Genotype by Trait Associations among Drought Tolerant Maize Inbred Lines

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Abstract

Twelve tropical, yellow maize inbred lines identified as drought tolerant were evaluated in multi environments, including managed drought, rain fed and irrigated conditions. The objective was to study genotype-trait associations across environments. A 3×4 α-lattice design with two replications was used in each environment. Data were recorded for twenty-one traits. Combined analysis of variance using data from all environments was done for all traits using the GLM procedure in SAS version 9.3. Genotype by trait associations were revealed using the genotype main effect plus genotype-by-environment biplot model in GENSTAT 14th Edition. Inbred lines which were associated with high grain yield and related desirable traits such as a low drought susceptibility index under managed drought were DMR-M-81, DMR-M-88, FA6, GPM36 and M39. Across the diverse environments, DMR-M-84, DMR-M-88, FA6 and GPM36 were associated with grain yield and/or its related traits. The inbred lines associated with desirable traits could be evaluated for combining ability in order to know their desirability in cultivar development. These inbred lines could be used as female parents in seed production programmes since high productivity and drought tolerance are important qualities of female parents in seed production.

Keywords: maize (*Zea mays* L.), inbred lines, drought tolerance, trait profiles

1. Introduction

Drought is the most important abiotic constraint to maize grain production worldwide, where most of the 160 million hectares which is put under maize is rainfed (Bänziger, Edmeades, Beck, & Bellon, 2000; Edmeades, 2013). Development of drought tolerant maize germplasm is critical to alleviate drought impacts on maize production (Edmeades, 2013). In breeding drought tolerant maize hybrids that would sustain production under climatic changes, identification of parents and knowing their attributes through characterization is a prerequisite (Chen, Xu, Velten, Xin, & Stout, 2012). There is evidence that use of drought tolerant inbred lines in hybrid development can lead to a significantly higher proportion of hybrid progenies that exhibit good performance under drought and other stresses like low soil nitrogen (Betrán, Beck, Bänziger, & Edmeades, 2003; Meseka, Menkir, Ibrahim, & Ajala, 2013), and this indicate the importance of the inbred-hybrid approach in developing stress tolerant hybrids (Kirkham, Suksayretrup, Wassom, & Kanemasu, 1984).

Genotype by trait biplot analysis is an application of the genotype plus genotype × environment interaction (GGE) biplot technique (Yan, Hunt, Sheng, & Szlavnics, 2000) and can be used for analysis of multi-trait data (Yan & Kang, 2003). Using this method, the data in a genotype by trait table can be displayed as a biplot, thereby exhibiting trait associations (Yan & Rajcan, 2002), as well as genotype trait profiles (Yan & Kang, 2003; Yan & Fregeau-Reid, 2008). This tool has been used to evaluate genotypes and explore trait associations in various crops as reported by Yan and Rajcan (2002), Rubio, Cubero, Martin, Suso, and Flores (2004), Oladejo, Akinwale and Obisesan (2011), and other authors. A study of genotype by trait associations among maize inbred lines using biplots can be used to visualize trait profiles of particular genotypes which helps in knowing their strengths and weaknesses, and this technique can be utilized in selection of parents in a breeding programme (Yan & Fregeau-Reid, 2008; Yan & Kang, 2003; Yan & Tinker, 2006). Twelve tropical yellow maize inbred lines

that were selected for drought tolerance in a 2011-2012 drought screening trial (unpublished) were used in this study. The objective was to study genotype by trait associations among the inbred lines under drought and across environments.

2. Materials and Methods

2.1 Germplasm and Environments

Twelve maize inbred lines (Table 1) that were identified as drought tolerant in a 2011-2012 dry season drought screening trial were used in this study. All the inbred lines are maintained at University of Agricultural Sciences, Dharwad, under the All India Coordinated Maize Improvement Project (AICMIP). Three locations in Karnataka, India, were used for evaluation trials, and these are Agricultural Research Station (ARS) Arabhavi, ARS Bailhongal and Main Agricultural Research Station (MARS) Dharwad. There were a total of seven environments, and an environment was considered as a combination of location, season and water regime (Table 2).

Table 1. Twelve drought tolerant inbred lines that were evaluated in multi-environmental trials

Code	Inbred line	Pedigree	Origin
G1	DMR-M-81	CI-4	International Centre for Maize and Wheat Improvement (CIMMYT)
G2	M4	KDMI-16	All India Coordinated Maize Improvement Project (AICMIP), ARS Arabhavi
G3	FA6	ARYP-73	AICMIP, ARS Arabhavi
G4	DMR-M-83	CI-5	CIMMYT
G5	GPM36	ARYP-36	Indian Institute of Maize Research, ICAR, Winter nursery, Hyderabad (IIMR, Hyderabad)
G6	DMR-M-88	CM-501	ICAR-Indian Institute of Maize Research (IIMR), New Delhi
G7	DMR-M-84	KDMI-10	AICMIP, ARS Arabhavi
G8	M39	ARYP-39	AICMIP, ARS Arabhavi
G9	M53	ARYP-53	Zonal Agricultural Research Station, Mandya, University of Agricultural Sciences, Bengaluru
G10	FA3	ARYP-70	AICMIP, ARS Arabhavi
G11	GPM43	ARYP-43	IIMR, Hyderabad
G12	GPM53	ARYP-53	IIMR, Hyderabad

Table 2. Description of environments used for evaluation of 12 drought tolerant maize inbred lines

Code	Location	Latitude N	Longitude E	Altitude (m)	Soil description	Season/water regime	Planting date
E1	ARS Arabhavi	16	74.5	585.2	Medium black clay loam of pH 8	2012-2013 dry season, managed drought	03-12-2012
E2	ARS Arabhavi	16	74.5	585.2	Medium black clay loam of pH 8	2012-2013 dry season, irrigated	03-12-2012
E3	ARS Arabhavi	16	74.5	585.2	Medium black clay loam of pH 8	2013 rainy season, rain fed, supplementary irrigation	01-08-2013
E4	MARS Dharwad	15.48	74.98	678	Medium deep black clay loam of pH 7.5	2013 rainy season, rain fed	01-07-2013
E5	ARS Bailhongal	16	75.5	680	Medium black, pH range is 7.2-8.4	2013 rainy season, rain fed	11-07-2013
E6	ARS Arabhavi	16	74.5	585.2	Medium black clay loam of pH 8	2013-2014 rainy season, managed drought	02-01-2014
E7	ARS Arabhavi	16	74.5	585.2	Medium black clay loam of pH 8	2013-2014 rainy season, irrigated	02-01-2014

2.2 Trial Establishment and Management

A 3×4 α-lattice design with two replications was used under each evaluation environment. An experimental unit was a two-row three-metre long plot which was occupied by a particular genotype (inbred line). A spacing of 0.6 m between rows and 0.2 m between planting hills within a row was used. Two seeds were placed per hill during planting, but thinning was done at three weeks after planting to one plant per hill giving rise to a plant population

of 83 333 plants ha^{-1}. In the managed drought stress trials, there was withdrawal of irrigation at 36 days after planting, and afterwards there was no more irrigation. This was done in order to impose drought stress at flowering and post-flowering stages. In the well-watered trial, irrigation water was applied after every 12 days to maintain optimal moisture conditions throughout the growing period. Fertilizer was applied at the following rates in all evaluation environments: 150 kg N ha^{-1}, 75 kg P ha^{-1}, 37.5 kg K ha^{-1}. At ARS Arabhavi, zinc sulphate was also applied at 10 kg ha^{-1} since the soil at that site is deficient of zinc. The trials were kept weed free mainly by hand weeding. Inter-row cultivation was done using a bullock drawn cultivator at four and eight weeks after planting. All packages of best practices were used to raise a good crop.

2.3 Data Collection

Data for twenty-one traits were recorded on a plot basis. Days to anthesis were determined as the number of days from planting date to the date when 50% of plants in a plot had fully emerged tassels and shedding pollen. Days to silking were determined as the number of days from planting date to the date when 50% of plants in a plot had emerged silks. Anthesis-silking interval was calculated by subtracting days to anthesis from days to silking. Days to physiological maturity were determined as the number of days from planting date to the date when 75% of plants in a plot had dry cob husks. Grain filling duration was calculated by subtracting days to silking from days to physiological maturity. Leaf rolling was visually scored under drought at two weeks before flowering using a 1 to 5 scale, 1 representing unrolled leaves and 5 representing lax leaves. Leaf senescence was scored visually under drought conditions on a 1 to 10 scale, where 1 represented green leaves and 10 represented completely senesced leaves. Ear height was measured at physiological maturity as distance in centimetres from the base of the plant to the insertion of the top (uppermost) ear of the same plant and mean of six plants was recorded. Plant height was measured at physiological maturity as the distance in centimetres from base of plant to the first tassel branch of the same plant, and a mean of six plants was recorded. Tassel size was visually scored from the milk to dough stages of grain filling, on a 1 to 5 scale where 1 represented very small tassel with few branches and 5 represented a large tassel with many branches. Lodging was visually scored at maturity using a 1 to 5 scale where 1 represented no lodging of plants, and 5, extreme lodging. Ears per plant were determined by counting the number of ears with at least one kernel in a plot, and dividing by the total number of plants. Ear aspect was visually rated on a scale of 1 to 5, where 1 represented clean, uniform, large, and well-filled ears and 5, ears with most undesirable (diseased, insect damaged, small, partially filled, and variable) features. Ear length was determined as the measurement of the length of an ear in centimetres, and a mean length for six ears was recorded. Ear diameter was determined as the measurement of the maximum girth of the ear using vernier calipers and mean of six ears was recorded in centimetres. Kernel row number was observed in the central part of the ear and mean of six ears was recorded. Kernels per ear row was observed and a mean of six ears was recorded. Kernels per ear was counted manually and the average for six ears was recorded. Kernel weight per ear was determined by weighing shelled kernels from six ears and getting an average for a single ear. Grain yield was determined as kernel weight per plot in tons per hectare, adjusted to 15% moisture content. Drought susceptibility index for grain yield was calculated as follows:

$$DSI = \left(\frac{1-Ys}{Yc}\right) \bigg/ \left(\frac{1-Ysm}{Ycm}\right) \qquad (1)$$

Where, *Ys* is mean grain yield of a genotype under managed drought stress, *Yc* is mean grain yield of the same genotype under well-watered conditions, *Ysm* is mean grain yield of all genotypes under managed drought stress, and *Ycm* is mean grain yield of all genotypes under well-watered conditions.

2.4 Data Analysis

2.4.1 Analysis of Variance

The PROC GLM procedure of SAS 9.3 (SAS Institute, 2010) was used for analysis of variance. Combined data from all environments and for all traits observed across environments were subjected to analysis of variance. The LSMEANS statement was used to calculate adjusted means for the inbred lines, and the TUKEY option was used at 5% probability level when mean separation was necessary.

2.4.2 Genotype by Trait Associations

The genotype by trait associations were analysed following Yan and Rajcan (2002), using GENSTAT 14th Edition (Payne et al., 2011). This was done using trait least square means under managed drought, and least squares means computed from across all environments. The GGE biplot model based on singular value decomposition was used to determine genotype by trait associations, and is presented as:

$$(Y_{ij} - \mu - \beta_j)\big/ S_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \qquad (2)$$

Where, Y_{ij} is the genetic value of the combination between genotype i and trait j, μ is the grand mean, β_j is the jth trait main effect, and $\mu + \beta_j$ is the mean across all genotypes for the jth trait (Yan & Rajcan, 2002). The terms λ_1 and λ_2 are the singular values for the first principal component (PC1) and second principal component (PC2), respectively; ξ_1 and ξ_2 are eigenvectors of the ith genotype for PC1 and PC2, respectively. The components η_{j1} and η_{j2} are eigenvectors of the jth trait for the principal components PC1 and PC2, respectively; S_j is the phenotypic standard deviation of the jth trait, and ε_{ij} is the residual associated with the combination of the ith genotype and the jth trait.

3. Results

3.1 Analysis of Variance

Combined analysis of variance across all the environments in which the traits were observed revealed that environment and genotype effects were significant for majority of traits (Table 3). Genotype-by-environment interaction effects were not significant for most of the traits, except for days to physiological maturity (DTM), tassel size (TS) and grain yield (GY) (Table 3). The mean performance of the twelve inbred lines for various traits across all environments is shown in Table 4.

3.2 Genotype by Trait Analysis

The genotype by trait biplots, Figures 1 and 2 show how the genotypes performed in respect of particular traits under managed drought and across all the environments, respectively. Genotypes that are associated or are in the same sector with particular traits were the best performers for those traits. Vertex genotypes are either the best or the worst in terms of expression of particular traits. The results of genotype by trait biplot analysis across all the environments are substantiated by mean performance data for the genotypes across environments presented in Table 4.

Under managed drought, the genotype by trait biplot (Figure 1) accounted for a total of 55.43% of the total variation in the standardized data set, which was partitioned as follows: 34.99% explained by the first principal component (PC1) and 20.43% explained by the second principal component (PC2). Easily noticeable associations were between genotypes G6 (DMR-M-88) and G8 (M39) with high levels in grain filling duration (GFD), kernel row number (KRN), kernels per ear row (KER), kernels per ear (KPE), ears per plant (EPP), kernel weight per ear (KWE), and low levels in drought susceptibility index (DSI), days to anthesis (AD), days to silking (SD) and days to physiological maturity (DTM). Genotypes G3 (FA6) and G7 (DMR-M-84) were found to be associated with high values for grain yield (GY) and plant height (PH), and also low values for drought susceptibility index (DSI). Further, under the same environmental conditions, genotypes G1 (DMR-M-81) and G5 (GPM36) were associated with high levels in ear diameter (ED), ear height (EH), and low levels in ear aspect (EA), leaf senescence (LS) and leaf rolling (LR). Genotype G4 (DMR-M-83) was associated with a constellation of undesirable attributes, *viz.* high values in drought susceptibility index (DSI), lodging (LOD), ear aspect (EA) and leaf rolling (LR).

Across all the seven evaluation environments, genotype-by-trait analysis revealed associations as presented in Figure 2. The first principal component (PC1) explained 38.42% of the of the standardized data set, and the second principal component explained 21.50% of the variation, while both the PC components accounted for 59.91% of the variation. Genotypes G3 (FA6), G5 (GPM36), G6 (DMR-M-88), and G7 (DMR-M-84) were strongly associated with kernels per ear (KPE), kernels per ear row (KER), ear length (EL), kernel row number (KRN), plant height (PH), and grain yield (GY). Genotypes G1 (DMR-M-81), G2 (M4), and G9 (M53) were associated with high values in ear diameter (ED), days to anthesis (AD), days to silking (DS), days to physiological maturity (DTM), and low values in lodging (LOD) and ear aspect (EA).

Table 3. Mean sum of squares from analysis of variance for traits of twelve inbred lines evaluated across diverse environments

Character	Environment (E) DF	MS	Replication (R) in (E) DF	MS	Block (E × R) DF	MS	Genotype (G) DF	MS	G × E DF	MS	Error DF	MS
Days to anthesis	6	964.25***	7	6.95*	28	2.65	11	22.56***	66	1.90	49	2.76
Days to silking	6	1291.69***	7	10.85*	28	4.62	11	34.01***	66	2.76	49	4.07
Anthesis-silking interval	6	3.24***	7	0.001	28	0.002	11	0.004*	66	0.002	49	0.002
Days to physiological maturity	6	1291.12***	7	4.06	28	2.42	11	23.79***	66	4.85*	49	2.59
Grain filling duration	6	2236.41***	7	3.57	28	5.39	11	9.68*	66	7.40	49	4.79
Leaf rolling[b]	1	2.23***	2	0.21*	8	0.06	11	0.14**	11	0.16	14	0.03
Leaf senescence	1	2.34***	2	0.14	8	0.07	11	0.07	11	0.06	14	0.04
Plant height (cm)	6	14395.58***	7	313.23***	28	113.64*	11	352.95**	66	91.61	49	64.38
Ear height (cm)	6	3701.81***	7	162.46***	28	59.42*	11	139.34***	66	47.65	49	30.70
Tassel size	6	0.43***	7	0.01	28	0.02***	11	0.12***	66	0.02***	49	0.01
Lodging	6	1.68***	7	0.05	28	0.05	11	0.19***	66	0.06	49	0.03
Ears per plant	6	1.93***	7	0.06*	28	0.03	11	0.01	66	0.03	49	0.16
Ear aspect	6	0.99***	7	0.12**	28	0.05	11	0.34***	66	0.11	49	0.04
Ear length	6	175.72***	7	1.92	28	1.51	11	2.73	66	1.87	49	1.62
Ear diameter	6	3.13***	7	0.15	28	0.06	11	0.51***	66	0.14	49	0.08
Kernel row number	6	6.92***	7	1.08	28	0.49	11	2.85**	66	1.02	49	1.05
Kernels per ear row	6	565.36***	7	23.30*	28	6.84	11	25.56	66	15.86	49	10.49
Kernels per ear	6	123545.83***	7	7282.45*	28	1981.92	11	9354.21**	66	4285.92	49	3261.54
Kernel weight per ear (g)	6	30573.70***	7	1150.63***	28	205.24	11	671.23**	66	334.25	49	233.60
Grain yield (t ha^{-1})	6	154.23***	7	5.08***	28	1.41	11	4.53***	66	2.07**	49	1.01
Drought susceptibility index	1	0.01	2	0.12**	8	0.05*	11	0.04*	11	0.03	14	0.01

Note. * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$; DF = Degrees of freedom; MS = Mean squares. [b] Leaf rolling and leaf senescence were observed only under drought situation.

Table 4. The least square means (LSMEANS) with respect to grain yield and secondary traits of twelve inbred lines evaluated across different growing environments

Code	Name	Days to anthesis	Days to silking	Anthesis-Silking Interval (days)	Days to physiological maturity	Grain filling duration (days)	Leaf rolling	Leaf senescence	Drought susceptibility index	Plant height (cm)	Ear height (cm)	Tassel size
G1	DMR-M-81	68.17a	71.21a	3.05a	106.12a	34.90ab	3.29ab	4.92	1.06a	139.38ab	66.94a-c	3.65ab
G2	M4	67.45ab	69.64ab	2.19ab	103.12a-c	33.48b	2.67b	4.79	1.23a	135.37ab	66.35a-c	3.33a-c
G3	FA6	66.17a-c	68.64ab	2.48ab	103.26a-c	34.62ab	2.29ab	5.42	0.91a	139.19ab	68.69ab	3.30bc
G4	DMR-M-83	65.74a-c	67.64ab	1.90ab	101.62c	33.98b	4.92a	7.29	1.16a	126.35b	62.09a-c	2.69de
G5	GPM36	64.63bc	66.57bc	1.94ab	101.72bc	35.15ab	2.91ab	5.31	1.03a	143.95a	71.36a	3.91a
G6	DMR-M-88	64.13c	66.14bc	2.02ab	101.52c	35.37ab	3.68ab	5.52	0.93a	138.59ab	63.63a-c	3.26bc
G7	DMR-M-84	64.45bc	67.50bc	3.05ab	102.76bc	35.26ab	2.54ab	5.42	1.07a	132.97ab	66.45a-c	3.87a
G8	M39	65.45a-c	66.43bc	0.98ab	102.12bc	35.69ab	3.04ab	4.54	0.92a	137.29ab	63.19a-c	2.58e
G9	M53	67.89a	69.43ab	1.54ab	104.04a-c	34.61ab	3.01ab	5.61	0.90a	127.04b	68.81a	3.13bc
G10	FA3	65.80a-c	67.86ab	2.06ab	104.27ab	36.41ab	3.20ab	5.10	1.17a	125.37b	59.16bc	3.00cd
G11	GPM43	65.96a-c	67.64a-c	1.68ab	103.04a-c	35.40ab	3.26ab	6.23	1.16a	132.53ab	60.60bc	2.91cd
G12	GPM53	64.30c	64.64c	0.34bab	101.84bc	37.20a	3.70ab	6.22	0.97a	124.16b	57.37c	3.00cd
Mean		65.845	67.780	1.935	102.952	35.173	3.208	5.531	1.042	133.517	64.553	3.220
SEm		0.138	0.582	0.378	0.464	0.632	0.179	0.282	0.033	2.316	2.466	0.084
P-value		<.0001	<.0001	0.0339	<.0001	0.0465	0.0083	0.1432	0.0317	<.0001	0.0001	<.0001
CV (%)		2.523	2.975	3.269	1.563	6.223	14.833	11.965	11.135	6.010	8.583	6.423

Table 4. Continued

Code	Name	Lodging	Ears per plant	Ear aspect	Ear length	Ear diameter	Kernel row number	Kernels per ear row	Kernels per ear	Kernel weight per ear	Grain yield (t ha⁻¹)
G1	DMR-M-81	1.00c	0.66	2.35a-c	12.20	4.15a-c	13.58a	25.76a	353.10a	72.41ab	3.46ab
G2	M4	2.14a-c	0.68	1.90c	11.81	4.16ab	14.11a	27.26a	383.48a	83.50a	4.48ab
G3	FA6	1.04c	0.74	2.14bc	13.14	3.92a-c	13.37a	28.56a	384.77a	79.72ab	3.91ab
G4	DMR-M-83	2.39a	0.62	3.58a	11.58	3.60c	13.32a	25.57a	341.60a	63.10b	2.76b
G5	GPM36	2.16ab	0.67	1.90c	13.03	4.13a-c	14.00a	28.98a	407.73a	90.76a	4.55a
G6	DMR-M-88	1.56a-c	0.76	2.87a-c	12.89	4.19ab	14.12a	28.98a	410.29a	82.44ab	4.50ab
G7	DMR-M-84	2.18ab	0.68	3.28ab	12.82	3.85a-c	14.59a	29.43a	428.75a	69.49ab	3.39ab
G8	M39	2.14a-c	0.71	2.24bc	12.34	4.06a-c	13.46a	28.45a	382.50a	79.04ab	3.73ab
G9	M53	1.92a-c	0.66	2.37bc	11.58	4.28a	13.06a	24.70a	329.45a	73.43ab	3.46ab
G10	FA3	1.58bc	0.67	2.63a-c	11.52	4.07a-c	13.12a	26.25a	349.04a	72.10ab	3.36ab
G11	GPM43	2.17a-c	0.69	2.94ab	12.60	3.80bc	13.96a	26.61a	375.64a	74.89ab	3.18ab
G12	GPM53	1.97a-c	0.69	2.60a-c	12.41	3.89a-c	13.10a	28.30a	368.00a	73.35ab	3.08ab
Mean		1.854	0.686	2.568	12.326	4.009	13.648	27.404	376.195	76.186	3.656
SEm		0.158	0.047	0.174	0.367	0.084	0.296	0.935	16.486	4.412	0.291
P-value		<.0001	0.8680	<.0001	0.1051	<.0001	0.0082	0.0164	0.0056	0.0055	0.0001
CV (%)		16.537	23.561	16.121	10.327	7.247	7.511	11.818	15.181	20.062	27.533

Note. Means followed by the same letter(s) within a column are not significantly different at 5% level of significance.
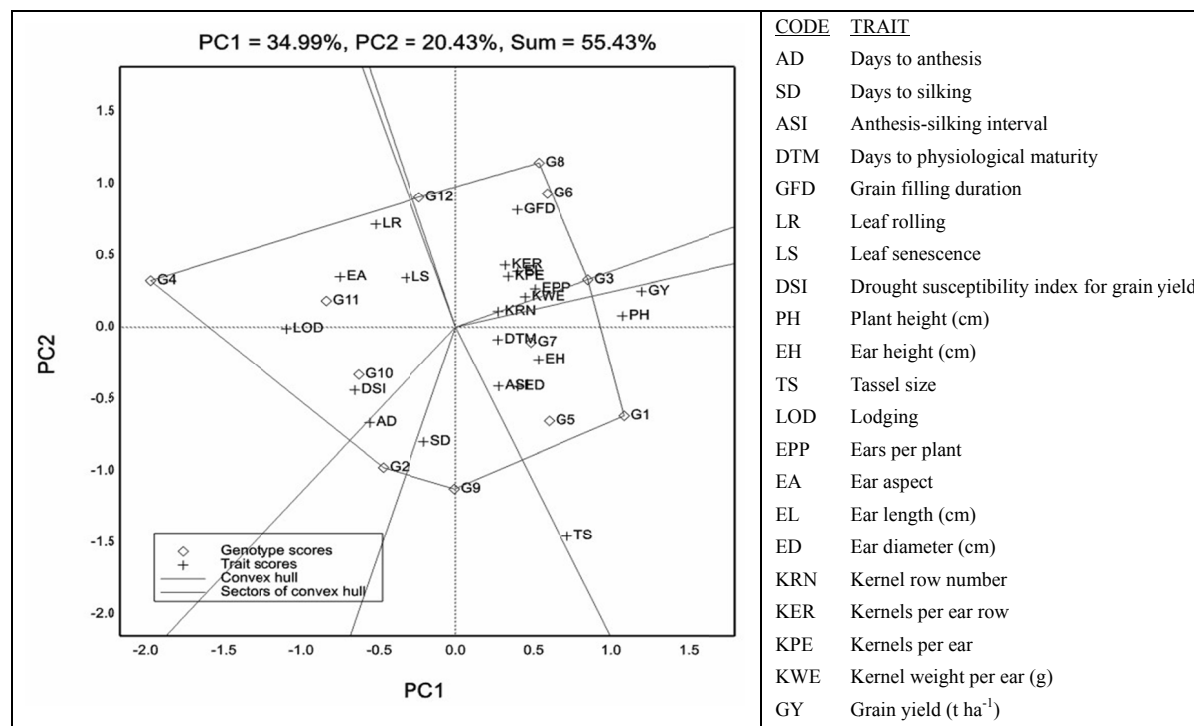

Figure 1. A polygon view genotype-by-trait biplot showing 12 tropical maize inbred lines and 21 traits observed under managed drought environments over two seasons. Genotypes are represented by diamond shaped markers and traits are represented by plus signs. Genotype codes are explained in Table 1 and in the text
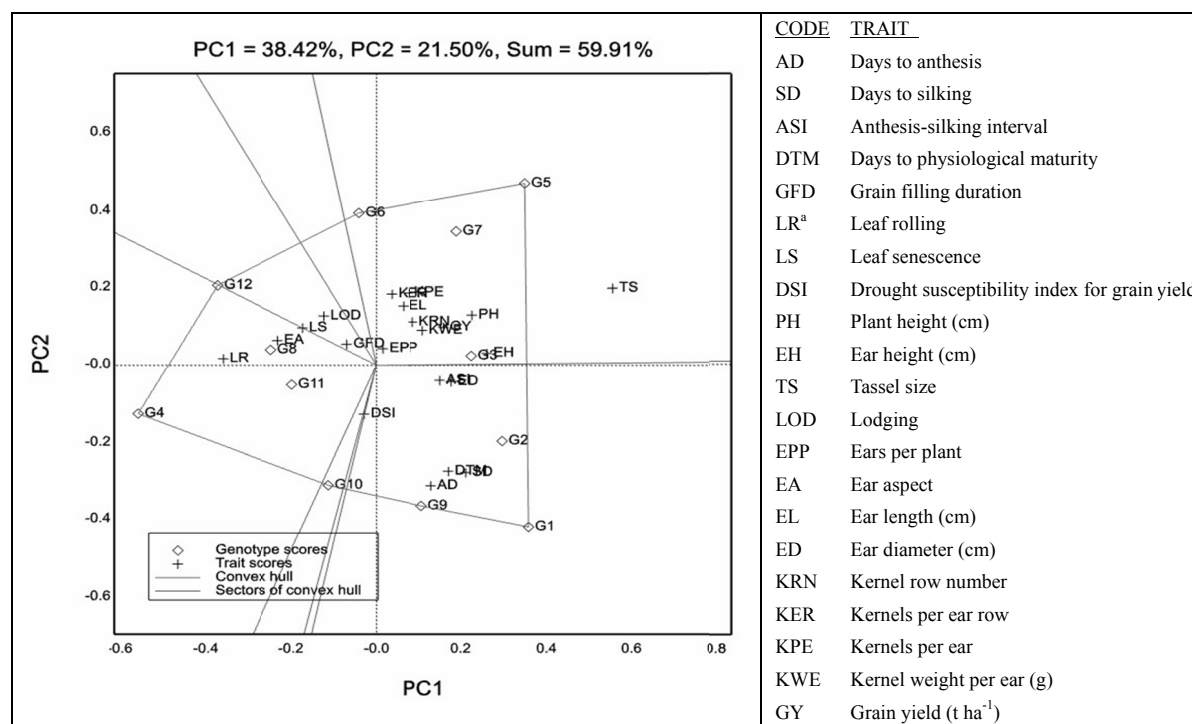
Figure 2. A polygon view genotype-by-trait biplot showing 12 tropical maize inbred lines and 21 traits observed across seven diverse environments. Genotypes are represented by diamond shaped markers and traits are represented by plus signs. Genotype codes are explained in Table 1 and in the text

Note. [a] LR and LS were observed only under managed drought.

4. Discussion

4.1 Analysis of Variance

Significance of environmental effects implies that the level of expression of traits across the environments was different. Significant genotypic effects suggest that the inbred lines possess different allelic combinations for expression of the traits. The genotypes responded differently in regard to expression of DTM, TS, and GY across environments; however for majority of traits, responses of genotypes were the same across environments.

4.2 Genotype by Trait Analysis

The genotype by trait biplot can offer visual comparison of genotypes for multiple traits, since trait profiles especially for genotypes that are located far away from the biplot origin are shown (Yan & Rajcan, 2002; Yan & Kang, 2003; Yan & Frégeau-Reid, 2008).

4.2.1 Genotype by Trait Analysis under Drought and across Environments

Genotypes G6 (DMR-M-88) and G8 (M39) were found to be superior in inherent component traits of grain yield *viz.* kernel row number, kernels per ear row and kernel weight per ear under drought, thus may produce high yielding hybrids if used in hybrid development programmes targeting drought tolerance. This is true if there is a positive correlation between inbred lines and their hybrid progenies in respect of grain yield; however in other studies, for example, Betrán et al. (2003), such a correlation was found to be relatively low. For other traits, for example, ear traits which are potentially involved in grain yield determination, the inbred-hybrid correlation has been found to be relatively high (Betrán et al., 2003; Betrán, Ribaut, Beck, & Gonzalez De León, 2003; Oyekunle, Badu-Apraku, Hearne, & Franco, 2015). It remains therefore necessary to carry out a combining ability analysis study in order to observe whether the inbred lines are able to transmit genes for their associated traits to their hybrid offspring. Early maturity, which is one of the characteristics of these inbred lines (DMR-M-88 and M39), is one of the most important attributes for crops exposed to early terminal drought stress (Harrison, Tardieu, Dong, Messina, & Hammer, 2014), and incorporating this trait in drought tolerance breeding programmes may help stabilize grain yields in farmers' fields. Ears per plant (EPP), which is also associated with these genotypes under drought (Figure 1), is a reliable secondary trait for selection of drought tolerant materials, and high values

for this trait are desirable (Bänzinger et al., 2000). A low value in drought susceptibility, a feature associated with G3 (FA6) and G7 (DMR-M-84) means these genotypes are drought tolerant as was confirmed by Grzesiak et al. (2012). Low values in leaf senescence (LS) and leaf rolling (LR) as exhibited by genotypes G1 (DMR-M-81) and G5 (GPM36) are some of the traits that are important for identification of drought tolerant materials (Bänzinger et al., 2000). Three genotypes *viz.* G3 (FA6), G5 (GPM36), G6 (DMR-M-88), and G7 (DMR-M-84) were superior in inherent component traits of grain yield namely, kernel row number, kernels per ear row and kernel weight per ear across environments, thus may produce high yielding hybrids if used in hybrid development programmes targeting adaptation to diverse environments.

4.2.2 Implications on Selection of Parents

The GT biplots showed rich information that can be utilized by breeders, especially in selection of parents for a breeding programme aimed at improving particular traits, as was pointed by Yan and Fregeau-Reid (2008), Yan and Kang (2003), and Yan and Rajcan (2002). Under managed drought, genotypes G6 (DMR-M-88), G8 (M39), G3 (F6), G5 (GPM36), and G1 (DMR-M-81) appeared to have good attributes, and would be used as parents in a hybridization programme meant to generate drought tolerant hybrids. Across diverse environments, the genotypes G3 (FA6), G5 (GPM36), G6 (DMR-M-88), and G7 (DMR-M-84), which are associated with grain yield and its inherent component traits could be used as parents in hybrid development programmes targeting stable and high yielding hybrids, as was suggested by Meseka, Menkir and Ibrahim (2008). However, since it is not possible to know the desirability of inbred lines for use as parents based solely on their individual performance (Bertan, Carvalho, & Oliveira, 2007), the ability of the identified inbred lines to transmit genes for the traits they are associated with to their offspring (combining ability) needs to be evaluated.

The inbred lines such as G3 (FA6), G5 (GPM36), G6 (DMR-M-88), and G7 (DMR-M-84), which are associated with grain yield and its inherent component traits would be desirable if they are used as female parents in hybrid seed production. This assertion is supported by Beck (2002) who highlighted that high seed yield is one of the very important attributes of a female (seed) parent lines in maize hybrid seed production. The lines G3 and G6 also have an added advantage of being good performers under drought (Figure 1), which is another important attribute of a female parent in seed production as emphasized by Frey (1981). As pointed by D'Andrea, Otegui, and De La Vega (2008), in selecting inbred lines for use in a hybrid breeding programme, both agronomic traits and grain yield *per se* are important. Hallauer and Miranda Filho (1988) further asserted that vigorous and highly productive inbred lines are very important in seed production since they determine the producibility of a hybrid, and decrease the costs of single-cross hybrid seed production. The results of this study should be considered in future breeding programmes involving some or all the inbred lines evaluated.

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