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RESEARCH ARTICLE

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Study on Applicability of Genotype × Yield × Trait (GYT) Biplots over Genotype × Trait (GT) Biplots in Selection of Maize Hybrids across Soil Moisture Regimes

Ashok Singamsetti[1], J.P. Shahi[1], P.H. Zaidi[2], K. Seetharam[2]

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ABSTRACT

Background: A large area of the maize production in Indo-Gangetic plains of India exposes alternative and combination of prolonged drought spells and heavy rainfall situation due to uncertainty of monsoon patterns. In such context, breeding for maize hybrids with cross-tolerant to both low and excess soil moisture stresses remain the ultimate alternative.

Methods: Evaluation of 75 maize hybrids planted at Banaras Hindu University, India during the subsequent *Rabi* and *Kharif* seasons of 2017 and 2018, respectively. The hybrids were evaluated for acquiring information on inter-trait associations among yield and yield-related traits under different soil moisture regimes. The trials were planted in alpha-lattice design and managed stress was imposed and data recorded.

Result: As our investigation was the evident of weak correlations among the traits studied, genotype × trait (GT) biplots are not advisable to select/ discard the genotypes under moisture stress conditions. The goodness of fit for GT biplots constructed under studied moisture conditions were almost poor because of fair to moderate correlations among the traits. To accomplish this problem of weak associations, genotype × yield × trait (GYT) technique was advisable to perform the precise selection of genotypes under studied environments. The investigation emphasized on accuracy and adequacy in implementing of GYT biplots for characterizing and selecting suitable hybrids.

Key words: Correlation, Drought, GT biplots, GYT biplots, Waterlogging.

INTRODUCTION

Approximately, 15 million farmers in India directly engaged in maize cultivation, and 45 million metric tons of maize production was targeted by the year 2022 to meet the nation's demand. But, only 15% of the cultivated area of maize is under proper irrigation and water availability at crucial growth stages has been a greater challenge to achieve sustainability in maize production (Sah *et al.* 2020). On other side, the crop grown during the summer-rainy seasons in the Indo-Gangetic plains critically face waterlogging due to contingent flooding and continuous rainfall. In South and South-East Asia alone, around 18% of the total maize cultivating area is frequently affected by floods (Zaidi *et al*. 2008). Maize is comparatively more sensitive to moisture stresses such as drought and waterlogging at flowering and knee-high stage, respectively that leads to severe yield losses through poor seed set because of barrenness or reductions in kernels rows and kernels per ear (Bolaños and Edmeades, 1993).

The study of correlations along with variability would assist the plant breeder in improving a character that brings simultaneous improvement in other characters. Al-Naggar *et al.* (2020) conducted an experiment to evaluate nineteen maize genotypes in two seasons with two irrigation regimes such as well-watered and water stressed at flowering stage. Similarly, field experiments were carried out by Nelimor *et al.* (2020) over two years on 66 extra-early maize landraces under drought, heat, combined stresses and stress-free conditions. Although, a numerous works reported on genetic variability and correlation studies in maize, but the present experiment was aimed to decipher the effect of soil moisture on associations among yield and other corresponding traits. Dealing with data of several traits from a multi-environment test is a challenge due to presence of unfavourable associations among traits (Yan *et al*., 2019). Since, non-linear distribution of data and poor correlations among traits under stress conditions, selection of genotypes based on genotype × trait (GT) biplots was not accurate. To overcome

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[1] Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, Uttar Pradesh, India.

[2] The International Maize and Wheat Improvement Center (CIMMYT), ICRISAT Campus, Hyderabad-502 324, Telangana, India.

Corresponding Author: Ashok Singamsetti, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, Uttar Pradesh, India.
Email: ashoks.setti10@bhu.ac.in

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the weak inter trait association, a novel tool of genotype × yield × trait (GYT) biplot was proposed to visualize the yield-trait combinations that increase the goodness of fit for the biplots (Yan and Frégeau-Reid, 2018). Sofi *et al.* (2021) studied to assess the comparative efficiency of GYT approach over GT approach in genotypic selection on multiple traits in common bean. The objective of the investigation was to estimate the magnitude of genetic variability and interrelationships among grain yield and its attributing traits among 75 maize hybrids under low, optimal and excess soil moisture condition; and construction of GT and GYT biplots for individual moisture condition to visualize the variability and association of traits and yield-trait combinations for the test hybrids.

MATERIALS AND METHODS

A set of 75 maize hybrids including five checks shown in Table 1 were developed from a CIMMYT's germplasm pool of 600 diverse maize lines majorly sourced from Asian tropical and subtropical regions that crossed with two elite testers *viz*, CML451 and CL02450 through biparental crossing pattern. These genotypes were evaluated under four environments in two seasons, under three soil moisture regimes such as optimal (OSM), low (LSM) and excess soil moisture (ESM) at Varanasi during the *Rabi* 2017-18 and *Kharif* 2018. Test environments E1 and E2 were planted in last week of December in *Rabi* 2017 under LSM and OSM, respectively whereas E3 and E4 in the first week of July in *Kharif* 2018 under OSM and ESM conditions, respectively. The experimental layout was alpha-lattice design (0, 1) with two replications. Managed drought stress and waterlogging stress imposed based on the abiotic stress phenotypic manuals by CIMMYT (Zaman-Allah *et al*., 2016; Zaidi *et al*., 2016). Manual sowing was done with 4 m in row length and two in row number and spacing was 60 × 20 cm. The phenotypic data on days to 50% anthesis (ANTH), days to 50% silking (SILK), anthesis-silking interval (ASI), shoot length (SL), chlorophyll content (SPAD), ear length (EL), number of kernels per row (NKPR), test weight (TW) and grain yield per hectare (GY) was recorded. Shelling and moisture percent for each plot were estimated for conversion of fresh weight of ears without husk in to grain yield per hectare (GY, in t/ha) at 15% moisture.

The data were subjected to ANOVA by general linear mixed model (GLMM). The data subjected to PROCGLM of SAS with the RANDOM statement (SAS, 2009). In the statistical model, replications and incomplete blocks within replication were considered as random, while the genotypes, soil moisture conditions within season was treated as a fixed factor. Soil moisture condition of the crop growing period was nested within 'season' factor. The model followed by Rusinamhodzi *et al*. 2020 was used in experiment. Magnitude and direction of association among the yield and its component traits were estimated by Pearson's correlation method. To visualize the genetic variability among test hybrids under the three test environments, a principal

Table 1: List of maize genotypes evaluated under different soil moisture conditions

Code	Genotype name	Code	Genotype name	Code	Genotype name
1	ZH161271	26	ZH161042	51	ZH161478
2	ZH161475	27	ZH161079	52	ZH161456
3	ZH161493	28	ZH161076	53	ZH161484
4	ZH161464	29	ZH161039	54	ZH161463
5	ZH161409	30	ZH161047	55	ZH15449
6	ZH161361	31	ZH161100	56	ZH161196
7	ZH161485	32	ZH161045	57	ZH161194
9	ZH161384	34	ZH161060	59	ZH161068
10	ZH161418	35	ZH161054	60	ZH161129
11	ZH161276	36	ZH161053	61	ZH161077
12	ZH161311	37	ZH161083	62	ZH161066
13	ZH161358	38	ZH161120	63	ZH161137
14	ZH161303	39	ZH161038	64	ZH161078
15	ZH161438	40	ZH161054	65	ZH161114
16	ZH161382	41	ZH161051	66	ZH161043
17	ZH161434	42	ZH161054	67	ZH161184
18	ZH161377	43	ZH161082	68	ZH161050
19	ZH161458	44	ZH161063	69	ZH161207
20	ZH161452	45	ZH161093	70	ZH161089
21	ZH161473	46	ZH161071	71	P3502
22	ZH161289	47	ZH161210	72	DKC9144
23	ZH161471	48	ZH161102	73	NK30
24	ZH161285	49	ZH161398	74	P339
25	ZH161135	50	ZH161410	75	Hytech 5106

component analysis (PCA) of standardized data was carried to display the individual trait and yield × traits relationships. To generate GT and GYT biplots, standardization of two-way table of genotype and trait data was carried out as per procedure given in Yan *et al*. (2010), Yan and Frégeau-Reid (2018) and Yan *et al*. (2019). Correlation analysis and construction of GT and GYT biplots were performed through 'metan' version 1.8.1 package (Olivoto and L'ucio, 2020) in RStudio (RStudio, 2020).

RESULTS AND DISCUSSION

Analysis of variance

The mean squares of grain yield and its related traits showed the significant variation for the studied maize genotypes and soil moisture within the season (Table 2). This revealed significant progress could be achieved by selection for the improvement of studied traits with desirable performance. Morphological traits had ample amount variation among genotypes and also at genotype-by-environment level indicated as interaction of genotype with soil moisture in the respective season that results substantial differences in the trait expression. Thus, the genetic variability reported in this experiment could be exploited by maize breeders to develop improved cultivars suitable to the particular moisture conditions.

The range and mean values for each trait for 75 maize hybrids under test environments explained the impact of moisture level on the trait's expression (Fig 1). A very few outliers for measured traits were probably the result of inconsistent expressions indicated stress severity and

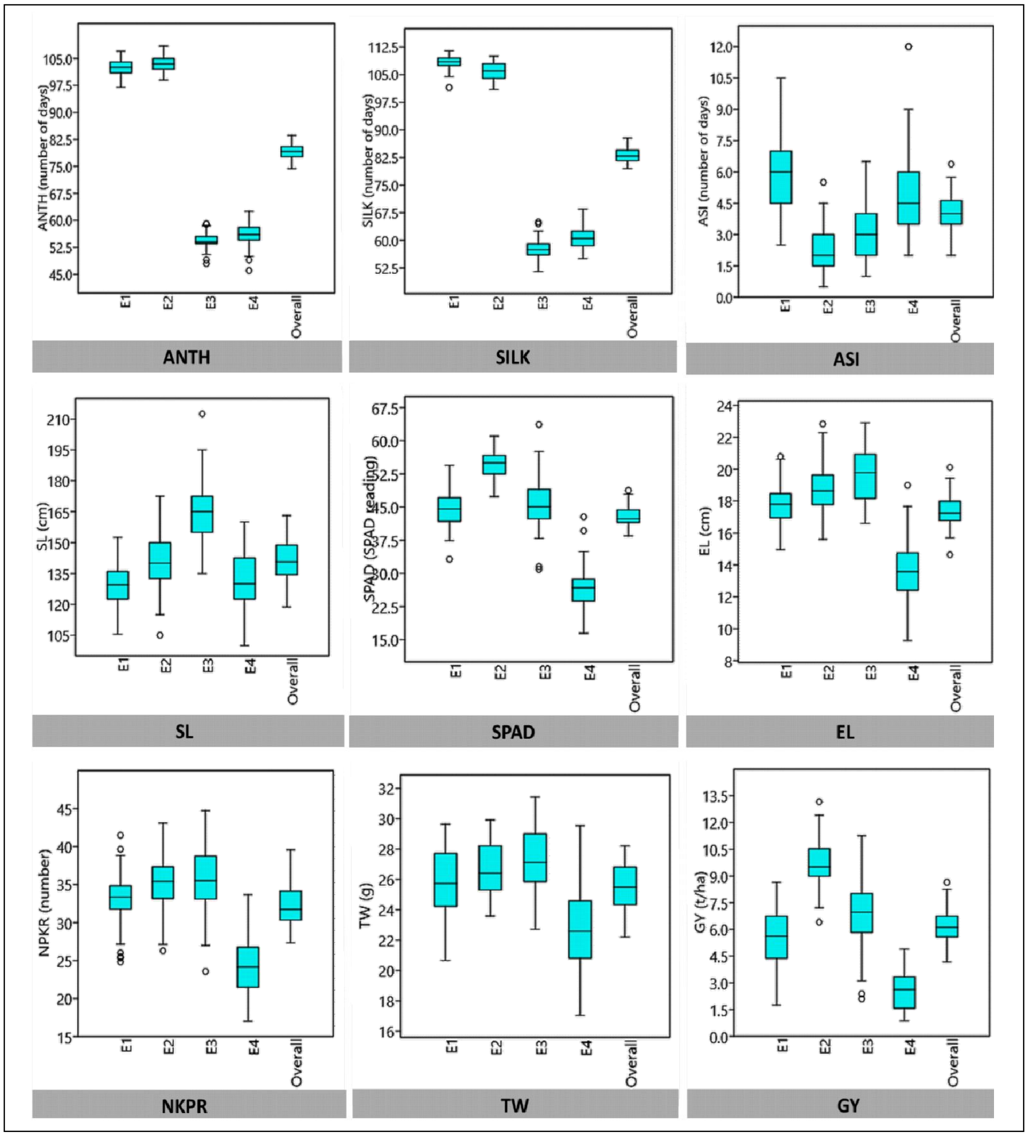


Fig 1: Mean performances of yield and other secondary traits under each test environment.

E1, *Rabi* 2017-18 under low soil moisture; E2, *Rabi* 2017-18 under optimal soil moisture; E3, *Kharif* 2018 under optimal soil moisture; E4, *Kharif* 2018 under excess soil moisture.

genotype-by-soil moisture interaction. A large variation in ANTH and SILK in two seasons was observed, that exhibited delayed maturity in winter maize crop due to a prolonged cold period at the early stages of crop growth from seedling to knee-high stage. According to grain yield, hybrids *viz*, 22 (ZH161289) followed by 30 (ZH161047) and 36 (ZH161053) recorded highest under waterlogging, whereas 36 (ZH161053) followed by 41 (ZH161051) and 9 (ZH161384) showed maximum under drought. Hybrids 22 (ZH161289), 30 (ZH161047) and 49 (ZH161398) had highest yield under optimal whereas 22 (ZH161289), 30 (ZH161047) and 36 (ZH161053) identified as top yielders across test environments.

Correlation studies

Under drought (E1), GY had significant positive and a fair association with NKPR and SL, whereas a significant and negative correlation with SILK and ASI (Table 3). ANTH had a strong positive association with SILK and a strong negative correlation with ASI and TW. The results revealed that SPAD and EL were not showed significant association with any other trait studied under drought. Under waterlogging (E4), GY showed a significant and positive correlation with SL, EL, NKPR and TW, whereas a significant negative association with ANTH and SILK. A moderate positive correlation observed for ANTH with SILK and a fair relationship with ASI positively. SL showed fair positive association with SPAD and a poor positive association with NKPR. EL recorded a moderate positive correlation with NKPR and TW along with GY, while a poor negative correlation with ANTH. Correlation coefficients estimated for mean values of traits evaluated under both optimal environments (E2 and E3). GY had moderate level of negative correlation with ANTH, SILK and ASI and a positive and significant association with EL, TW, NKPR and SPAD. The flowering traits *viz*, ANTH, SILK and ASI showed negative and fair association with SPAD, TW, EL and NKPR. Traits such as EL, NKPR and SPAD showed a fair positive

Table 2: Mean sum squares of grain yield and other secondary traits from ANOVA.

Source of variation	df	ANTH	SILK	ASI	SL	SPAD	EL	NKPR	TW	GY
GEN	74	28.97***	26.24***	5.33***	738.77***	37.08*	7.27***	50.84***	16.66***	7.04***
REP	1	14.72*	4.86	2.66	2934.88**	0.47	62.41***	1.55	3.37	3.92*
BLK(REP)	8	5.41*	4.25	0.61	113.43	16.81	0.71	2.83	2.00	2.97*
SEA(SMC)	3	114813.08***	115281.22***	400.42***	38331.47***	20564.34***	1008.84***	3958.97***	617.21***	1296.52***
GEN×SEA(SMC)	222	5.00***	7.11***	4.43***	187.97***	36.34*	3.47***	21.67***	7.07***	2.69***
RESIDUAL	291	3.08	3.39	2.20	118.79	28.56	0.72	3.96	1.4	1.29

***= Significant at 0.1% (p<0.001), **= Significant at 1% (p<0.01), *= Significant at 5% (p<0.05), df: Degrees of freedom; GEN: Genotypes; REP: Replications; BLK: Block; SEA: Season; SMC: Soil moisture condition.

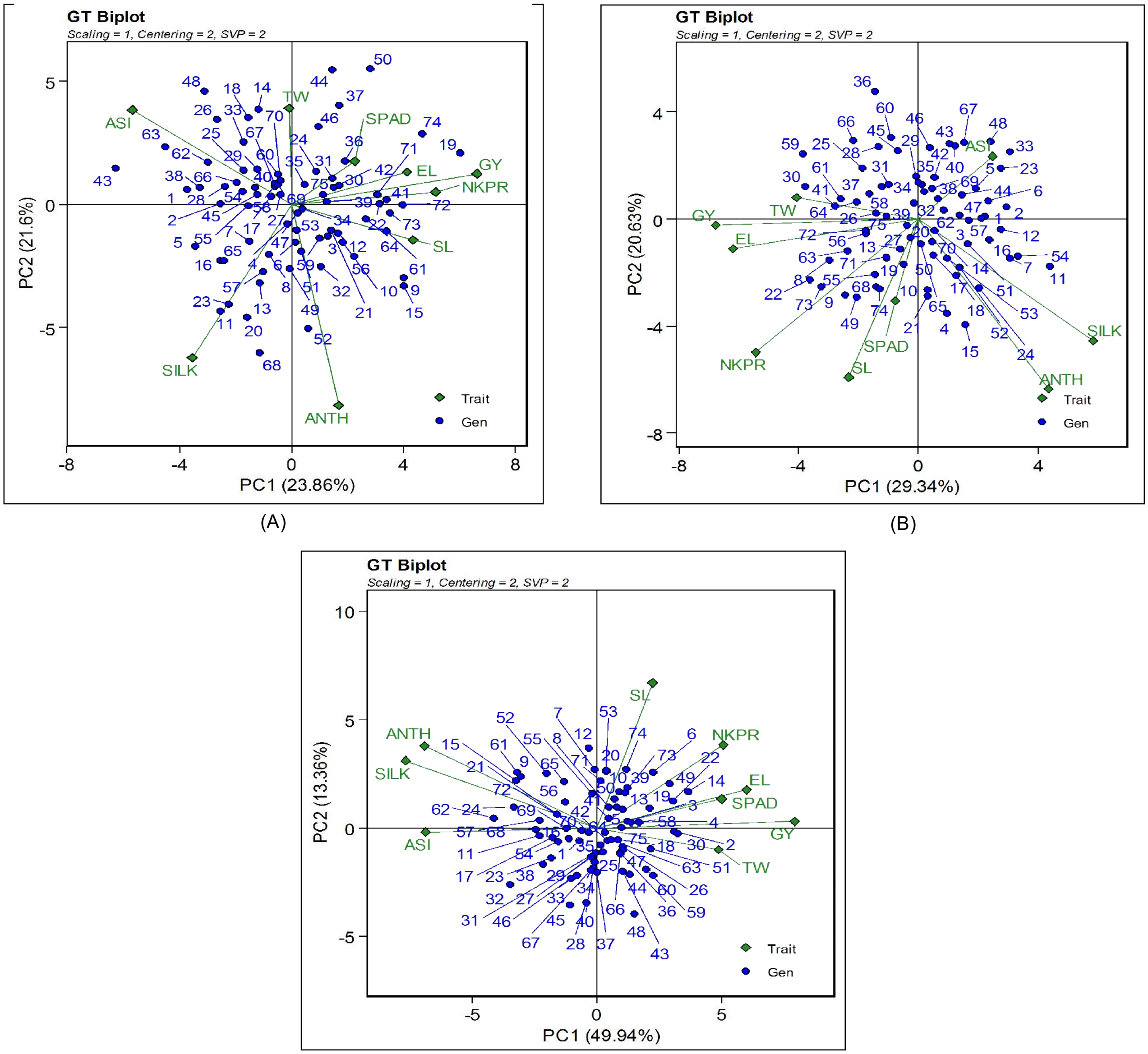
Table 3: Correlation among grain yield and other secondary traits under soil moisture condition.

	ANTH	SILK	ASI	SL	SPAD	EL	NKPR	TW	GY
(a) Correlations under stress (above the diagonal: waterlogging; below the diagonal: drought)									
ANTH	**1.00**	0.77***	-0.29*	0.21	-0.01	-0.24*	0.06	-0.10	-0.34**
SILK	0.62***	**1.00**	0.39***	0.08	-0.03	-0.22	-0.05	-0.18	-0.45***
ASI	-0.61***	0.24*	**1.00**	-0.18	-0.02	0.02	-0.17	-0.12	-0.19
SL	0.18	-0.12	-0.35**	**1.00**	0.23*	0.12	0.40***	-0.04	0.26*
SPAD	-0.11	-0.10	0.03	0.04	**1.00**	0.02	0.24*	-0.23**	-0.01
EL	-0.03	-0.10	-0.06	0.01	0.22	**1.00**	0.59***	0.40***	0.41***
NKPR	0.01	-0.10	-0.11	0.10	0.10	0.41***	**1.00**	0.19	0.43***
TW	-0.26*	-0.29**	0.03	0.05	-0.13	-0.06	-0.18	**1.00**	0.25*
GY	0.03	-0.32**	-0.37**	0.24*	0.16	0.22	0.39***	0.11	**1.00**
(b) Correlations under optimal (above the diagonal) and across all the environments (below the diagonal)									
ANTH	**1.00**	0.97***	0.49***	0.01	-0.41***	-0.46***	-0.27*	-0.37*	-0.67***
SILK	0.90***	**1.00**	0.69***	-0.05	-0.42***	-0.53***	-0.35**	-0.44***	-0.77***
ASI	-0.33**	0.11	**1.00**	-0.20	-0.27*	-0.50***	-0.44***	-0.46***	-0.77***
SL	0.35**	0.27**	-0.20	**1.00**	0.15	0.20	0.24*	0.14	0.27*
SPAD	0.14	0.16	0.02	0.15	**1.00**	0.43***	0.36**	0.19	0.48***
EL	-0.07	-0.15	-0.17	0.19	0.11	**1.00**	0.45***	0.16	0.58***
NKPR	0.25**	0.13	-0.31**	0.45**	0.31**	0.58***	**1.00**	0.22	0.51***
TW	-0.31**	-0.34**	-0.04	-0.15	-0.29**	0.06	-0.31**	**1.00**	0.57***
GY	-0.24*	-0.35**	-0.20	0.30**	-0.06	0.26*	0.27*	0.15	**1.00**

Note: ***, ** and * Significant at *p*-value 0.001, 0.01 and 0.05 respectively.

relation with each other under the optimal soil moisture environment. GY had a poor positive correlation with NKPR, EL and SL whereas fair to poor negative correlation with ANTH and SILK across all the test environments including low, optimal and excess soil moisture.

A significant negative association recorded between grain yield and flowering traits (ANTH and SILK) under all the moisture conditions, while ASI had significant negative correlation under drought. It explained the importance of ASI in development of drought tolerant maize cultivars. The longer gap between anthesis and silking resulted in failure of proper seed set due to poor availability of viable pollen for late emerged female flowers. Campbell *et al.* (2014) reported shorter ASI is genetically correlated with increased drought tolerance by studying the effect of water availability on flowering behavior under moisture regimes. Longer ASI values are owing to the delay of silk extrusion, premature lodging and reduced rates of net photosynthesis arising from oxidative damage to chloroplasts (Nelimor *et al.* 2020). The relationship between grain yield and ASI in our study was in agreement with previous reports on maize under



(A)

(B)

(C)

Fig 2: Genotype by trait (GT) biplot illustrating the relationship between PC1 and PC2 for 75 genotypes and nine traits under (a) low soil moisture (b) excess soil moisture (c) optimal soil moisture.

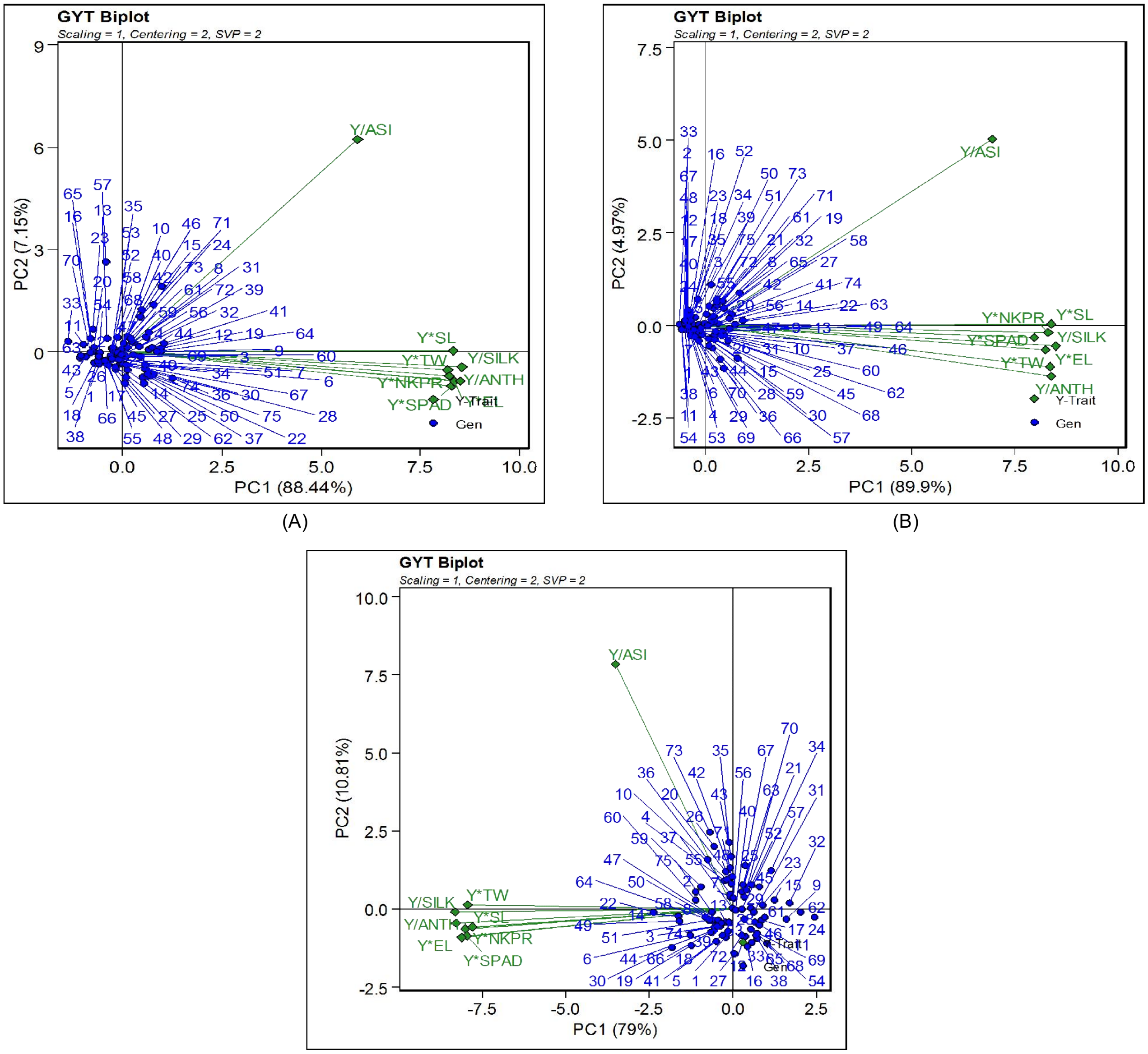
PC1 and PC2, principal components 1and 2 respectively; Scaling = 1, Centering = 2 and SVP = 2 represented the biplot was based on singular value decomposition of trait-standardized data and trait-focused singular value partition. Goodness of fit for biplot (a) 45.46%, (b) 49.97% and (c) 63.30%.

drought (Edmeades and Daynard, 1979) and under waterlogging conditions (Zaidi *et al.* 2007). Direct selection of characters like SL, EL and NKPR would results in promising yields under varied moisture conditions. The strong association between phenological traits and grain yield under water deficit conditions than under optimal moisture conditions was reported by Sah *et al.* (2020).

GT and GYT biplots

According to GT biplots, the first two PCs explained 45.46% of total variability under LSM, whereas 49.97% and 63.3% under ESM and OSM conditions, respectively (Fig 2a-c). In case of GYT biplots, first two PCs contributed around 95% under LSM and ESM, whereas 90% under OSM (Fig 3a-c). For example, biplot (Fig 2a) constructed for performance of genotype under drought environment showed that GY was positively correlated with EL, SL, NK, PR and negatively with ASI and SILK. Almost zero correlation was found for GY with TW and ANTH. Also the biplot depicted the cultivars *viz*, 19 (ZH161458), 72 (DKC9144), 41 (ZH161051), 39 (ZH161038), 73 (NK30) and 22 (ZH161289) *etc*. were recorded higher values for traits *viz*, NKPR, SL, EL and GY.

The accuracy of biplots was based on goodness of fit that generally indicated by the sum of PCs involved in the



(A)

(B)

(C)

Fig 3: Genotype by yield*trait (GYT) biplot illustrating the relationship between PC1 and PC2 for 75 genotypes and nine traits under (a) low soil moisture (b)excess soil moisture (c) optimal soil moisture.

PC1 and PC2, principal components 1and 2 respectively; Scaling = 1, Centering = 2, and SVP = 2 represented the biplot was based on singular value decomposition of trait-standardized data and trait-focused singular value partition. Goodness of fit for biplot (a) 95.59%, (b) 93.87%and (c) 89.81%.

biplot construction. The goodness of fit for the GT biplots constructed under all the studied moisture conditions were almost poor due to fair to moderate correlations among the traits. To accomplish the problem of weak associations, GYT technique was advisable to perform the precise selection of genotypes under studied environments. However, each trait combined with yield is more acceptable than yield per se alone or each trait alone in case of multiple trait evaluation. Correlations among yield-trait combinations are obviously greater than the trait-associations as the result of presence of yield as a common component. This could be observed by the presence of acute angles between yield-trait vectors in the GYT biplots (Fig 3a-c). The studied hybrids can be depicted graphically on GYT biplots based on these strong yield-trait correlation values. The GYT biplots showed the enhanced goodness of fit than the GT biplots. Around 90-95% goodness of fit that explained very good adequacy in biplot construction was recorded for all the soil moisture environments. Further, ranking and selection of genotypes could be proceeded with respect to desirable yield-trait combinations by plotting polygon view and mean-stability plot with similar interpretations of GGE biplots (Yan and Tinker, 2005).

CONCLUSION

The measured traits had ample amount variation among genotypes and also at genotype-by-environment level indicated as interaction of genotype with soil moisture in the respective season that results substantial differences in the trait expression. To overcome the problem of weak associations in GT biplots under stress environments, GYT technique was desirable to perform the precise selection and genotype ranking pattern of genotypes under test environments where the grain yield is targeted.

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Conflict of interest

The authors declare no conflict of interest.

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