

# Genotype By Environment Interaction and Stability Analysis for Maize Hybrids in North Western Himalayas Ecology

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**KeyWords** Maize (*Zea mays* L), Genotype x Environment interaction, Yield Stability Index, Ranking Sum and Stability

**Abbreviations** AMMI – Additive main effects and Multiplicative Interaction; ASV – AMMI stability value; RS – Ranking sum, YSI- Yield stability index, GGE - genotype + genotype \* environment

## Abstract

Genotype (G) x Environment (E) interaction of 25 medium maturity maize hybrids tested at three environments in North-Western Himalayas was analyzed to identify stable high yielding hybrids for mid hill conditions. The G x E interaction was studied using different stability statistics viz; Additive main effects and multiplicative interaction (AMMI), AMMI stability value (ASV), rank sum (RS) and yield stability index (YSI). Combined analysis of variance shows that genotype, environment and G x E interaction are highly significant. This indicated possibility of selection of stable genotypes across the environments. The results of AMMI analysis indicated that first two principal components (PC1-PC2) were highly significant ( $P < 0.05$ ). The partitioning of TSS (total sum of squares) exhibited that the environment effect was a predominant source of variation followed by genotypes and GxE interaction, suggesting the possible existence of different environment groups. The first two interaction principal component axis (IPCA) cumulatively explained 82.87% of total interaction effect. The study revealed that G11 and G7 were found to be stable based on all stability statistics and GGE biplot assessment. Based on GGE biplots, it is concluded that E3 is best environment for testing the hybrids for wider adaptability and E2 and E1 locations can be used to identify location specific hybrids. Grain yield is positively and significantly correlated with rank-sum (RS) and yield stability index (YSI). The above mentioned stability statistics could be useful for identification of stable high yielding genotypes, whereas, GGE biplots facilitated visual comparisons of high yielding genotypes across the multi-environments.

## Introduction

Maize or Indian corn (*Zea mays* L.) is an important cereal crop of the world after wheat and rice (Morris et al., 1999). It has a wider range of uses than any other cereals as animal feed, human food and for industrial purposes (White and Johnson, 2003). It belongs to the family Poaceae and the tribe Maydeae and originated in Mexico and evolved from teosinte (*Zea Mexicana*) (De Wet and Harlan, 1972). It is also known as miracle crop. It has very high yield potential as compared to other cereals and, that is why it is referred to as "queen of cereals". In India, it is grown in an area of about 8.67 million hectares with an overall production of 23.68 million tonnes and productivity of 2564 Kg/ha (Anonymous, 2016).

It is cultivated in diverse agro-climatic conditions across the world. It is cultivated in the tropics, sub-tropics and temperate regions; from sea level to > 4000 m above sea level, under irrigated to semi-arid conditions. Maize is staple food in African countries and in other part of

the world it is mainly utilized in feed industry. Maize ranks first among cereal food crops in world production (868 million tons from 168 million hectares) followed by wheat and rice. It represents 38% of the total grain production as compared to 30% for wheat and 20% for rice (FICCI, 2014).

Maize improvement programme is heavily based on exploitation of heterosis for grain yield. Per se performance of the inbred lines, source population from where it derived and genetic diversity between the inbred lines are major factors determining success of single cross hybrid development programme (Edmeades et al., 2001). The search for hybrid combinations with high grain yield adapted across the environments is one of the most important objectives of the breeders. Allelic homeostasis seems to be essential for stability and adaptability of single cross hybrids across the environmental regimes. Multi-environment evaluation experiments are essential to evaluate grain yield and to quantify adaptability and stability of the hybrids since this is complex trait and highly influenced

by environments (Edmeades et al., 2000). Changes in the relative behaviour of the genotype in different environments are usually noticed if experiments are conducted over the years and locations, and the phenomenon is generally referred to as genotype by environment interaction (G×E). The higher G × E interaction makes it difficult to select genotypes that produce high grain yield across the environments. Due to changing climate and inclement weather conditions throughout the year in general and during the cropping season in particular, the criteria for selection based on general as well as specific stability and adaptability parameters seems to be more relevant in improvement programme specifically in case of single cross hybrids, where only two parents are involved. Further, fragile ecosystem of North-Western Himalayas, where maize is cultivated under rain fed conditions and influenced by macro as well as micro environmental conditions and altitudinal variation, necessitate identifying maize hybrids which could perform uniformly across the zone. The development of hybrids/varieties, which can be adapted to a wide range of diversified environments, is the ultimate goal of plant breeders.

Genotype adaptability and stabilization of maize production under ecosystem of North-Western Himalayas over to environmental fluctuations is vital. Thus, evaluation of maize genotypes for yield stability under varying environmental conditions has become an essential part of breeding programme. Genotype by environment interaction has been studied previously by various researchers (Zubair and Ghafoor, 2001; Ramburan et al., 2011; Kumar et al., 2014).

Many statistical methods for quantifying genotypes (G), environment (E) and their interaction are available (Gauch, 2013). However, a method called (AMMI) has been found particularly useful in visualizing G × E effects graphically (Jha et al., 2013 and Kumar et al., 2014).

The AMMI model increases the probability of selection high yielding genotypes. The other stability statistics like AMMI stability value (ASV) has been taken into consideration (Purchase et al., 2000) because AMMI model does not make any provision for quantitative stability measure, which is essential to quantify and rank the genotypes for their stability. Apart from this, another stability statistics i.e. yield stability index (YSI) which incorporates both mean yield and stability in a single criterion (Farshadfar, 2011) has been used to measure the stability of tested genotypes. Hence, the objective of this study was to find out the stable genotypes across the environment using different stability statistics and to find out the interrelationship among these stability

statistics as well confirmation of stability of tested genotypes through GGE biplot display.

### Materials and Methods

The material for the present investigation comprised of 23 newly developed single crosses along with two released checks of maize viz., one composite Bajaura Makka and one single cross maize hybrid of private sector Bio 9544 (Table 1).

**Table 1 - Locations used for evaluation of medium maturity hybrids**

Location/ Parameters	Kangra	Bajaura	Udhampur
Altitude	700.00m	1090.00m	634.00m
Latitude	32°09'N	32°20'N	32°54'N
Longitude	76°22'E	77°00'E	75°09'E
Total Rainfall (mm)	1317.5	420.00	807.2
Average Temp °c (Max)	32.05	30.1	32.05
Average Temp °c (Min)	21.80	18.27	21.22

Note: Data for maize crop season Kharif 2016

### Agronomical trials

All the 25 genotypes were evaluated in randomized complete block design (RCBD) with three replications during Kharif 2016 at three locations namely Bajaura, Kangra (Hmachal Pradesh) and Udhampur (Jammu & Kashmir) located at different altitudes in north-western Himalayas (Table 2). Performance evaluation experiments were conducted at in plot size of 3.12 meter<sup>2</sup> at Kangra (E1), 4.8 meter<sup>2</sup> at Udhampur (E2) and 3.0 meter<sup>2</sup> at Bajaura (E3) with spacing of 60x 20cm line to plant basis under rainfed conditions at Kangra and Udhampur, whereas, three supplementary irrigation were provided at Bajaura during no rainfall period. All the locations were considered as different environments as there were difference in average rainfall, mean temperature, humidity and soil type. All the necessary agronomic and cultural practices were timely followed to ensure good plant stand. At harvest grain yield was recorded on plot basis and then converted to yield Kg/ha. The fertilizer dose was applied @ 120:60:40 of N: P: K Kg/ha. The entire dose of P, K along with 50% of N was applied as basal dose, while the rest of 50% of N was applied in two split doses, one 35 days after sowing (knee-height stage) and other at flowering stage of crop.

**Table 2 - Code and Pedigree of maize hybrids along with their source of seed**

1	G1	LMH-1615	CSKHPKV, HAREC, Bajaura
2	G2	LMH-1715	CSKHPKV, HAREC, Bajaura
3	G3	LMH-1815	CSKHPKV, HAREC, Bajaura
4	G4	KMH-13-17	CSKHPKV, SAREC, Kangra
5	G5	PMH-35	CSKHPKV, Palampur
6	G6	PMSW4	SKUAST, Srinagar
7	G7	LMH-1915	CSKHPKV, HAREC, Bajaura
8	G8	LMH-2015	CSKHPKV, HAREC, Bajaura
9	G9	PMH-48	CSKHPKV, Palampur
10	G10	LMH-2115	CSKHPKV, HAREC, Bajaura
11	G11	KMH-13-79	CSKHPKV, SAREC, Kangra
12	G12	LMH-2215	CSKHPKV, HAREC, Bajaura
13	G13	LMH-2315	CSKHPKV, HAREC, Bajaura
14	G14	PMSY-3	SKUAST, Srinagar
15	G15	LMH-2415	CSKHPKV, HAREC, Bajaura
16	G16	KMH-13-15	CSKHPKV, SAREC, Kangra
17	G17	LMH-2515	CSKHPKV, HAREC, Bajaura
18	G18	LMH-2615	CSKHPKV, HAREC, Bajaura
19	G19	UDMH-1220	SKUAST, Udhampur
20	G20	UDMH-121	SKUAST, Udhampur
21	G21	LMH-2715	CSKHPKV, HAREC, Bajaura
22	G22	KMH-13-5	CSKHPKV, SAREC, Kangra
23	G23	UDMH-123	SKUAST, Udhampur
24	G24	BajauraMakka	CSKHPKV, HAREC, Bajaura
25	G25	BIO-9544	Bioseed Pvt. Ltd.

### Statistical analyses

Grain yield (Kg/ha at 15% moisture) was used for AMMI analysis using software GENSTAT 12.0 (Genstat, 2009). AMMI analysis was based on model by (Gauch, 2006) and GGE was based on the model for two principal components (Yan and Kang, 2003). The combined ANOVA for all three locations was done to estimate the variations in the genotypes under study and partitioning of G x E interaction. AMMI combines ANOVA into single model with additive and multiplicative parameters.

### AMMI stability value (ASV)

AMMI model suffers from limitations that it does not provide quantitative measure of stability; however, such measures are essential in order to quantify and rank genotypes according to their yield stability. The AMMI stability values (ASV) were calculated to study the stability of genotypes across the environments following the formula of Purchase et al. (2000). The lower stability value indicated high stability and *vice versa*.

### Rank-Sum (RS)

Rank-sum was calculated using following formula (Farshadfar and Elyasi, 2012):

RS = Rank mean (R) + Standard deviation of rank (SDR)

Low value of RS was taken as most stable genotypes with high yield.

### GGE -Biplot

The GGE biplot is modification of AMMI analysis which provides graphical display and is considered as an

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} + (IPCA1 \text{ score})^2 + (IPCA2 \text{ score})^2}$$

Where  $\frac{SS_{IPCA1}}{SS_{IPCA2}}$  is the weight given to the IPCA1-

innovative methodology for applied plant breeding. This methodology uses a biplot to show the factors (G + GE) that are important in genotype evaluation and also source of variations in GEI analysis of multi environment trials (METs) data (Yan et al., 2000). In the present study, genotype –focused scaling was used in visualizing for genotypic comparison, with environment –focused scaling for environment comparison. The statistical analysis was done using software GENSTAT 12.0.

### Results and Discussion

#### Additive main effects and Multiplicative Interaction

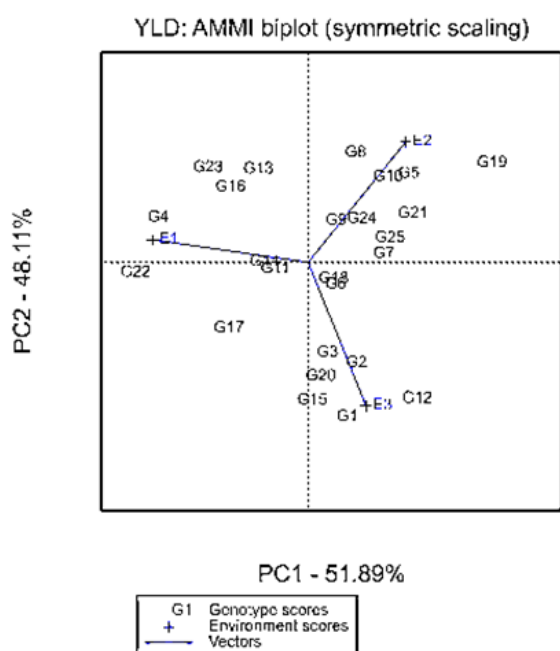
The combined analysis of variance showed significant differences for environment, genotype and interactions. The AMMI analysis of variance for grain yield (Kg/ha) of 25 maize genotypes was tested in three environments. The AMMI results show that 35.29% of total sum of squares was attributed to environmental effects, 27.90% to genotypic effect and 24.30% to G x E interaction as shown in Table 3. The analysis revealed that variances due to environments, genotypes and G x E interactions were highly significant ( $P \leq 0.05$ ). The large sum of squares for environments indicated that the environments were diverse, with difference among environmental means (Rodriguez et al., 2008, Bahrami et al., 2009; Kumar et al., 2014). The AMMI model exhibited significant G x E interaction. G x E variance is partitioned into two principal components (PC1 and PC2). Cumulatively these two principal components

**Table 3 - AMMI analysis of variance over three environments**

Source	Df	SS	MS	Variation % explained
Treatments	74	584515947	7898864**	
Genotypes	24	186381953	7765915**	27.90
Environments	2	235757297	117878649**	35.29
Blocks	6	17858806	2976468**	24.30
Interactions	48	162376696	3382848**	
IPCA1	25	84249938	3369998**	58.99
IPCA2	23	78126759	3396816**	23.88
Error	144	65576731	455394	
Total	224	667951485	2981926	

\*\* Significant at 5 % probability level

explained 82.87% variation; PC1 accounted for 58.99% and PC2 23.88% (Table 3). This indicated sufficient approximation of data by the two PC scores for grain yield of genotypes in different environments.



**Fig. 1 - Biplot of 25 genotypes and three environments for grain yielding using genotype and environmental scores**

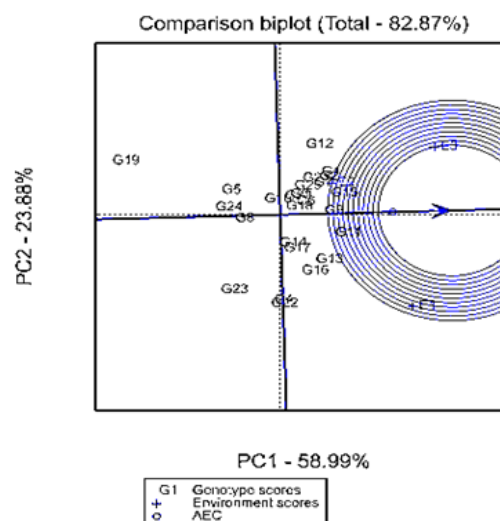
The biplot of IPCA1 against IPCA2 was given in Figure 1. In addition, the AMMI analysis selected best genotypes in each environment namely G13 in E1, G21 in E2 and G1 in E3 (Table 4). In Figure 1, the IPCA scores of both the genotypes and environments were plotted against the grain yield for the genotypes and the environments.

The values of yield and different stability parameters viz; IPCA1, IPCA2, ASV, YSI and RS for the 25 maize genotypes are given in Table 4. To find out

the relationship among different parameters, rank correlation was performed. Grain yield is positively and significantly correlated with yield stability index (YSI) and rank sum (RS) ( $P \leq 0.05$ ), but not with AMMI stability value (ASV); the correlation of YSI with all parameters is significant ( $P \leq 0.05$ ) (Table 5).

### Genotype and genotype per environment Assessment

Ranking based on the genotype –focused scaling assumed that stability and mean yield were equally important (Yan, 2002). The best candidate genotypes were expected to have high mean grain yield with stable performance across all test locations. In practice, such genotypes are very rare to find. Therefore, high yielding and relatively stable genotypes can be considered as reference for genotype evaluation (Yan and Tinker, 2006).



**Figure 2 - GGE biplot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability**

IPCA1s were sufficient to predict accurate AMMI model. The genotype G11 is high yielder and ranks first based on ASV, YSI and RS with values of 8.61, 5 and 5.46 respectively followed by G9 with values 8.13, 5 and 5.87 respectively (Table 4). Hence, G11 is stable genotype followed by G9. The genotype will be stable across all the environments with its score near to zero in the interaction of IPCA1 versus IPCA2 (Sanni et al., 2009).

The genotype focused comparison of genotypes revealed that G11 fell near to the central circle indicating its high yield potential and relative stability compared to the rest of the genotypes evaluated in this study (Figure 2). In addition, genotype G9 fell closer to the ideal genotype, suggesting that this genotype is also high yielding and stable (Figure 2). An

**Table 4 - Yield, first and second IPCAs, ASV, YSI and RS of 23 genotypes and two checks**

S. No.	Name	Pedigree	GY	IPCA1	IPCA2	ASV	YSI	RS
1	G1	LMH-1615	8131	4.95	-27.03	28.3	30	11.17
2	G2	LMH-1715	8233	6.58	-17.61	19.36	19	9.96
3	G3	LMH-1815	7597	1.53	-15.78	16.33	23	15.35
4	G4	KMH-13-17	7380	-27.99	7.83	29.94	42	15.21
5	G5	PMH-35	6682	15.71	15.49	22.72	40	18.76
6	G6	PMSW4	7907	2.95	-3.88	5.02	14	11.36
7	G7	LMH-1915	8431	11.38	1.5	11.82	1	6.21
8	G8	LMH-2015	6954	6.42	19.09	20.74	37	18.46
9	G9	PMH-48	8676	3.04	7.28	8.13	5	5.87
10	G10	LMH-2115	7558	11.3	14.93	19.29	26	15.11
11	G11	KMH-13-79	8702	-8.27	-1.2	8.61	5	5.46
12	G12	LMH-2215	7982	16.41	-23.83	29.80	33	13.20
13	G13	LMH-2315	8514	-11.31	16.25	20.39	16	7.10
14	G14	PMSY-3	7512	-10.23	0.05	10.54	22	13.90
15	G15	LMH-2415	8325	-1.91	-24.15	24.95	24	8.72
16	G16	KMH-13-15	8189	-16.17	13.12	21.45	25	9.44
17	G17	LMH-2515	7391	-16.44	-11.56	20.7	33	15.50
18	G18	LMH-2615	7694	1.82	-2.88	3.51	14	13.73
19	G19	UDMH-1220	4463	29.45	17.34	35.2	50	24.40
20	G20	UDMH-121	7406	-0.41	-19.95	20.55	31	16.11
21	G21	LMH-2715	8316	15.65	8.45	18.32	16	9.44
22	G22	KMH-13-5	7132	-32.76	-1.77	33.79	44	16.94
23	G23	UDMH-123	6413	-20.11	16.52	26.81	43	12.99
24	G24	Bajaura Makka	6366	6.74	7.57	10.44	29	21.16
25	G25	BIO-9544	8051	11.65	4.21	12.76	18	11.69

GY-Grain yield, IPCA-Interaction principal component axis, ASV- AMMI stability value, YSI-Yield stability index, RS- Rank sum

environment is more desirable if it is located closer to the ideal environment (Table 6). Thus, using the ideal environment as the centre, concentric circles are drawn to visualize the distance between each environment as the ideal environment (Yan, 2001). Figure 2 indicated that E3 which fell near the centre of concentric circles was an ideal test environment in terms of being the most representative of the all environments under study to discriminate genotypes.

GGE biplot also identified G11 and G9 as highest yielding genotypes and most stable genotypes (Figure 2.). The general adaptability of these high yielding maize hybrids may be due to diversity of parents, allelic homeostasis and complementation of the grain yield related genes of the parents. The biplot of the two IPCAs does not show the best adapted genotype and/or genotypes to most environments. The genotypes suitable for ENV 1 were G13, G16, G11 and G4,

whereas G21, G9, G7 and G13 were best for ENV 2. The best genotypes with respect to E3 were G1, G15, G12 and G2. Considering the environments tested in the study, no single environment had both IPCA1 and IPCA2 scores close to zero line (Figure 1). This indicated that all the environments had potential for large G x E interaction. The significant correlation of grain yield (GY) with rank sum (RS) and yield stability index (YSI) ( $P \leq 0.05$ ) indicated the good potential of these statistics for selecting the most stable high yielding genotypes. In addition, visual interpretation of GE interaction also facilitated the genotype recommendations (Figure 2). Based on GGE biplot assessment, only these two genotypes viz., G11 and G9 were also identified as most stable and high yielding. Hence, the experiment conducted on 25 maize genotypes in three environments G11 was found to be stable and high yielding using all the stability parameters and GGE biplot assessment followed by G9 and could be grown



**Table 5 - Correlation matrix of four stability measures**

Variables	GY	ASV	YSI	RS
GY		0.385	0.835**	0.933**
ASV			0.804**	0.388
YSI				0.793**
RS				

\*\*Significant at 5% probability level

under mid- hills of the north western Himalayas agro-ecologies where these were tested and other area of similar conditions

**Table 6 - AMMI selections of genotypes per environment**

No.	Environment	Mean (kg/ha)	Score	First four AMMI selections		
				1	2	3
1	E1	6803	-58.79	G13	G16	G11
2	E2	6943	36.95	G21	G9	G7
3	E3	9041	21.84	G1	G15	G12

### Conclusions

Combined analysis of variance shows that genotype, environment and G x E interaction are highly significant indicating the existence of a wide range of variation between the genotypes, environments and their interactions. The existence of such significant G x E interaction indicated possibility of selection of stable genotypes across the environments. The genotype G11 is high yielder and ranks first based on ASV, YSI and RS followed by G9 and could be grown under mid- hills of the north western Himalayas agro- ecologies where these were tested and other area of similar conditions. It was also observed that test environment E3 could be an ideal in terms of being the most representative of the all environments under study to discriminate genotypes. This information could be useful in performance trials by identifying the best test environment under limited resources. In addition, it was concluded that there is no difference between AMMI and GGE biplot analysis in evaluating experimental maize hybrids and test environments in this study and both methods can be used successfully in determining suitable location for maize hybrids in the environments under mid- hills of the north western Himalayas agro- ecologies.

### References

Anonymous 2016. Annual progress report. ICAR-IIMR, Ludhiana. pp. 11.  
Bahrami S, Bihanta MR, Solouki M, 2009. Adaptation and stability analysis of hulless

barley (*Hordeum vulgare* L.) genotypes in temperate regions of Iran. *Trakia Journal of Sciences I*: 8-17.

De Wet JMJ, Harlan JR, 1972. Origin of maize: the tripartite hypothesis *Euphytica* 21: 271-279.

Edmeades GO, Bolanos J, Elings A, Ribaut JM, Banziger M, Westgate M E, 2000. Physiology and modeling kernel set in maize, "The role regulation of the anthesis-silking interval in maize", pp. 43-73. Westgate ME, Boote BJ, eds, CSSA Special Publication 29, CSSA, Madison, WI.

Edmeades GO, Copper M, Lafitte R, Zinselmeier C, Ribaut JM, Habben JE, Lolfer C, Banziger M, 2001. *Crop science: Progress and Prospects*, "Abiotic stress and staple crops", pp. 137-154.

Nosberger J, Geiger HH, Struic PC, eds., *Proc. of Third Int. Crop Sci. Congress*, 17-21 August, 2000. CAB Int., Wallingford, Oxon, U. K.

Farshadfar E, 2011. Chromosomal localization of the genes controlling adaptation in *Agropyron elongatum* using AMMI-based simultaneous selection index of yield and yield stability. *Int. J. Plant. Breed.* 5(2): 80-83

Farshadfar E, Elyasi P, 2012. Screening quantitative indicators of drought tolerance in bread wheat (*Triticum aestivum* L.) landraces. *Eur J of Exper Biol* 2: 577-584.

FICCI 2014. Website: [www.ficci.com/publicationpage.asp](http://www.ficci.com/publicationpage.asp). Accessed on 1st Jan., 2014.

Gauch H G 2006. Statistical analysis of yield trials by AMMI and GGE. *Crop Science* 53: 1860-1869

Gauch H G 2013. A simple protocol for AMMI analysis of yield trials. *Crop Science* 53: 1860-1869

Gauch HG, Zobel R W, 1996. AMMI analysis of yield trials. In Kang MS, Gauch (eds.) *Genotypes by environment interaction*. CRC Press. Boca Raton, EL.

Genstat 2009. *Genstat for Windows* (12th Edition) Introduction. VSN International, Hemel Hempstead.

Jha SK, Singh NK, Aggarwal PK, 2013. Additive main effects and multiplicative interaction analysis for grain yield of short duration maize hybrids in North -Western Himalayas. *Indian J. Genetics* 73: 29-35

Kumar R, Singode E, Chikkappa GK, Yadav OP, 2014. Assessment of genotype x environment interactions for grain yield in maize hybrids in rainfed environments. *SABRAO Journal of Breeding and Genetics* 46: 292-214

- Morris ML, Risopoulous J, Beck D, 1999. Genetic changes in farmer – recycled maize seed: A review of the evidence, CIMMYT Econ, Working Paper No. 99-07. Mexico, D.F., CIMMYT. pp. 1
- Purchase JL, Hatting H, Vandeventer CS, 2000. Genotype x environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: Stability analysis of yield performance. *South African Journal of Plant and Soil* 17: 101-107
- Ramburan S, Zhou M, Labuschagne M, 2011. Interpretation of genotype × environment interactions of sugarcane: Identifying significant environmental factors. *Field Crops Research* 124: 392-399.
- Rodriguez M, Rau D, Papa R, Attene G, 2008. Genotype by environment interactions in barley (*Hordeum vulgare* L.): different responses of landraces, recombinant inbred lines and varieties to Mediterranean environment. *Euphytica* 163: 231-247
- Sanni KA, Ariyo OJ, Ojo DK, Gregorio G, Somado EA, Sanchez I, Sie M, Futakuchi K, Ogunabayo SA, Guel RG, Wopereis MCS, 2009. Additive main effects and multiplicative interaction analysis of grain yield performance in rice genotypes across environments. *Asian J. Plant Sci.* 8(1): 48-53.
- White PJ, Johnson LA, 2003. *Corn: Chemistry and Technology*, 2ndEdn, American Association of Cereal Chemists, St. Paul, M. N. USA., ISBN – 13: 9781891127335, Pages: 892
- Yan W 2001. GGE biplot - a windows application for graphical analysis of multi-environment and other types of two-way data. *Agron. J.* 93: 1111-1118
- Yan W 2002. Singular value partitioning in biplot analysis of multi environmental trial data. *Agronomy Journal* 94: 990-996
- Yan W, Hunt LA, Sheng Q, Szlavnic Z, 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Sci.* 40: 597-605
- Yan W, Kang M S, 2003. *GGE Biplot Analysis: A graphical tool for breeders, geneticists, and agronomists*. CRC Press, Boca Raton, FL.
- Yan W, Tinker NA, 2006. *Biplot analysis of multi environment trial data: Principles and applications*. *Can. J. Plant Sci.* 86: 623-645
- Zubair M, Ghafoor A 2001. Genotype x Environment interaction in mung bean. *Pak. J. Bot* 33(2): 187-190