Genetic Variability and AMMI Bi-Plot Analysis in Bread Wheat Based on Multi-location Trials Conducted under Drought Conditions across Agro-climatic Zones of India

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Abstract Wheat grown globally under different agro-ecological conditions and drought conditions has emerged as a priority research area for developing genotypes in the near future. In this research, 36 genotypes, including checks (HW 2004, HD 2888, PBW 175 and NI 5439) were tested at 12 locations covering four mega wheat growing zones of India, followed by augmented design under drought conditions, during the crop season 2012/13. The main objective of this research was: to estimate variability parameters and correlation; determining the closeness of experimental sites; and identification of site specific adapted wheat genotypes. Our research findings revealed higher broad-sense heritability for plant height (89-98%) and thousand grain weight (80-93%) in all four zones of India. Herein positive and significant phenotypic correlation was found between thousand grain weight and grain yield; while days to heading, days to maturity and plant height were negatively correlated with grain yield under peninsular zone comparable to other zones. Based upon mean yield across locations, the genotypes MACS 6348 (25 q/ha); HD 3043 and AKAW 4635 (24 q/ha each) were found better than others. AMMI analysis revealed that locations; Kota, Sagar, Indore and Niphad were very close to each other and five genotypes were found to be stable in these locations. The locations; Ranchi, Delhi, Gurdaspur and Pune had also been very close to each other and we have identified seven stable genotypes for these locations. Our findings would be very spectacular for wheat breeders conducting multi-location trials. Herein; the promising genotypes identified for different locations could serve as donors to develop the multi-parent advanced generation integrated cross populations to stack genes/alleles conferring drought tolerance.

Keywords Wheat; MLTs; Heritability; AMMI; Drought; India

Background

Bread wheat is one of the world’s most important cereal crops, serving as the staple food source for nearly 30% of the human population globally. Wheat production during 2000-2008 decreased by 5.5%, primarily owing to climatic changes (Lobell et al., 2011), in last 5-10 years, and worldwide wheat production was not sufficient to meet demand (FAO, 2013). It is predicted that the global population would exceed a billion by 2050, therefore, researchers have a challenge of increasing wheat production by about 70% to meet future demands (Tilmam et al., 2002; Foley et al., 2011). In view of global food security, identification of suitable and efficient plant type for coping with climatic changes is foremost important aspect and to address such issues, there is need of new high yielding wheat varieties; that would display both high intrinsic yield stability under drought stress and have the capacity to adapt to future climatic changes. Developing superior genotypes for complex traits, such as yield under stressed environments encompassing component traits that are often controlled by multiple, small QTLs and/or several epistatic QTLs, are the need of time.

Despite international efforts, progress is still slow and thus wide yield gaps between drought prone areas and ideal production regions for most of the crops including wheat. Previous workers have also reported that tolerance to drought is a complex quantitative trait that involves multiple chromosome regions (Mir et al., 2012). It is further complicated by the fact that the degree of drought effects on plant growth depends on timing, duration and intensity of drought and different traits may be required for different patterns of drought (Passioura, 2012). Genetic gain for grain yield under
drought affected environment is estimated nearly half of the yield under irrigated environments (Rajaram et al., 1996). In addition to poor or erratic rainfall, the wheat growing areas of developing countries, suffer from poor soils, aggressive diseases, and sometimes extreme heat or cold. During green revolution, these areas were not covered, hence moderate yield in these areas (Lantican et al., 2002). By 2020, demand for wheat in marginal environments will be rise 40%, as compared to current levels (Rosegrant et al., 2001), thus the demand is unlikely to be met unless wheat productivity in these environments is increased (Lantican et al., 2002). It is difficult to make progress for yield and yield component traits under drought, because these are complex traits and are highly influenced by environmental factors and are characterized by low heritability and large genotype-by-environment interactions under drought conditions (Smith et al., 1990).

Researchers usually focus on G×E interaction, whenever selecting the genotypes for general adaptation and crossover G×E interaction for the specific adaptation (Matus–Cadiz et al., 2003). Numerous approaches have been proposed to harness G×E interaction, and these include joint regression developed by Finlay and Wilkinson (1963); Eberhart and Russell (1966) and Perkins and Jinks (1968). AMMI developed by Gauch (1992), and genotype main effects and genotype × environment interaction (GEI) developed by Yan et al., (2000). It has always been challenging to define how new genotypes would respond under various climatic conditions, without graphically presenting the data, when many cultivars are evaluated across many sites, seasons and years (Yan et al., 2001). Mainly two types of bi-plots were extensively utilized to visualize G×E interactions, and these are AMMI and GGE bi-plots (Yan et al., 2000). However, applications of two bi-plots in research have been debated by Gauch et al., (2008) and Yang et al., (2009).

Dissimilarities among the two approaches are that GGE bi-plots, analysis can capitalize on location-centered principle component analysis (PCA) while, AMMI analysis is denoted as double-centered principle component analysis. Additive main effects and multiplicative interaction were found suitable to utilize both the main and G×E interaction effects in the MLTs more effective and efficient than any other statistical model. Herein, AMMI bi-plot according to Gauch (2013) is used for understanding complex G×E interactions, inclusive of mega-environment delineation and selecting genotypes to exploit narrow adaptations as well as enhancing accuracy in recommendations, repeatability and genetic gains. In this research, our main focus was on identifying high yielding and stable genotypes for favorites/ adverse locations, so as to use these in breeding programmes. The objectives of this study include; estimation of variability parameters for yield and yield related traits along with correlation; determining the closeness of experimental sites along with site specific adapted wheat genotypes by using AMMI model under drought conditions.

1 Results
1.1 Analysis of variance and mean yield performance
The results of analysis of variance (ANOVA) presented in Table 1 revealed that the mean sum of squares due to entries (including checks); checks; entries (excluding checks); checks versus entries showed significant effect under all the four zones (central, northeastern plains, northwestern plains and peninsular zone) and for all the traits. Researchers are usually interested only in entries (excluding checks), for which high mean sum of squares were found under plain zone for all aforementioned traits. The trend for specific trait was different, as apparent from Table 1, where days to heading had a high mean sum of squares from highest to lowest in the respective zone (PZ > NWPZ > CZ > NEPZ); for days to maturity (CZ > PZ > NWPZ > NEPZ); for plant height (PZ > CZ > NEPZ > NWPZ); for thousand grain weight (PZ > NEPZ > CZ > NWPZ); and for grain yield (PZ > NEPZ > CZ > NWPZ) thereby suggested that zonal variations existed for each trait.

Based on means over the locations for each zone (CZ, NEPZ, NWPZ and PZ) the performance of all 36 genotypes varied and has been presented in Table 2. It is apparent from table that, in central zone, the UAS 324 occupied the first rank with mean yield 30 q/ha, followed by K 0815 and HI 1572 with mean yield 29q/ha that occupied the second rank. The performance of these 36 genotypes differed in the northeastern plains zone, whereas, several genotypes ranked first (AKAW 4635, HD 2888© and MACS...
Table 1 Analysis of variance (ANOVA) for yielding traits of bread wheat tested over four zones of India under drought conditions

| Source of variation       | D.F. | Location | Mean sum of squares |                  |                  |                  |
|---------------------------|------|----------|---------------------|------------------|------------------|------------------|
|                           |      |          | Days to heading     | Days to maturity | Plant height (cm)| Thousand grains weight (g) | Grain yield (q/ha) |
| Total entries             | 35   | CZ       | 36.68**             | 56.06**          | 47.36**          | 13.86**          | 9.33*            |
|                           |      | NEPZ     | 12.67*              | 12.79*           | 35.07**          | 15.13**          | 12.45*           |
| Total entries (including checks) (t) |      | NWPZ     | 52.54**             | 12.20*           | 10.88**          | 14.05**          | 8.74*            |
|                           |      | CZ       | 98.02**             | 32.14**          | 53.13**          | 23.79**          | 11.98*           |
|                           |      | NEPZ     | 18.02**             | 1.40             | 60.24**          | 27.27**          | 13.59*           |
|                           |      | PZ       | 12.67*              | 12.79*           | 35.07**          | 15.13**          | 12.45*           |
| Total checks ©            | 3    | NEPZ     | 9.81*               | 9.44*            | 34.29**          | 13.84*           | 0.81             |
|                           |      | NWPZ     | 11.53*              | 7.15*            | 70.46**          | 36.77**          | 7.34*            |
|                           |      | PZ       | 12.06*              | 0.27             | 6.77*            | 18.71**          | 6.27             |
|                           |      | CZ       | 37.67**             | 34.69**          | 41.26**          | 12.34**          | 8.78*            |
| Total entries (excluding checks) (e) | 31   | NWPZ     | 55.42**             | 12.64*           | 10.53**          | 11.29*           | 8.60*            |
|                           |      | NEPZ     | 11.14*              | 12.53*           | 21.99**          | 15.41**          | 11.01*           |
|                           |      | PZ       | 97.59**             | 33.95**          | 51.71**          | 23.49**          | 13.16**          |
|                           |      | CZ       | 83.38**             | 53.06**          | 66.84**          | 22.89*           | 7.88*            |
| Checks vs entries (c vs e) | 1    | NWPZ     | 66.95**             | 33.31**          | 14.42*           | 12.38*           | 19.23**          |
|                           |      | NEPZ     | 35.98**             | 19.95*           | 53.48**          | 20.26*           | 18.22*           |
|                           |      | PZ       | 53.94**             | 33.95**          | 51.71**          | 23.49**          | 13.16**          |
| Error (er)                | 4    | NEPZ     | 2.95                | 7.95             | 1.98             | 0.53             | 2.05             |
|                           |      | NWPZ     | 2.25                | 2.28             | 5.33             | 1.48             | 0.70             |
|                           |      | PZ       | 5.45                | 4.28             | 0.53             | 0.83             | 0.58             |

*,** Significant at 5 and 1% probability level respectively. DF= Degree of freedom.
| Area of adaptation / Zones | Genotypes (code) | Parentage | Production conditions | CZ | NEPZ | NWPZ | PZ | Across Zones |
|----------------------------|------------------|-----------|----------------------|----|------|------|----|---------------|
|                            |                  |           |                      | M. R.| M. R.| M. R.| M. R.| M. R.         |
| HD 3045 (G1)               | BOW/2°C 306/HW 2004/PBW 175 | IR,TS    |                      | 21  | 10   | 3    | 21  | 23 3          |
| DT 187 (G2)                | TL 2861/HW 2041//TR 125/JNIT 140/JNIT 140 | REF,TS  |                      | 22  | 9    | 16   | 25  | 8    14 8 19 7 |
| UAS 324 (G3)               | BUC/MN72253//PASTOR/3/BABAX | REF,TS   |                      | 30  | 1    | 9    | 30  | 15 7 23 3      |
| UAS 325 (G4)               | MILAN/S87230//BABAX/NI 5439 | REF,TS   |                      | 22  | 9    | 19   | 31  | 2    19 3 23 3 |
| NW 4075 (G5)               | K-9107/Chirya-7   | REF,TS   |                      | 19  | 12   | 21   | 3   | 3    18 4 22 4 |
| WH 1096 (G6)               | PASTOR/MILAN//KAUZ/3/BABAX | IR,TS    |                      | 21  | 10   | 22   | 2   | 5    8 12 10 20 6 |
| K 0815 (G7)                | UP 2003/K 8020    | REF,TS   |                      | 29  | 2    | 20   | 4   | 24   9 15 7 22 4 |
| K 0818 (G8)                | K 8027/K 9465/K 8027/K 9465 | REF,TS   |                      | 24  | 7    | 20   | 4   | 29   4 13 9 21 5 |
| All Zones                  |                  |           |                      |     |      |      |     |               |
| NI AW 1548 (G9)            | VORONA/CNO79//KAUZ/3/MILAN | REF,TS   |                      | 26  | 5    | 22   | 2   | 26   7 17 5 23 3 |
| UP 2767 (G10)              | UP 2382/VL 721   | REF,TS   |                      | 22  | 9    | 20   | 4   | 25   8 13 9 20 6 |
| UP 2768 (G11)              | UP 2523/LFN/IS8.57//PRL/3/HAHN | REF,TS |                      | 21  | 10   | 20   | 4   | 26   7 15 7 20 6 |
| MP 1228 (G12)              | MP 1053/HDR199/CPAN4117/HW2004 | REF,TS |                      | 25  | 6    | 17   | 7   | 23   10 17 5 21 5 |
| MP 1229 (G13)              | HW2033/HD1999/CPAN4177/HW2004 | REF,TS |                      | 24  | 7    | 20   | 4   | 33   1 12 10 22 4 |
| MACS 6530 (G14)            | Selections from RS 943 | REF,TS   |                      | 25  | 6    | 20   | 4   | 27   6 20 2 23 3 |
| RW 3682 (G15)              | BL 1961/NL 867   | REF,TS   |                      | 28  | 3    | 22   | 2   | 27   6 17 5 23 3 |
| HWU 639 (G16)              | ATTL//HW 2045//UP 2425 | REF,TS |                      | 23  | 8    | 21   | 3   | 25   8 13 9 20 6 |
| JSW 183 (G17)              | HP 1731/HW 2004  | REF,TS   |                      | 24  | 7    | 16   | 8   | 25   8 19 3 21 5 |
| HI 1572 (G18)              | SKAUZ/2/FCT      | REF,TS   |                      | 29  | 2    | 13   | 9   | 26   7 21 1 22 4 |
| MP 1230 (G19)              | HW2004/HBWN166/GW190/HW2023/HDR199 | REF,TS |                      | 26  | 5    | 17   | 7   | 27   6 17 5 22 4 |
| HW 2004 (G20)              | C 306*7/TR 380-14*7/3AG14 | REF,TS |                      | 28  | 3    | 21   | 3   | 23   10 20 2 23 3 |
| AKAW 4635 (G21)            | PASTOR/DHARWAR DAY | REF,TS |                      | 26  | 5    | 25   | 1   | 27   6 19 3 24 2 |
| North Eastern Plain Zone   |                  |           |                      |     |      |      |     |               |
| (NEPZ)                     |                  |           |                      |     |      |      |     |               |
| HP 1927 (G22)              | RL 6043/RAJ 3765/HUW 516 | REF,TS |                      | 26  | 5    | 18   | 6   | 31   2 15 7 22 4 |
| HD 2888® (G23)             | C306/T. sphaerococcum/HW 2004 | REF,TS |                      | 20  | 11   | 25   | 1   | 26   7 18 4 22 4 |
| Northern Hills Zone (NHZ)   |                  |           |                      |     |      |      |     |               |
| TL 2968 (G24)              | TL 2702/TL 2421 | REF,TS |                      | 20  | 11   | 17   | 7   | 28   5 16 6 20 6 |
| Northern West Plain Zone    |                  |           |                      |     |      |      |     |               |
| (NWPZ)                     |                  |           |                      |     |      |      |     |               |
| HD 3043 (G25)              | PJJN/BOW/OPATA2/3/CROC1/Ae.squarrosa(224)//opata | IR,TS |                      | 23  | 8    | 21   | 3   | 33   1 18 4 24 2 |
| HD 3044 (G26)              | C 306/PBW 175/2/PBW 175 | REF,TS |                      | 26  | 5    | 20   | 4   | 30   3 17 5 23 3 |
| Peninsular Zone (PZ)        |                  |           |                      |     |      |      |     |               |
| K 0817 (G32)               | K 8027/HUW 533   | REF,TS   |                      | 24  | 7    | 20   | 4   | 22   11 17 5 20 6 |
| NI AW 1549 (G33)           | KAUZ/2/CHEN/BCN/MILAN | REF,TS |                      | 26  | 5    | 21   | 3   | 24   9 19 3 20 6 |
| MP 1227 (G34)              | Hy 11/HW 2010//NI 5439/CPAN 1220/PBW 168 | REF,TS |                      | 25  | 6    | 16   | 8   | 25   8 21 1 22 4 |
| MACS 6348 (G35)            | Selections from RS 940 | REF,TS |                      | 26  | 5    | 25   | 1   | 31   2 18 4 25 1 |
| NI 5439® (G36)             | NI 8883/MP 1055  | REF,TS   |                      | 23  | 8    | 16   | 8   | 21   19 3 22 4 |

Where, IR= Irrigated, RF= Rainfed, TS= Timely Sown; M= Mean yield (quintals/hectare) and R= Ranking of the genotype.
6348) with mean grain yield performance of 25 q/ha. Similarly, second rank genotypes were, WH 1096, NIAW 1598, RW 3682, PBW 175© and K 0817; as all these genotypes had mean yield performance of 22 q/ha. The ranking pattern under NWPZ was different as there were two first ranking genotypes (MP 1229 and HD 3043) with mean yield of 33 q/ha; and three genotypes (UAS 325, HP 1927, MACS 6348) were second ranking with mean yield of 31 q/ha. Top ranking genotypes under peninsular zone also differed, as first ranking genotypes were (HD 3045, HI 1572 and MP 1227) with mean yield of 21 q/ha; whilst second ranking genotypes included (MACS 6350, HW 2004 © and PBW 644) with mean yield performance of 20 q/ha.

1.2 Genetic variability and phenotypic correlation

The results revealed that genotypic variability was moderate to high for all the traits that promoted us for further analysis. The mean performance based on three centers in each zone and range for all of each trait is presented in Table 3. It is apparent from Table 3, that wide range were found for all the traits under all studied zones. For days to heading lowest range (12 days) found in the northeastern plain zone with mean of 81 days, and highest range were observed under peninsular zone (34 days) with a mean value of 60 days. Days to maturity also have a wide range of variation as central zone with the lowest range (11 days) and with mean of 146 days, while highest range (25 days) found in peninsular zone with mean value of 98 days. Plant height exhibited lowest range of 17 cm in case of northeastern plain zone with mean 81 cm, and highest range (48 cm) for this trait were found in central zone with mean 85 cm. The thousand grains weight and grain yield didn’t have much variation in range as well as for mean in all zones. It explained that studied genotypes have wide range of variation for flowering, maturity and plant height under all four zones while thousand grain weight and grain yield have less variation and hence these two traits less influenced by location effects.

As expected, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation for all the traits, thereby indicating that expression of the traits was highly influenced by the environmental effects (Table 3). Highest estimates of PCV and GCV were observed for days to heading (11.42 and 10.76%) in peninsular zone; for days to maturity (6.54 and 6.43%) in central zone; for plant height (9.68 and 9.39%) also in central zone; for thousand grains weight (10.50 and 10.12%) in peninsular zone; and for grain yield highest phenotypic coefficient of variation (12.56%) and genotypic coefficient of variation (11.94%) was estimated in peninsular zone. Over the zones, higher genotypic coefficient of variation was observed for days to heading (with range of 2.60-10.76%) and moderate for thousand grains weight (5.70-10.12%) and for grain yield (6.82-11.94%). Higher PCV and GCV indicated that the visible variation in the expression of traits was not only due to genotypes alone, but also due to the varying influence of the environment (Table 3).

The phenotypic correlation coefficients of days to heading, days to maturity, plant height and 1000-grain weight with grain yield under all four zones is presented in Table 3. If the association is positive, improvement in one character will simultaneously bring about an improvement in another. However, the negative association with grain yield is useful for plant height, maturity duration and days to heading, where a genotype with shorter height and early duration will be advantageous under drought conditions. The positive and significant correlation was found between thousand grains weight and grain yield under northeastern plain zone (0.37*) and peninsular zone (0.41*), while other three traits showed negative and significant correlation with grain yield. Days to heading showed negative correlation under central zone (−0.48**) and peninsular zone (−0.58**); days to maturity under northwestern plains zone (−0.43**) and peninsular zone (−0.44**); and similarly plant height exhibited significant, but a negative correlation with grain yield under peninsular zone (−0.36*) thus indicating that early maturing with shorter height genotypes having better yielding ability under worst drought conditions.

It is apparent from Table 3, that thousand grains weight was positively correlated with grain yield; hence selection based on higher seed weight might lead to better yield under drought conditions. Days to heading and days to maturity that were negatively correlated with grain yield, indicated that under stressed environments, early heading and early maturity might
Table 3 Estimates of range, mean, variability, heritability, genetic advance as a percentage of mean for yielding traits and phenotypic correlation with grain yield

| Traits                       | Locations | Estimates | R<sub>gy</sub> |
|------------------------------|-----------|-----------|--------------|
|                              |           | Range     | Mean | PCV | GCV | h<sup>2</sup><sub>b</sub>(%) | GA |          |
| Days to heading              | CZ        | 26         | 74   | 5.75 | 5.33 | 86         | 10.31 | – 0.48** |
|                              | NEPZ      | 12         | 81   | 3.34 | 2.60 | 60         | 14.20 | – 0.10   |
|                              | NWPZ      | 24         | 92   | 5.46 | 5.22 | 91         | 20.40 | – 0.12   |
|                              | PZ        | 34         | 60   | 11.42| 10.76| 89         | 21.35 | – 0.58** |
|                              | CZ        | 11         | 146  | 6.54 | 6.53 | 98         | 19.44 | – 0.27   |
|                              | NEPZ      | 15         | 123  | 2.57 | 1.96 | 61         | 11.09 | – 0.16   |
|                              | NWPZ      | 12         | 144  | 1.82 | 1.49 | 67         | 12.51 | – 0.43** |
|                              | PZ        | 25         | 98   | 4.20 | 3.65 | 75         | 9.58  | – 0.44** |
|                              | CZ        | 48         | 85   | 9.68 | 9.39 | 94         | 19.31 | – 0.24   |
|                              | NEPZ      | 17         | 81   | 5.16 | 4.86 | 89         | 19.44 | – 0.18   |
|                              | NWPZ      | 38         | 92   | 7.80 | 7.39 | 90         | 14.59 | – 0.20   |
|                              | PZ        | 32         | 66   | 7.44 | 7.36 | 98         | 15.38 | – 0.36*  |
|                              | CZ        | 11         | 43   | 6.07 | 5.72 | 89         | 11.06 | 0.15     |
|                              | NEPZ      | 16         | 43   | 6.22 | 6.00 | 93         | 11.98 | 0.37*    |
| Plant height (cm)            | NWPZ      | 12         | 42   | 6.38 | 5.70 | 80         | 10.52 | 0.21     |
|                              | PZ        | 15         | 33   | 10.50| 10.12| 93         | 19.76 | 0.41*    |
|                              | CZ        | 11         | 23   | 8.96 | 8.39 | 88         | 16.33 | -        |
| Thousand grains weight (g)   | NWPZ      | 12         | 19   | 12.23| 10.09| 70         | 9.94  | -        |
|                              | PZ        | 10         | 28   | 7.43 | 6.82 | 84         | 12.74 | -        |
| Grain yield (q/ha)           | NEPZ      | 13         | 19   | 12.56| 11.94| 90         | 23.50 | -        |

Note: Where, h<sup>2</sup><sub>b</sub> = Heritability in broad sense, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, GA = Genetic advance as per cent of mean, Range = (Highest – Lowest), R<sub>gy</sub> = Phenotypic correlation with grain yield, *, ** Significant at 5 and 1% probability level respectively.
lead to yield improvement, similarly, plant height was also negatively correlated with grain yield and therefore, dwarf genotypes might be gave higher yield under drought conditions.

1.3 Stability analysis by AMMI model
Bi-plot analysis is the most powerful interpretive tool for AMMI models. In this study, AMMI bi-plot for studying the stability of 36 genotypes (G1 to G36) tested at 12 (L1 to L12) locations of India under drought environmental conditions were followed. The mean grain yield values of each genotype across locations presented in Table 2 indicated that the genotypes MACS 6348 with 25 q/ha; HD 3043 and AKAW 4635 with 24q/ha had highest yield potential, while DT 187 with 19q/ha had lower yield potential. The results of AMMI bi-plot (Figure 1) indicate that the locations, scores are joined to the origin by side lines. The locations with short spokes (L11: Dharwad and L7: Ludhiana) don’t exert strong interactive forces. Whereas, locations (L3: Indore and L8: Delhi) with long spokes exert strong interaction among each other.

Figure 1 Additive main effects and multiplicative interaction bi-plot for environment scaling using 36 wheat genotypes (including checks) for grain yield tested at three different centers each from central zone, northeastern plain zone, northwestern plain zone and peninsular zone under drought conditions
An example of this is shown in Figure 1, where the points representing the locations (L1 to L12) are connected to the origin. The locations L11 (Dharwad) and L7 (Ludhiana) had short spokes and hence they don’t exert strong interactive forces. The genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes moving far apart may either differ in mean yield or show a different pattern of response over the locations. Hence, the genotypes near origin are not sensitive to genotype × location interactions; those distant from the origins are more sensitive and exhibited large genotype × location interactions.

In the present study, G20 (HW 2004); G3 (UAS 324); G29 (PBW 175); G25 (HD 3043); G24 (TL 2968); G17 (JSW 133) and G34 (MP 127) were more responsive, owing to be away from the origin. Whereas, the genotypes namely G14 (MACS 6350); G8 (K 0818); G9 (NIAW 1548) and G 22 (HP 1927) were close to the origin and thus were non-sensitive to environmental interactive forces.

It is apparent from Figure 1, that location spokes that are close to each other show highly correlated response. Whereas, genotypes which are close to the spokes of locations, exhibited highly stable performance for these locations. Based on this idea, the locations L1 (Kota); L2 (Sagar); L3 (Indore) and L10 (Niphad) were very close to each other and genotypes close to these locations were G7 (K 0815); G19 (MP 1230); G31 (MP 3299); G14 (MACS 6350) and G3 (UAS 324). Similarly, locations L6 (Ranchi), L8 (Delhi), L9 (Gurdaspur) and L12 (Pune) were correlated to each other and stable performing genotypes for these locations included; G8 (K0818); G9 (NIAW 1548); G26 (HD 3044); G15 (RW 3682); G1 (HD 3045); G29 (PBW 175) and G25 (HD 3043). Other locations that were very diverse are: L5 (Kanpur) and stable genotype was G36 (NI 5439); for L4 (Sabour) the genotypes were G23 (HD 2888) and G6 (WH 1096); for L7 (Ludhiana) genotype G22 (HP 1927); and for location L11 (Dharwad) the genotype G30 (WH 1095) exhibited stable performance for grain yield under drought conditions.

2 Discussion

Highest broad-sense heritability was estimated for plant height, thousand grain weight coupled with moderate genetic advances in all four zones of India. For plant height, the heritability was in the range of 89-98% with 14-19% genetic advance; whereas, for thousand grains weight broad-sense heritability (80-93%) with genetic advance of (10-19%) was estimated. The moderate values of heritability and genetic advance were observed for days to heading (60-91% and 10-21%); and days to maturity (61-98% and 9-19%) in all four zones of India (Table 3).

High broad-sense heritability coupled with moderate genetic advance and high genotypic coefficient of variation was observed for plant height in all zones of India; hence it showed good scope for improvement by selecting this trait (Table 3). However, other traits as grain weight, heading days and maturity days exhibited moderate heritability with low genetic advance, which may be due to non-additive gene action and presence of lower genotype and environment interaction, therefore, in such cases simple selection may not be rewarding and planned hybridization followed by selecting desirable transgressive segregants will be advantageous option.

Similar to our findings, high heritability for plant height, days to heading, thousand grains weight, and spike length was reported by Singh et al., (2014). The high heritability coupled with high genetic advance for plant height and thousand grains weight was reported by Ranjana and Suresh (2013). High estimates of broad-sense heritability (>80%) were recorded in parents and F1s populations for tillers, plant height, thousand grain weight and grain yield (Singh et al., 2013). Higher estimates of heritability for grain yield also reported by earlier researchers and indicated that significant genotype by environment interactions exist under drought conditions (McIntyre et al., 2010). The heritability (>75%) for days to heading, thousand grain weight, harvest index under irrigated, rain-fed and drought conditions was also reported by (Dodig et al., 2012). The moderate values of broad-sense heritability estimated for grain yield (45%) under drought conditions have been reported (Abdolshahi et al., 2015).

The correlation coefficients for grain yield, implying that improving one or more of the traits could result in higher grain yield in case of durum wheat was reported by Yagdi and Sozen (2009), while plant...
height showed significant and positive association with grain yield (Singh et al., 2010). The significant and positive correlation of number of tillers and 1000-grain weight with grain yield was reported by Singh et al., (2014). Grain yield was also found significantly and positively correlated with tillers, biological yield, harvest index and thousand grains weight (Arya et al., 2013).

In this research, the genotype × location interaction was analyzed with the aid of the AMMI model for grain yield stability and also similar study was conducted earlier (Ramburn et al., 2011). An AMMI bi-plot, which hinges on environment focused scaling, was depicted to assess the pattern of environments. The environment principle component 1 had both positive and negative scores, as also reported by Yang et al., (2009). The environment principle component 2 had both positive and negative scores, and this leads to disproportionate genotypic yield differences across locations. We have found total seven genotypes (HW 2004, UAS 324, PBW 175, HD 3043, TL 2968, JSW 133 and MP 127) that were better responsive and four genotypes (MACS 6350, K 0818, NIAW 1548 and HP 1927) were non-sensitive to the location interaction.

It was surprising that all the locations in the present study were positively correlated because the angles among them were less than 90°, and similar results were also reported earlier (Kaya et al., 2006). In a situation where the same trait is measured on the same genotypes under different locations, indirect selection could be practiced based on stability patterns. The highest estimates of correlation between test locations suggest that indirect selection for the grain yield might be applied across the testing sites. For instances the higher yielding genotypes at the Kota location may also perform similar at the Sagar, Indore and Niphad; similar to this higher yielding genotypes at the Ranchi location that also exhibited good performance at the other three locations as Delhi, Gurdaspur and Pune.

The estimates of significant correlation between locations indicated that there is a possibility of reducing testing sites without significantly affecting the validity of the data. An environment that is more representative of other testing environment is the one with a smaller angle with the average environment axis (Yan and Tinker, 2006). The L1 (Kota) was the most representative followed by L7 (Ludhiana), whilst L3 (Indore) and L8 (Delhi) was the least representative. The locations are both discriminating and representative such as L7 (Ludhiana), might be used for selecting generally adapted genotypes and the discriminating and non-representative locations such as L3 (Indore) and L8 (Delhi) could be useful for selecting specific adapted genotypes, if the target locations are grouped into mega locations. Also, the discriminating and non-representative locations might be used for discarding unstable genotypes, if the target location is a single mega environment. The results similar to this study were also reported by Thokozile et al., (2014). In order to meet the demand of food for the faster growing population, faster breeding programme with precision phenotyping over locations and harnessing the potential benefits of MAS in wheat are essential aspects to characterize traits under specific situations i.e. drought conditions. Multi-location trials and making use of the next generation genomic approach for untapped genetic variation in wheat for developing genotypes suited to the drought conditions might be useful. Besides this there is a requirement to develop multi-parent advanced generation intercross population (MAGIC) by using aforementioned genotypes might perform better under drought conditions, across locations. Moreover, these next generation populations can also be used for scanning the genomic region for drought tolerance. The work on developing MAGIC populations in wheat have been already initiated and are underway for field testing (Huang et al., 2012; Mackey et al., 2014).

3 Material and Methods
3.1 Field materials and experimentation sites
We selected a set of 36 diverse genotypes, including four standard checks used in India, particularly for drought conditions (HW 2004, HD 2888, PBW 175 and NI 5439) ensuring that the test material has diverse adaptability across zones or for a specific zone; and suited for two production conditions (irrigated timely sown and rainfed timely sown). The passport data of all the test genotypes along with parentage, production conditions, area of adaptations, mean yields over the locations and also ranking are presented in Table 2. For conducting this study, twelve locations were identified, representing all four zones.
Table 4: Meteorological and agro-climatic conditions of the tested locations

| Zone | State       | Location (code) | Longitude | Latitude  | Altitude (m) | Soil type                        | Temperature °C (Min- Max), during growing period | % Humidity (Min- Max), during growing period |
|------|-------------|-----------------|-----------|-----------|--------------|----------------------------------|-----------------------------------------------|-----------------------------------------------|
| CZ   | RAJASTHAN   | KOTA (L1)       | 75° 50'E  | 25° 80'N  | 279          | Clay loam                        | 10-42                                         | 19-74                                         |
|      | MADHYA PRADESH | SAGAR (L2)    | 78° 71'E  | 23° 83'N  | 587          | Black soil                       | 11-37                                         | 25-49                                         |
|      | MADHYA PRADESH | INDORE (L3)   | 75° 50'E  | 22° 43'N  | 537          | Medium black soil                | 8-38                                          | 23-54                                         |
| NEPZ | BIHAR       | SABOUR (L4)    | 74° 06'E  | 32° 80'N  | 60           | Sandy soil                       | 15-34                                         | 38-95                                         |
|      | UTTAR PRADESH | KANPUR (L5)   | 80° 33'E  | 26° 46'N  | 123          | Moderately saline and sodic      | 7-38                                          | 45-71                                         |
|      | JHARKHAND  | RANCHI (L6)    | 85° 33'E  | 23° 35'N  | 644          | Red gravelly and sandy           | 9-35                                          | 36-63                                         |
| NWPZ | PUNJAB       | LUDHIANA (L7)  | 75° 85'E  | 30° 88'N  | 239          | Sandy Loam                      | 2-30                                          | 44-74                                         |
|      | DELHI        | DELHI (L8)     | 77° 23'E  | 28° 60'N  | 212          | Peaty and Marshy                 | 7-36                                          | 26-90                                         |
|      | PUNJAB       | GURDASPUR(L9)  | 75° 25'E  | 31° 91'N  | 237          | Reddish loamy                   | 19-44                                         | 40-76                                         |
| PZ   | MAHARASHTRA  | NIPHAD (L10)   | 73° 80'E  | 20° 08'N  | 560          | Black soil                      | 10-33                                         | 36-60                                         |
|      | KARNATAKA   | DHARWAD (L11)  | 75° 08'E  | 15° 35'N  | 660          | Red sandy, Sandy loam            | 15-36                                         | 55-75                                         |
|      | MAHARASHTRA  | PUNE (L12)     | 73° 85'E  | 18° 52'N  | 552          | Lateritic Soil                  | 11-36                                         | 36-58                                         |

Note: Where, CZ= Central zone; NEPZ= North eastern plain zone; NWPZ= North western plain zone; PZ=Peninsular zone
of India (CZ, NEPZ, NWPZ and PZ) based on latitude, longitude, altitude, soil types, temperature and relative humidity. These twelve locations covered nine wheat growing states of India such as, Madhya Pradesh (Sagar and Indore); Maharashtra (Niphad and Pune); Punjab (Ludhiana and Gurdaspur); Delhi (Delhi); Uttar Pradesh (Kanpur); Bihar (Sabour); Rajasthan (Kota); Jharkhand (Ranchi); Karnataka (Dharwad) also possessing a wide range of environments as locations. Salient features of all the locations/sites are presented in Table 4, and it is apparent from the table, that all the locations represented a wide range of variation for the environments.

3.2 Experimental design and data collection
For this research, we planted 32 genotypes following augmented design having four checks (HW 2004, HD 2888, PBW 175 and NI5489) in six-row plots of 6.0 m length with 23 cm row to row spacing and 10 cm spacing between plants and within a row. There were four blocks at each site, comprising of 4 checks along with 8 test genotypes; and same set of checks was replicated in each block following separate randomization plan for each site. Recommended agricultural practices were followed to raise good crop and fully genotypic expression.

Data were recorded on five important metric traits, namely: days to heading (days), days to maturity (days), plant height (cm), thousand grains weight (g) and grain yield (q/ha). Days to heading and maturity were recorded on the plot basis counting number of days from sowing until 50% of the spikes (heading) in each plant had completely emerged above the flag leaves. While, days to maturity was recorded as the number of days from planting until 50% of the peduncles in each plot had turned yellowish (physiological maturity). The plant height was recorded as the average of twenty values of individual random plant measured in centimeter from the soil surface to the tip of the spike excluding awns. The grain yield was recorded as the total weight of seed yield from each plot divided by the plot area and expressed as q/ha; similarly, thousand grains weight was taken based on random sample drawn from each plot yield where thousand seeds were counted with the help of seed counter and weighed through electronic weighing balance. There was a similar pattern of phenotyping were followed for all the other phenological traits across the locations.

3.3 Statistical analyses
The adjusted mean values were subjected to analysis of variance to test the level of significance. Analysis of variance (ANOVA) for estimating phenotypic and genotypic coefficients of variation, heritability, genetic advance as per cent of mean for all the five traits, and phenotypic correlation with grain yield was performed as per latest available software (SAS, 2011). The AMMI analysis was computed using the same mean values to assess relationships among genotypes, locations and G×E interaction [AMMI model as described by Zobel et al., (1988), Gauch and Zobel (1988), and Crossa (1990)]. This analysis uses principal component analysis (PCA) to decompose the multiplicative effects (G × E) interaction into a number of interaction principal components axes (IPCA). The AMMI analysis was performed using IRRI-STAT software (ver. 5.0) developed by the International Rice Research Institute (IRRI).

Authors’ contributions
Dr. Bhudev Singh Tyagi, supervise all the activities for this research work and Dr. Muneendra Kumar Singh, is the corresponding author of this research article and he developed the idea that how to write article from trial data sets. Dr. Gyanendra Singh, helps in editing and improving the quality of this article. Dr. Rajendra Kumar, have a main role for collecting meteorological data from different locations. Dr. Ajay Verma, was mainly involved in analyzing the multi-location data. Dr. Indu Sharma, is the director of this institute and she gave the permission to write the research article by using trial data.

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References
Abdolshahi R., Nazari M., Safarian A., Sadat-hosssini T.S., Salarpour M. and Amiri H., 2015, Integrated selection criteria for drought tolerance in wheat (Triticum aestivum L.) breeding programs using discriminant analysis. Field Crops Research, 174: 20-29
http://dx.doi.org/10.1016/j.fcr.2015.01.009

Arya S., Mishra D.K. and Bornare S.S., 2013, Screening genetic variability in advance lines for drought tolerance of bread wheat (Triticum aestivum L.). The Bioscan, 8(4):1193-1196

Crosa J., 1990, Statistical analysis of multi-location trials. Advances in
Agronomy, 44:55-85
http://dx.doi.org/10.1016/S0004-2898(88)80916-8

Dodig D., Zoric M., Kobiljski B., Savic J., Kandic V., Quarrie S. and Barnes J., 2012, Genetic and association mapping study of wheat agronomic traits under contrasting water regimes. International Journal of Molecular Sciences, 13:6167-6188
http://dx.doi.org/10.3390/ijms13051617

Eberhart S.A. and Russell W.A., 1966, Stability parameters for comparing cultivars. Crop Science, 6:36-40
http://dx.doi.org/10.2135/cropsciresearch1966.001183X000600010011x

FAO 2013, Food and Agriculture Organization (FAO) of the United Nations, FAO cereal supply and demand brief.

Finlay K.W. and Wilkinson G.N., 1963, The analysis of adaptation in a plant breeding programme. Australian Journal of Agricultural Research, 14:742-754
http://dx.doi.org/10.1071/AR9630742

Foley J.A., Ramankutty N., Brauman K.A., Cassidy E.S., Gerber J.S.,FS., Suryanarayanan R., Haddad L., Howe P.J., Osmond C.B., Rosswall T., Ruane A.K., Schmid huber.ca
http://dx.doi.org/10.1038/nature10452

Gauch H.G., 1992, Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, Netherlands. p. 278.

Gauch H.G., 2013, A simple protocol for AMMI analysis of yield trials. Crop Science, 53:1860-1869
http://dx.doi.org/10.2135/cropsciresearch2013.04.0241

Gauch H.G., Piepho H.P. and Annicchiarico P., 2008, Statistical analysis of yield trials by AMMI and GGE: Further considerations. Crop Science, 48:866-889
http://dx.doi.org/10.2135/cropsciresearch2007.09.0513

Gauch H.G. and Zobel R.W., 1988, Predictive and postdictive success of statistical analyses of yield trials. Theoretical and Applied Genetics, 76:1-10
http://dx.doi.org/10.1007/BF00288824

Huang B.E., George A.W., Forrest K.L., Kilian A., Hayden M.J., Morell M.K. and Cavanagh C.R., 2012, A multi-parent advanced generation inter-cross population for genetic analysis in wheat. Plant Biotechnology Journal, 10:826-839
http://dx.doi.org/10.1111/j.1467-7652.2012.00702.x

Kaya Y., Akcura M. and Taner S., 2006, GGE biplot analysis of multi-environment yield trials in bread wheat. Turkish Journal of Agriculture, 30:325-337

Lanican M.A., Pangali P.L. and Rajaram S., 2002, Are marginal environments catching up? In: Ekboir J (ed) CIMMYT world wheat overview and outlook 2000-2001. Developing no-till packages for small-scale farmers. CIMMYT, Mexico, DF.

lobell D.B., Schlenker W., and Costa-Roberts J., 2011, Climate trends and global crop production since 1980. Science, 333:616-620
http://dx.doi.org/10.1126/science.1204531

Mackay I.J., Bansept-Blaser P., Barber T., Bentley A.R., Cockram J., Gosman N., Greenland A.J., Horsnell R., Howells R., O'Sullivan D.M., Rose G.A. and Howell P.J., 2014, An eight-parent multi-parent advanced generation inter-cross population for winter-sown wheat: creation, properties and validation. G3, 4:1603-1610
http://dx.doi.org/10.1534/g3.114.012963

Matus-Cadiz M.A., Huc P., Peron C.E. and Tyler R.T., 2003, Genotype x environment interaction for grain color in hard white spring wheat. Crop Science, 43:219-226
http://dx.doi.org/10.2135/cropsciresearch2003.2190

McIntyre C.L., Mathews K.L., Rattey A., Chapman S.C., Drenth J., Ghaderi M., Reynolds M. and Shorter R., 2010, Molecular detection of genomic regions associated with grain yield and yield-related components in an elite bread wheat cross evaluated under irrigated and rain-fed conditions. Theoretical and Applied Genetics, 120:527-541
http://dx.doi.org/10.1007/s00122-009-1173-4

Mir R., Zaman-Allah M., Sreevatsulvi N., Trethowan R. and Varshney R., 2012, Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. Theoretical and Applied Genetics, 125:625-645
http://dx.doi.org/10.1007/s00122-012-1904-9

Passiourea J.B., 2012. Phenotyping for drought tolerance in grain crops: when is it useful to breeders? Functional Plant Biology, 39:851-859
http://dx.doi.org/10.1071/FP12079

Perkins J.M., and Jinks J.L., 1968, Environmental and genotype-environmental interactions and physical measures of the environment. Heredity, 25:29-40
http://dx.doi.org/10.1038/hdy.1970.4

Rajaram S., Braun H.F. and Ginkel VM., 1996, CIMMYT's approach to breed for drought tolerance. Euphytica, 92-175
http://dx.doi.org/10.1007/BF00022840

Ramburan S., Zhou M. and Labuschagne M., 2011, Interpretation of genotype × environment interactions of sugarcane: Identifying significant environmental factors. Field Crops Research, 124:392-399
http://dx.doi.org/10.1016/j.fcr.2011.07.008

Ranjan and Suresh K., 2013, Study of genetic variability and heritability over extended dates of sowing in bread wheat (Triticum aestivum L.). Research in Plant Biology, 3:33-36

Rosegrant M.W., Paisner M.S., Meijer S. and Witcover J., 2001, Global food projections to 2020: emerging trends and alternative futures. International food policy research institute (IFPRI), Washington, DC.

SAS Institute Inc. 2011. Base SAS® 9.3 Procedures Guide. Cary, NC: SAS Institute Inc.

Singh B.N., Vishwakarma S.R. and Singh V.K., 2010, Character association and path analysis in elite lines of wheat (Triticum aestivum L.). Plant Archives, 10(2): 845-847

Singh G., Kulsheerthna N., Singh B.N., Setter T.L., Singh M.K., Saharan M.S., Tyagi B.S., Verma A. and Sharma I., 2014, Germplasm characterization, association and clustering for salinity and waterlogging tolerance in bread wheat (Triticum aestivum). Indian Journal of Agricultural Sciences, 84 (9):1102-1110

Singh M.K., Sharma PK., Tyagi B.S. and Singh G., 2013, Genetic analysis for morphological traits and protein content in bread wheat (Triticum aestivum L.) under normal and heat stress environments. Indian Journal of Genetics and Plant Breeding, 73(3):320-324
http://dx.doi.org/10.3956/j.0975-6006.73.3.047

Smith M.E., Coffman W.R. and Baker T.C., 1990, Environmental effects on selection under high and low-input conditions. In: Kang MS (ed) Genotype-by-environment interaction and plant breeding. Louisiana State University, Baton Rouge, LA, USA, 261-272.

Thokozile N., Liezel H., Cosmo M., Peter S., Charles M. and Maryke L., 2014, Genotype x Environment interaction of maize grain yield using AMMI-bi-plots. Crop Science, 54:1992-1999
http://dx.doi.org/10.2135/cropsciresearch2013.07.0448

Tilman D., Cassman K.G., Matson P.A., Naylor R. and Polasky S., 2002, Agricultural sustainability and intensive production practices. Nature, 418:671-677
http://dx.doi.org/10.1038/nature01014

Yagdi K. and Sozen E., 2009, Heritability, variance components and correlations of yield and quality traits in durum wheat (Triticum durum Desf.). Pakistan Journal of Botany, 41(2): 753-759

Yan W., Cornelius P.L., Cross J. and Hunt H.L., 2001, Two types of GGE
biplot for analyzing multi-environment trial data. Crop Science, 41:656-663
http://dx.doi.org/10.2135/cropsci2001.413656x
Yan W., Hunt L.A., Sheng Q. and Szlavnics Z., 2000, Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science, 40:597-605
http://dx.doi.org/10.2135/cropsci2000.403597x
Yan W. and Tinker N.A., 2006, Biplot analysis of multi-environment trial data: Principles and applications. Canadian Journal of Plant Science, 86:623-645
http://dx.doi.org/10.4141/P05-169
Yang R.C., Crossa J., Cornelius P.L. and Burgueno J., 2009, Biplot analysis of genotype × environment interaction: Proceed with caution, Crop Science, 49:1564-1576
http://dx.doi.org/10.2135/cropsci2008.11.0665
Zobel R.W., Wright M.G. and Gauch H.G., 1988, Statistical analysis of yield trial. Agronomy Journal, 80:388-393
http://dx.doi.org/10.2134/agronj1988.0002196200800030002x