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Adaptability of Wheat Genotypes under Multi-environment Trials for Northern Hills Zone

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Abstract

Adaptability of wheat genotypes viewed by mixed model together with factor analytic under restricted irrigated late sown trials for the Northern Hills Zone of the country. Analytic measures marked VL892, VL3010 & HS627 as of high yield and better adaptability across major locations of this zone while VL3011 and VL3012 of specific adaptations as per year 2015-16. Biplot analysis expressed stable yield of HS625, HS490 and HPW433 genotypes. Kalimpong and Dhaulakuan, would be suitable environments for stable yield of genotypes while Malan, Imphal and Bajura observed as larger contributor to the G x E interactions. HPW433 had specific adaptations to Kalimpong, Shimla and Dhaulakuan while HS626 for Imphal and Bajura, whereas HS625 identified for Malan. Wheat genotypes HS490, HS660 andVL 3017 had expressed high yield and better adaptability as compared to VL892, UP3017during second year (2017-18) of study.HPW495, VL3016 and HS660 genotypes as positioned near the origin would be of stable nature as compared to HS490, HS661, VL892 and UP3017 had maintained distance from origin in biplot analysis. VL3017 had specific adaptations to Imphal, Malan and Bajura while VL3018 would be for Una, Almora and Dhaulakaun whereas HS662 identified for Shimla, Majhera and Kalimpong. Environments Una with Almora and Dhaulakuan, Bajurawith Imphal and Malan, Shimla with Majhera and Kalimpong would show similar performance of genotypes as acute angle observed among environment rays.

Keywords: BLUE, BLUP, Mixed Models, PRVG, MHVG , MHPRVG

1. Introduction

Wheat (*Triticum aestivum*) has been established as one of the most important cereal crops at world level. Wide adaptation and cultivation of crop across all the continents of world enabled to harvest the record production. Bread wheat covers more than 95% of the total production and provides 19% of calories and 21% of proteins (Igrejas and Branlard, 2020). Still big gap had been anticipated between the demand and annual wheat production in the scenario of climate change with shortage of water. One of the main objectives of wheat breeding programs is to recommend / identify genotypes with high yield and adaptable behavior to the range of environmental conditions (Burgueno et al., 2007). Selection of the promising genotype may be affected by genotype x environment interactions (G×E) (Crespo et al., 2017). Quite large number of statistical methods have been developed for the G×E interactions evaluation; though the final choice of the suitable method depends on

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the experimental design, number of environments and level of precision (Crossa et al., 2006, Hernandez et al., 2019). Number of well known advantages has been associated with mixed models analysis procedure. The foremost is to avoid the consequences of inappropriate models and statistical tests. Few studies had acknowledged the presence of both fixed and random effects in experimental designs for field trials. Analysis procedure of mixed models would be an appropriate analysis to producing correct results including correct standard errors of differences between treatment means.Mixed models with genotypes and environments as the major effects (at least one of which is random) and random G×E interactions (Cullis et al., 2014) had been observed as method of choice (Burgueno et al., 2011). Factor analytic models under mixed approach performed with a restricted maximum likelihood/best-linear unbiased predictor (REML/BLUP) procedure adequately explains the major effects and interactions (Friesen et al., 2016). The advantage of this approach is related to its ability to address missing data and the heterogeneity of residual and genotypic (co)variances. These models are also notable for allowing the inclusion of heteroscedastic residues of genetic values, which constitute an important aspect to be considered in the analyses (Nuvunga et al., 2015). It is known that the heterogeneity of variances among genotypes is affected by the heterogeneity of variances among environments and vice versa. Furthermore, this model has been useful for summarizing the covariance pattern in multivariate data. FA models exhibited a superior performance in the study of G x E interactions (Kelly et al. 2007; Piepho et al., 2008; Kleinknecht et al., 2011). However, these studies were limited to comparisons between models and the structures of genetic variance, and covariance matrices with heterogeneous variances FA model adopted in this study captures a more complex covariance structure with regard to the genetic effect, which provides accurate predictions, for MET analysis. The prime objective of this study was to use the linear mixed model together with FA variance– covariance structure to identify adaptable and high yielder wheat genotypes for the Northern Hills Zone of the country.

2. Materials and Methods

Wheat is cultivated in the hills at different altitudes suited to fit under different crop rotations as per specific adaptations at different elevations. Northern Hills Zone encompasses the hilly terrain of Northern region extending from Jammu & Kashmir to North Eastern States. NHZ comprises J&K (except Jammu and Kathuadistt.); Himachal Pradesh (except Una and Paonta Valley); Uttarakhand (except Tarai area); Sikkim, hills of West Bengal and North Eastern states. Advanced wheat genotypes were evaluated in field trials at major locations of the zone during cropping season's viz. 2015-16 and 2017-18 as details are reflected in tables 1 and 2 for ready reference. Randomized block design with three replications were used for research field trials and recommended agronomical practices had followed to harvest good crop. More over grain yield was further analysed as per recent analytic adaptability measures.

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

$$Y = Xb + Z_r r + Z_g g + e$$

where X is the incidence matrix for the fixed effects of environments and Z_r & Z_g 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, 2006)

Simple and effective measure for adaptability is based on

Table 1: Parentage and location details under multi environmental trials (2015-16)

Genotype	Parentage	Locations	Latitude	Longitude	Altitude
HS 625	(CM H82A.1294/2*KAUZ/MUNIA/CHTO/3/MILAN)	Bajaura	31°50'N	77°9'E	1103.85
HPW 433	(VL832/PBW498)	Dhaulakuan	30°16' N	74°56'E	
HS 627	(69-1 776/663//2*BCN/3/7*BCN/4/PARUS/PASTOR)	Imphal	24°81' N	93°93' E	786
HPW 432	(HS295/FLW2-1)	Kalimpong	27° 4' N	88° 28' E	1121
VL 3010	(RAJ4083/NESSER/SAULES:KU32)	Malan	32°08' N	76°35'E	846
VL 892	(WH542/PBW226)	Shimla	31°10' N	77°17'E	2,276
HS 626	(CHEN/AE.SQUARROSA(TAUS)/BCN/3/BAV92/4/BERKUT)				
VL 3012	(RAJ4132/SW89.3218//AGRI/NAC//VL900)				
UP 2955	(RAJ 4132 / HPW 155/TAS T/S PRW//TL176.73 /7 /SOTY)				
HS 490	(HS364/HPW 114 //HS240//HS346)				
VL 3011	(RAJ4132/SW89.3218//AGRI/NAC/ /VL900)				

Table 2: Parentage and location details under multi environmental trials (2017-18)

Genotype	Parentage	Locations	Latitude	Longitude	Altitude
VL 3017	(RWP2008-31/VL895)	Almora	29° 35' N	79° 39'E	1610
UP 3017	(FRANCOLIN#1/BAJ#1)	Bajaura	31°50'N	77°9'E	1103.85
VL 3016	(KA/NAC//TRCH/3/DANPHE)	Dhalakuan	30°16' N	74°56'E	
HS 662	(SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/5/CNO79//PF70353/ MUS/3/PASTOR/4/BAV92)	Gangtok	27° 20' N	88° 36' E	1509
HS 490	(HS364/HPW114//HS240//HS346)	Imphal	24°81° N	93°93 E	786
VL 892	(WH542/PBW226)	Kalimpong	27° 4' N	88° 28' E	1121
HS 661	(HS295*2/FLW20//HS295*2/FLW13)	Majhera	29° 16' N	80° 5' E	1532
HS 660	(PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1)	Malan	32°08' N	76°35'E	846
VL 3018	(FRNCLN/NIINI#1//FRANCOLIN#1)	Ranichauri	28° 43' N	81°02' E	2200
HPW 459	(HPW249/HPW211)	Shimla	31°10' N	77°17'E	2276
		Una	31°46' N	76°27° E	369

the relative performance of genetic values (PRVG) across environments. Resende (2007) considered the yield & stability, described the MHVG method (harmonic mean of genetic values) and based on the harmonic mean of the genotypic values. The lower the standard deviation of genotypic performance across environments, the greater is the harmonic mean of genotypes. For the use of mixed models, Resende (2007) proposed the simultaneous analysis of stability, adaptability and yield based on the harmonic mean of the relative performance of the genotypic values (MHPRVG). The MHPRVG combines the methods PRVG and MHVG, simultaneously. Consequently, the selection for higher values of the harmonic mean results in selection for both yield and stability.

$PRVG_{ij} = VG_{ij} / VG_{i}$

$MHVG_{i} = \text{Number of environments} / \sum^{k}_{i}=1\times1/X_{i}$

$MHPRVG_{i.} = \text{Number of environments} / \sum^{k}_{j}=1\times1/PRVG_{ij}$

VG_{ij} is the genotypic value of the i genotype, in the j environment, expressed as a proportion of the average in this environment. PRVG and MHPRVG values were multiplied by the general mean (GM) to have results in the same magnitude as of the average wheat 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 and Cullis, 2018). Quite popular and widely cited ASReml-R package was exploited to fit models which use the average information algorithm for REML (Gogel et al., 2018).

3. Results and Discussion

3.1. First year (2015-16)

Average yield of genotypes as per BLUPs identified VL892, HS627 andVL3010as of high yield with better adaptations while VL3011&HPW432 expressed low yield. Ranking of genotypes based on harmonic mean of BLUP's selected VL892, VL3010&HS627as better adapted genotypes at the same time pointed out suitability of VL3011&VL3012for specific adaptations (Table 4). Average of genotypes based on BLUE's pointed towards VL892, HS627 andVL3010as desirable genotypes whereas as Harmonic mean observed advantages for VL 892, VL3010&HS627. Genotypes VL892, VL3010&HS627were pointed out by PRVG as well as by PRVG*GM for the better adaptable behavior and VL3011&VL3012of low adaptability under restricted irrigated late sown conditions for Northern Hills Zone. Most cited analytic measures HMPRVG and HMPRVG*GM marked VL892, VL3010 &HS627as of high yield and better adaptability across major locations of this zone while VL3011&VL3012for low degree of adaptation. Consensus has been observed among analytic measures PRVG, MHVG, MHPRVG, and HM-UP for the classification of wheat genotypes (Table 3).

Only marginal variation in average yield of wheat genotypes had been observed as per BLUP and BLUE across locations of zone for restricted irrigated late sown conditions (Figure 1). Relatively lower yield of genotypes were estimated as per Best Linear Unbiased predictors except for UP2995 &VL3011. Moreover, the heights of standard error of genotypes were more or less same under fixed and random effects of genotypes.

Genotypes or environments located near the origin of the coordinate system in the Biplot presentations were considered more stable; however, the greater the distance from the source the lower the stability related to the grain yield character; these effects are due to the nature of the G x E interaction (Duarte and Vencovsky, 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). Biplot analysis based on first two highly

Table 3: Analytic measures of adaptability for wheat genotypes (2015-16)

Genotype	BLUP	Rk	HM-UP	Rk	BLUE	Rk	HM-UE	Rk	PRVG	Rk	PRVG×GM	Rk	HPVRG	Rk	HPVRG× GM	Rk
HS 625	24.53	7	22.54	7	24.59	7	22.73	5	0.9881	7	24.66	7	0.9874	7	24.64	7
HPW 433	25.66	5	23.01	4	25.86	5	23.14	4	1.0217	5	25.50	5	1.0202	4	25.46	4
HS 627	26.21	2	23.52	3	26.23	2	23.31	3	1.0457	3	26.10	3	1.0420	3	26.01	3
HPW 432	23.29	10	21.35	9	23.36	9	21.48	9	0.9390	9	23.44	9	0.9321	9	23.26	9
VL 3010	26.19	3	24.37	2	26.17	3	24.40	2	1.0711	2	26.73	2	1.0492	2	26.19	2
VL 892	27.05	1	24.93	1	27.25	1	25.07	1	1.0995	1	27.44	1	1.0856	1	27.10	1
HS 626	25.32	6	22.71	6	25.25	6	22.37	7	1.0136	6	25.30	6	1.0010	6	24.98	6
VL 3012	23.80	8	20.30	10	23.62	8	19.72	11	0.9330	10	23.29	10	0.9190	10	22.94	10
UP 2955	23.45	9	21.55	8	23.22	10	21.50	8	0.9474	8	23.65	8	0.9420	8	23.51	8
HS 490	25.77	4	22.81	5	25.87	4	22.70	6	1.0248	4	25.58	4	1.0166	5	25.37	5
VL 3011	23.28	11	20.20	11	23.15	11	19.86	10	0.9162	11	22.87	11	0.9067	11	22.63	11

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)

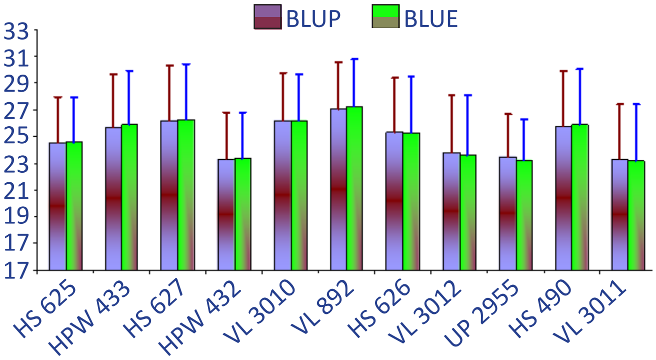

Figure 1: Average yield of wheat genotypes along with standard errors (2015-16)

significant Interaction Principal Components expressed stable yield of HS625, HS490 and HPW433 genotypes. VL3010, and VL3011 would be good for specific adaptations. These two significant interaction principal components, accounted for 86.1 % of total GxE interaction sum of squares (Figure 2). Kalimpong and Dhaulakuan, would be suitable environments for stable yield of genotypes. Environments Malan, Imphal and Bajura observed as larger contributor to the G x E interactions, because as positioned relatively away from the origin.

Genotypes and environments placed in proximity have positive associations as these observations would enable to identify specific adaptations of the genotypes. HPW433 had specific adaptations to Kalimpong, Shimla and Dhaulakuan while HS626 for Imphal and Bajura, whereas HS625 identified for Malan. Bajura with Imphal, Kalimpong with Dhaulakuan, Shimla with Kalimpong would show similar performance of genotypes as expressed acute angles among rays connecting these environments. Malan had an obtuse angle with Imphal this would express opposite performance of genotypes i.e. HS626 will not be of choice for Malan.

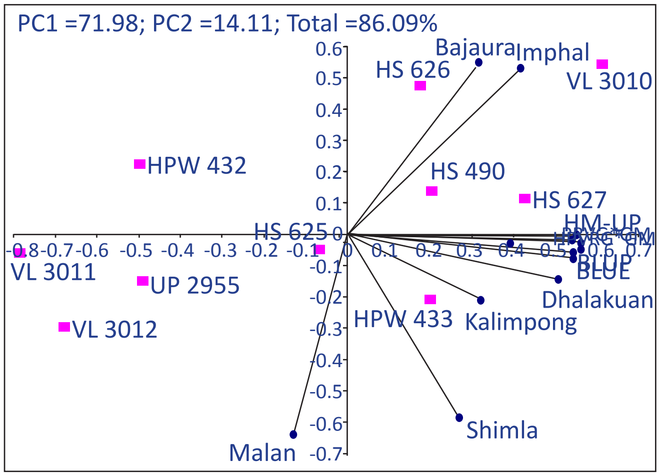

Figure 2: Biplot analysis of wheat genotypes vis-a-vis environments (2015-16)

3.2. *Second year (2017-18)*

Mean yield of genotypes based on their BLUP values identified HS490,VL3017and HS660 with high yield and better adaptations while UP3017, HS661would be with low realization of yield. The ranking of genotypes as per harmonic mean of BLUP's selected HS490, HS662andHS660 with better adaptations whereas also pointed out suitability of VL892, UP3017for specific adaptations (Table 4). Average of genotypes based on BLUE's identified HS490,HS 660 and VL3017while Harmonic mean observed advantages for HS490,HS661 &HS660. Genotypes pointed out by PRVG as well as by PRVG*GM for better adaptability wereHS490,HS662 andHS660along with lower adaptability UP3017, VL892of under irrigated timely sown conditions. Analytic measures

Table 4: Analytic measures of adaptability for wheat genotypes (2017-18)

Genotype	BLUP	Rk	HM-UP	Rk	BLUE	Rk	HM-UE	Rk	PRVG	Rk	PRVG× GM	Rk	HPVRG	Rk	HPVRG× GM	Rk
VL 3017	20.82	2	15.41	6	20.75	3	15.05	6	1.0236	4	20.23	4	0.9910	3	19.58	3
UP 3017	17.80	10	14.53	9	17.27	10	13.73	9	0.9042	10	17.87	10	0.8917	9	17.62	9
VL 3016	19.81	5	14.94	8	19.89	5	15.02	7	0.9850	5	19.46	5	0.9479	8	18.73	8
HS 662	19.49	6	16.57	2	19.10	7	15.31	5	1.0349	2	20.45	2	0.9876	4	19.52	4
HS 490	21.89	1	17.90	1	22.20	1	18.68	1	1.1367	1	22.46	1	1.0991	1	21.72	1
VL 892	19.43	7	12.82	10	19.58	6	12.95	10	0.9538	9	18.85	9	0.7851	10	15.51	10
HS 661	18.82	9	15.89	4	19.07	8	16.45	2	0.9819	7	19.40	7	0.9513	6	18.80	6
HS 660	20.69	3	16.06	3	20.81	2	16.13	3	1.0318	3	20.39	3	1.0185	2	20.13	2
VL 3018	19.91	4	15.02	7	19.90	4	14.67	8	0.9831	6	19.43	6	0.9504	7	18.78	7
HPW 459	18.94	8	15.46	5	19.02	9	15.66	4	0.9649	8	19.07	8	0.9516	5	18.80	5

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

HMPRVG and HMPRVG×GM marked HS490, HS660 and VL 3017 high yield and better adaptability across major wheat producing zone of the country while VL892, UP3017 for low degree of adaptation. PRVG, MHVG, MHPRVG, HM-UP measures had classified productive wheat genotypes (Oliveira et al., 2017).

More or less same yield levels of wheat genotypes were seen as per BLUP and BLUE across locations of zone (Figure 3). Relatively higher as well as lower yield of genotypes were estimated as per Best Linear Unbiased Predictors except HS662 & UP3017. Moreover, the heights of standard error of genotypes were same under fixed and random effects of genotypes.

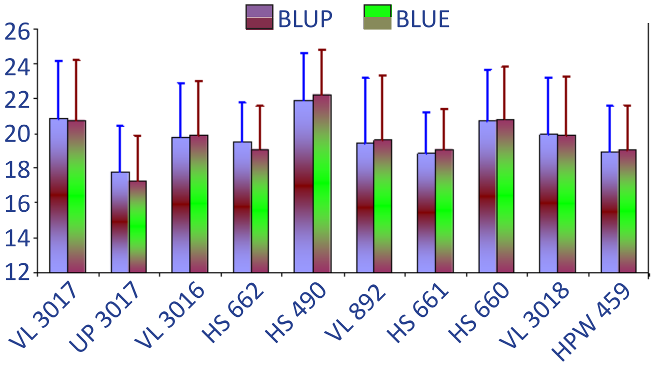

Figure 3: Average yield of wheat genotypes along with standard errors (2017-18)

First two significant interaction principal components, accounted for 72.7% of total G×E interaction sum of squares (Figure 4). Biplot analysis considering first two highly significant Interaction principal components expressed stable yield of HPW495, VL3016 and HS660 genotypes as positioned near the origin. HS490, HS661, VL892 and UP3017 genotypes positioned far from origin though high yielder would be of unstable nature in general may be good for specific adaptations. Environments Majhera, Shimla, Kalimpong and Gangtok would be suitable for stable yield performance of evaluated genotypes. Environments Almora, Malan and Dhaulakuan observed as larger contributor to the G×E interactions, because as positioned relatively away from the origin.

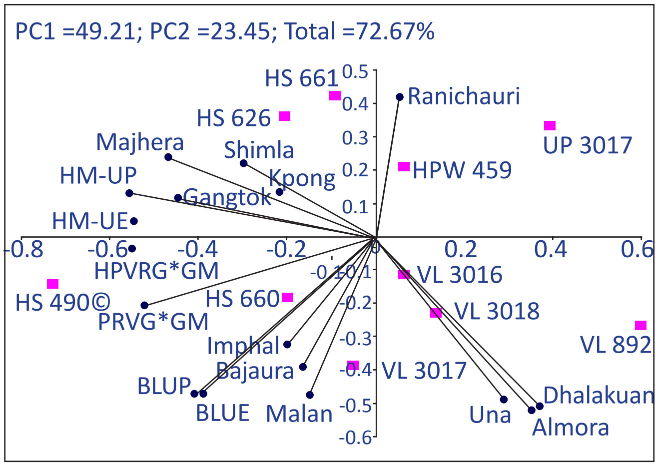

Figure 4: Biplot analysis of wheat genotypes vis-a-vis environments (2017-18)

Genotypes and environments placed in proximity have positive associations as these observations would enable to identify specific adaptations of the genotypes. VL3017 had specific adaptations to Imphal, Malan and Bajura while VL3018 would be for Una, Almora and Dhaulakuan whereas HS662 identified for Shimla, Majhera and Kalimpong and HPW495 for Ranichauri location. Environments Una with Almora and Dhaulakuan, Bajurawith Imphal and Malan, Shimla with Majhera and Kalimpong would show similar performance of genotypes as acute angle observed among environment rays. Gangtok had an angle of 180 degree with Almora this would express opposite performance of genotypes i.e. VL3018 will not suitable for Gangtok.

The different analytic measures to estimate the adaptability of advanced wheat genotypes allow identifying and recommending efficient genotypes to the best environments to obtain increased yield (Mendes et al., 2012). Prime objective of wheat improvement is to identify genotypes with wider adaptations as well as good average yield even in heterogeneous environments. Although, these conditions are not easy to satisfy, to increase wheat productivity at national level, it is very important to recommend wheat genotypes as per specific adaptations (Silveira et al., 2018). Proper exploitation of these specific positive interactions in rational manner contributes to improve wheat productivity in Northern Hills Zone of the country.

4. Conclusion

Adaptability of wheat genotypes had been studied by recent analytic measures while considering BLUE and BLUP of genotypes yield. Marginal yield differences had observed in yield of wheat genotypes. Biplot analysis portrayed the close affinity of analytic measures based on BLUE and BLUP estimates. Performance of genotypes had not differed significantly while analysinggenotypes performance as fixed or mixed effects models. Specific and general adaptation of genotypes, in biplot graphical analysis, to various environmental conditions will help to increase wheat production of zone

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