

Biplot Analysis of Advanced Wheat Genotypes in Northern Eastern Plains Zone

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ABSTRACT

The biplot analyses methods of AMMI & GGE were applied to analyze multi-environment trials data for advanced wheat genotypes evaluated under northern eastern plains zone of the country. The combined analysis of variance showed that the interaction effect of genotypes with environment accounted for 57.3% of total variation. Genotypes PBW 693 and NW 5054 with mean yields greater than the overall mean and low IPC1 scores had a high combination of yield and stability performances. Based on the angles between environment vectors, the Patna, Coochbehar and Ranchi, Malda as well as Shillongani, Jalalgarh separated in a three groups highly correlated among themselves. The vertex genotypes in GGE biplot study were HD 3128, K 0307, NW 5054, HD 2733 and UP 2855 as these genotypes were farthest from the origin of the biplot.

Highlights

- Highly significant environment effect accounted for 75.4 % of total sum of squares (TSS).
- G×E accounted for 16.5% of TSS and was about fifteen times the G effect.
- IPC1 contributed 29.54% of G×E interaction.
- PBW 693 and NW 5054 expressed yields greater than overall mean accompanied low IPC1 scores desirable combination of yield and stability performances.
- Environments Patna, Coochbehar and Ranchi, Malda as well as Shillongani, Jalalgarh separated in a three groups showed high correlation among themselves.
- Obtuse angles of environments Varanasi with IARI Pusa, Kalyani with Shillongani and Patna with Ranchi indicated a negative correlation.

Keywords: Biplot analysis, AMMI, GGE, stability estimates

Multi-environment trials (MET) are conducted to evaluate yield stability performance of genetic materials under different environmental conditions (Yan *et al.* 2000; Yan and Rajcan 2002). Usually a genotype grown in various environments will show yield fluctuations. These differences are influenced by the different environmental conditions and referred as genotype-by-environment (G×E) interaction (Allard and Bradshaw 1964). However, significant cross over type genotype environment interaction reduces the genetic progress in plant breeding programs (Comstock and Moll 1963).

Numerous methods for judging the performance of

genotypes have been commonly used i.e. regression coefficient (Finlay and Wilkinson 1963), sum of squared deviations from regression (Eberhart and Russel 1966), stability variance (Shukla 1972), coefficient of determination (Pinthus, 1973), coefficient of variability (Francis and Kanneberg 1978) and additive main effects and multiplicative interaction (AMMI) (Zobel *et al.* 1988; Gauch 2006) to reveal patterns of interactions effects. The AMMI model uses analysis of variance (ANOVA, an additive model) to characterize genotype and environment main effects and principal component analysis (a multiplicative model) to characterize



their interactions (IPCA). The AMMI analysis has been shown to be effective as it captures major portion of the $G \times E$ sum of squares and estimates the main and interaction effects. The AMMI-1 biplot allow comparison with the output of other statistical methods presenting both yield and stability statistics simultaneously. It has been proposed that GGE biplot analysis was a useful method for the analysis of GE interactions (Fanet *et al.* 2007; Laffont *et al.* 2007; Yan and Kang 2003; Samonte *et al.* 2005) and had been exploited in the variety evaluation of wheat (Yan and Hunt, 2001; Yan *et al.* 2000).

Yan *et al.* (2000) developed GGE biplot for graphical display of $G \times E$ interaction pattern of MET data. GGE biplot analysis considers both genotype (G) and GE interaction effects (Yan *et al.* 2000). GGE biplot method is based on principal component analysis (PCA) to allow visual examination of the relationships among the test environments, genotypes and the GE interactions.

The main objectives of the present study was to (i) evaluate the performance of thirteen wheat genotypes under fifteen different growing conditions using biplot methodologies, (ii) compare the yield levels of each genotype in relation to ideal genotype and (iii) examine the classification of test environments vis-a-vis genotype discrimination.

MATERIALS AND METHODS

Thirteen advanced wheat genotypes were grown in 15 environmental conditions pertaining to Northern eastern plains zone of the country during 2013-14. More over the details on the wheat genotypes and environmental conditions are given in Table 1. The plant materials were evaluated in randomized complete block designs with four replications. Evaluations were conducted for several agronomic traits, but yield in all the considered environments were used for detailed study.

The effects of genotype (G), environment (E) and $G \times E$ interactions were calculated by combined analysis of variance (ANOVA) to estimate variance component for G, E and $G \times E$ interactions. Three stability parameters were derived from grain yield for stability analysis. The stability of yield performance for each genotype was calculated using the following methods. Annicchiarico (2002) suggested a reliable genotype characterized by having consistently high yield across environments.

The environmental variance, S^2_x [Roemer (1917) cited in Becker and Leon (1988)], is one of the stability measures for the static stability concept (Lin *et al.* 1986), was calculated for genotypes across environments. Genotype with minimum variance is considered as stable. Superiority index (P_i), which is an estimate of genotype adaptability over environments, is determined by utilizing the highest-yielding genotypes within each environment as a reference point. Genotypes with the largest yield difference from the reference genotype will have the highest P_i values (Lin and Binns 1988). The Wricke's (1962) ecovalence, which shows the contribution of a genotype to the interaction sum of squares, can be used as a measure of stability. A low ecovalence (W^2_i) value indicated high relative stability.

RESULTS AND DISCUSSION

The highly significant ($P < 0.01$) differences among all sources of variation were obtained from combined ANOVA analysis (Table 2). The environment (E) effect was accounted for 75.4 % of total sum of squares (TSS). The $G \times E$ was accounted for 16.5% of TSS and was greater about fifteen times than the G effect. Larger the interaction, as comparison to genotype effect, suggests the possibility of different mega-environments (Yan and Kang, 2003). This result supported the differential yield performance among wheat genotypes across testing environments due to the presence of $G \times E$ interaction. MET data may constitute a mixture of cross over and non-cross over types of interactions, the cross over type indicate the change in yield ranking of genotypes across environments whereas other shows constant yield rankings of genotypes across environment (Yan and Hunt, 2001; Matus-Cadiz *et al.* 2003).

This is supported by the fact that the $G \times E$ mean grain yield varied from 28.8 to 58.9 q/ha, while the genotype mean grain yield varied from 55 to 62 q/ha. The highest yield performance was observed for DBW39, PBW677 and PBW693, while the lowest was obtained by DBW98. The genotype HD2733 with high-yielding performance had good stability performance based on cultivar superiority while UP2855 with static stability. The genotype K1006 was low-yield performance were more stable as Wricke's ecovalence.



Table 1: Details of genotypes and environments

Genotype code	Genotype name	Parentage	Environment codes	Details	Latitude	Longitude
G1	DBW 98	PBW65/2*PASTOR//PBW55O	E1	Kanpur	26°29'N	80°18'E
G2	HD 3127	PBW343/C HO IX/Star/3/H E I/3*C NO79//2*SERI	E2	Faizabad	26°47' N	82°12' E
G3	PBW 693	WH890-AE.UMB.3732AMPH./CS(S)//WL711NN/3/*PBW343	E3	Varanasi	25° 20' N	83° 03' E
G4	HD 3128	VL849/HW5015	E4	Barabanki	26°94'N	81°.19'E
G5	HD 2733	ATTI LA/3/TU I/CARC//C H E N/C HTO/4I/ATT ILA	E5	Araul	26°92'31''N	80°19'60'' E
G6	NW 5054	TH E LI N//2*ATTI LA*2/PASTOR	E6	Iaripusa	25°.98'0 N	85°67' E
G7	WH 1132	PBW65/2*PASTOR	E7	Sabour	25° 23' N	87° 07' E
G8	DBW 39	ATTILA/HUI	E8	Patna	25°30' N	85°15' E
G9	UP 2855	PBW565/UP2565	E9	Ranchi	23°21'N	85°20'E
G10	HUW 661	W15.92/4/ PASTO R//H XL7 573/ 2*BAU/3/WB LL1	E10	Coochbehar	26°19'86'' N	89°23'53'' E
G11	PBW 677	PFAU/MILAN/5/CHEN/A.SQUARROSA//BCN/3/VEE#7/BOW/4/PASTOR	E11	Kalyani	22°57'N	88°20'E
G12	K 0307	K8321/UP2003	E12	Burdhwan	23°15' N	87°52' E
G13	K 1006	PBW343/HP1731	E13	Malda	25° 2' N	88° 8' E
			E14	Jalalgarh	25°94'36''N	87°53'46''E
			E15	Shillongani	26° 21' N	90°45' E

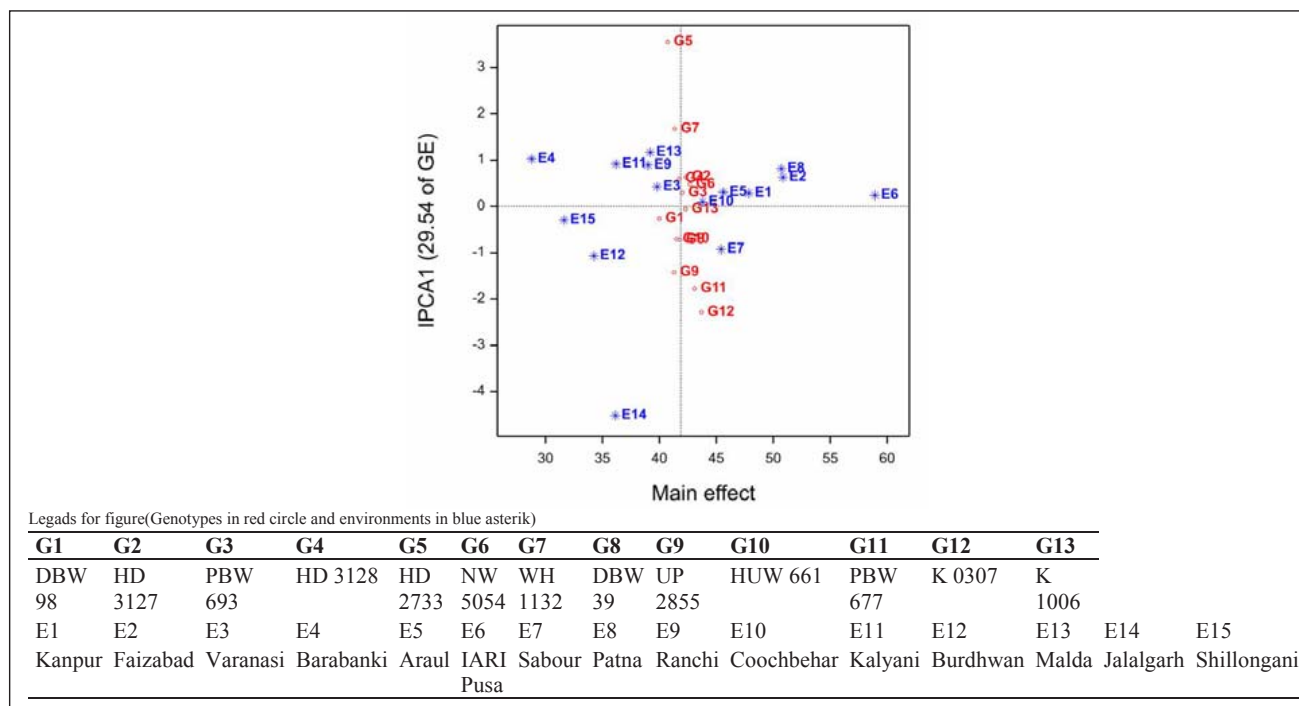


Fig. 1: AMMI-1 biplot of first IPCA scores against genotypes and environmental means

Table 2: Analysis of variance for yield of 13 genotypes in fifteen environments

Source	Degree of freedom	Sum of squares	Mean Sum of squares	Variance ratio	F probability	% TSS
Total	779	64476	82.8			
Treatments	194	59906	308.8**	43.06	<0.001	
Genotypes	12	688	57.3**	7.99	<0.001	1.07
Environments	14	48583	3470.2**	223.83	<0.001	75.35
Block	45	698	15.5	2.16	<0.001	
Interactions	168	10635	63.3**	8.83	<0.001	16.49
IPCA 1	25	3141	125.6	17.52	<0.001	
IPCA 2	23	2509	109.1	15.21	<0.001	
Residuals	120	4984	41.5	5.79	<0.001	
Error	540	3872	7.2			

TSS, total sum of squares, ** significant at $P < 0.01$

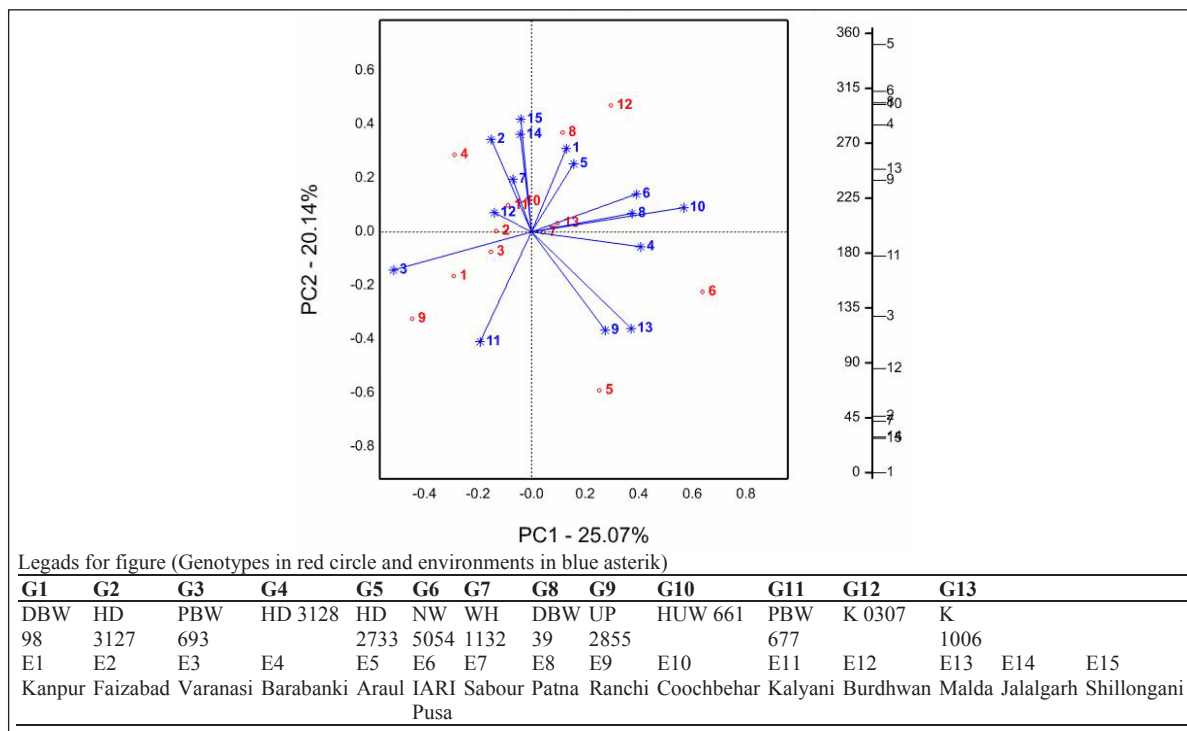


Fig. 2: Biplot depicts the relationship among test environments

In the AMMI-1 biplot analysis represents simultaneously both main effects (G and E) and stability (IPC1) of genotypes (Fig. 1). The IPC1 accounted for a total of 29.54% of the G×E interaction. Genotypes PBW 693 and NW 5054 with mean yields greater than the overall mean and low IPC1 scores had a high combination of yield and stability performances. Genotypes HD 3127 and HD 3128 were similar to PBW 693 and NW 5054 in the main effect but tended to contribute more to GE interaction. The two genotypes PBW 677 and K 0307, with mean yields less than the overall mean and

with the highest distance from the IPC1 = 0 level, tended to contribute highly to GE interaction and accordingly can be regarded as the most unstable genotypes.

Fig. 2 provides the summary of the interrelationships among the test environments. The lines that connect the biplot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation



Table 3: Meanyield and three stability parameters for wheat genotypes

Genotype	Genotype mean	Cultivar superiority	Static stability	Wricke's ecovalence
DBW 98	40.00	40.74	54.16	137.0
HD 3127	42.31	27.86	91.74	154.9
PBW 693	42.01	27.48	82.88	105.0
HD 3128	41.74	32.57	105.22	252.6
HD 2733	40.73	53.82*	96.78	427.1
NW 5054	42.68	30.59	97.87	340.9
WH 1132	41.34	36.11	90.72	157.7
DBW 39	41.80	26.57	95.46	192.6
UP 2855	41.29	32.28	45.44*	280.1
HUW 661	41.51	28.51	78.15	79.5
PBW 677	43.10	18.53	86.21	177.3
K 0307	43.70*	18.03	73.57	276.0
K 1006	42.30	26.04	59.27	78.0*

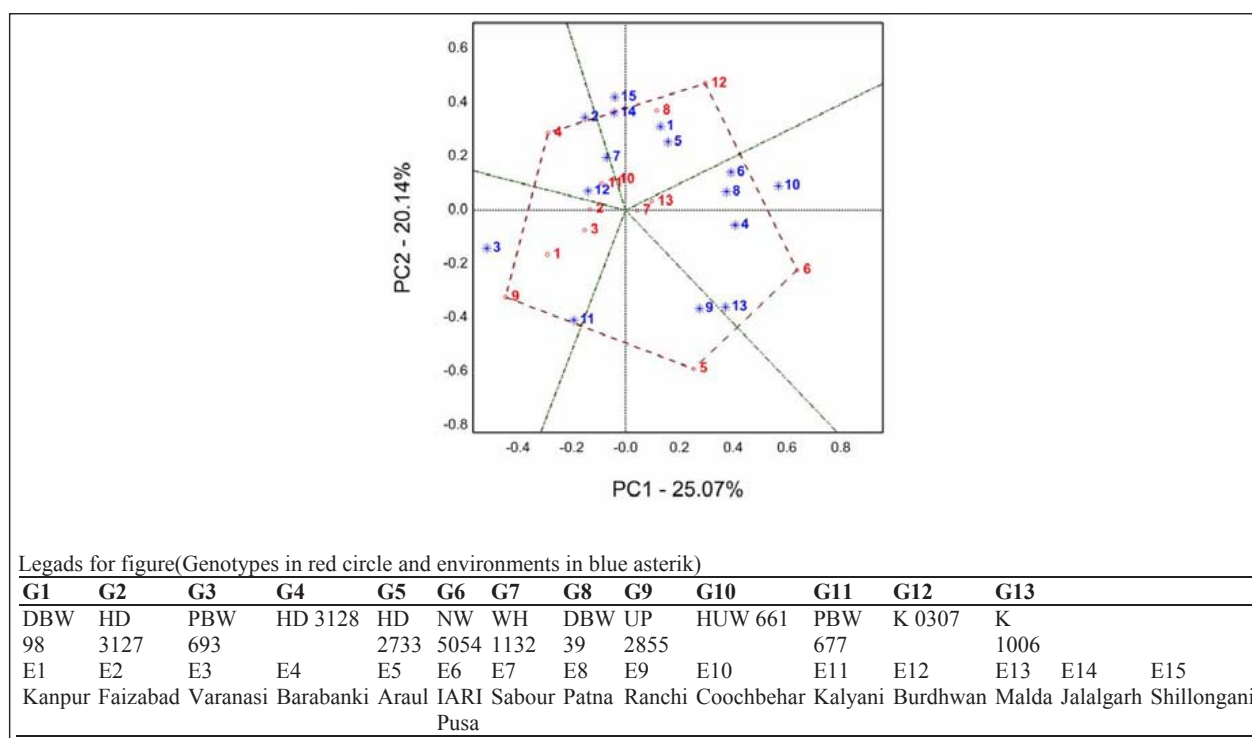


Fig. 3: Polygon view of genotype – environment interaction

coefficient between them (Kroonenberg 1995; Yan and Rajcan 2002). Acute angles indicate a positive correlation, obtuse angles for negative correlation and right angles show no correlation (Yan and Kang 2003). A short vector may indicate that the test environment (Burdhwan) is not related to other environments. Based on the angles between environment vectors, the Patna, Coochbehar and Ranchi, Malda as well as Shillongani, Jalalgarh

separated in a three groups highly correlated among themselves from other clusters of environments. The environments Varanasi with IARI Pusa, Kalyani with Shillongani and Patna with Ranchi made an obtuse angle, which indicates a negative correlation between the responses of genotypes to these environments.

Polygon was formed by connecting the vertex genotypes in respective sectors with straight

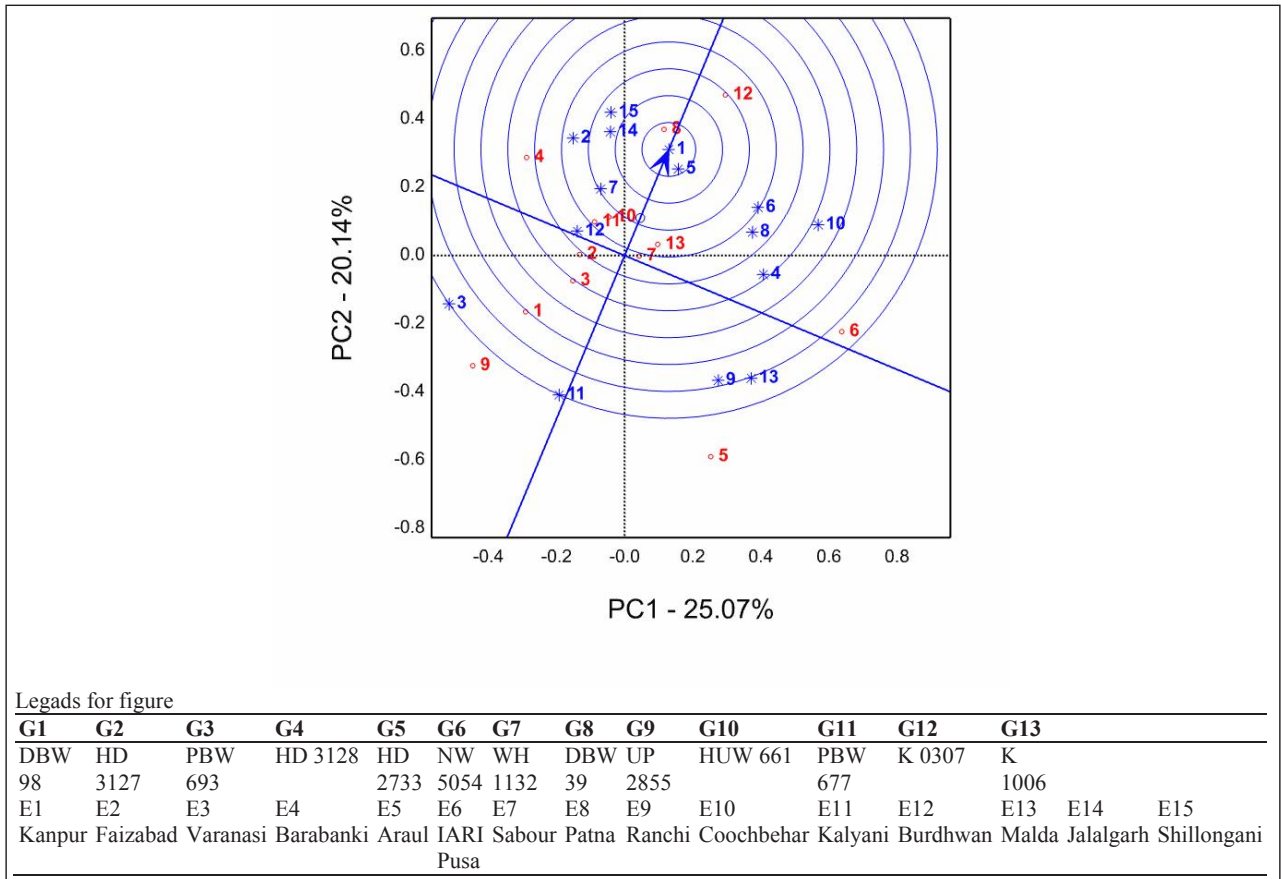


Fig. 4: Ranking of genotypes relative to ideal genotype 10

lines and the rest of the genotypes placed within the polygon. The partitioning of G×E interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 25.07% and 20.14% of GGE sum of squares, respectively, explaining a total of 45.21% variation. The vertex genotypes in this study were HD 3128, K 0307, NW 5054, HD 2733 and UP 2855. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang 2003). From the polygon view of biplot analysis of MET data the test environments fell in five sections. The first section contains the major test environments IARI Pusa, Patna, Coochbehar, Barabanki, Malda which had the genotype NW 5054 as the winner; the second section contains the environments Sabour, Shillongani, Jalalgarh Kanpur, Araul with DBW 39 as the best yielder. The test environment Ranchi was fallen in a separate section without any yielder.

Genotype with highest yield and stability value regarded as ideal genotype (Yan and Kang 2003).

Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero G×E (or highest stability), as represented by the dot with an arrow pointing to it (Fig. 4). An ideal genotype HUW 661 is located at the center of the concentric circles. Ideal genotype projection on the ATC x-axis is designed to be equal to the longest vector of all the genotypes. The ideal genotype is stable because its projection on the ATC y-axis is near zero. A genotype is more favorable if it is closer to the ideal genotype. The PBW 677 and K 1006 were near to the ideal genotype. Ranking of other genotypes based on the ideal genotype was WH 1132>HD 3127>PBW 693>HD 3128. In other words, the lower yielding genotypes (UP 2855&HD 2733) were unfavorable because they are far from the ideal genotype.

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