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MULTI-TRAIT SELECTION OF TROPICAL MAIZE GENOTYPES UNDER OPTIMUM AND ACIDIC SOIL CONDITIONS

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SUMMARY

Increasing maize production by expanding to marginal areas in the tropics faces substantial challenges, such as drought and acidic soil. Acidic soils may have low availability of plant nutrients because of the soil's low pH and heavy metals. This study aimed to a) elucidate the response of maize genotypes under optimum and acidic soil, b) determine the correlation between several tolerance indices, and c) predict the response to selection performance based on multiple traits. Thirty-six genotypes, including six checks, laid out in an augmented RCBD, had three replications for the checks under optimum and acidic soil conditions in Bogor, Indonesia. Acidic soil induced late flowering and reduced agronomic performance and yield traits. Genotype, environment, and genotype-byenvironment interaction (GEI) had highly significant (P < 0.01) effects on yield and several traits. G05, G15, and G20 were tolerant and high-yielding genotypes evaluated and ranked using tolerance indices. The mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP), and stress tolerance index (STI) showed significant correlations with yield under both conditions. The multi-trait genotype-ideotype distance index (MGIDI) suggested that genotypes G15 and G20 were better selections in acidic soil, whereas G05's was better in the tolerance index values. Using tolerance indices can help determine the most tolerant genotypes, whereas the multiple-trait index enables researchers to assess the performance of genotypes and identify the most effective traits. These two parameters require recommendations as tools for describing tolerant genotypes in acidic soils in tropical maize breeding programs.

Keywords: Abiotic stress, maize breeding, MGIDI, tolerance indices

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Key findings: The multiple-trait combination index enables researchers to identify desired maize genotypes adapted to optimum and acid soil conditions and elucidate their strengths and weaknesses. Several tolerance indices, i.e., MP, HM, GMP, and STI, revealed correlations with yield in optimum and acid soil conditions.

INTRODUCTION

Maize is an agricultural commodity plant vital for its high economic value. In several sectors of human needs, maize has served for food, bio-energy, industrial materials, animal feed, and other purposes (Sun *et al.*, 2020; Maitra and Singh, 2021). Globally, maize is a complex supply chain traded for food and feed (BfR, 2019). Maize has the highest production, reaching 1.2 billion tons in 2021 (FAO, 2022), with the top maize-producing countries being the United States, Brazil, and China. Indonesia has an average national maize productivity reaching 5.7 t ha⁻¹ in 2021 (BPS, 2021).

The environment is an influential factor affecting maize growth and productivity. Several studies have reported that the genotype-by-environment interaction significantly affects maize yield (Mafouasson et al., 2018). Acidic soils provide abiotic stress and have low pH and less available plant nutrients (Agegnehu et al., 2021). Plants experience poisoning owing to heavy metals, essential nutrient deficiencies, and increased susceptibility to drought, which can reduce crop productivity (Tandzi et al., 2018). Heavy metals are potentially toxic to plants, inhibiting the absorption of nutrients, such as Ca, Mg, and P, because they interfere with root growth and photosynthate mobilization (Sikirou et al., 2016). Acidic soils cause stunted plant growth, early leaf senescence, flowering, and poor anthesis-silking interval synchronization, reducing biomass and yield components, such as cob weight and kernel size (Steiner et al., 2012; Vasconcellos et al., 2021).

Maize breeding has served to obtain varieties that can adapt to and tolerate abiotic stress using conventional and biotechnological approaches (Sheoran, 2022). The tolerance of maize to stress is discernible using tolerance indices, such as tolerance index (TOL), stress tolerance index (STI), and stress susceptibility index (SSI) (Azrai *et al.*, 2022). The yield is the chief trait of maize. Therefore, maize genotypes are prospects for having tolerance and high yield potentials under stress conditions (Makumbi *et al.*, 2018).

Evaluation by identifying the agronomic and physiological traits that affect maize yield can also be helpful for genotypic selection under abiotic stress (Liu and Qin, 2021). Another consideration when selecting maize varieties is the preferences of consumers and industries. Maize selection using multiple traits could benefit more efficient decision-making by weighing the traits' desired economic values (Dermail et al., 2022). Olivoto and Nardino (2021) proposed the multitrait genotypeideotype distance index (MGIDI), which selects an appropriate genotype based on information from several traits. The presented study sought to a) elucidate the response of maize genotypes under optimum and acidic soil conditions, b) determine the correlation between several tolerance indices, and c) predict the response to selection based on multiple traits.

MATERIALS AND METHODS

The genetic materials used in this study consisted of 18 hybrid genotypes, 12 inbred lines, and six hybrid varieties as checks (BISI 18, JHG02, P21, P27, NK Perkasa, and NK Sumo). A complete list of the genetic materials used is available in Table 1. Two varied experimental conditions comprised the study, with the first trial on the optimum soil condition conducted at the Leuwikopo Experimental Station of IPB (6°33'50.8" S; 106°43'29.7" E), Bogor and the second trial on acidic soil transpired at the Cikabayan Experimental Station of IPB (6°33'05.7" S; 106°42'55.3" E), Bogor, from September 2022 to February 2023. The detailed parameters for both conditions appear in Table 2. Organic fertilizer and dolomite applications had rates of

Code	Genotype	Code	Genotype
G01	L152/L26	G19	Mr14
G02	L152/Nei	G20	Nei
G03	L152/P2B	G21	B1
G04	L15/L26	G22	B2
G05	L15/Nei	G23	B4B
G06	L22/L26	G24	L15
G07	L22/Nei	G25	L152
G08	L26/B2	G26	L22
G09	L26/L15	G27	L26
G10	L26/L45	G28	P10
G11	L28/Nei	G29	P13
G12	L45/L15	G30	P2A
G13	L45/P42	G31	BISI 18
G14	L68/L15	G32	JHG02
G15	Mr14/B1	G33	P21
G16	Mr14/P10	G34	P27
G17	Nei/L22	G35	NK Perkasa
G18	Nei/P2	G36	NK Sumo

Table 1. List of maize parental lines, hybrid genotypes, and check varieties.

 Table 2. Description of the optimum and acidic soil environments.

Parameter	Optimum conditions	Acidic soil conditions
Soil type	Alluvial	Alluvial
Altitude (masl)	± 189 masl	± 164 masl
pH H ₂ O	5.26	4.28
pH KCL	4.80	4.03
C-organic (%)	1.88	1.25
N-total (%)	0.22	0.17
AI-dd (cmol AI/kg)	0.00	2.10
H-dd (cmol H/kg)	0.23	0.63
P potential (mg P ₂ O ₅ /100g)	98.76	69.10
K potential (mg K ₂ O/100g)	32.41	12.57

10 t ha⁻¹ and 1 t ha⁻¹, respectively, under optimum conditions, whereas no addition of organic fertilizer or dolomite for the acidic soil. The experimental design used an augmented randomized complete block design with three blocks and repeated checks in each block. The planting distance was 75 cm between rows and 25 cm within rows. The first fertilizer application at 7 days after planting (DAP) used urea fertilizer (46% N) at 150 kg ha⁻¹ and NPK Phonska (15% N, 10% P, 12% K, 10% S) at a rate of 350 kg ha⁻¹. The second fertilization applied at 28 DAP used urea (46% N) at 150 kg ha⁻¹. Harvesting proceeded when most plants reached physiological maturity, as indicated by a black layer appearance in the grain.

Ten collected plant samples for each genotype became the source of phenotypic

data. The observed traits consisted of days to anthesis/DTA; anthesis-silking interval/ASI; plant height/PH (cm, measured as the distance from ground level to the node bearing the flag leaf); ear height/EH (cm, measured as the distance from ground level to the node bearing the uppermost ear); stem diameter/SD (mm, measured at the first node); leaf length/LL (cm, measured at the first leaf after the uppermost ear); leaf width/LW (cm, measured at the first leaf after the uppermost ear); stay green/SG; ear length/EL (cm); ear diameter/ED (mm); a number of ear rows/ER; number of kernels per row/KR; husk cover/HC (scoring from one [very good] to five [very poor]); ear aspect/EA (scoring from one [very five [very poor]); [boop to shelling percentage/SP; moisture content/MC (%); thousand-grain weight/1000 GW (g), and the

grain yield/Y, with calculations using the following formula (CIMMYT, 2004):

 $Yield (t ha^{-1}) = \frac{10000}{PS} \times \frac{100 - MC}{100 - 15} \times \frac{EW}{1000} \times SP$

Where: MC is the actual moisture content of the harvested grain, PS is the harvested plot size (m^2) , EW is the ear yield per plot (kg), and SP is the shelling percentage.

Data analysis employed the F-test to understand the genotype and environment main effects and the interaction effect. Tolerance indices, genotype rankings, and genotype × tolerance indices continued to determine suitable indices for selecting genotypes, including tolerance index (TOL) (Rosielle and Hamblin, 1981); harmonic mean (Schneider *et al.*, 1997); (HM) stress susceptibility index (SSI) (Fischer and Maurer, 1978); and mean productivity (MP), geometric mean productivity (GMP), and stress tolerance index (STI) (Fernandez, 1992). Applying the method of Yan and Rajcan (2002) aided in studying the genotype × tolerance indices interaction. The Pearson correlation helped clarify the relationship between yield in conditions and tolerance indices.

The multitrait genotype-ideotype distance index (MGIDI) served to select genotypes under optimum acidic soil conditions (Olivoto and Nardino, 2021). The selection traits used included ASI, SG, EA, HC, ER, SP, and Y. The grain yield was weighted as two, while the other traits as one. Assessment of the strengths and weaknesses of each genotype was according to the proportion of MGIDI index values of the genotype explained by the selection traits. The broad-sense heritability (H) (Stansfield, 1991), genetic advance (GA) (Singh and Chaudhary, 1979), and genetic advance as a percentage of the mean (GAM) (Shukla et al., 2006) of each selection trait under optimum and acid conditions incur calculations. The heritability categories are low (less than 20%), moderate (20%-50%), or high (>50%) (Stansfield, 1991). Classifying the selection trait GAM, values consisted of low (less than 10%),

moderate (10%–20%), and high (greater than 20%) (Johnson *et al.*, 1955).

The software packages used for statistical analyses were SAS OnDemand for Academics (welcome.oda.sas.com), RStudio (R version 4.1.2), and Microsoft Excel. SAS OnDemand for Academics served in the analysis of variance, and using Microsoft Excel continued for further calculation of variance estimates, heritability, and tolerance indices. Utilizing RStudio drew the 3D scatter plot with the "scatterplot3d" R package (Ligges and 2003), and for analyses of Maechler, correlations, genotype × tolerance indices, MGIDI, and selection differential with the "metan" R package (version 1.18.0) (Olivoto and Lúcio, 2020).

RESULTS

Combined analysis of variance

The combined analysis of agronomic traits, yield, and yield components under optimum and acidic soil conditions is accessible in Table 3. The environment significantly affected all agronomic traits except ER and MC. Genotype (G) caused a significant effect on all yield and yield components except MC. A significant genotype-by-environment interaction (G \times E) for some agronomic traits appeared, and most yield and yield components indicated that genotype responses varied over changing environments. The mean DTA and ASI in the acidic soil environment (DTA 61.7 and ASI 1.3) were higher than those in the optimum environment (DTA 55.9 and ASI 0.4) (Table 4). However, the mean agronomic and yield traits of maize plants grown in the acidic soil environment were lower in the optimum setting.

Maize genotypes' tolerance to acidic soil conditions

Hybrids G33, G15, G05, G31, and G02 and inbred lines G20, G24, and G26 were the best selections based on the ranking summary

Source	df	Agronomic traits							
Source	ui	DTA	ASI	PH	EH	SD	LL	LW	SG
Environments (E)	1	<.0001	0.021	0.002	0.003	0.003	0.0003	0.0002	0.003
Blocks/Environments	4	0.838	0.150	0.021	0.005	0.002	0.110	0.350	0.098
Genotype (G)	35	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Candidate (V)	29	<.0001	<.0001	<.0001	0.002	<.0001	<.0001	<.0001	<.0001
Checks (C)	5	0.0001	<.0001	0.015	0.028	0.001	0.040	<.0001	0.355
V vs C	1	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
GxE	35	0.020	0.099	0.551	0.726	0.006	0.008	0.033	0.003
V x E	29	0.032	0.546	0.584	0.768	0.041	0.014	0.057	0.007
СхЕ	5	0.058	0.005	0.317	0.360	0.0002	0.013	0.037	0.277
(V vs C) x E	1	0.019	0.009	0.455	0.505	0.948	0.112	0.053	0.0001
CV, %		2.35	6.49	9.92	12.69	6.72	4.94	5.14	24.43
â	df								
Sourco	df			Yi	eld and yie	eld compon	ients		
Source	df	EL	ED	Yi ER	eld and yie KR	eld compon SP	ients MC	1000GW	Y
Source Environments (E)	df 1	EL 0.001	ED 0.0001	Yi ER 0.247	eld and yie KR 0.0004	eld compor SP 0.008	MC 0.395	1000GW 0.001	Y 0.0002
Source Environments (E) Blocks/Environments	df 1 4	EL 0.001 0.156	ED 0.0001 0.608	Yi ER 0.247 0.170	eld and yie KR 0.0004 0.545	eld compon SP 0.008 0.164	MC 0.395 0.911	1000GW 0.001 0.882	Y 0.0002 0.181
Source Environments (E) Blocks/Environments Genotype (G)	df 1 4 35	EL 0.001 0.156 <.0001	ED 0.0001 0.608 <.0001	Yi ER 0.247 0.170 <.0001	eld and yie KR 0.0004 0.545 <.0001	eld compor SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189	1000GW 0.001 0.882 0.001	Y 0.0002 0.181 <.0001
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V)	df 1 4 35 29	EL 0.001 0.156 <.0001 <.0001	ED 0.0001 0.608 <.0001 <.0001	Yi ER 0.247 0.170 <.0001 <.0001	eld and yie <u>KR</u> 0.0004 0.545 <.0001 <.0001	Eld compor SP 0.008 0.164 <.0001 <.0001	MC 0.395 0.911 0.189 0.146	1000GW 0.001 0.882 0.001 0.002	Y 0.0002 0.181 <.0001 <.0001
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C)	df 1 4 35 29 5	EL 0.001 0.156 <.0001 <.0001 0.011	ED 0.0001 0.608 <.0001 <.0001 0.020	Yi ER 0.247 0.170 <.0001 <.0001 <.0001	eld and yie <u>KR</u> 0.0004 0.545 <.0001 <.0001 0.003	eld compor SP 0.008 0.164 <.0001 <.0001 0.015	MC 0.395 0.911 0.189 0.146 0.375	1000GW 0.001 0.882 0.001 0.002 0.015	Y 0.0002 0.181 <.0001 <.0001 0.070
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C) V vs C	df 1 4 35 29 5 1	EL 0.001 0.156 <.0001 <.0001 0.011 <.0001	ED 0.0001 0.608 <.0001 <.0001 0.020 <.0001	Yi ER 0.247 0.170 <.0001 <.0001 <.0001 0.005	eld and yie <u>KR</u> 0.0004 0.545 <.0001 <.0001 0.003 <.0001	SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189 0.146 0.375 0.397	1000GW 0.001 0.882 0.001 0.002 0.015 <.0001	Y 0.0002 0.181 <.0001 <.0001 0.070 <.0001
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C) V vs C G x E	df 1 35 29 5 1 35	EL 0.001 0.156 <.0001 <.0001 0.011 <.0001 0.007	ED 0.0001 0.608 <.0001 <.0001 0.020 <.0001 0.023	Yi ER 0.247 0.170 <.0001 <.0001 0.005 0.011	eld and yie <u>KR</u> 0.0004 0.545 <.0001 <.0001 0.003 <.0001 0.013	SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189 0.146 0.375 0.397	1000GW 0.001 0.882 0.001 0.002 0.015 <.0001 0.059	Y 0.0002 0.181 <.0001 <.0001 0.070 <.0001 <.0001
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C) V vs C G x E V x E	df 1 4 35 29 5 1 35 29	EL 0.001 0.156 <.0001 <.0001 0.011 <.0001 0.007 0.004	ED 0.0001 0.608 <.0001 <.0001 0.020 <.0001 0.023 0.017	Yi ER 0.247 0.170 <.0001 <.0001 0.005 0.011 0.006	eld and yie <u>KR</u> 0.0004 0.545 <.0001 <.0001 0.003 <.0001 0.013 0.014	SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189 0.146 0.375 0.397 0.397 0.790 0.850	1000GW 0.001 0.882 0.001 0.002 0.015 <.0001 0.059 0.031	Y 0.0002 0.181 <.0001 <.0001 0.070 <.0001 <.0001 0.0002
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C) V vs C G x E V x E C x E	df 1 4 35 29 5 1 35 29 5	EL 0.001 0.156 <.0001 <.0001 0.011 <.0001 0.007 0.004 0.910	ED 0.0001 0.608 <.0001 <.0001 0.020 <.0001 0.023 0.017 0.372	Yi ER 0.247 0.170 <.0001 <.0001 0.005 0.011 0.006 0.870	eld and yie KR 0.0004 0.545 <.0001 <.0001 0.003 <.0001 0.013 0.014 0.530	SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189 0.146 0.375 0.397 0.790 0.850 0.765	1000GW 0.001 0.882 0.001 0.002 0.015 <.0001 0.059 0.031 0.783	Y 0.0002 0.181 <.0001 <.0001 0.070 <.0001 <.0001 0.0002 0.002
Source Environments (E) Blocks/Environments Genotype (G) Candidate (V) Checks (C) V vs C G x E V x C C x E (V vs C) x E	df 1 4 35 29 5 1 35 29 5 1	EL 0.001 0.156 <.0001 <.0001 0.011 <.0001 0.007 0.004 0.910 0.019	ED 0.0001 0.608 <.0001 <.0001 0.020 <.0001 0.023 0.017 0.372 0.087	Yi ER 0.247 0.170 <.0001 <.0001 <.0001 0.005 0.011 0.006 0.870 0.054	eld and yie KR 0.0004 0.545 <.0001 <.0001 0.003 <.0001 0.013 0.014 0.530 0.004	SP 0.008 0.164 <.0001	MC 0.395 0.911 0.189 0.146 0.375 0.397 0.790 0.850 0.765 0.055	1000GW 0.001 0.882 0.001 0.002 0.015 <.0001 0.059 0.031 0.783 0.922	Υ 0.0002 0.181 <.0001

Table 3. Summary of ANOVA (p-values) of agronomic and yield traits of maize.

DTA: days to anthesis; ASI: anthesis-silking interval - data transformed to log(x+5); PH: plant height; EH: ear height; SD: stem diameter; LL: leaf length; LW: leaf width; SG: stay green; EL: ear length; ED: ear diameter; ER: number of ear rows; KR: number of kernels per row; SP: shelling percentage; MC: moisture content; 1000GW: 1000 grain weight; Y: grain yield.

Condition				Agronon	nic traits			
Condition	DTA (d)	ASI (d)	PH (cm)	EH (cm)	SD (mm)	LL (cm)	LW (cm)	SG
Optimum	55.9 ±	0.4 ±	$175.35 \pm$	87.71 ±	21.63 ±	86.81 ±	10.09 ±	$14.3 \pm$
	1.5	0.87	16.63	15.49	1.69	4.37	0.79	3.93
Acid Soil	61.7 ±	1.3 ±	126.78 ±	$57.01 \pm$	16.8 ±	71.55 ±	8.5 ±	8.4 ±
	2.32	0.49	24.91	9.84	1.95	6.5	0.54	3.93
p-value	<.0001	0.021	0.002	0.003	0.003	0.000	0.000	0.003
			•	Yield and yiel	d components	8		
Condition	EL (cm)	ED (cm)	ER	KR	SP (%)	MC (%)	1000 GW (g)	Y (t ha ⁻¹)
Optimum	16.84 ±	47.22 ±	14.8 ±	33.60 ±	0.81 ±	$15.37 \pm$	294.97 ±	5.41 ±
	1.49	2.97	1.2	2.04	0.01	0.19	0.05	0.98
Acid Soil	$13.3 \pm$	$41.63 \pm$	$14.50 \pm$	$29.2 \pm$	0.80 ±	$15.31 \pm$	$234.25 \pm$	$2.64 \pm$
	1.72	2.45	0.87	3.52	0.02	0.77	0.07	0.9
p-value	0.001	0.000	0.247	0.000	0.008	0.395	0.001	0.000

Table 4. Mean of agronomic and yield traits in maize under optimum and acid soil conditions.

Values are least square means \pm SE; DTA: days to anthesis; ASI: anthesis-silking interval, data transformed to log(x+5); PH: plant height; EH: ear height; SD: stem diameter; LL: leaf length; LW: leaf width; SG: stay green; EL: ear length; ED: ear diameter; ER: number of ear rows; KR: number of kernels per row; SP: shelling percentage; MC: moisture content; 1000GW: 1000 grain weight; Y: grain yield.

Genotype	Y _P	Ys	TOL	MP	HM	GMP	SSI	STI
Hybrids								
G01	8.44	3.20	5.25	5.82	4.64	5.19	1.19	0.49
G02	8.62	4.87	3.76	6.74	6.22	6.48	0.84	0.76
G03	2.16	1.80	0.36	1.98	1.96	1.97	0.32	0.07
G04	7.96	2.49	5.47	5.23	3.80	4.45	1.32	0.36
G05	7.52	5.58	1.94	6.55	6.41	6.48	0.49	0.76
G06	4.05	2.29	1.76	3.17	2.92	3.04	0.84	0.17
G07	6.70	4.19	2.51	5.45	5.16	5.30	0.72	0.51
G08	8.57	2.30	6.27	5.44	3.63	4.44	1.41	0.36
G09	7.95	2.75	5.20	5.35	4.09	4.68	1.26	0.40
G10	6.47	1.64	4.83	4.06	2.62	3.26	1.43	0.19
G11	7.54	3.17	4.37	5.36	4.47	4.89	1.11	0.43
G12	4.16	1.34	2.82	2.75	2.02	2.36	1.30	0.10
G13	5.61	4.73	0.87	5.17	5.13	5.15	0.30	0.48
G14	7.26	3.72	3.54	5.49	4.92	5.19	0.94	0.49
G15	7.59	5.53	2.07	6.56	6.40	6.48	0.52	0.76
G16	7.47	3.67	3.80	5.57	4.92	5.23	0.98	0.50
G17	9.47	2.24	7.23	5.85	3.62	4.60	1.47	0.38
G18	7.64	3.11	4.53	5.38	4.42	4.88	1.14	0.43
G31	8.19	4.66	3.54	6.42	5.94	6.18	0.83	0.69
G32	8.35	3.82	4.53	6.09	5.24	5.65	1.04	0.58
G33	7.95	5.29	2.66	6.62	6.35	6.49	0.64	0.76
G34	9.18	4.73	4.44	6.95	6.24	6.59	0.93	0.79
G35	9.61	5.07	4.53	7.34	6.64	6.98	0.91	0.88
G36	10.01	3.37	6.65	6.69	5.04	5.81	1.27	0.61
Lines								
G19	1.75	0.96	0.80	1.35	1.24	1.29	1.10	0.91
G20	2.34	1.60	0.74	1.97	1.90	1.94	0.76	2.05
G21	1.00	0.58	0.42	0.79	0.73	0.76	1.01	0.32
G22	0.93	0.73	0.20	0.83	0.82	0.83	0.51	0.37
G23	1.23	0.28	0.95	0.76	0.46	0.59	1.85	0.19
G24	1.24	0.82	0.42	1.03	0.99	1.01	0.81	0.55
G25	0.58	0.75	-0.16	0.66	0.65	0.66	-0.68	0.24
G26	1.04	0.87	0.18	0.96	0.95	0.95	0.41	0.49
G27	2.18	0.33	1.85	1.26	0.57	0.85	2.04	0.39
G28	0.73	1.16	-0.44	0.94	0.89	0.92	-1.44	0.46
G29	1.20	0.31	0.90	0.75	0.49	0.61	1.80	0.20
G30	2.01	1.12	0.89	1.56	1.43	1.50	1.07	1.22
Soloctod	G36, G35,	G05, G16,	G03, G13,	G35, G34,	G35, G05,	G35, G34,	G13, G03,	G35, G34,
Selected	G17, G34,	G33, G35,	G06, G05,	G02, G36,	G15, G33,	G33, G05,	G05, G15,	G33, G05,
nybrids	G02	G02	G15	G33	G34	G15	G33	G15
Selected	G20, G27,	G20, G28,	G28, G25,	G20, G30,	G20, G30,	G20, G30,	G28, G25,	G20, G30,
lines	G30	G30	G26	G19	G19	G19	G26	G19
Ranking summary	G33, G15, G	G05, G31, G02	2; G20, G24, G	G26				

Table 5. Selected genotype of maize based on acid soil tolerance indices.

 Y_P : yield under optimum conditions; Y_S : yield under acidic soil conditions; TOL: tolerance index; MP: mean productivity; HM: harmonic mean; GMP: geometric mean productivity; SSI: stress susceptibility index; STI: stress tolerance index.

(Table 5). Based on the polygon diagram of genotype \times tolerance indices, G03, G05, G10, G12, G13, G17, G35, and G36 (Figure 1a) and G20, G23, G25, G27, and G28 (Figure 1b) were superb genotypes compared with the others. Hybrid G05 was more desirable in Y_s,

hybrid G35 in HM, STI, GMP, and MP, and hybrid G17 and G36 in SSI and TOL. The inbred line G20 was superior in Y_p , Y_s , MP, STI, GMP, and HM, and G23 and G27 were best in TOL and SSI indices.



Figure 1. Polygon diagram of maize genotypes to tolerance indices studied under acidic soil.



Figure 2. Pearson correlation between tolerance indices: a) hybrids; b) inbred lines, evaluated under acid soil stress.

Correlations between tolerance indices

The mean yield values under optimum (Y_P) and acidic soil conditions (Y_s) indicated significant correlations (r = 0.42, P < 0.05) in maize hybrids (Figure 2a) but not in inbred lines (r =0.28, p > 0.05) (Figure 2b). The Y_P showed a substantial link with all tolerance indices (P < 0.05), whereas Y_s has no significant connections with the TOL and SSI. The correlation between the TOL and SSI was noteworthy. MP, HM, GMP, and STI differed significantly. Tolerance indices with high and significant correlations (P < 0.05) with Y_p and Y_s were MP, HM, GMP, and STI.



Figure 3. MGIDI index analysis for the 18 maize hybrids: a) under optimum conditions; b) under acidic soil conditions; c) using tolerance index.



Figure 4. MGIDI index analysis for the 12 maize inbred lines: a) under optimum conditions; b) under acidic soil conditions; c) using tolerance index.

Multitrait genotype-ideotype distance index and predicted genetic advance

Three hybrids and two lines gained selection based on the MGIDI for each condition and using tolerance index (TOL), with a selection intensity of 15%. Genotypes G17, G08, and G01 (optimum conditions), G15, G07, and G13 (acid soil conditions), and G05, G03, and G13 (using tolerance index) were best options (Figure 3). Meanwhile, G20 and G19 (optimum conditions), G20 and G28 (acid soil conditions), and G28 and G25 (using tolerance index) were the best-selected lines. Line G20 attained selection in both evaluation environments (Figure 4). The selection differential (SD) of the hybrids were 27% (optimum conditions) and 47.9% (acidic soil conditions), whereas the SD of the inbred lines were 51.2% (optimum conditions) and 74.1% (acidic soil conditions) (Table 6).

The heritability for each selection trait was generally high and moderate under both conditions. The predicted genetic advance (GA) of hybrids ranged from 0.02 to 4.26 under optimum conditions and from 0.03 to 2.76 under acidic soil conditions. The foreseen genetic advance as a percentage of the mean (GAM) of hybrids was relatively high (>20%) in both situations. The GA of lines ranged from 0.09 to 2.45 in optimum conditions and from 0.09 to 2.43 in acidic soil conditions. ER, SP, and EA, under optimum conditions, and SP and ER, under acidic soil conditions, had GAM values below 20%.

Factor Traita		Samaa	Caal		Mean pe	rformance			<u> </u>	CAM	
Factor	Traits	Sense	Sense	Goal	Xo	Xs	SD	SD%	— н	GA	GAIVI
Optimum	o conditions	s (hybrids)									
FA1	EA	-	Yes	2.34	1.79	-0.55	-23.60	61.88	0.64	27.21	
FA1	Y_{P}	+	Yes	6.96	8.83	1.88	27.00	85.63	2.14	30.76	
FA2	ASI	-	Yes	1.18	0.59	-0.59	-49.70	76.36	1.32	111.84	
FA2	SP	+	Yes	0.83	0.84	0.01	1.07	80.20	0.02	2.29	
FA2	HC	-	Yes	1.61	1.11	-0.50	-30.90	53.72	0.92	57.45	
FA3	SG	+	Yes	18.40	22.70	4.34	23.60	65.67	4.26	23.17	
FA3	ER	+	Yes	15.60	16.20	0.67	4.30	62.00	1.16	7.46	
Acidic so	il condition	s (hybrids)									
FA1	SG	+	Yes	9.70	13.90	4.18	43.10	50.86	2.76	28.43	
FA1	HC	-	Yes	1.96	1.11	-0.85	-43.30	33.51	0.47	24.20	
FA2	ASI	-	Yes	1.48	1.06	-0.42	-28.50	90.36	1.37	92.62	
FA2	ER	+	Yes	15.90	17.00	1.04	6.54	89.10	2.27	14.30	
FA2	SP	+	No	0.81	0.78	-0.03	-3.16	79.44	0.03	4.27	
FA3	Ys	+	Yes	3.26	4.82	1.56	47.90	80.00	1.56	47.97	
FA3	EA	-	Yes	1.91	1.45	-0.46	-24.20	67.17	0.76	39.96	
Optimum	o conditions	s (lines)									
FA1	ASI	-	Yes	0.95	0.06	-0.89	-93.70	85.53	1.89	198.92	
FA1	SG	+	No	4.81	1.83	-2.98	-61.90	46.95	2.45	50.98	
FA1	ER	+	No	13.70	13.10	-0.61	-4.46	47.20	0.75	5.48	
FA1	SP	+	No	0.78	0.78	0.00	-0.32	98.68	0.09	11.63	
FA1	EA	-	Yes	2.83	2.61	-0.22	-7.88	43.44	0.37	12.97	
FA2	HC	+	Yes	1.14	0.56	-0.58	-50.80	57.94	1.05	91.78	
FA2	Y_{P}	+	Yes	1.35	2.04	0.69	51.20	86.56	2.24	165.79	
Acidic so	il condition	s (lines)									
FA1	EA	_	Yes	2.64	1.42	-1.22	-46.40	79.30	1.13	42.97	
FA1	Ys	+	Yes	0.79	1.38	0.59	74.10	78.67	1.49	188.44	
FA2	ASI	-	Yes	1.42	0.86	-0.56	-39.50	96.51	2.43	171.36	
FA2	ER	+	Yes	12.20	13.50	1.32	10.80	88.29	2.17	17.82	
FA2	HC	-	Yes	1.89	1.16	-0.72	-38.30	62.72	1.19	62.72	
FA3	SG	+	Yes	5.44	5.78	0.34	6.15	44.66	2.28	41.94	
FA3	SP	+	Yes	0.77	0.79	0.01	1.51	95.71	0.09	11.86	

Table 6. Predicted genetic advance of maize based on MGIDI selection.

ASI: anthesis-silking interval; SG: stay green; ER: number of ear rows; HC: husk cover; EA: ear aspect; SP: shelling percentage; Y_P : yield under optimum conditions; Y_S : yield under acidic soil conditions; X_0 : mean of population; X_S : mean of selected genotypes; SD: selection differential; H: heritability of broad sense; GA: predicted genetic advance; GAM: predicted genetic advance as percentage of mean.

The strengths and weaknesses of selected genotypes

The strengths and weaknesses view of selected hybrids under optimum conditions (Figure 5a) revealed that the performance of choice hybrids G17 and G08 showed strengths related to factor FA2 with ASI, HC, and SP. The hybrid G01 revealed strengths related to the FA3 factor with SG and ER. Under acidic soil conditions (Figure 5b), hybrid G07 exhibited abilities related to feature FA2 with ASI, ER, and SP, whereas G13 and G15 showed strengths related to factor FA3 with EA and Y_S . Meanwhile, using the tolerance index (Figure 5c), hybrid G13 demonstrated strengths related to issue FA2 with Y_{TOL} , ASI, and EA; G03 showed strengths related to factor FA4 with SP, and G05 exhibited intensities related to factors FA2, and F4 with Y_{TOL} , ASI, EA, and SP. The lines under optimum conditions (Figure 6a) show that line G19 has strengths related to factor FA1 with ASI, SG, ER, SP, and EA, whereas G20 exhibits strengths related to aspect FA2 with HC and Y_P . Lines G20 and G28, selected under acid soil conditions (Figure 6b),



Figure 5. The strengths and weakness view of selected hybrids based on MGIDI: a) optimum condition; b) acidic soil conditions; c) using tolerance index.



Figure 6. The strengths and weakness view of selected inbred lines based on MGIDI: a) optimum conditions; c) acidic soil conditions; c) using tolerance index.

demonstrate strengths related to issue FA2 that holds ASI, ER, and HC. Meanwhile, lines G28 and G25, selected based on the tolerance index, exhibited vigor linked to FA3 containing ER and SP (Figure 6c).

DISCUSSION

The environment is an influential factor in the performance of maize agronomic traits, yield, and yield components (Shojaei *et al.*, 2022). Variations in environmental factors, such as soil pH and nutrient content, between the two environments used in this study impacted the phenotypic performance of maize genotypes. The interaction between genotype and

environment is crucial for determining the performance of genotypes requiring further testing for stability using regression analysis and GGE biplot to explain the interaction, assess the potential yield, and know the adaptability of genotypes across various environments (Kumar *et al.*, 2015; Mafouasson *et al.*, 2018; Zaki and Ahmed, 2023).

Yield is one of the most critical quantitative traits in maize. In this study, the mean yield decreased in the acidic soil environment compared with the optimum conditions. Previous studies have reported yield reductions ranging from 36% to 51% in Latin America-Asia and 36% to 40% in Cameroon due to acid soil stress (Tandzi *et al.*, 2018; Amzeri *et al.*, 2020). The genotypes

showed delayed and asynchronous flowering under acidic soil conditions, as indicated by the anthesis-silking interval. The effect of abiotic stress on maize flowering can affect the optimal expression of yield-related traits (Maazou *et al.*, 2016). The poor performance of maize genotypes in acidic soils has pointed to the toxicity of heavy metals and nutrient deficiency. Consequently, plant growth in acidic soils tends to worsen, leading to drought stress and premature aging of plants (Sikirou *et al.*, 2016).

Developing superior maize genotypes is the goal of selection and breeding programs, particularly in tropical and subtropical regions with acidic soil conditions. Evaluating maize genotypes under optimum and acidic soil conditions is necessary to select tolerant genotypes under acidic soil settings. Fernandez (1992) reviewed several formulas of tolerance indices to choose genotypes, including TOL, SSI, SI, HM, and MP, showing the relevance of using STI. In this study, genotype selection happened by ranking maize genotypes based on their adjusted values for each index to determine the desired genotypes based on the tolerance indices. Shojaei et al. (2022) and Karaman (2019) used a polygon diagram with genotype × tolerance indices methods to identify the selected genotypes under stress

conditions. This method supports the selection of genotypes from each index, the results of which were close to those of the ranking method, such as the G20 line, superior to MP, STI, GMP, and HM.

The average yields of each genotype under both conditions and tolerance index (TOL) have a projection in a three-dimensional scatter plot in Figure 7, showing that hybrids G05 and G15 (Figure 7a) and inbred line G20 (Figure 7b) were genotypes that had the best yield retention in both optimum and acidic soil conditions. The ranking summary of all tolerance indices showed the same results, with G15, G05, and G20 (Nei) being tolerant to acidic soil conditions. Future research should focus on studying these genotypes' morphophysiological adaptation and tolerance to acidic soil conditions.

Several tolerance indices indicated significant correlations with yields under optimum (Y_P) and acidic soil (Y_S) conditions, such as, MP, HM, GMP, and STI. Tandzi *et al.* (2015) reported significant correlations between STI, GMP, MP, and the Y_P and Y_S of maize genotypes evaluated under acidic soil conditions, while Azrai *et al.* (2022) found a significant correlation between STI and yield in both surroundings.



Figure 7. The average yield under optimum (Y_P) and acid soil conditions (Y_S) and tolerance index (TOL) of maize genotypes: a) hybrids; b) inbred lines.

The multitrait genotype-ideotype distance index (MGIDI) is a new method used considers for genotype screening that secondary traits and yields to identify the best genotypes. This method performs selection using genotype and ideotype distances formulated by the breeder, which can be a solution to weighting coefficients for economic traits or multicollinearity issues in other selection methods (Olivoto and Nardino, 2021). Olivoto et al. (2022) reported that this selection method has advantages in terms of genotype ranking, strengths easy and weaknesses view, and the option to weigh each trait in genotype ranking. Several previous studies have reported the utility of this method in selecting superior genotypes under abiotic stress and mega-environments (Maranna et al., 2021; Singamsetti et al., 2023).

Genotype selection in this study involves dividing between maize hybrids and lines under optimum and acid soil conditions and using the tolerance index (TOL). Using the tolerance index to select maize genotypes with multiple traits identified the differences between genotypes under optimum and acidic soil conditions. The selected hybrids may need further probing in a multi-environment trial to elucidate adaptability and stability, while the selected inbred lines can test for combining ability. Heritability was moderate to high, with high GA and GAM for several traits. Analysis of heritability, GA, and GAM helped estimate the effectiveness of attributes in selecting superior genotypes (Magar et al., 2021).

The MGIDI model could better identify multiple traits for genotyping and enable breeders to simplify the selection process by considering the strengths and weaknesses of attributes in maize breeding programs in multienvironments (Yue *et al.*, 2022). For example, hybrid G15, evaluated under acidic soil conditions, showed strengths related to FA3, which consists of EA and Y_s traits, but had a weakness related to FA2, consisting of ASI and HC features. It indicated that the G15 genotype had high yield values but lacked synchronization in ASI and a less favorable husk cover of the ear. Such information may be valuable for maize breeders to identify superior genotypes for their breeding programs.

CONCLUSIONS

The genotype, environment, and GFL significantly affected vield and several agronomic traits on tropical maize evaluated under optimum and acidic soil conditions. G05, G15, and G20 were the most tolerant under acidic soil stress and high yield under both conditions, assessed based on tolerance indices. The MP, HM, GMP, and STI are indices significantly correlated with yield in both settings. G08, G01, G17, G19, and G20 (optimum conditions), G15, G07, G13, G20, and G28 (acidic soil conditions), and G05, G03, G13, G28, and G25 (using the tolerance index) were best-selected using the MGIDI method. This method is recommendable for determining the appropriate genotypes by considering their strengths and weaknesses.

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