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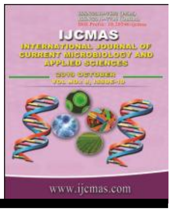

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Analytic Measures for Adaptability of Wheat Genotypes for Northern Hills Zone of Country by Mixed Model Approach

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ABSTRACT

Adaptability of wheat genotypes studied by mixed model methodology under rainfed sown trials for the Northern Hills Zone of the country. Analytic measures marked HS612, HPW430, VL2023 & HS507 as of high yield and better adaptability across major locations of this zone while HS615 & HS617 for low degree of adaptation as per year 2015-16. Biplot analysis expressed stable yield of HPW349 and HPW441 genotypes. Majhera, Ranichauri and Khudwani, would be suitable environments for stable yield of genotypes. HPW442 had specific adaptations to Dhaulakuan and Berthin while HP441 for Almora and VL907 for Malan and Ranichauri, whereas HPW349 and HS634 identified for Khudwani. Genotypes HS631, HS632, VL2030 & VL 2025 were of high yield and better adaptability across major locations of this zone while HS 635 & VL 2028 with lower level of adaptation during 2016-17. Biplot analysis considered 86.1 % of total GxE interaction sum of squares marked HS507, HS634, HS636 and UP2991 genotypes of stable yield. HPW447 had specific adaptations to Wadhura, and Khudwani while VL2030 & VL2025 for Almora, whereas VL2027, UP2990 & VL2028 identified for Bajaura. Third year of study 2017-18 identified HS562 & VL907 with yield and better adaptability. Biplot analysis observed UP2953, HPW428 and HS613 as desirable genotypes for yield and adaptability. VL2021, HS616, HS507, HPW425 and HPW426 had specific adaptations to Shimla and VL2020, VL2024, HS613 would be for Almora and Malan, whereas HPW426 identified for Khudwani. Analytic measures based on Harmonic means showed suitability to identify the better adaptive genotypes with high yield.

Keywords

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

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Introduction

Knowledge about the genotype–by-environments interaction (GxE) effects is necessary for efficient plant breeding strategies (Burgueño *et al.,* 2007). One of main challenges faced by Indian farmers is the wide yield variation caused by environmental conditions i.e. related to climate and soils quality that affects the crop performance (Crespo *et al.,* 2017). These factors may cause low genotypic adaptability which is very common in quantitative traits *viz.,* yield. The expected marginal means obtained across several environmental are calculated to drop out the environmental nuisance factors

(Crossa *et al.*, 2006). Evaluation of genotypes under multi-environment trials (METs) is exploited in breeding programs to study the stability and adaptability of genotypes along with performance prediction in different environments (Oliveira *et al.*, 2017).

GxE may be understood as the phenomenon where the genotypes show different responses across the environments cause to it the ranking of genotypes altered in the target environments (Nuvunga *et al.*, 2018). Quite large number of methods has been cited in literature to predict yield in different locations (Silveira *et al.*, 2018). Among the statistical methods used for MET analysis mixed models approach based on factor analysis or FA structure has been very well appreciated as allows genotypes and GxE interactions as random effects and environment is fixed (Kelly *et al.*, 2007; Burgueño *et al.*, 2011; Friesen *et al.*, 2016; Nuvunga *et al.*, 2018). FA method has offered advantages as compared to traditional analysis methods in the plant breeding (Piepho *et al.*, 2008; Meyer, 2009; Smith & Cullis, 2018).

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. In general sowing is done for Northern Hills Zone under rainfed conditions in October/November with residual moisture and harvesting takes place in May/June. Development of high yielding varieties for moisture stress condition is the major objective of wheat improvement programmes in NHZ. Region encompasses the hilly terrain of Northern region extending from Jammu & Kashmir to North Eastern States. NHZ comprises J&K (except Jammu and Kathua distt.); 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, 2016-17 and 2017-18 as details are reflected in tables 1, 2 & 3 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 were further analysed as per recent analytic adaptability measures (Fig. 1).

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)

The variance-covariance matrices R and E are $R = \Sigma_r \otimes I_r$ and $E = \Sigma_e \otimes I_{rg}$, where I_r and I_{rg} are the identity matrices of order *r* and *r* x *g*, respectively, $\Sigma_r = \text{diag}\ (\sigma^2_{rj}, j = 1,2, \dots, e)$ and $\Sigma_e = \text{diag}\ (\sigma^2_{ej}, j = 1,2, \dots, e)$; σ^2_{rj}, σ^2_{ej} are the replicate and residual variances within the *j*th environment, respectively, and $\otimes$ is the Kronecker (or direct) product of the two matrices.

The factor analytic structure for G in terms of a few unobservable factors can be expressed as $\sum_{k=1}^{t} \delta_{ik} X_{jk}$ + d_{ij}, where δ_{ik} is the *k*th random regression coefficient of the *i*th genotype (loading or genotypic sensitivity) to the *k*th unobserved (latent) variable related to the *j*th environment (environmental potentiality), X_{jk} and d_{ij} is the residual interaction term. In matrix notation, the vector of genotypic effects is represented by $g = \Delta x + d$ so that the variance-covariance of g is $V(g) = \Delta V(x) \Delta' + D$ and, since $V(x) = I$, $V(g) = \Delta\Delta' + D$. The factor analytic model implies that the variance of the effect of *i*th genotype is $\sum_{k=1}^{t} \delta_{jk}^{2}$ $+d_i$ and the covariance of the effects of genotypes i and i' is $\sum_{k=1}^{t} \delta_{ik} \delta_{ik}$.

Simple and effective measure for adaptability is based on 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.

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

$MHVG_i$ = Number of environments / $\sum_{i=1}^{k} \frac{1}{X_i}$

$MHPRVG_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$

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 ASReml-R package using residual maximum likelihood (REML) along with estimation / prediction of the fixed as well as random effects (Smith and Cullis, 2018).

Results and Discussion

First year (2015-16)

Average yield of genotypes as per BLUPs identified HS612, HS507, HPW430 and VL2021 of better adaptations along with high yield while HS615 & UP2952 expressed low yield. Ranking of genotypes based on harmonic mean of BLUP's selected HS612, HPW430 VL2024 & VL2023 as better adapted genotypes at the same time pointed out suitability of HS615 & HS617 for specific adaptations (Table 4). Average of genotypes based on BLUE's pointed towards HS612, HPW430, HS507 and VL2021 as desirable genotypes whereas as Harmonic mean observed advantages for HS612, HPW430, VL2024 and VL2020. Adaptability measures PRVG & PRVG*GM pointed out HS612, HPW430, HS507 and VL2023 for the better adaptable behavior and HS615 & HS617 of low adaptability under rainfed timely sown conditions for Northern Hills Zone.

Analytic measures HMPRVG and HMPRVG*GM marked HS612, HPW430, VL2023 & HS507 as of high yield and better adaptability across major locations of this zone while HS615 & HS617 for low degree of adaptation. Consensus has been observed among analytic measures PRVG, MHVG, MHPRVG and HM-UP for the classification of wheat genotypes (Table 4).

Only marginal variation in average yield of wheat genotypes had been observed as per BLUP and BLUE across locations of zone for rainfed timely sown conditions (Figure 2). Relatively comparable yield of genotypes were estimated as per Best Linear Unbiased predictors except for HS612 & HPW430. 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 stable; however, the more distant from the source the lower the stability of the wheat yield; these effects are due to the nature of the G x E interaction. 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 significant Interaction Principal Components expressed stable yield of HPW349 and HPW441 genotypes. HS507, HS562, HS634 and VL907 would be good genotypes for specific adaptations. These two significant interaction principal components, accounted for 90.3 % of total GxE interaction sum of squares (Figure 5). Majhera, Ranichauri and Khudwani, would be suitable environments for stable yield of genotypes. Environments Bajura, Malan and Dhaulakuan 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. HPW442 had specific adaptations to Dhaulakuan and Berthin while HP441 for Almora and VL907 for Malan and Ranichauri, whereas HPW349 and HS634 identified for Khudwani. Berthin with Dhaulakuan, Ranichauri with Malan, Majhera with Arkot would show similar performance of genotypes as expressed acute angles among rays connecting these environments. Malan had an obtuse angle with Khudwani this would express opposite performance of genotypes i.e. HPW349 will not be of choice for Malan.

Second year (2016-17)

Mean yield of genotypes based on BLUPs pointed towards HPW447, HS631, HS632 & VL2030 of better adaptations along with high yield while HS635 & HS637 expressed low yield. Ranking of genotypes based on harmonic mean of BLUP’s selected HS631, HS632, VL2030 & VL2025 as better adapted genotypes at the same time pointed out suitability of HS 635 & VL2028 for specific adaptations (Table 5). Mean yield of genotypes as per BLUE’s identified HS631, HPW447, HS632 & VL2030 as desirable genotypes whereas as Harmonic mean observed advantages for HS631, HS632, VL2030 & VL2025. PRVG as well as by PRVG*GM pointed out HS631, HS632, HPW447 & VL2030 for the better adaptable behavior and HS635 & VL2028 of low adaptability for Northern Hills Zone. Recent measures of adaptability HMPRVG and HMPRVG*GM marked HS631, HS632, VL2030 & VL2025 of high yield and better adaptability across major locations of this zone while HS635 & VL2028 as for low degree of adaptation. Consensus has been observed among analytic measures PRVG, MHVG, MHPRVG, and HM-UP for the classification of wheat genotypes (Table 6).

Variation in average yield of wheat genotypes had been observed as per BLUP and BLUE across locations of zone (Figure 3). Relatively higher yield of genotypes were estimated as per Best Linear Unbiased Estimators except for HPW444 & HS637. Moreover, the heights of standard error of genotypes were more under fixed effects of genotypes.

Biplot analysis based on first two highly significant Interaction Principal Components expressed stable yield of HS507, HS634, HS636 and UP2991 genotypes. HPW447, VL2028 and HS637 would be good for specific adaptations. First two significant interaction principal components contributed 86.1 % to total GxE interaction sum of squares (Figure 6). Malan and Bajaura would be suitable environments for stable yield of genotypes. Environments Shimla, Wadhua and Khudwani positioned relatively away from the origin.

Genotypes and environments placed in proximity have positive associations enable to identify specific adaptations. HPW447 had specific adaptations to Wadhura, and Khudwani while VL2030 & VL2025 for Almora, whereas VL2027, UP2990 & VL2028 identified for Bajaura. Malan with Almora and Bajaura whereas Wadura with Khudwani would show similar performance of genotypes as expressed acute angles among rays connecting these environments. Shimla had an obtuse angle with Wadura this would express opposite performance of genotypes i.e. HPW447 will not be of choice for Shimla.

Third year (2017-18)

Mean yield of genotypes by considering BLUP values identified HS562 & HPW442 of better adaptations along with high yield while HS507 expressed low yield. Ranking of genotypes based on harmonic mean of BLUP's selected VL907 & HS562 as better adapted genotypes at the same time pointed out suitability of HS634 for specific adaptations (Table 6). Average of genotypes based on BLUE's pointed towards HS562 & HPW441 as desirable genotypes whereas as Harmonic mean observed advantages for VL907 & HS562. PRVG as well as by PRVG*GM pointed out HS562 & VL907 for the better adaptable behavior and HS634 of low adaptability under rainfed conditions of Northern Hills Zone. Most cited analytic measures HMPRVG and HMPRVG*GM marked HS562 & VL907 of high yield and better adaptability across major locations of this zone while HS634 as for low degree of adaptation. Analytic measures PRVG, MHVG, MHPRVG, and HM-UP showed consensus for the classification of wheat genotypes (Table 6).

Marginal variation in average yield of wheat genotypes had been observed as per BLUP and BLUE across locations of zone for rainfed sown conditions (Figure 4). Relatively more yield of genotypes was estimated as per Best Linear Unbiased Estimators except for HS634 & HPW441. Moreover, the heights of standard error of genotypes were more under fixed effects of genotypes.

Biplot analysis based on first two highly significant Interaction Principal Components observed stable yield of genotypes UP2953, HPW428 and HS613. Genotypes HS612, HS615 and HPW427 would be good for specific adaptations. These two significant interaction principal components, accounted for 84.4 % of total GxE interaction sum of squares (Figure 7). Shimla and Malan would be suitable environments for stable yield of genotypes. Environments Almora and Khudwani positioned relatively away from the origin.

Genotypes and environments placed in proximity would have positive associations. VL2021, HS616, HS507, HPW425 and HPW426 had specific adaptations to Shimla and VL2020, VL2024, HS613 would be for Almora and Malan, whereas HPW426 identified for Khudwani.

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

Genotype	Parentage	Locations	Latitude	Longitude	Altitude
HPW 425	(VL832/WH423)	Almora	29° 35' N	79° 39'E	1610
VL2022	(EC635640)	Khudwani	33° 70' N	75°10' E	1590
VL2019	(RWP2002-2/SW89.3218//AGRI/NAC//VL905)	Malan	32°08' N	76°35' E	846
HPW431	(HPW42/HPW236)	Shimla	31°10' N	77°17' E	2276
HPW430	(HPW249/HPW211)				
UP2953	(WBLL1/KUKUNA//TACUPETO F2001/3/KIRITATI)				
VL2024	(W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/MUNAL)				
VL2023	(ATTILA/3/WEAVER*2/TSC//WEAVER/4/ATTILA/PASTOR)				
HPW427	(VL616/FLW3)				
HS616	(SOKOLL/3/PASTOR//HXL7573/2*BAU)				
HS612	(SERI.1B*2/3KAUZ*2/BOW//KAUZ*2/5/CNO79/PF70354/MUS/3/PASTOR/4/BAV92)				
HPW429	(ESWYT(2008)115/HPW211)				
HS507©	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)				
HPW426	(HPW155/HD29)				
UP2952	(MILAN/S87230//BAV92*2/3/AKURI)				
HS615	(BERKUT/HTG)				
HPW428	(HPW155/HD29)				
HS613	(WBM1587/VL824)				
HS614	(HPW155/CHINESE LINE 14)				
HS617	(PASTOR/3/CROC-1/AE.SQUARROSA(224)//OPATA/4/BERKUT)				
VL907©)	(DYBR 1982-83/842 ABVD 50/VW 9365//PBW 343				
VL2020	(KLEIBER/2*FL80/DONSK.POLL/AKAW4006)				
VL2021	(KLEIBER/2*FL80/DONSK.POLL/GW2000-18)				
HS618	(BERKUT/HTG)				

Table.2 Parentage and location details under multi environmental trials (2016-17)

Genotype	Parentage	Locations	Latitude	Longitude	Altitude
HS 631	(WHEAR/VIVITSI//WHEAR)	Almora	29° 35' N	79° 39'E	1610
HS 632	(HS240*2/FLW20(LR19)//HS240*2/FLW13(YR15)	Bajaura	31°84'N	77°16 'E	1099
HS 633	(HS240*2/FLW20(LR19)//HS240*2/FLW13(YR15)	Khudwani	33° 70' N	75°10' E	1590
HS 634	(PBW343*2/KUKUNA/5/CNO79//PF73054/MUS/3/PASTOR/4/BAV92)	Malan	32°08' N	76°35'E	846
HS 635	(PFAU/MILAN/5/CHEN/AE.SQUARROSA(TAUS)//BCN/3/VEE#7/BOW/4/PASTOR)	Shimla	31°10' N	77°17'E	2276
HS 636	(PASTOR//KAUZ/6/CNDO/R143//ENTE/MEX1-2/3/AEGILOPSSQUARROSA(TAUS)/4/WEAVER/5/2*KAUZ)	Wadura	21° 18' N	77° 41' E	508
HS 637	(PRL/2*PASTOR)				
HPW 441	(NAC/TH.AC//3*MIRLO/BUC/4/PASTOR)				
HPW 442	(LONG291*2/PASTOR)				
HPW 443	(PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1)				
HPW 444	(AZAR2/4/CROC_1/AE.SQUARROSA (205)//BORL95/3/2*MILAN/5/BERKUT)				
HPW 445	(PBW575/HPW251)				
HPW 446	(BOW/URES//KEA/3/SITE)				
HPW 447	(HPW266/HPW249)				
VL 2025	(LBPY04-1/RAJ4132//HS490)				
VL 2026	(GW366/KS82W428/SWM75740//UP2739)				
VL 2027	(RAJ4083/SKAUZ/HATUSA//VL900)				
VL 2028	(FRANCOLIN#1*2/MUU)				
VL 2029	(MUNAL#1/FRANCOLIN#1)				
VL 2030	(KA/NAC//TRCH/3/DANPHE#1)				
UP 2990	(UP2744/WL711//PBW644)				
UP 2991	(SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SOKOLL/WBLL1)				
VL 907	(DYBR1982-8384ABVD50/VW9365//PBW343)				
HS 507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)				

Table.3 Parentage and location details under multi environmental trials (2017-18)

Genotype	Parentage	Locations	Latitude	Longitude	Altitude
HPW 349	(NAC/TH.AC//3*MIRLO/BUC/4/2*PASTOR)	Akrot	31°4'N	76°1'E	425
HS 634	(PBW343*2/KUKUNA/5/CNO79//PF73054/MUS/3/PASTOR/4/BAV92)	Almora	29° 35' N	79° 39 'E	1610
VL 907	(DYBR1982-83842ABVD50/VW9365//PBW343)	Bajaura	31°84 'N	77°16'E	1099
HS 507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)	Berthin	31°50 'N	77°9 'E	1103.85
HPW 441	(NAC/TH.AC//3*MIRLO/BUC/4/PASTOR)	Dhaulakuan	30°16' N	74°56'E	468
HPW 442	(LONG291*2/PASTOR)	Khudwani	33° 70' N	75°10' E	1590
HS 562	(OASIS/SKUAZ//4*BCN/3/2*PASTOR)	Majhera	29° 16' N	80° 5' E	1532
		Malan	32°08' N	76°35'E	846
		Ranichauri	28° 43' N	81°02' E	2200
		Shimla	31°10' N	77°17'E	2276

Table.4 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
HPW 425	27.22	6	24.63	7	27.15	6	24.36	8	1.0737	7	26.90	7	1.0601	8	26.56	8
VL2022	21.66	21	20.36	21	21.37	21	20.03	21	0.8685	22	21.76	22	0.8653	21	21.68	21
VL2019	23.76	16	23.67	10	23.85	16	23.79	10	0.9991	13	25.03	13	0.9599	16	24.05	16
HPW431	22.56	20	21.10	18	22.45	19	20.89	18	0.9041	19	22.65	19	0.8987	19	22.52	19
HPW430	28.16	3	25.60	2	28.40	2	25.82	2	1.1078	2	27.76	2	1.1047	2	27.68	2
UP2953	25.74	12	22.24	16	25.68	13	21.83	16	0.9988	14	25.02	14	0.9688	14	24.28	14
VL2024	26.56	8	25.36	3	26.77	7	25.51	3	1.0777	6	27.00	6	1.0676	6	26.75	6
VL2023	27.73	5	25.30	4	27.76	5	25.29	5	1.0938	4	27.41	4	1.0861	3	27.21	3
HPW427	22.67	19	20.12	22	22.33	20	19.13	23	0.8927	20	22.37	20	0.8728	20	21.87	20
HS616	26.24	10	23.58	13	26.41	10	23.53	12	1.0303	11	25.81	11	1.0217	11	25.60	11
HS612	29.23	1	28.46	1	29.75	1	29.08	1	1.1991	1	30.04	1	1.1839	1	29.66	1
HPW429	24.57	15	23.66	11	24.67	15	23.74	11	1.0000	12	25.06	12	0.9924	12	24.87	12
HS507	28.28	2	24.93	6	28.25	3	24.80	6	1.0977	3	27.50	3	1.0805	4	27.07	4
HPW426	26.66	7	23.63	12	26.71	8	23.50	13	1.0387	9	26.03	9	1.0287	10	25.77	10
UP2952	21.11	23	20.93	19	20.91	23	20.76	19	0.8812	21	22.08	21	0.8558	22	21.44	22
HS615	19.55	24	19.04	24	19.31	24	18.74	24	0.8103	24	20.30	24	0.7851	24	19.67	24
HPW428	26.05	11	21.91	17	25.82	11	21.29	17	0.9955	15	24.94	15	0.9669	15	24.23	15
HS613	25.71	13	24.29	9	25.75	12	24.35	9	1.0316	10	25.85	10	1.0305	9	25.82	9
HS614	23.55	18	20.62	20	23.19	18	20.10	20	0.9112	18	22.83	18	0.9005	18	22.56	18
HS617	21.21	22	20.04	23	21.01	22	19.73	22	0.8578	23	21.49	23	0.8474	23	21.23	23
VL907	23.56	17	23.33	14	23.61	17	23.42	14	0.9819	17	24.60	17	0.9557	17	23.95	17
VL2020	26.54	9	25.20	5	26.66	9	25.37	4	1.0685	8	26.77	8	1.0652	7	26.69	7
VL2021	27.86	4	24.62	8	28.25	4	24.60	7	1.0896	5	27.30	5	1.0710	5	26.83	5
HS618	25.16	14	22.78	15	25.21	14	22.68	15	0.9904	16	24.82	16	0.9844	13	24.67	13

BLUP (average of values); HM-UP (Harmonic mean of BLUP); 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.5 Analytic measures of adaptability for wheat genotypes (2016-17)

Genotype	BLUP	Rk	HM-UP	Rk	BLUE	Rk	HM-UE	Rk	PRVG	Rk	PRVG*GM	Rk	HPVRG	Rk	HPVRG*GM	Rk
HS 631	31.62	2	29.69	1	31.95	1	30.11	1	1.0789	1	31.55	1	1.0755	1	31.45	1
HS 632	31.46	3	29.65	2	31.84	3	30.08	2	1.0755	2	31.45	2	1.0707	2	31.31	2
HS 633	29.07	13	26.97	13	30.19	6	28.33	6	0.9892	14	28.93	14	0.9832	15	28.75	15
HS 634	29.20	10	26.82	18	28.87	15	25.72	21	0.9888	15	28.91	15	0.9859	12	28.83	12
HS 635	26.67	24	24.66	24	26.28	24	24.12	24	0.9074	24	26.53	24	0.8960	24	26.20	24
HS 636	28.89	14	27.25	11	29.02	12	27.48	13	0.9895	13	28.93	13	0.9843	13	28.78	13
HS 637	27.50	23	26.52	20	27.13	23	26.05	19	0.9635	21	28.17	21	0.9343	21	27.32	21
HPW 441	27.95	20	26.89	15	27.69	20	26.45	17	0.9701	20	28.37	20	0.9583	20	28.02	20
HPW 442	29.15	11	26.94	14	28.98	13	26.63	15	0.9909	12	28.98	12	0.9866	11	28.85	11
HPW 443	28.73	17	26.09	21	28.67	17	25.99	20	0.9750	19	28.51	19	0.9627	19	28.15	19
HPW 444	27.78	21	25.32	22	27.37	22	24.44	23	0.9388	22	27.45	22	0.9339	22	27.31	22
HPW 445	28.41	19	27.17	12	28.54	19	27.56	12	0.9781	18	28.60	18	0.9757	18	28.53	18
HPW 446	28.66	18	27.89	8	28.88	14	28.14	8	1.0033	10	29.34	10	0.9834	14	28.76	14
HPW 447	31.63	1	26.86	17	31.91	2	26.29	18	1.0578	3	30.93	3	1.0221	5	29.89	5
VL 2025	30.29	5	28.89	4	30.42	5	28.92	4	1.0447	5	30.55	5	1.0362	4	30.30	4
VL 2026	30.13	6	27.82	9	30.16	7	27.67	10	1.0225	8	29.90	8	1.0187	8	29.79	8
VL 2027	30.10	7	27.99	7	30.15	8	27.83	9	1.0290	6	30.09	6	1.0205	7	29.84	7
VL 2028	27.63	22	24.71	23	27.53	21	24.70	22	0.9346	23	27.33	23	0.9169	23	26.81	23
VL 2029	28.81	15	26.74	19	28.80	16	26.65	14	0.9805	17	28.67	17	0.9783	16	28.61	16
VL 2030	30.72	4	29.24	3	30.97	4	29.47	3	1.0562	4	30.88	4	1.0521	3	30.76	3
UP 2990	29.90	8	28.10	6	30.00	9	28.22	7	1.0218	9	29.88	9	1.0210	6	29.86	6
UP 2991	29.11	12	27.66	10	29.06	11	27.57	11	0.9992	11	29.22	11	0.9984	10	29.19	10
VL 907	29.61	9	28.48	5	29.78	10	28.79	5	1.0238	7	29.94	7	1.0183	9	29.78	9
HS 507	28.76	16	26.88	16	28.63	18	26.57	16	0.9809	16	28.68	16	0.9773	17	28.58	17

BLUP (average of values); HM-UP (Harmonic mean of BLUP); 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.6 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
HPW 349	26.51	3	17.62	4	26.51	5	17.08	5	0.9943	4	26.24	4	0.9937	4	26.22	4
HS 634	26.28	5	15.78	7	26.94	3	16.25	7	0.9438	7	24.91	7	0.9232	7	24.36	7
VL 907	25.91	6	19.27	1	26.24	7	19.65	1	1.0402	2	27.45	2	1.0222	2	26.97	2
HS 507	25.66	7	17.54	5	26.32	6	17.91	4	0.9816	6	25.90	6	0.9711	6	25.63	6
HPW 441	26.46	4	18.21	3	27.15	2	18.59	3	1.0120	3	26.71	3	1.0112	3	26.68	3
HPW 442	26.70	2	17.24	6	26.78	4	16.93	6	0.9867	5	26.04	5	0.9811	5	25.89	5
HS 562	27.20	1	18.74	2	28.23	1	19.54	2	1.0414	1	27.48	1	1.0387	1	27.41	1

BLUP (average of values); HM-UP (Harmonic mean of BLUP); 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)

Fig.1 Agro climatics zones for wheat cultivation in country

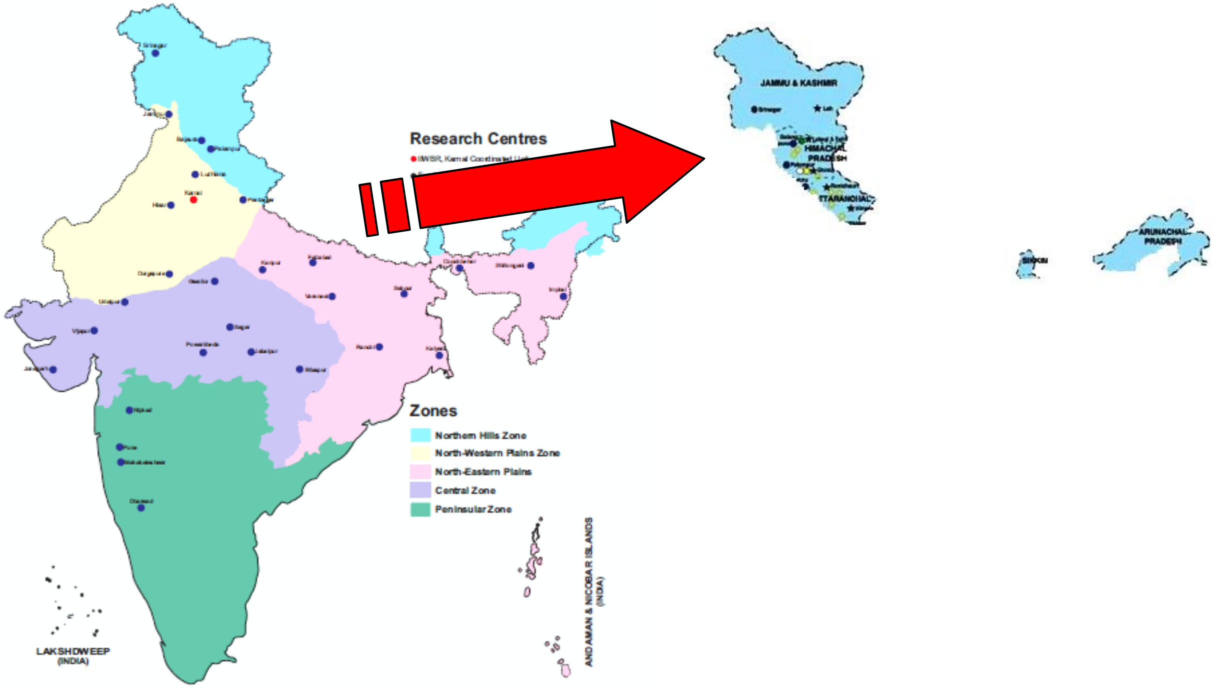


Fig.2 Average yield of wheat genotypes along with standard errors (2015-16)

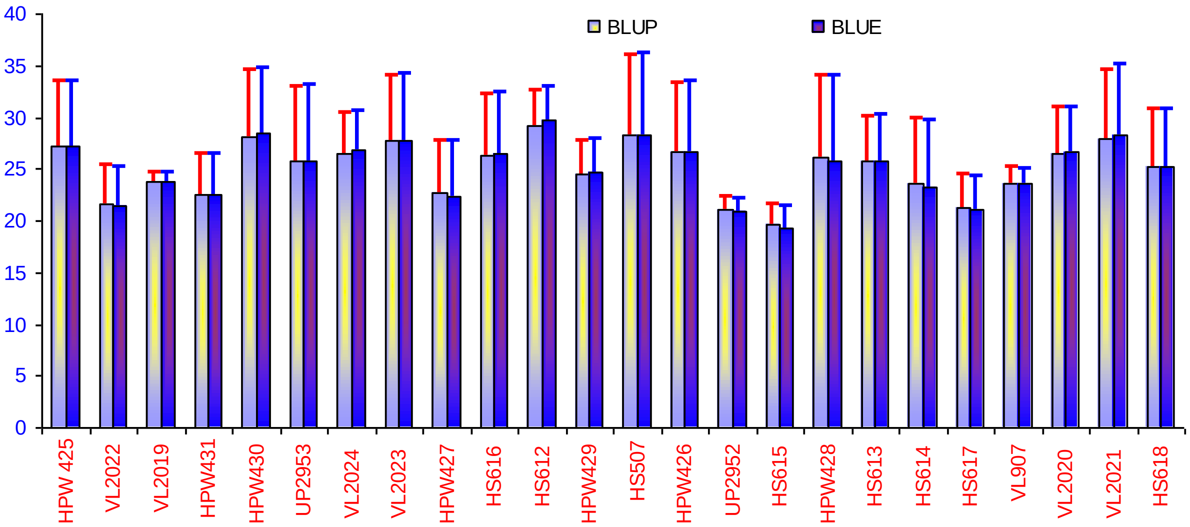


Fig.3 Average yield of wheat genotypes along with standard errors (2016-17)

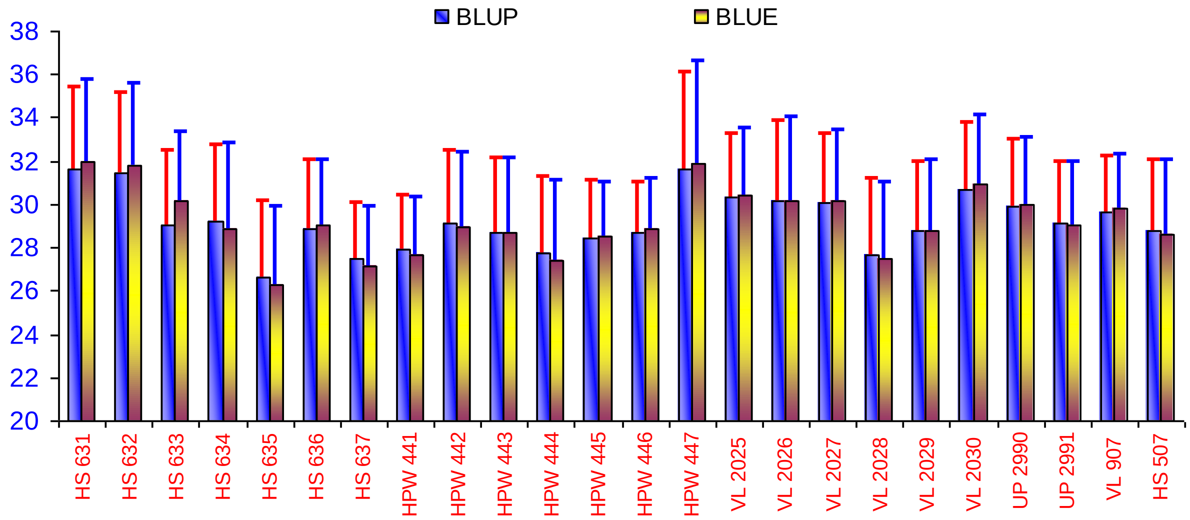


Fig.4 Average yield of wheat genotypes along with standard errors (2017-18)

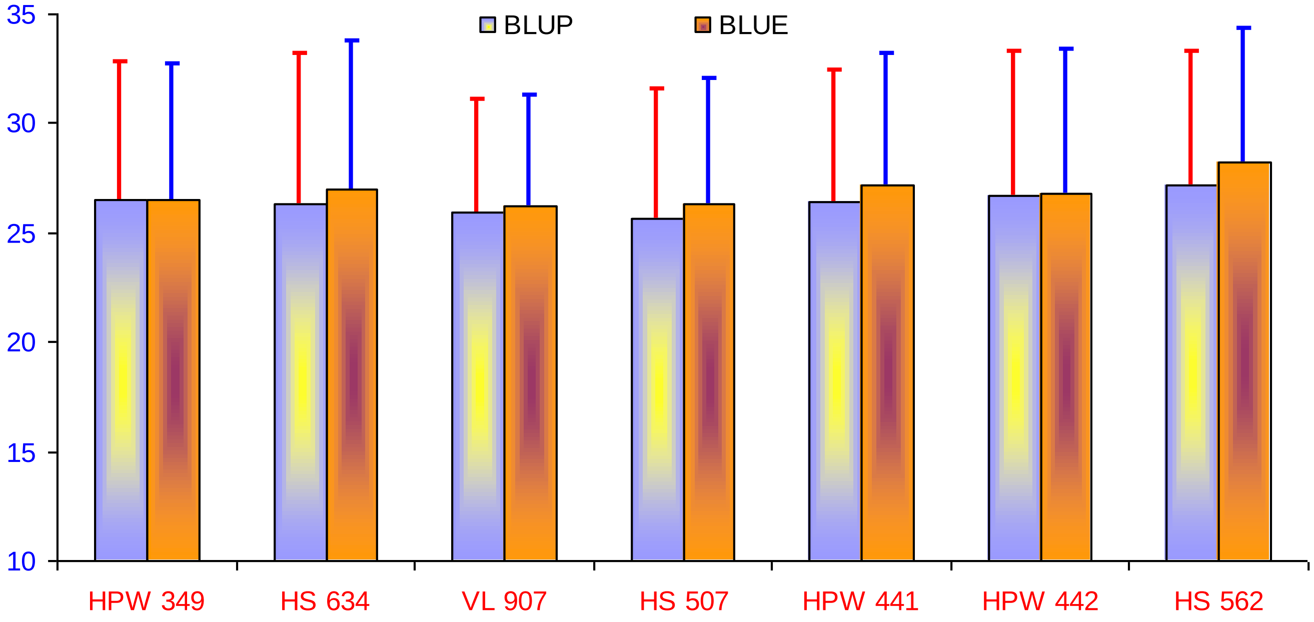


Fig.5 Biplot analysis of wheat genotypes vis-à-vis environments for irrigated timely sown trials (2015-16)

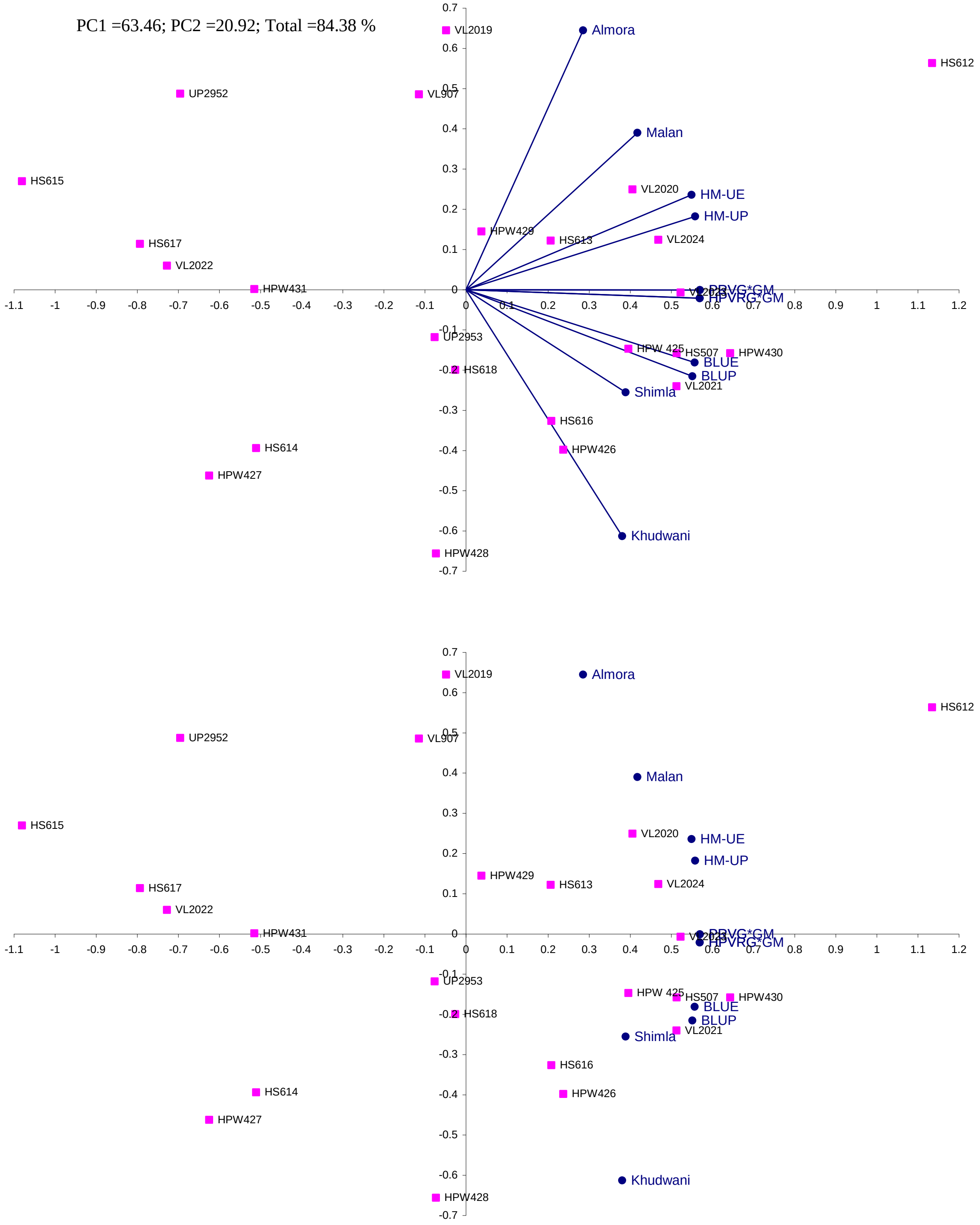


Fig.6 Biplot analysis of wheat genotypes vis-à-vis environments for irrigated timely sown trials (2016-17)

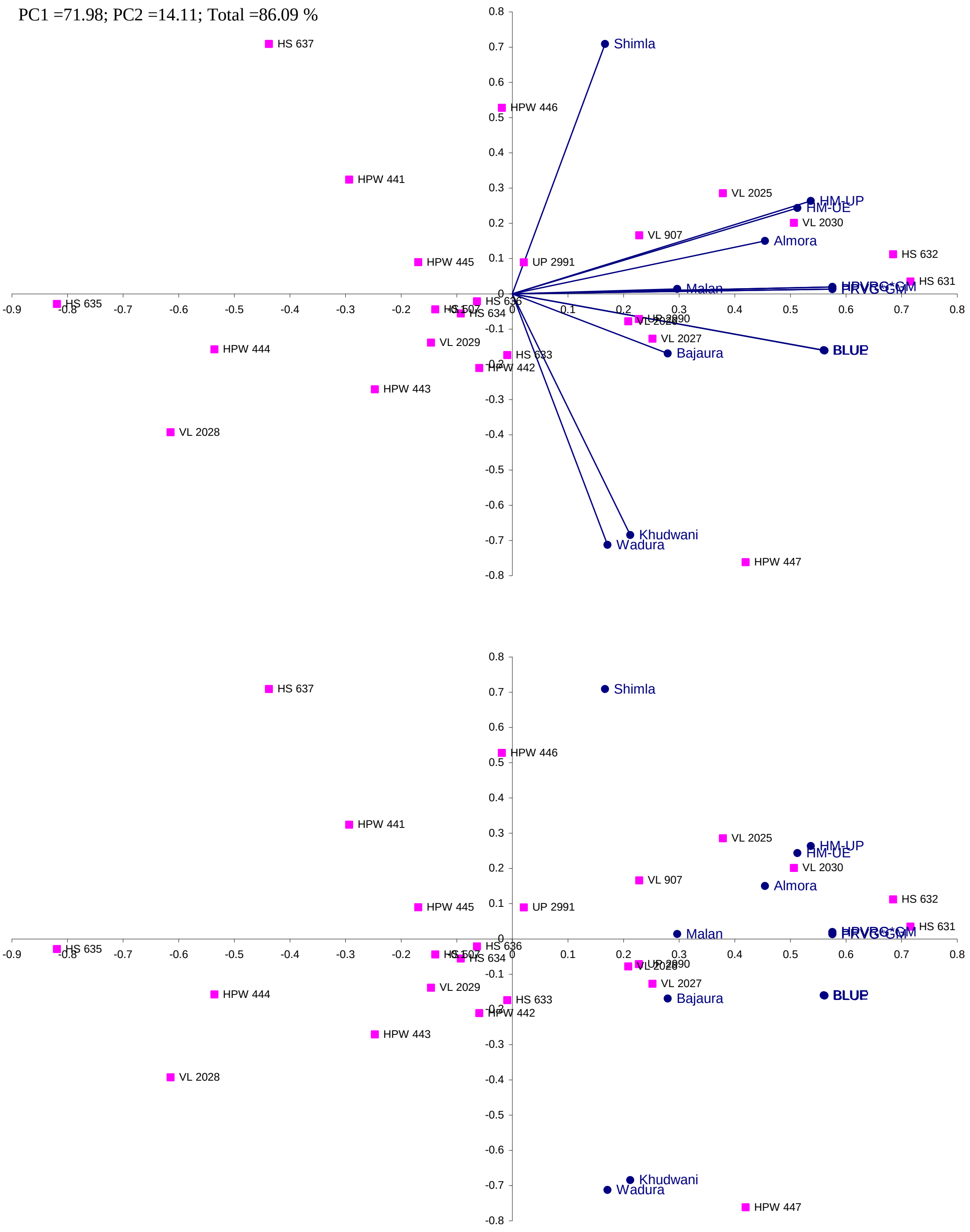
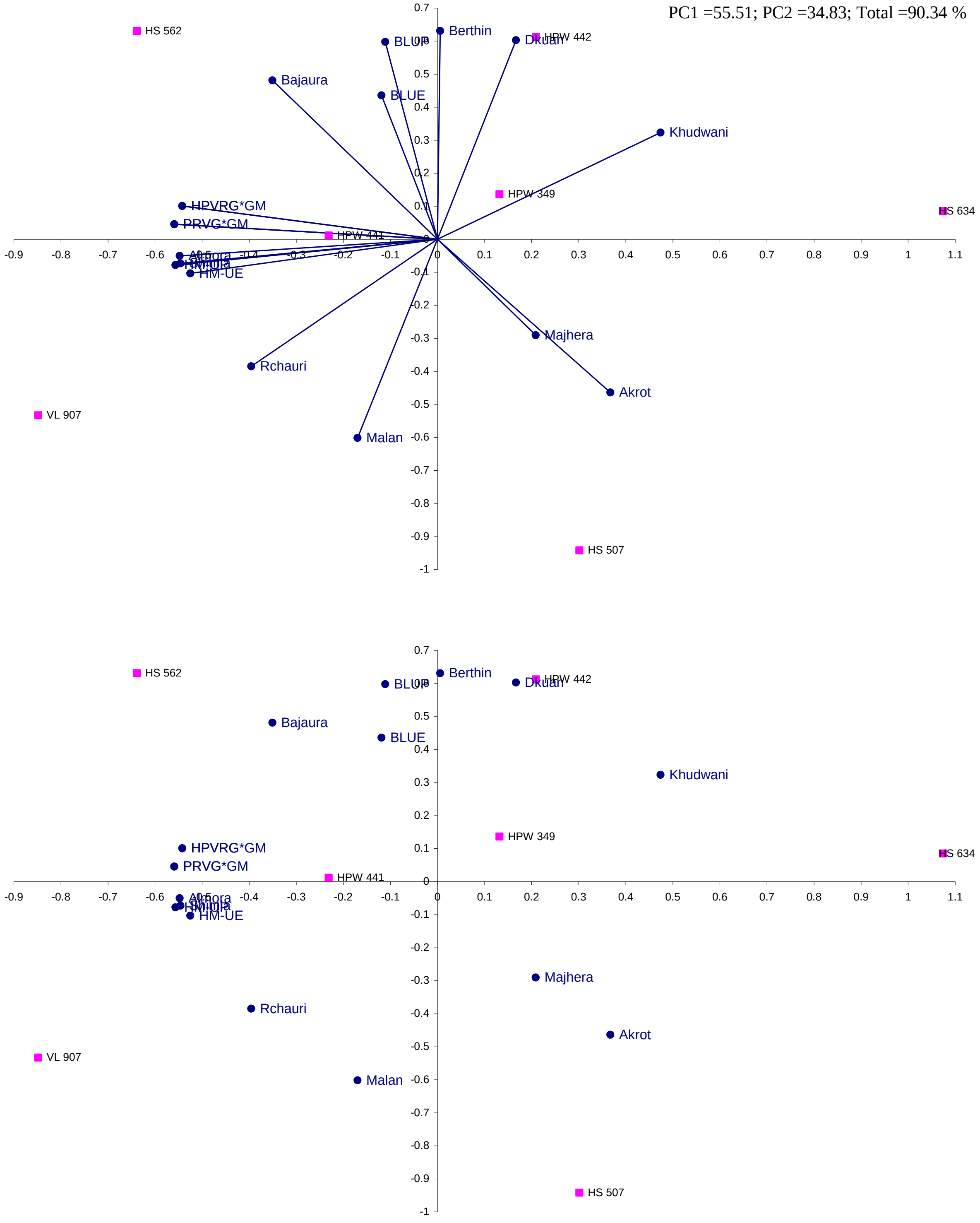


Fig.7 Biplot analysis of wheat genotypes vis-à-vis environments for irrigated timely sown trials (2017-18)



Malan with Almora, Shimla with Khudwani would show similar performance of genotypes as expressed acute angles among rays connecting these environments. Khudwani had an obtuse angle with Almora this would express different performance of genotypes for both locations.

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 (Kleinknecht *et al.,* 2011) in rational manner contributes to improve wheat productivity in Northern Hills Zone of the country.

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