAR/AE.SQUARROSA (783)/4/GOV/AZ//MUS/3/SARA/5/MYNA/VUL//JUN |
| G16 | HEILO//MILAN/MUNIA/3/2*WHEAR/SOKOLL |
| G17 | WAXWING//INQALAB 91*2/KUKUNA/3/WBLL1*2/TUKURU/8/2*NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA |
| G18 | HUW234+LR34/PRINIA*2//SNLG/3/BOKOTA |
| G19 | CHEN/AE.SO//WEAVER/3/SSERI/4/TOBA97/PASTOR/5/MUU #1/6/KACHU #1//PI 610750/SASIA/3/KACHU |
| G20 | COPIO/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA |
| G21 | SAUAL/YANAC//SAUAL/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA |
| G22 | PRL/2*PASTOR/3/2*TRCH/SRTU//KACHU |
| G23 | FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD #1//INQALAB 91*2/TUKURU |
| G24 | PRL/2*PASTOR//SUNSTATE/4/2*ATTILA*2/PBW65//PIHA/3/ATTILA/2*PASTOR |
| G25 | BAV92//IRENA/KAUZ/3/HUITES/4/DOLL*2/5/FRET2/KUKUNA//FRET2/3/TNMU/4/FRET2*2/SHAMA |
| G26 | TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/TRCH/SRTU//KACHU |
| G27 | KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL/5/PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA/6/KACHU/SAUAL |
| G28 | SAUAL/MUTUS//KINGBIRD #1/3/SAUAL/MUTUS |
| G29 | SAUAL/MUTUS*2/3/TRCH/SRTU//KACHU |
| G30 | SAUAL/MUTUS*2//PICAFLOR #1 |
| G31 | C80.1/3*BATAVIA//2*WBLL1/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES*2/6/TRCH/SRTU//KACHU |
| G32 | ROLF07*2/KIRITATI*2//PICAFLOR #1 |
| G33 | FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/TRCH/SRTU//KACHU |
| G34 | FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/TRCH/SRTU//KACHU |

| | |
|-----|--|
| G35 | ATTILA*2/PBW65*2//WHEAR/3/TRCH/SRTU//KACHU/8/ALD/CEP75630//CEP75234/PT7219/3/BUC/BJY/4/CBRD/5/TNMU/PF85487/6/PBW343*2/KUKUNA/7/CNO79//PF70354/MUS/3/PASTOR/4/BAV92 |
| G36 | BCN/RIALTO//2*MUNAL #1 |
| G37 | CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92 |
| G38 | BAVIS/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/ PASTOR//MILAN/KAUZ/3/BAV92 |
| G39 | SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SHAMA//PARUS/PASTOR |
| G40 | W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92 |
| G41 | BECARD #1/BAVIS |
| G42 | WBLL1*2/BRAMBLING/3/SOKOLL//SUNCO/2*PASTOR |
| G43 | PASTOR//HXL7573/2*BAU/3/WBLL1/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92 |
| G44 | OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/SOKOLL//SUNCO/2*PASTOR/7/SOKOLL//SUNCO/2*PASTOR |
| G45 | SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI |
| G46 | GLADIUS/5/2*W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1 |
| G47 | CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/2*BAVIS #1 |
| G48 | D67.2/PARANA 66.270//AE.SQUARROSA (320)/3/CUNNINGHAM/4/PASTOR/SLVS/5/SUNCO/2*PASTOR//EXCALIBUR/ 6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92 |
| G49 | LIVINGSTON/5/2*W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1 |
| G50 | MUNAL #1*2//SOKOLL/WBLL1 |

Table 3. ANOVA for AMMI analysis of 50 diverse genotypes in 16 environments.

| Source of variation | df | MS | F | Prob |
|---------------------|--------|----------|--------|-------|
| Environments | 15.00 | 13159.79 | 549.15 | <0.00 |
| Genotypes | 49.00 | 120.81 | 5.04 | <0.00 |
| G x E | 735.00 | 78.60 | 3.28 | <0.00 |
| PC1 | 63.00 | 219.75 | 9.21 | <0.00 |
| PC2 | 61.00 | 127.06 | 5.32 | <0.00 |
| PC3 | 59.00 | 120.43 | 5.05 | <0.00 |
| PC4 | 57.00 | 109.51 | 4.59 | <0.00 |
| PC5 | 55.00 | 89.77 | 3.76 | <0.00 |
| PC6 | 53.00 | 73.10 | 3.06 | <0.00 |
| PC7 | 51.00 | 56.43 | 2.36 | <0.00 |
| PC8 | 49.00 | 48.82 | 2.05 | <0.00 |
| PC9 | 47.00 | 44.36 | 1.86 | <0.00 |
| PC10 | 45.00 | 38.07 | 1.59 | <0.00 |
| Residuals | 800.00 | 23.96 | NA | NA |

(b_i) less than unity with non-significant deviations from regression. Genotypes G14 and G26 exhibited stable performance across the environments suggested by

their higher mean performance than population mean, regression coefficient (b_i) near to unity with non-significant deviations from regression. Kumar *et al.* (2017) identified genotype K 612 to be stable as it had superior mean performance, regression coefficient greater than unity with non-significant deviation from regression coefficient. Another genotype K 9162 was the highest yielding and stable genotype along with early maturity (118 days) and has potential for late planting conditions.

3.3. Stability analysis by AMMI model

The AMMI model is widely used in the stability analysis as it provides an initial diagnosis of the model to be fit into multi- environmental evaluation (Zobel *et al.* 1988, Crossa *et al.* 1990). Analysis of variance (ANOVA) revealed significant role of the additive main effects *i.e.*, genotype and environment on the total variation of the traits (Table 3). The multiplicative analysis revealed that, all the 10 interaction principal components were significant. The first two interaction principal components cumulatively explained 37.38% of interaction. Graphical representation (biplot) employed by using PCA1 and PCA2 to ascertain environmental variation and to interpret the genotype-environment interactions (Fig.3).

Table 4. Stability parameters (Eberhart and Russell model for grain yield of 50 genotypes in 16 locations

| Genotype | Mean | SD | CV (%) | bi | S ² di |
|----------|-------|-------|--------|------|-------------------|
| G1 | 49.28 | 10.75 | 21.81 | 0.80 | 22.91 |
| G2 | 47.74 | 13.29 | 27.84 | 1.07 | 14.85 |
| G3 | 47.29 | 8.66 | 18.31 | 0.60 | 18.13 |
| G4 | 50.57 | 12.35 | 24.41 | 0.95 | 24.58 |
| G5 | 50.79 | 13.13 | 25.84 | 1.04 | 21.62 |
| G6 | 46.75 | 15.36 | 32.86 | 1.25 | 20.82 |
| G7 | 48.46 | 9.23 | 19.05 | 0.69 | 13.36 |
| G8 | 48.67 | 10.21 | 20.98 | 0.65 | 40.87 |
| G9 | 48.54 | 12.13 | 24.99 | 0.90 | 30.73 |
| G10 | 49.99 | 12.75 | 25.50 | 1.04 | 9.30 |
| G11 | 48.94 | 12.99 | 26.55 | 1.02 | 23.90 |
| G12 | 48.69 | 13.21 | 27.14 | 1.05 | 20.70 |
| G13 | 47.69 | 12.07 | 25.30 | 0.88 | 36.35 |
| G14 | 49.91 | 12.46 | 24.97 | 1.01 | 11.52 |
| G15 | 45.58 | 10.20 | 22.37 | 0.73 | 23.76 |
| G16 | 49.99 | 13.00 | 26.00 | 1.08 | 4.19 |
| G17 | 50.56 | 15.53 | 30.72 | 1.26 | 24.60 |
| G18 | 49.97 | 10.27 | 20.55 | 0.81 | 7.75 |
| G19 | 48.80 | 11.58 | 23.73 | 0.96 | 2.25 |
| G20 | 51.77 | 15.21 | 29.37 | 1.14 | 53.20 |
| G21 | 48.95 | 13.22 | 27.00 | 1.03 | 25.02 |
| G22 | 48.87 | 16.14 | 33.03 | 1.28 | 37.56 |
| G23 | 50.45 | 12.32 | 24.43 | 1.03 | 1.74 |
| G24 | 49.94 | 11.78 | 23.59 | 0.90 | 22.65 |
| G25 | 45.49 | 13.94 | 30.64 | 0.96 | 65.90 |
| G26 | 51.10 | 12.55 | 24.55 | 1.00 | 14.81 |
| G27 | 47.08 | 14.88 | 31.60 | 1.19 | 24.79 |
| G28 | 51.28 | 12.89 | 25.13 | 1.06 | 6.96 |
| G29 | 52.81 | 13.89 | 26.31 | 1.12 | 18.06 |
| G30 | 50.52 | 14.24 | 28.19 | 1.19 | 6.66 |
| G31 | 47.97 | 13.43 | 27.99 | 1.01 | 38.65 |
| G32 | 49.70 | 12.29 | 24.73 | 0.98 | 15.26 |
| G33 | 45.66 | 15.38 | 33.69 | 1.22 | 32.02 |
| G34 | 46.95 | 12.80 | 27.26 | 0.91 | 47.97 |
| G35 | 52.14 | 15.85 | 30.39 | 1.21 | 49.95 |
| G36 | 49.05 | 13.01 | 26.52 | 1.02 | 24.11 |
| G37 | 48.39 | 12.55 | 25.93 | 0.95 | 30.96 |
| G38 | 46.97 | 10.84 | 23.09 | 0.82 | 19.28 |
| G39 | 47.71 | 12.58 | 26.37 | 0.83 | 60.24 |
| G40 | 51.41 | 11.96 | 23.27 | 0.93 | 18.68 |

| | | | | | |
|-----|-------|-------|-------|------|-------|
| G41 | 49.75 | 13.85 | 27.83 | 0.97 | 60.83 |
| G42 | 49.07 | 12.83 | 26.14 | 1.04 | 13.28 |
| G43 | 50.35 | 12.76 | 25.34 | 1.06 | 2.97 |
| G44 | 48.20 | 10.84 | 22.49 | 0.71 | 43.87 |
| G45 | 52.16 | 13.21 | 25.32 | 1.02 | 28.31 |
| G46 | 47.50 | 14.91 | 31.39 | 1.19 | 27.32 |
| G47 | 53.98 | 15.03 | 27.85 | 1.21 | 24.19 |
| G48 | 51.46 | 13.76 | 26.74 | 1.02 | 43.56 |
| G49 | 48.72 | 13.30 | 27.29 | 1.07 | 16.36 |
| G50 | 53.12 | 15.33 | 28.85 | 1.15 | 54.00 |

Genotypes with PCA1 scores near zero showed very less interaction across environments. Similarly, environments with PCA1 scores near zero displaying little interaction across genotypes and generally show less discrimination among the genotypes (Crossa *et al.* 1990). Jabalpur and Durgapura are the distinct environments compared to other locations (Fig.3).

The genotypes *i.e.*, G10, G14, G18, G23, G26, G30 and G47 showed greater stability since they found very close to the origin (Fig.3). The genotypes which have the longest vectors were adapted to specific environments and contributed to more diversity. The genotypes appearing close together on the plot have almost similar mean grain yield over all the locations while the genotypes placed far apart may either differ in mean grain yield or show a different pattern of response over the locations. Hence, the genotypes near to the origin are not sensitive to genotype \times environment interactions whereas those distant from the origins are more sensitive and exhibit large genotype \times environment interactions. The genotypes located near the centre of the bi-plot contributed less to GE interaction, while cultivars having longer vectors, showed the greatest contribution to GE interaction (Letta *et al.* 2008). The distance from the origin exhibits the amount of interaction by genotypes either over environments or by environments over genotypes (Yan and Kang 2003). The genotypes *viz.*, G20, G33, G35, G37, G41, G44, G46 and G48 expressed interaction on higher side (positively or negatively). The genotypes at vertex were the winners in the environment included in that sector (Yan and Tinker, 2006). The genotypes that results in both high mean grain yield and high stability termed as an ideal genotype, should possess both high mean performance and high stability across environments. The environment with short spike (Pantnagar, Vijapur, Hisar and Junagadh) does not exert strong interactive forces. While the environment with long spike (Jabalpur, Powarkheda, Durgapura, Ludhiana) exert strong interaction among each other.

Table 5. Mean grain yield (q/ha⁻¹) performance of 50 genotypes for grain yield across 16 locations

| Entry | Delhi | Karnal | Pantnagar | Hisar | Ludhiana | Durgapura | Faizabad | Kota | Powarkheda | Vijapur | Junagadh | Jabalpur | Pune | Indore | Bilaspur | Dharwad |
|-------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| G1 | 53.61 | 40.67 | 49.42 | 44.71 | 56.07 | 48.96 | 38.04 | 59.90 | 78.96 | 44.58 | 51.22 | 47.43 | 55.41 | 48.01 | 38.47 | 32.94 |
| G2 | 43.89 | 45.26 | 43.48 | 55.88 | 50.82 | 58.33 | 41.67 | 74.27 | 68.75 | 26.50 | 56.33 | 29.08 | 55.81 | 37.89 | 35.28 | 40.64 |
| G3 | 43.61 | 40.04 | 42.43 | 50.92 | 51.95 | 49.48 | 40.64 | 58.75 | 61.04 | 40.00 | 55.90 | 57.20 | 55.00 | 37.15 | 36.11 | 36.45 |
| G4 | 53.54 | 42.99 | 50.18 | 54.21 | 66.53 | 71.88 | 32.00 | 63.02 | 65.63 | 32.42 | 55.35 | 44.27 | 56.16 | 43.94 | 35.83 | 41.24 |
| G5 | 63.82 | 43.26 | 48.43 | 60.92 | 61.10 | 63.54 | 38.16 | 58.02 | 80.25 | 38.42 | 53.32 | 40.97 | 50.25 | 41.33 | 28.96 | 41.91 |
| G6 | 58.26 | 38.74 | 34.88 | 63.29 | 50.50 | 55.21 | 37.98 | 68.44 | 74.37 | 31.83 | 55.87 | 28.00 | 54.44 | 42.58 | 25.56 | 28.05 |
| G7 | 47.78 | 41.11 | 47.25 | 56.92 | 59.45 | 52.60 | 35.02 | 58.96 | 58.33 | 35.08 | 56.12 | 48.00 | 57.78 | 48.36 | 37.01 | 35.49 |
| G8 | 53.33 | 48.53 | 37.13 | 50.13 | 44.72 | 72.40 | 45.59 | 62.08 | 54.17 | 42.33 | 52.62 | 33.53 | 59.16 | 43.63 | 36.04 | 43.35 |
| G9 | 56.32 | 43.92 | 46.03 | 35.79 | 47.03 | 57.29 | 41.67 | 71.04 | 70.83 | 35.67 | 60.58 | 34.27 | 56.03 | 44.93 | 35.90 | 39.38 |
| G10 | 48.96 | 48.10 | 42.48 | 50.00 | 61.53 | 60.94 | 39.37 | 70.00 | 72.92 | 33.08 | 47.25 | 43.70 | 65.19 | 48.60 | 34.38 | 33.40 |
| G11 | 46.39 | 44.15 | 50.25 | 47.67 | 60.37 | 69.79 | 40.34 | 54.06 | 81.25 | 37.17 | 50.65 | 37.77 | 53.25 | 41.79 | 31.53 | 36.64 |
| G12 | 44.17 | 38.08 | 46.80 | 52.04 | 56.35 | 59.90 | 41.36 | 61.67 | 84.47 | 33.00 | 49.57 | 49.87 | 52.19 | 42.40 | 29.86 | 37.29 |
| G13 | 40.13 | 45.68 | 44.85 | 43.33 | 62.15 | 48.44 | 36.53 | 73.33 | 62.08 | 37.50 | 60.08 | 28.50 | 56.81 | 40.98 | 35.76 | 46.81 |
| G14 | 50.42 | 43.14 | 37.63 | 57.25 | 56.70 | 63.02 | 37.56 | 56.67 | 81.15 | 38.25 | 61.60 | 39.97 | 52.47 | 43.10 | 34.38 | 45.31 |
| G15 | 36.88 | 46.90 | 40.10 | 43.21 | 45.30 | 50.00 | 30.50 | 55.73 | 67.71 | 36.17 | 59.92 | 47.03 | 54.59 | 38.03 | 32.51 | 44.71 |
| G16 | 50.83 | 43.51 | 48.38 | 57.79 | 59.58 | 66.67 | 41.06 | 61.35 | 79.17 | 35.33 | 52.17 | 33.77 | 56.88 | 37.21 | 35.00 | 41.10 |
| G17 | 52.78 | 47.76 | 49.98 | 64.58 | 50.07 | 71.35 | 33.82 | 62.81 | 85.05 | 31.17 | 53.35 | 31.03 | 60.97 | 38.94 | 34.86 | 40.49 |
| G18 | 47.85 | 42.00 | 48.10 | 51.21 | 61.95 | 53.13 | 33.94 | 67.81 | 68.13 | 41.92 | 55.90 | 50.10 | 57.09 | 42.34 | 39.10 | 38.91 |
| G19 | 45.83 | 46.56 | 43.88 | 53.08 | 58.82 | 56.77 | 46.68 | 65.42 | 71.67 | 38.83 | 54.13 | 32.73 | 58.44 | 34.00 | 34.79 | 39.14 |
| G20 | 46.46 | 48.92 | 40.73 | 56.58 | 50.23 | 63.54 | 36.23 | 72.60 | 86.30 | 29.25 | 52.73 | 63.37 | 62.50 | 46.83 | 36.53 | 35.51 |
| G21 | 56.25 | 49.89 | 37.00 | 55.58 | 55.33 | 60.42 | 37.98 | 76.98 | 62.08 | 33.92 | 56.80 | 27.65 | 55.94 | 42.33 | 33.47 | 41.52 |
| G22 | 47.08 | 46.42 | 28.83 | 71.50 | 60.67 | 60.94 | 41.67 | 69.58 | 75.00 | 24.25 | 56.95 | 30.88 | 57.50 | 41.29 | 36.60 | 32.79 |
| G23 | 51.74 | 45.81 | 41.78 | 61.96 | 57.32 | 60.94 | 39.25 | 72.40 | 70.00 | 30.75 | 53.00 | 44.00 | 59.19 | 43.40 | 34.65 | 40.99 |
| G24 | 42.57 | 50.06 | 46.13 | 51.58 | 43.05 | 66.67 | 38.04 | 72.50 | 70.83 | 35.08 | 53.77 | 46.55 | 58.84 | 44.80 | 36.53 | 42.00 |
| G25 | 46.11 | 42.44 | 41.05 | 51.04 | 31.58 | 38.02 | 30.19 | 72.19 | 80.21 | 31.75 | 48.57 | 40.10 | 55.97 | 40.03 | 37.15 | 41.49 |
| G26 | 49.86 | 46.88 | 49.93 | 59.54 | 65.52 | 58.33 | 31.40 | 65.46 | 68.75 | 32.92 | 54.62 | 39.43 | 68.47 | 46.90 | 34.79 | 44.85 |
| G27 | 39.38 | 43.36 | 39.93 | 43.67 | 55.68 | 44.79 | 38.35 | 71.88 | 84.54 | 34.67 | 52.23 | 31.58 | 62.59 | 40.05 | 32.08 | 38.44 |
| G28 | 58.47 | 44.75 | 41.38 | 58.54 | 52.18 | 65.63 | 39.25 | 68.54 | 75.00 | 35.42 | 61.27 | 43.27 | 57.69 | 43.95 | 28.96 | 46.19 |
| G29 | 51.74 | 44.78 | 45.78 | 61.17 | 56.27 | 70.83 | 41.55 | 72.71 | 77.29 | 37.42 | 68.87 | 47.77 | 53.09 | 46.84 | 31.46 | 37.36 |
| G30 | 54.10 | 49.83 | 41.78 | 52.79 | 62.00 | 60.42 | 40.22 | 70.42 | 80.42 | 30.75 | 50.78 | 46.02 | 62.00 | 43.76 | 33.61 | 29.39 |
| G31 | 45.56 | 46.96 | 41.40 | 46.00 | 47.55 | 49.48 | 42.27 | 75.73 | 78.13 | 31.08 | 49.10 | 50.48 | 56.31 | 43.48 | 36.60 | 27.38 |
| G32 | 52.15 | 44.24 | 36.68 | 50.92 | 64.37 | 63.54 | 39.86 | 68.65 | 65.83 | 43.92 | 54.38 | 32.25 | 60.81 | 41.75 | 30.42 | 45.41 |
| G33 | 48.61 | 47.43 | 33.95 | 45.58 | 59.43 | 48.96 | 37.44 | 63.33 | 83.33 | 32.25 | 50.32 | 16.87 | 54.72 | 34.70 | 34.44 | 39.21 |
| G34 | 49.31 | 48.43 | 41.45 | 54.00 | 64.72 | 59.38 | 38.41 | 58.85 | 56.25 | 33.08 | 54.73 | 18.33 | 61.59 | 42.75 | 36.88 | 33.08 |
| G35 | 61.81 | 46.32 | 44.13 | 70.67 | 68.70 | 61.46 | 34.54 | 72.29 | 70.83 | 42.17 | 57.23 | 20.13 | 64.88 | 42.38 | 35.28 | 41.46 |
| G36 | 51.67 | 45.25 | 43.98 | 64.42 | 52.77 | 59.38 | 37.14 | 58.85 | 75.00 | 45.50 | 55.23 | 23.67 | 58.28 | 43.28 | 31.46 | 38.99 |
| G37 | 48.26 | 54.29 | 49.40 | 55.25 | 54.32 | 37.50 | 38.16 | 65.10 | 78.34 | 38.92 | 51.13 | 33.27 | 58.63 | 42.36 | 33.89 | 35.44 |
| G38 | 53.26 | 43.92 | 40.03 | 50.88 | 59.20 | 39.06 | 39.55 | 61.67 | 71.88 | 35.33 | 45.68 | 43.25 | 52.47 | 45.39 | 28.75 | 41.25 |
| G39 | 44.03 | 42.14 | 32.85 | 45.00 | 66.82 | 42.19 | 40.34 | 54.48 | 79.17 | 50.75 | 51.03 | 41.08 | 57.97 | 35.70 | 30.42 | 49.35 |
| G40 | 59.72 | 54.74 | 41.98 | 56.50 | 69.20 | 64.06 | 41.55 | 59.48 | 72.92 | 34.17 | 52.12 | 47.43 | 53.38 | 40.91 | 34.24 | 40.15 |
| G41 | 49.51 | 49.13 | 41.38 | 49.75 | 63.90 | 36.98 | 41.97 | 65.63 | 80.42 | 31.42 | 51.33 | 56.57 | 67.09 | 38.68 | 34.03 | 38.20 |
| G42 | 44.72 | 47.97 | 46.43 | 46.50 | 56.67 | 60.42 | 38.89 | 69.06 | 77.08 | 49.33 | 53.70 | 33.90 | 56.75 | 37.45 | 31.11 | 35.20 |
| G43 | 49.38 | 54.36 | 48.68 | 48.54 | 60.88 | 57.29 | 40.70 | 66.15 | 77.08 | 31.50 | 58.55 | 41.80 | 60.94 | 40.34 | 32.99 | 36.49 |
| G44 | 43.13 | 49.54 | 33.00 | 51.17 | 39.88 | 44.27 | 47.40 | 64.69 | 71.88 | 39.67 | 56.85 | 53.13 | 59.53 | 41.71 | 35.00 | 40.38 |
| G45 | 63.26 | 48.81 | 49.10 | 53.58 | 56.12 | 69.79 | 36.23 | 70.63 | 70.83 | 44.17 | 59.25 | 27.23 | 60.41 | 42.06 | 35.63 | 47.48 |
| G46 | 53.61 | 47.56 | 46.30 | 48.21 | 62.75 | 71.88 | 35.02 | 60.10 | 77.08 | 28.33 | 50.05 | 31.92 | 46.81 | 36.16 | 26.60 | 37.66 |
| G47 | 46.67 | 55.25 | 42.30 | 65.88 | 63.40 | 63.54 | 34.42 | 76.25 | 85.42 | 52.92 | 61.30 | 43.70 | 58.09 | 37.39 | 32.22 | 44.86 |
| G48 | 60.21 | 53.63 | 47.28 | 53.38 | 63.22 | 73.44 | 30.19 | 56.88 | 80.21 | 47.67 | 50.97 | 43.50 | 52.34 | 38.04 | 29.72 | 42.68 |
| G49 | 45.69 | 48.96 | 43.83 | 56.25 | 61.78 | 61.46 | 37.44 | 75.54 | 72.71 | 36.58 | 48.35 | 40.43 | 44.63 | 35.48 | 31.18 | 39.19 |
| G50 | 57.29 | 47.79 | 49.50 | 78.96 | 70.67 | 53.65 | 40.16 | 58.54 | 83.33 | 43.67 | 58.10 | 33.42 | 63.44 | 38.79 | 35.35 | 37.33 |
| Mean | 50.20 | 46.40 | 43.19 | 54.17 | 57.14 | 57.96 | 38.36 | 65.81 | 74.08 | 36.76 | 54.42 | 39.00 | 57.42 | 41.48 | 33.67 | 39.30 |

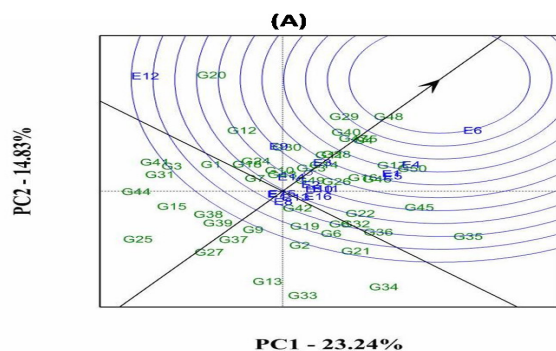


Fig 5 Ranking of genotypes with reference to ideal genotypes

The environmental locations *viz.*, Pantnagar, Vijapur, Hisar and Junagadh had short spikes and hence they do not exert strong interactive forces.

3.5. Stability analysis by GGE model

3.5.1. Discriminating ability and representativeness of environments

According to Yan and Thinker (2006), a long environmental vector had high discriminating ability whereas short vectors had low discrimination. It also identifies the test environment that effectively spots the superior genotypes for mega environments along with its representativeness (Yan *et al.* 2007). The vector length that is the absolute distance between the marker of an environment and the plot origin is a measure of the discriminating ability as the longer vector the discrimination of the environment increases. Therefore, regarding grain yield, test locations Durgapura and Jabalpur were identified as the most discriminating (informative), whereas Pune was least discriminating (Fig.4). The distance between two environments indicates their dissimilarity in discriminating ability among genotypes. If two test locations are consistently highly correlated across the years, one location can be eliminated from the analysis without losing much genotypic information (Farshadfar *et al.* 2013; Rakshit *et al.* 2014). Close relationship between the test environments may be removed from multilocation testing of cultivars as they will generate the similar information. This will help in optimal allocation of the scarce resources during multi-location trial allocation (Rakshit *et al.* 2012). In the bi-plot, the environments (Indore, Karnal, Kota, Pune, Dharwad, Faizabad) have environmental vectors of similar length whereas the environments (Hisar, Delhi, Ludhiana) have environmental vectors of similar length and other have environments vectors of dissimilar length. Thus most of the test environments are highly discriminating for grain yield. The earlier study (Sabaghnia *et al.* 2013) also

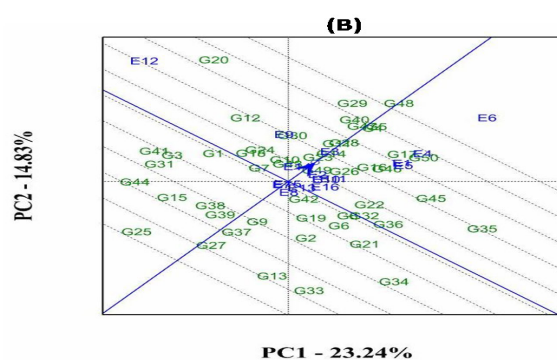


Fig 6 Bi-plot for mean VS stability

reported that the length of locations vector can be used to estimate the standard deviation within each location. Observed mixture of crossover and non-crossover types of GEI in Multi- environment (MET) data is of very common occurrence (Rao *et al.* 2011) and is indicative if existence of mega-environment within the testing locations. Discrimination ability of the location is measured by the length of the environment vectors and in the present study testing locations can be ranked from top to bottom *viz.*, Durgapura > Jabalpur > Hisar > Ludhiana = Delhi > Powarkheda > Pantnagar > Kota = Indore > Vijapur = Karnal > Dharwad = Faizabad > Pune.

3.5.2. Assessment of Ideal environment :

The environment that has both high mean yield and high stability is called an ideal environment. Accordingly environments closer to the ideal environment on the biplot are regarded as more favorable than others (Farshadfar *et al.* 2013). The ideal environment should be most discriminative and more representative of the largest environment. The centre of the concentric circle is an ideal test environment (Fig.4). This is a point on the Average environmental axis (AEA) in the positive direction (more representative), with a distance to the biplot origin equal to the longest vector of all environments (most informative) reported by Yan and Tinker (2006). In the present study, no environment was located at the centre of the AEA therefore no environment is considered absolutely stable (Fig.4), but the Durgapura environment is to be considered a best environment because it is located near the centre of AEA. Moreover, Hisar, Delhi, Ludhiana, Pantnagar, Powarkheda, Indore, Karnal, Dharwad, Jabalpur and Vijapur are located in the above average sector. Whereas Pune, Kota and Faizabad are below average in term of grain yield and were poorest environments for selecting cultivars adapted to the whole region. Therefore, biplot for ideal environment indicated that Durgapura, Hisar, Delhi, Ludhiana, Pantnagar, Powarkheda, Indore, Karnal, Dharwad, Jabalpur and Vijapur were favorable

environments because they located in the above average sector in biplot that can be recommended testing of bread wheat genotypes.

3.5.3. Which-won-where and mega environment identification:

The GGE biplot Which-Won-Where (Fig.4), which is based on a tester-centered (G + GE) table, without any scaling and it is row metric preserving. Several researchers (Yan *et al.* 2000; Yan and Timker, 2006; Rakshit *et al.* 2012; 2014) also reported that the most attractive feature of GGE biplot is which-won-where analysis in which crossover genotype \times environment interactions (GEI), mega-environment differentiation and specific adaptation of genotypes are graphically represented. The polygon (biplot of which-won-where) is formed by joining the markers of the genotypes that are farthest from the biplot origin, such that all other genotypes are placed within polygon and also a set of equality and/or perpendicular lines drawn from biplot origin to each side of the polygon. These equality and/or perpendicular lines divide the polygon into several sectors. All the genotypes in biplot were arranged in such a way that some of them were on the vertex and the rest were inside the polygon. The winning genotype for each sector is the one located at the perspective vertex (Fig.5). The genotype located at the vertices of the polygon revealed the best or the poorest in one or other environment (Yan and Tinker, 2006). These vertex genotypes were the most responsive genotypes because they have the longest distance from the origin of biplot. The responsive genotypes were those having either the best or poorest performance in one or all environments (Yan and Rajcan, 2002) falling within the sectors. In the present investigation, "Which-Won-Where" biplot divided by equality lines into seven (7) sectors with eight genotypes viz., G25, G28, G33, G34, G35, G44, and G48 as the vertex genotypes (Fig.5). All the 16 testing locations were spread in five sectors within the biplot, six in one, three each in two separate and two each in two separate sector and this may be probably due to latitudinal and longitudinal differences. The environments viz., Hisar, Delhi, Ludhiana, Dharwad, Vijapur and Karnal fall in one sector in which G35 was the winning genotype. This means that G35 was the best genotype for these above environments. The environments viz., Kota and Pune fall in the sector in which G33 was the vertex genotype; Pantnagar and Durgapur fall in the sector in which G48 was the vertex genotype; Powarkheda and Indore fall in the sector in which G29 was the vertex genotype and Faizabad fall in the sector in which G25 was the vertex genotype. No environment fall into sectors with G34 and G44 as the vertices, indicating that these genotypes were

not the best in any environments. Similar findings were reported earlier (Rakshit *et al.* 2012; 2014; Singh *et al.* 2019). The present investigation also showed that instead of conducting multi-location trials (MLTs) across closely related locations, near similar conclusion could be drawn from fewer locations clustered within a mega-environment (ME). However, reported grouping of environments need to be reconfirmed using MLTs data over larger years of the data as demonstrated by Casanoves *et al.* (2005). The environments within the same sector share the same winning genotype and environment in different sector share different winning genotypes. The identification of best genotype for each location using which-won-where was earlier reported in dry bean (Mathobo and Marais, 2017).

In light of the cited logical conclusion, it can be concluded that high yielding and stable genotypes efficiently selected based on the three stability parameters bi-plot models (Eberhart and Russell model, GGE and AMMI) using multi-environmental trial (MET) data. All the testing locations showed their suitability to be used for conducting multi-location trials on the basis of their distinctness and representativeness. It was also observed that the genotype which is giving stable performance for one environment not necessarily be stable for yield in other environment. Among the tested materials, G48 ranked best for (Durgapura and Pantnagar); G29 (Powarkheda); G35 (Hisar, Delhi and Ludhiana) based on grain yield among all genotypes. Durgapura was observed as an ideal and representative environment for studying yield stability in bread wheat.

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