Analytic Measures of Adaptability for Wheat Genotypes Evaluated under Restricted Irrigation Timely Sown Conditions for Central Zone of India

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ABSTRACT

Background: Wheat improvement program of the country identify genotypes with specific and general adaptations to ensure sustain yield for food security of the people. Yield behavior of promising wheat genotypes were studied at twelve locations of Central Zone of the country under restricted irrigation timely sown conditions.

Methods: Recent analytic measures of adaptability viz., Relative Performance of Genetic Values (PRVG), Harmonic Mean of Genetic Values (MHVG) and Harmonic Mean of the Relative Performance of Genotypes (MHPRVG) were compared by considering Best Linear Unbiased Predictors (BLUP) of genotypes based on mixed model approach.

Result: Genotypes MP3288, BRW3775 and DBW110 had been marked by analytic measures PRVG, MHVG, MHPRVG, HM for high yield and better adaptability across locations as per first year (2016-17) findings. HI8791 and DBW110 genotypes occupied places near to the origin in Biplot graphical analysis. Specific adaptations of genotype HI8791 for Sagar and Dhanduka locations were observed. DBW110 would be suitable for Jabalpur, Gwalior and Udaipur locations, whereas BRW3775 identified for Kota, Sanosora and Vijaipur. Genotypes GW495, GW322, HI8713 and GW1339 had achieved high yield and better adaptability during the year (2017-18). The genotype UAS466 had expressed specific adaptations to Jabalpur and Gwalior, whereas HI8627 for Bhopal and Udaipur, NIAW3170 were identified for Indore and Vijaipur, DDW47 for Sanosora, Dhanduka and Pratapgarh. The recent analytic measures based on harmonic means of the relative performance of predicted genetic values have been observed as an appropriate to identify the better adaptive genotypes with higher yield.

Key words: Mixed model, REML/BLUP, HMGV, RPGV, HMRPGV.

INTRODUCTION

Wheat is one of the largest cultivated cereals at the world level. Crop improvement programs aim to identify or recommend genotypes with higher yield accompanied with stable performance for specific and general adaptations (Crespo et al., 2017). Estimates of variance components (genetic and environmental) and prediction of genotypic values are of paramount importance for identification of appropriate genotypes (Friesen et al., 2016).

Under multi environments trials, procedures based on restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) have been established as an effective tools to assess genotypic performance, as most of times, environmental effects are considered of random nature (Hernández et al, 2019). Since 1990s, the methods of mixed models have been cited more in plant breeding trials. These procedures allow a most robust and proper estimation of genetic and environmental effects, as well as the prediction of genotypic values in a non-biased way (Hu, 2014). In addition, mixed model procedures reduce the noise of unbalanced designs as well as of the non-additive traits, features often observed in plant breeding trials (Oliveira et al., 2017). In this context, this study aims to utilize REML/BLUP-based procedures to estimate variance components, genetic parameters and genotypic performance of wheat genotypes in Central Zone of country under restricted irrigated timely sown conditions.

MATERIALS AND METHODS

Central Zone of India is known for the premium quality wheat having typically hard lustrous grains with high gluten strength and comprises of states of Madhya Pradesh, Chhattisgarh, Gujarat, Rajasthan (Kota and Udaipur divisions) and Jhansi division of Uttar Pradesh. The promising wheat genotypes were evaluated under restricted irrigated timely sown conditions under advanced varietal trials during the cropping seasons of 2016-17 and 2017-18 at the twelve major...
locations of this zone. Details of genotypes and locations were reflected in Tables 1 and 2 for completeness.

The yield of ‘g’ genotypes evaluated at ‘e’ environments with ‘r’ replications can be modeled as follows (Hernandez et al., 2019):

\[ Y = Xb + Zr + Zg + e \]

Where X is the incidence matrix for the fixed effects of environments and Zr and Zg are the incidence matrices for the random effects of replicates within sites and genotypes within sites that combine the main effects of genotypes and GxE interaction. Vector b denotes fixed effect of environments and vectors r, g and e are the random effect of replicates within environments, genotypes within environments and residuals within environments, respectively. These effects are assumed to be random and normally distributed with zero mean vectors and variance-covariance matrices R, G, E respectively, such that the joint distribution of r, g and e is multivariate normal (Crossa et al., 2004 and 2006).

Simple and effective measure for adaptability (PRVG) is based on the relative performance of genetic values across environments. Resende (2007) while considering the yield and stability described the MHVG method (Harmonic Mean of Genetic Values). The lower the standard deviation of genotypic performance across environments, the greater is the harmonic mean of genotypes. Under mixed model methodology, (MHPVRG) consider simultaneously stability, adaptability and yield based on the harmonic mean of the relative performance of the genotypic values. MHPVRG combined PRVG and MHVG simultaneously, penalizing genotype instability, similarly to the PI measure of Lin and Binns (1988).

\[ PRVG_{ij} = \frac{VG_{ij}}{VG_i} \]

\[ MHVG = \frac{\text{Number of environments}}{\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}} \]

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VGj is the genotypic value of ‘j’ genotype, in the ‘j’ environment, expressed as a proportion of the average in this environment. PRVG and MHPVRG values were multiplied by the general mean (GM) to have results in the same magnitude as of the average yield in order to facilitate interpretation (Verardi et al., 2009). Estimation of the variance components were carried out by using residual maximum likelihood (REML) along with estimation / prediction of the fixed as well as random effects (Smith et al. 2018). Quite

| Genotype | Parentage | Environments | Latitude | Longitude | Altitude |
|----------|-----------|--------------|----------|-----------|----------|
| BRW3775  | (PFAU/SERI.1B//AMAD/3/WAXWING/4/BABAX/LR42/BABAX*3/KURUKU) | Bhopal    | 23° 15’ N | 77° 24’ E | 496 m    |
| UAS385   | (GW344/UAS239/DWR162) | Bilaspur | 22° 4’ N | 82° 9’ E | 264 m    |
| UAS462   | (DWR1006/Hl8671//UAS415) | Banswara | 23° 32’ N | 74° 26’ E | 216 m    |
| Hi8791   | (H11531/H18498/H18627) | Dhandhuka | 22° 22’ N | 71° 59’ E | 24 m     |
| Hi8627   | (HD4672/PDW233) | Gwalior   | 26° 13’ N | 78° 10’ E | 213 m    |
| MP3288   | (DOVE/BUC/DL788-2) | Indore    | 22° 43’ N | 75° 51’ E | 550 m    |
| DBW110   | (KIRITATI/4/2*SER11B*2/3/KAUZ*2/BOW//KAUZ) | Jabalpur | 23° 10’ N | 79° 55’ E | 403 m    |
|          |           | Kota       | 25° 21’ N | 75° 86’ E | 271 m    |
|          |           | Sagar      | 23° 50’ N | 78° 44’ E | 525 m    |
|          |           | Sanosara   | 21° 72’ N | 71° 76’ E | 89 m     |
|          |           | Udaipur    | 24° 34’ N | 73° 41’ E | 585 m    |
|          |           | Vijapur    | 23°33’ N  | 72°45’ E | 129.4 m  |

Table 2: Parentage details of wheat genotypes along with environmental conditions (2017-18).

| Genotype | Parentage | Environments | Latitude | Longitude | Altitude |
|----------|-----------|--------------|----------|-----------|----------|
| DDW47    | (PBW34/RAJ1555/PDW314) | Sagar      | 23° 50’ N | 78° 44’ E | 525 m    |
| MP1331   | (PBW343*2/KUKUNA/KITE) | Sanosara  | 21° 72’ N | 71° 76’ E | 89 m     |
| UAS466   | (AMRUTH/BIJAGA YELLOW/ASKW299-16) | Bhopal    | 23° 15’ N | 77° 24’ E | 496 m    |
| NIAW3170 | (SKOLL/ROLF07) | Bilaspur  | 22° 4’ N | 82° 9’ E | 264 m    |
| DBW110   | (KIRITATI/4/2*SER11B*2/3/KAUZ*2/BOW//KAUZ) | Dhandhuka | 22° 22’ N | 71° 59’ E | 24 m     |
| MP3288   | (DOVE/BUC/DL788-2) | Gwalior   | 26° 13’ N | 78° 10’ E | 213 m    |
| Hi8627   | (HD4672/PDW233) | Indore    | 22° 43’ N | 75° 51’ E | 550 m    |
|          |           | Jabalpur   | 23° 10’ N | 79° 55’ E | 403 m    |
|          |           | Kota       | 25° 21’ N | 75° 86’ E | 271 m    |
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|          |           | Udaipur    | 24° 34’ N | 73° 41’ E | 585 m    |
|          |           | Vijapur    | 23°33’ N  | 72°45’ E | 129.4 m  |

Table 1: Parentage details of wheat genotypes along with environmental conditions (2016-17).
popular and widely cited ASReml-R package was exploited to fit models which use the average information algorithm for REML (Cullis et al. 2014).

**RESULTS AND DISCUSSION**

**First Year (2016-17)**

The genotypes viz., MP3288, BRW3775 and DBW110 were identified as high yielder with wider adaptability based on BLUP yield value while UAS462, UAS385 recorded low yield. Ranking of genotypes based on harmonic mean of BLUP’s, the genotypes MP3288, BRW3775 and DBW110 were identified as better adapted genotypes whereas UAS462 and HI8627 suitable for specific locations (Table 3). Mean yield of genotypes based on BLUE’s selected MP3288, DBW110 and HI8791 whereas Harmonic mean expressed advantages for MP3288 and DBW110. The genotypes namely MP3288, BRW3775 and DBW110 were found to be better adaptable genotypes based on PRVG and PRVG*GM whereas UAS462, UAS385 recorded low adaptability under restricted irrigated timely sown conditions across major locations of wheat producing zone of the country. Similar results was already reported by Silveira et al., (2018).

Grain yield of wheat genotypes differed to large extent as per BLUP and BLUE values across zone for studied conditions (Fig 1). Relatively lower yield of genotypes were estimated as per Best Linear Unbiased Predictors. Moreover, the heights of standard error of genotypes were less under fixed effects assumptions of genotypes.

First two highly significant interaction principal components accounted for 83.77 % of total GxE interaction sum of squares (Fig 3). Biplot analysis based on two highly significant interaction principal components expressed stable yield of HI8791 and DBW110 as these genotypes were po-sitioned near the origin. UAS462, UAS385 and MP3288 genotypes placed far from origin though high yielder would be of unstable nature in general may be good for specific adaptations. Environments namely Bhopal, Indore, Vijapur and Sagar would be suitable for stable yield performance of evaluated DBW110 and MP3288 genotypes. Whereas, Bhanswara, Bilaspur and Kota were found to be larger contributors to the G x E interactions due to they positioned relatively far from the origin.

Genotypes and environments placed in proximity have positive associations as these relations enable to identify specific adaptations of the genotypes. HI8791 had specific adapta-tions in the locations of Sagar and Dhanduka while DBW110 would be suitable for Jabalpur, Gwalior and Udaipur, whereas BRW3775 identified for Kota, Sanosora and Vijapur. Environments Sagar with Dhanduka, Kota with Bhopal, Banswara with Bilaspur, Vijapur with Sanosora and Indore would show similar performance of genotypes as these locations have been placed in proximity to each other. Banswara had an angle of 180 degree with Danduka, this
would express opposite performance of genotypes i.e. HI8627 will not be of choice for Dhandhuka, similarly behavior of UAS835 will not appropriate for Banswara.

**Second Year (2017-18)**

Based on BLUP values, the genotypes were NIAW3170, HI8627 and MP3288 were identified as desirable while the genotypes DBW110 and MP1331 are low yielders (Table 4). On harmonic mean the genotypes NIAW3170, HI8627, DDW47 were selected as high yielding genotype at the same time the genotypes MP1331, DBW110 expressed lower yield. Mean and harmonic mean of genotypes as per BLUE values, the genotypes NIAW3170, HI8627 and DDW47 were selected as better adaptable genotypes along with high yield. The genotypes namely DBW110 and MP1331 would be suitable for specific adaptations though expressed relatively lower yield.

NIAW3170, HI8627 and MP3288 genotypes were pointed out by PRVG as well as by PRVG*GM for better adaptability and MP1331, DBW110 as of low adaptability across major locations under central zone of the country. HMPRVG and HMPRVG*GM marked GW495, GW322,
### Table 3: Adaptability measures based on BLUP for wheat genotypes (2016-17).

| Genotype  | BLUP  | Rk | HM-UP  | Rk | BLUE  | Rk | HM-UE  | Rk | PRVG  | Rk | PRVG*GM | Rk | MHPRVG | Rk | MHPRVG*GM | Rk |
|-----------|-------|----|--------|----|-------|----|--------|----|-------|----|---------|----|---------|----|-----------|----|
| BRW3775   | 39.61 | 2  | 37.65  | 2  | 38.57 | 4  | 36.89  | 3  | 1.0979| 2  | 41.24   | 2  | 1.0043 | 2  | 37.73     | 2  |
| UAS385    | 37.71 | 6  | 35.96  | 5  | 37.50 | 6  | 35.62  | 5  | 1.0414| 6  | 39.12   | 6  | 0.9625 | 5  | 36.16     | 5  |
| UAS462    | 36.42 | 7  | 33.99  | 7  | 35.92 | 7  | 33.64  | 7  | 1.0023| 7  | 37.65   | 7  | 0.9149 | 7  | 34.37     | 7  |
| H18791    | 39.13 | 4  | 36.42  | 4  | 39.30 | 3  | 36.30  | 4  | 1.0800| 4  | 40.57   | 4  | 0.9761 | 4  | 36.67     | 4  |
| H18627    | 38.36 | 5  | 35.59  | 4  | 37.84 | 5  | 35.08  | 6  | 1.0576| 5  | 39.73   | 5  | 0.9554 | 6  | 35.89     | 6  |
| MP3288    | 40.97 | 1  | 38.42  | 1  | 40.43 | 1  | 37.77  | 1  | 1.1318| 1  | 42.52   | 1  | 1.0296 | 1  | 38.68     | 1  |
| DBW110    | 39.51 | 3  | 37.27  | 3  | 39.40 | 2  | 37.13  | 2  | 1.0931| 3  | 41.06   | 3  | 0.9960 | 3  | 37.41     | 3  |

BLUP (average of values); MHVG (Harmonic mean of the genotypic values); PRVG (Relative performance of genotypic values); GM (Overall average); MHPRVG (Harmonic mean of the relative performance of the predicted genotypic values); Rk (rank of genotypes).

### Table 4: Adaptability measures based on BLUP for wheat genotypes (2017-18).

| Genotype  | BLUP  | Rk | HM-UP  | Rk | BLUE  | Rk | HM-UE  | Rk | PRVG  | Rk | PRVG*GM | Rk | MHPRVG | Rk | MHPRVG*GM | Rk |
|-----------|-------|----|--------|----|-------|----|--------|----|-------|----|---------|----|---------|----|-----------|----|
| DDW47     | 37.85 | 4  | 36.83  | 3  | 38.02 | 3  | 37.04  | 2  | 1.0174| 3  | 38.22   | 3  | 1.0131 | 3  | 38.06     | 3  |
| MP1331    | 36.25 | 6  | 33.35  | 7  | 36.29 | 6  | 33.44  | 7  | 0.9497| 7  | 35.68   | 7  | 0.9349 | 7  | 35.12     | 7  |
| UAS466    | 37.34 | 5  | 35.70  | 5  | 37.51 | 5  | 35.85  | 5  | 0.9924| 5  | 37.28   | 5  | 0.9907 | 5  | 37.22     | 5  |
| NIAW3170  | 39.05 | 1  | 37.80  | 1  | 39.14 | 1  | 37.92  | 1  | 1.0468| 1  | 39.32   | 1  | 1.0418 | 1  | 39.13     | 1  |
| DBW110    | 36.11 | 7  | 34.31  | 6  | 35.68 | 7  | 33.73  | 6  | 0.9569| 6  | 35.95   | 6  | 0.9550 | 6  | 35.87     | 6  |
| MP3288    | 37.93 | 3  | 36.27  | 4  | 37.99 | 4  | 36.02  | 4  | 1.0091| 4  | 37.91   | 4  | 1.0070 | 4  | 37.83     | 4  |
| H18627    | 38.43 | 2  | 37.03  | 2  | 38.33 | 2  | 36.83  | 3  | 1.0277| 2  | 38.60   | 2  | 1.0230 | 2  | 38.43     | 2  |

BLUP (average of values); MHVG (Harmonic mean of the genotypic values); PRVG (Relative performance of genotypic values); GM (Overall average); MHPRVG (Harmonic mean of the relative performance of the predicted genotypic values); Rk (rank of genotypes).
H18713 and GW1339 as high yield and better adaptability genotypes across this zone while AKAW4924 and H11544 for low degree of adaptation. Predictions about the genotypic values can be made based only on a standard yield that includes stability and adaptability as reported by Verardi et al. (2009).

Average yield of genotypes across locations did not differed much on both procedures i.e. BLUE and BLUP (Fig 2). However, more or comparable yields were observed for three genotypes as compared to BLUE values. Heights of standard error of genotypes were more or less same under fixed and random effects assumptions.

The genotypes MP3288 and UAS466 were stable performer as po-sitioned near the origin of the biplot. On the other hand, genotypes MP1331 and DDW47 placed far from origin were unstable in nature. These genotypes may be good for specific adaptations.

First two significant interaction principal components, accounted for 92.14 % of total GxE interaction sum of squares, utilized for graphical representation in biplot analysis (Fig 4). The locations namely Vijapur, Indore and Jabalpur were observed as one of the largest contributors to the phenotypic stability of evaluated genotypes as these environments observed near to origin. Whereas, the environment-ments namely Sansora, Dhanduka, Powerkeda and Bhopal contributed largely to the G x E interactions, because as positioned far from intersection of axis in the AMMI2 biplot. Positive associations are anticipated among genotypes and environments as placed close to each other, this would assist to select specific genotypes. The genotype UAS466 had a specific adapta-tion to environments Jabalpur and Gwalior, whereas H18627 for the locations Bhopal and Udaipur. The genotype NI-AW3170 identified for Indore and Vijapur, DDW47 for Sansora, Dhanduka and Pratapgarh. The locations Gwalior with Jabalpur, Dhanduka with Partapgarh, Vijapur with Indore, Udaipur with Vijapur would show the similar performance of genotypes. Genotypes or environments located near the origin of the coordinate system would be more adaptable as per biplot analysis; however, the distance from the center is inversely related to stable performance. These type of effects and relations are due to the G x E interaction (Duarte and Vencovský, 1999). A genotype is considered adapted to a particular environment when it is situated in the same quadrant of the environment (Yan and Kang, 2003). Other associations among genotypes and environments would be observed as per the degree of angle for genotypes as well as environments.

CONCLUSION
Values of harmonic mean based on BLUP for 2016-17, genotypes MP3288, BRW3775 and DBW110 would be suitable for general UAS462 and HI8627 for specific locations. Measures considered BLUE values observed general adaptations of MP3288, BRW3775 and DBW110 and specificity associated with UAS462, UAS385 for restricted irrigation timely sown conditions. BLUP values of genotypes during 2017-18 identified NI-AW3170, HI8627, DDW47 for general whereas MP1331, DBW110 for specific locations. Genotypes NIAW3170, HI8627 and MP3288 for general and MP1331, DBW110 for specific locations as per BLUP’s values.

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