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Research article

Identification of adaptable sunflower (*Helianthus annuus* L.) genotypes using yield performance and multiple-traits index

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ABSTRACT

Sunflower is the most important oil crop ranked as fourth edible oil in the world. The study was conducted in Northern Ethiopia during 2017–2019 cropping seasons using randomized completely block design with three replications. The objective was to decipher the genotype by environment interaction (GEI) in multi-environment trials (MET) and identify adaptable sunflower genotypes. Combined ANOVA, AMMI ANOVA and Eberhart and Rusell regression were analyzed, and GGE bi-plots, AMMI1 and AMMI2 bi-plots, Principal component Analysis (PCA), multi-trait genotype–ideotype distance index (MGIDI), correlation network plot for sunflower traits were sketched. AMMI stability measures, Best Linear Unbiased Prediction (BLUP) based indexes; parametric and non-parametric statistics were computed using R-statistical software. In the AMMI ANOVA the main effects of the environment (E) (54.18 % SS), genotype (G) (16.9 % SS) and GEI (23.50 % SS) were significant ($p < 0.001$). The genotypic Likely-hood Ratio Test revealed significant for all traits. The AMMI bi-plot and the GGE bi-plots selected G10 and G2 as the most adaptable genotypes. CV, HMGV, RPGV, HMRPGV, P_i, GAI, KRS, $S^{(3)}$ and $S^{(6)}$ also identified G10 as the most stable genotype. Based on the MGIDI, G10 (MGIDI = 1.45) and G5 (MGIDI = 2.19) are selected and these genotypes are recommended for further cultivation in Tigray.

1. Introduction

Among the 51 *Helianthus* genus species [1], Sun flower (*Helianthus annuus* L.) and Jerusalem artichoke (*Helianthus tuberosus* L.) are the only exploited species in agriculture and are cultivated for seed oil and while the latter species is for feed and food of its tubers [2]. Sunflower is recognized as the most important oil crops and ranked as fourth edible oil in the world next to rapeseed, soybean and palm oil [3]. Sunflower oil which covers about 10 % of the total world consumption of plant-derived edible oil [4] varies because of environmental factors and contains an oil content of about: 39.6 %–48.3 % [5] and 39.26 % [6]. Furthermore, it is rich in fiber and possessing low caloric content and it also contains different levels of protein content 25 % [7] and 40–44 % [8]. Sunflower (*Helianthus annuus* L.) is among the highly adaptable crops because of it has deep roots, to get enough moisture and avoid erosion [1], and

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allopathic effect, to tolerate weeds [9].

The understanding of environmental and genotypic causes of GxE Interaction (GEI) is crucial and such occurrence of GEI is a challenge and an opportunity for plant breeders [10]. To develop new variety it is important to undertake a multi-environment trials (MET) on which, a set of genotypes are usually evaluated across many years and locations [11]. Execution of MET creates a room to breeders and agronomist to recognize ideotypes with a specific adaptability in many environments [12]. Generally, there are two main methods (parametric and non-parametric) for analyzing the interaction of G × E and stability of genotypes [13]. These methods has different advantages and limitations, that should be completed and supported by each other to select a stable and high yielding genotype by considering a number of identified variables for environmental interactions [14]. For this reason, both parametric and non-parametric methods are used for data analysis from multi environment trials [15–17]. AMMI [18] and GGE bi-plots [11] are also very important to identify desirable genotypes. While using the conventional AMMI model, if the explained variance in the first IPCA is lower, it may lead to a biased interpretation on the stability. To avoid such drawback [19] proposed a new stability index namely Weighted Average of Absolute Scores (WAASB), which integrates both AMMI and BLUP models. Piepho H.-P [20] suggested that BLUP (Best Linear Unbiased Predictor) should be used instead of AMMI to obtain a reliable estimates in METs. Moreover, Olivoto et al. [12], also reported that the predictive accuracy was higher when using the BLUP than any member of the AMMI family for real MET dataset.

Nowadays, selection desirable genotype considers multiple traits instead of grain yield only. Predominantly, MET analysis is executed with a special focus on a single trait, mainly yield, to select desired genotype [21,22]. However, the use of multiple traits to select desirable genotypes is more preferable [23–25]. Plant breeders are eager in search of high yielding genotype with better agronomic traits and such target genotype is considered as ideotype, which is introduced by Donald C.T [26]. In order to realize and get such ideotype genotype in MET [27] proposed a novel method named multi-trait genotype–ideotype distance index (MGIDI), which integrates the simultaneous selection for the stability of multiple traits into a single and easy-to-interpret index. This MGIDI is more recommended to select adaptable and high yielding genotype based on multiple traits [28] which could be better selection of genotypes for further breeding based on different traits.

In Ethiopia Sunflower, having an oil content of 25–33 % and seed yield of lower than 1.1 t/ha has been cultivated since the beginning of 19th centuries [29]. Sunflower oil yield and seed yield are highly variable across different environments and showed significant GEI on its grain yield [30,31]. Sunflower cultivation is a common practice in Ethiopia in general and in the study areas in particular. However, there are no improved varieties released for these areas and the observed performance variation across the growing seasons and locations is not studied very well yet. Therefore, the present study aimed (i) to decipher the GEI of sunflower genotypes and thereby (ii) to identify high yielding and stable genotypes in the lowlands of Tigray, Northern Ethiopia.

Table 1
AMMI based, BLUP based, Parametric and Non-parametric stability statistics used to analyze stability.

SNo	Stability Measure	Symbol	Value for Selection of Stable Genotype	Reference
1	AMMI stability value	ASV	Minimum	[36]
2	Sums of the absolute value of the IPCA scores	SIPC	Minimum	[37]
3	Averages of the squared eigenvector values	EV	Minimum	[37]
4	Absolute value of the relative contribution of IPCAs to the interaction	ZA	Minimum	[38]
5	Weighted Average of Absolute Scores	WAAS	Minimum	[39]
6	Harmonic Mean of Genotypic Values	HMGV	Maximum	[40]
7	Relative Performance of Genotypic Values and other as mentioned above	RPGV	Maximum	
8	Harmonic Mean of RPGV	HMRPGV	Maximum	
9	Wricke's Ecovalence	W*i*	Minimum	[41]
10	Shukla stability variance	σ2 (S2)	Minimum	[42]
11	Coefficient of Variation	CV	Minimum	[43]
12	Coefficients of determination	R2	Minimum	[44]
13	Geometric Adaptability Index	GAI	Maximum	[45]
14	Superiority index	Pi	Minimum	[46]
15	Eberhart and Russel regression coefficient	bi	bi = 1	[47]
16	Eberhart and Russel deviation from regrassion	S2di	Minimum	[47]
17	Kang's rank-sum	KRS	Minimum	[48]
18	Average rank differences in different environments	S(1)	Minimum	[49]
19	The variance among the ranks in different environments	S(2)	Minimum	
20	The sum of squares of rank for each genotype relative to the mean of ranks	S(3	Minimum	
21	The sum of the absolute deviations for each genotype relative to the mean of ranks	S(6)	Minimum	
22–25	Thennarasu non-parametric stability measures NP(1–4)	NP(1), NP(2), NP(3), NP (4),	Minimum	[50]

2. Materials and methods

2.1. Experimental material and method

The study was conducted in Tigray, Northern Ethiopia in four locations viz. Humera (14°15′N, 36°37′ E), Banat (13°48′ N, 36°30′ E), Kebabo (13°36′ N, 36°41′ E) and Sheraro (14°24′ N, 37°45′ E) during 2017–2019, 2017–2019, 2018–2019 and 2018 cropping seasons in the respective locations in a total of nine environments (Supplementary Table S1). In all environments the design was randomized completely block design (RCBD) with three replications. 15 sunflower genotypes, obtained from the breeding program of Humera Agricultural Research Center of the Tigray Agricultural Research Institute, Holleta Agricultural Research Center (standard check) and farmers' seed (local check), were used in the trial and are described in Saplimentary Table S2. Each experimental plot had 5 m length and five rows with 75 cm and 30 cm spacing between rows and plants respectively and all other agronomic practices were applied to each plot equally. Data on agro-morphological traits were taken from five randomly selected and representative plant in the middle of the plots. Similarly, data on grain yield were taken from the middle rows of each plot, excluding the two border rows, and total grain yield (kg/ha) was estimated for each genotype at each test environments.

2.2. Statistical analysis

A combined analysis of variance for grain yield was executed from the mean data of all environments to identify the existence of GEI and Tukey's HSD was performed to explain the significant differences among the genotypes' mean grain yields. Combined ANOVA, AMMI ANOVA and Eberhart & Rusell regression were analyzed, and GGE bi-plots, AMMI1 and AMMI2 bi-plots were sketched. The stability measures like AMMI related stability measures, BLUP based indexes; parametric and non-parametric stability statistics were analyzed to estimate the GEI for the fifteen sunflower genotypes. These stability statistics are described in Table 1 and the formulas are stated in Supplementary Table S3. Principal Component Analysis (PCA) was computed to identify association among the stability statistics using the 'factoextra' package [32] of R software 4.2.2. while all other data were analyzed with the assistance of R statistical environment version 4.2.2 [33] with the help of the "metan" package [34]. Moreover, "corrr" package version 0.April 4, 9000 [35] was employed to sketch the network plots of the pairwise correlation data frame.

Table 2

Combined ANOVA, AMMI ANOVA and Eberhart and Rusell Regression and Mean yield performance for fifteen sunflower genotypes.

Source	Df	SS	Mean Square	Explained Sum of Squares (%)		
				Total	GEI	GEI Cumulative
Combined ANOVA						
Rep	2	1687	843			
Gen	14	10320208	737158***			
Env	8	33101740	4137718***			
Gen:Env	112	14358055	128197***			
Residuals	268	3311284	12356			
Eberhart and Rusell Regression						
Total	134	19260001	143731			
Genotypes	14	3440069	245719***			
Env + (Gen x Env)	120	15819932	131833			
Env (linear)	1	11033913	11033913			
Gen x Env(linear)	14	984639	70331*			
Pooled deviation	105	3801379	36204			
AMMI analysis						
ENV	8	33101740	4137718***	54.18		.
REP(ENV)	18	151130	8396	.		.
GEN	14	10320208	737158***	16.89		.
ENV:GEN	112	14358055	128197***	23.5		.
PC1	21	6653949	316855***		46.3	46.3
PC2	19	2822295	148542***		19.7	66
PC3	17	1885572	110916***		13.1	79.1
PC4	15	1201051	80070***		8.4	87.5
PC5	13	746473	57421***		5.2	92.7
PC6	11	582676	52971***		4.1	96.8
PC7	9	312597	34733**		2.2	98.9
PC8	7	153441	21920^{ns}		1.1	100
Residuals	252	3161842	12547		.	.
Total	404	61092974	151220		.	.

Df: degree of freedom; SS: sum of squares; Gen: genotype; Env: environment; GEI: genotype-by-environment interaction.

Table 3
Genotypic values and ranks of the stability measures.

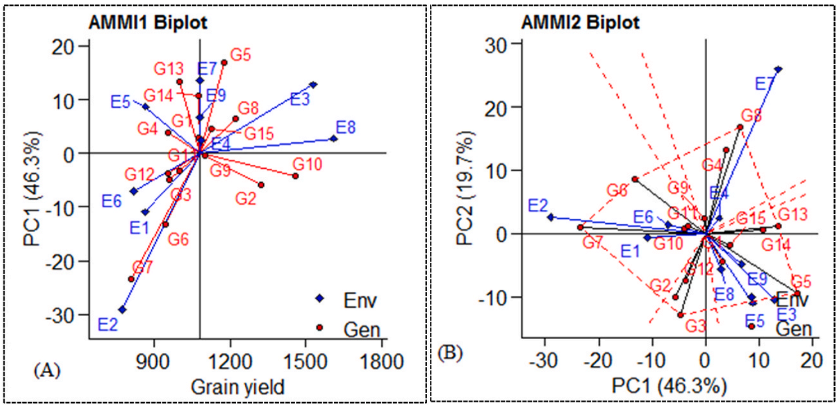
Gen	Yld	CV	σ 2	Wi	b_i	S^2d_i	R^2	ASV	SIPC	EV	ZA	WAAS	HMGV	RPGV
G1	1076.55	30.56	10544.1	287689	1.02	9460.44	0.89	8.34	26.99	0.03	0.11	3.44	993.54	1
G10	1457.9	19.7	15449.5	389721	0.86	12328.6	0.82	9.75	30.08	0.06	0.12	3.58	1403.57	1.38
G11	1001.91	22.78	11477.1	307095	0.71	1830.3	0.9	7.68	28.44	0.05	0.11	3.29	956.88	0.94
G12	957.44	38.8	43273.4	968457	1.03	41832.7	0.71	11.61	49.19	0.09	0.22	6.48	874.3	0.89
G13	998.19	49.23	62147.1	1361032	1.5	33845.6	0.86	31.72	42.11	0.09	0.25	8.57	773.7	0.89
G14	1075.05	37.33	32618.7	746840	1.21	26894.5	0.83	25.27	34.38	0.05	0.19	6.63	937.59	0.98
G15	1124.96	33.01	8344.15	241930	1.19	3345.25	0.95	10.71	22.23	0.03	0.1	3.34	1033.7	1.03
G2	1321.05	21.58	41717.4	936093	0.73	32712.8	0.6	16.87	43.48	0.08	0.22	6.93	1268.86	1.25
G3	958.95	41.74	34459	785120	1.19	29277.4	0.82	17.21	40.47	0.06	0.2	6.31	852.96	0.88
G4	952.59	38.05	32163.9	737381	1.05	30694.1	0.77	15.87	37.67	0.07	0.17	5.36	836.78	0.87
G5	1177.61	41.49	82985.8	1794475	1.39	65159.5	0.75	41.06	53.24	0.1	0.33	11.49	957.07	1.07
G6	946.79	20.22	74483	1617618	0.33	26064.9	0.28	32.53	48.56	0.08	0.31	10.61	920.87	0.91
G7	808.9	44.43	126482	2699192	0.59	106756	0.25	55.14	49.59	0.1	0.36	12.88	691.51	0.77
G8	1219.18	31.97	57838.8	1271418	1.04	56208.5	0.65	22.51	45.55	0.07	0.25	8.1	1115.39	1.13
G9	1101.31	32.34	7001.02	213993	1.14	3909.11	0.94	2.51	22.34	0.04	0.07	1.8	1018.23	1.01
Rank														
G1	7	5	3	3	1	4	4	3	3	2	4	4	6	7
G10	1	1	5	5	5	5	7	4	5	6	5	5	1	1
G11	9	4	4	4	11	1	3	2	4	4	3	2	8	9
G12	12	11	10	10	2	12	11	6	13	13	9	8	11	12
G13	10	15	12	12	14	11	5	12	9	12	11	12	14	11
G14	8	9	7	7	9	7	6	11	6	5	7	9	9	8
G15	5	8	2	2	8	2	1	5	1	1	2	3	4	5
G2	2	3	9	9	10	10	13	8	10	11	10	10	2	2
G3	11	13	8	8	7	8	8	9	8	7	8	7	12	13
G4	13	10	6	6	4	9	9	7	7	8	6	6	13	14
G5	4	12	14	14	12	14	10	14	15	14	14	14	7	4
G6	14	2	13	13	15	6	14	13	12	10	13	13	10	10
G7	15	14	15	15	13	15	15	15	14	15	15	15	15	15
G8	3	6	11	11	3	13	12	10	11	9	12	11	3	3
G9	6	7	1	1	6	3	2	1	2	3	1	1	5	6

Gen	HMRPGV	Pi	GAI	KRS	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$N^{(1)}$	$N^{(2)}$	$N^{(3)}$	$N^{(4)}$
G1	0.98	124608	1032.76	10	0.08	11.69	6.81	2.52	2.78	0.35	0.43	0.01
G10	1.36	7065.07	1433.22	6	0.03	17.28	0.29	0.38	3.33	3.33	2.52	0.02
G11	0.93	145778	979.17	13	0.19	16.5	13.5	3.5	2.78	0.31	0.41	0.02
G12	0.86	202315	906.48	22	0.03	23.53	24.88	5.16	3.67	0.31	0.44	0
G13	0.81	170529	872.75	22	0.08	24.94	23.84	5.05	4.11	0.51	0.51	0.01
G14	0.95	127919	1001.22	15	0.03	17.5	12.93	3.04	2.89	0.41	0.5	0
G15	1.03	95896.1	1074.93	7	0.03	15.61	7.51	2.16	3.11	0.52	0.5	0
G2	1.22	47241.1	1295.12	11	0.25	22.25	9.5	2.15	3.89	1.3	1.08	0.06
G3	0.85	199781	894.69	19	0.17	16.36	10.33	3.39	2.67	0.24	0.36	0.02
G4	0.84	185548	888.86	19	0.11	16.03	21.38	4.88	3.22	0.25	0.35	0.01
G5	0.98	112763	1062.53	18	0.03	32.25	18.83	3.86	4.78	1.19	0.85	0
G6	0.88	202654	931.33	27	0.08	21.61	17.34	4.39	3.78	0.38	0.48	0.01
G7	0.68	313955	737.76	30	0.19	27.69	44.4	8	4	0.29	0.39	0.02
G8	1.1	77603.4	1163.4	14	0.03	28.86	13.34	3.05	4.44	0.89	0.86	0
G9	1.01	105899	1055.54	7	0.11	13.36	3.59	1.44	3	0.43	0.48	0.02
Rank												

(*continued on next page*)

Table 3 (*continued*)

Gen	HMRPGV	Pi	GAI	KRS	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$N^{(1)}$	$N^{(2)}$	$N^{(3)}$	$N^{(4)}$
G1	6	7	7	4	8	1	3	5	2.5	6	5	9
G10	1	1	1	1	3.5	7	1	1	8	15	15	13
G11	9	9	9	6	13.5	6	9	9	2.5	5	4	14
G12	11	13	11	12	3.5	11	14	14	9	4	6	1
G13	14	10	14	13	8	12	13	13	13	10	11	6.5
G14	8	8	8	8	3.5	8	7	6	4	8	9	2
G15	4	4	4	2	3.5	3	4	4	6	11	10	3
G2	2	2	2	5	15	10	5	3	11	14	14	15
G3	12	12	12	10	12	5	6	8	1	1	2	12
G4	13	11	13	11	10.5	4	12	12	7	2	1	8
G5	7	6	5	9	3.5	15	11	10	15	13	12	4
G6	10	14	10	14	8	9	10	11	10	7	7	6.5
G7	15	15	15	15	13.5	13	15	15	12	3	3	10.5
G8	3	3	3	7	3.5	14	8	7	14	12	13	5
G9	5	5	6	3	10.5	2	2	2	5	9	8	10.5



AMMI1 Biplot

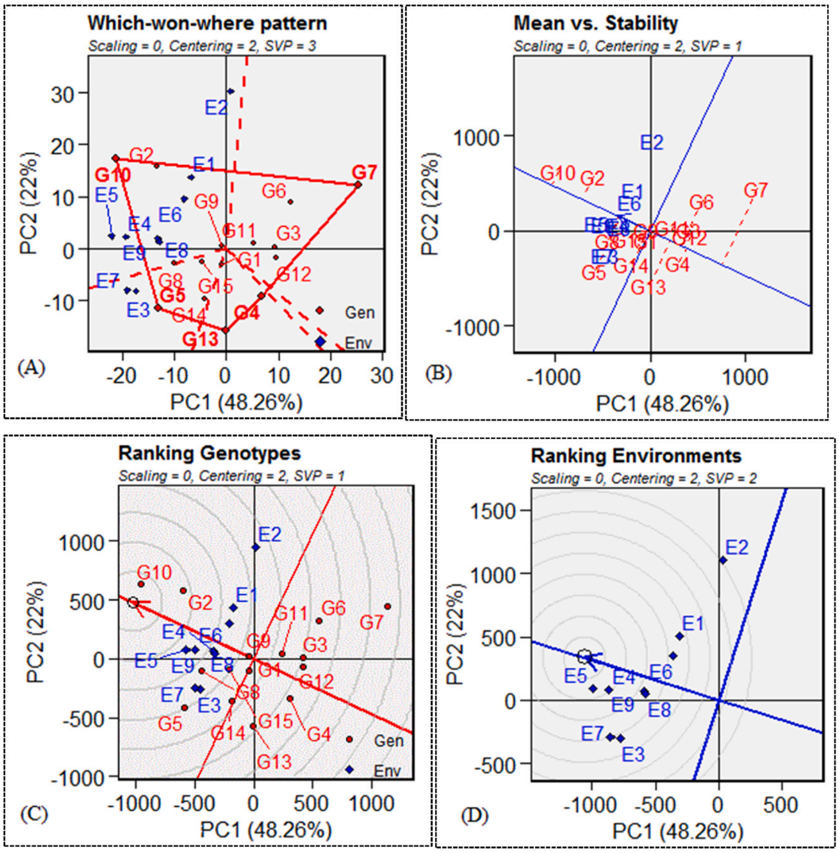
AMMI2 Biplot

Fig. 1. AMMI1 bi-plot showing Genotype and Environmental means against IPCA1 (A) and AMMI2 bi-plot showing PC1 versus PC2 indicating the stability of the Genotypes (B).

3. Results

3.1. Deciphering genotype-by-environment interaction

The results of the combined analysis of variance showed that the genotypes, environments and the GEI were significant ($p < 0.001$) (Table 2). In the model the GE interaction was further partitioned into linear and non-linear components. The G ($P < 0.001$) and GE (linear) ($P < 0.05$) mean sum squares were found significant, confirming the importance of both linear and non-linear sensitivity for the performance of the grain yield was correct. In the AMMI ANOVA the main effects of the environment (E) (54.18 % SS), genotype



Which-won-where pattern

Mean vs. Stability

Ranking Genotypes

Ranking Environments

Fig. 2. GGE bi-plot for yield of the sunflower genotypes. Which-won-where view (A); mean Vs stability (B); ranking of genotypes (C) and ranking of the environments (D).

(G) (16.9 % SS) and GEI (23.50 % SS) were highly significant ($p < 0.001$). Moreover, the GEI was partitioned in to seven significant principal components. G10 (1457.9 kg/ha), G2 (1321.05 kg/ha) and G8 (1219.18 kg/ha) are the top three high yielding genotypes correspondingly according to the yield rank while G7 (808.9 kg/ha) and G6 (946.79 kg/ha) are the low yielding genotypes and ranked as 15th and 14th respectively (Table 3).

3.2. AMMI and GGE model analysis

In the AMMI1bi-plot, Yan, W., and Tinker, N.A [51]. stated that genotypes and environments in the right side of the abscissa are high yielding genotypes and environments while those in the left side are low yielding genotypes and unfavorable environments. Accordingly, genotypes G10, G2, G8, G9, and G15 are high yielding genotypes while the other genotypes in the left side of the abscissa are low yielding genotypes (Fig. 1A). Genotypes with a longest vector length from the origin are unstable with highest contribution for the GEI interactions are unstable while genotypes with shorter vector length from the origin are stable genotypes [52]. Accordingly, in the AMMI2 bi-plot, showing 46.3 % and 19.7 % of PC1 and PC2 respectively, genotypes in the vertexes G3, G5, G6, G7, G8 and G13 are unstable genotypes and genotypes nearest to the origin G10, G1, G11 are stable genotypes (Fig. 1B).

The GGE bi-plot with PC1 (48.26 %) and PC2 (22 %) 70.26 % of total variation for grain yield. Yan, W., and Tinker, N.A. [51], described different GGE bi-plots and accordingly, in the which-won-where pattern (Fig. 2 A) five genotypes are in the vertexes and from which G10 laid in the

Sector where most of the environments laid is the winner genotype while the genotypes in the other sectors are low yielding genotypes in one or more environments. In the mean versus stability bi-plot G10 followed by G2 are the high yielding since they are nearest to the average-environment coordination [53] and stable genotypes because of they have short vectors from the AEC line (Fig. 2 B). Similarly (Fig. 2C), also recognized G10 followed by G2 as the most desirable genotypes since they are near to the AEC point and G7 is the most undesirable genotype since it is too far from the AEC point in the circle. On the other hand, G7 with longest vector and too far from the AEC point is the low yielding and unstable genotype. Regarding the environments, E5 is the ideal environment (Fig. 2 D) which may be important for sesame genotypes selection for their grain yield stability.

3.3. AMMI, BLUP, parametric and non-parametric based stability measures

Among the AMMI derived stability measures [39], genotypes with smallest values are considered as the most stable while genotypes with highest value are unstable. Accordingly, ASV, ZA and WAAS recognized G9 as the most stable genotype while SIPC and EV identified G15 as the most stable one. On the other hand, all of the AMMI related stability measures, except SIPC, identified G7 as the most unstable genotype followed by G5. Based on the BLUP related stability indexes of HMGV, RPGV and HMRPGV [54] both G10 and G2 had highest values of these stability indexes and ranked first and second indicating these are the most stable genotypes according to these indexes. On the other hand, G7 had the lowest value of all of these indexes declaring this genotype is the most unstable genotype (Table 3).

G10 and G2 with lower values of CV [43], Pi [46] and highest values of GAI [45], are the most stable genotypes while G7 as the most unstable one. Similarly, σ 2 [42], Wi [41] recognizes genotypes with smaller values as stable while those with larger values as unstable. Accordingly, G9 and G15 are the top two stable genotypes respectively. On the other hand, σ 2 and Wi identified G7 as the most unstable genotype ranked at the last. Based on the regression model, regression coefficients and deviation from regression (S2di) should be taken in to account for selecting a stable and high yielding genotype [47]. A given genotype with $bi = 1$, and deviation from regression $(S2di) = 0$ and high mean yield, is a superior genotype. Furthermore, according to Anandaraj et al. [55], if S2di is lower, the genotype is most stable and genotypes with any bi value and having significant S2di are unstable. Hence, in this study, G1, G11, G12 and G15 are the most stable genotypes, G6, and G7 as unstable ones and these genotypes are also low yielding genotypes and are

Table 4
Selected stable and high yielding sunflower genotypes based on the stability statistics groups.

Gen	Yld	AMMI	WAAS	BLUP	Parametric	Non-parametric	Average
G1	7	3 ^{b}	4	6.33	4.25	4.83 ^{a}	*4.90*
G2	2 ^{c}	9.75	10	2.00 ^{b}	7.25	10.22	6.87
G3	11	8	7	12.33	9.5	6.33	9.03
G4	13	7	6	13.33	8.5	7.50	9.22
G5	4	14.25	14	6.00	10.88	10.28	9.90
G6	14	12	13	10.00	10.88	9.17	11.51
G7	15	14.75	15	15.00	14.63	11.11	14.25
G8	3 ^{b}	10.5	11	3.00 ^{c}	7.75	9.28	7.42
G9	6	1.75	1 ^{a}	5.33	3.88 ^{b}	5.78 ^{c}	***3.96*** ^{c}
G10	1^{a}	5	5	1.00 ^{a}	3.75 ^{a}	7.17	***3.82*** ^{a}
G11	9	3.25 ^{c}	2 ^{b}	8.67	5.63	7.67	*6.03*
G12	12	10.25	8	11.33	10	8.28	9.98
G13	10	11	12	13.00	11.63	11.06	11.45
G14	8	7.25	9	8.33	7.63	6.17	7.73
G15	5	2.25 ^{a}	3 ^{c}	4.33	3.88 ^{b}	5.17 ^{b}	***3.94*** ^{b}

$^{A, b, c}$: Represents the first, second and third selected genotypes respectively.

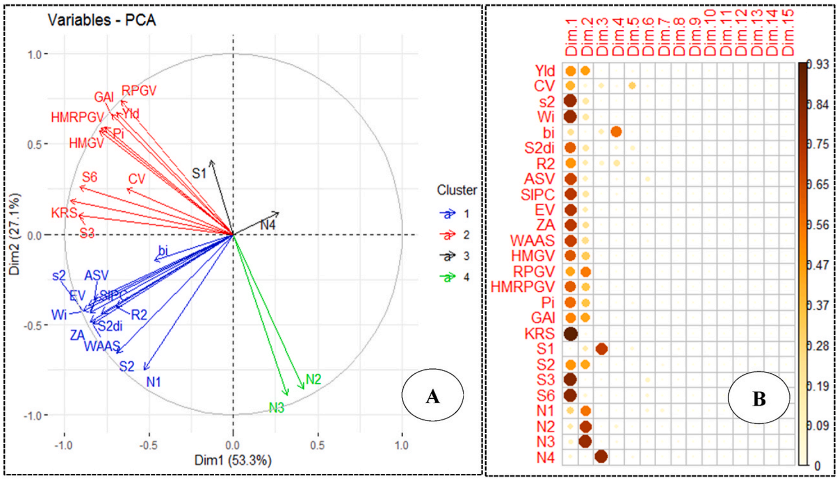


Fig. 3. Principal component analysis (PCA) based by-plot for various stability statistics: (A) Grouping of the stability statistics in the first two principal components; (B) The contribution of the stability statistics on the extracted PCs based on square cosine and squared coordinates.

Table 5

Likelihood Ratio Test, estimated variance components and genetic parameters of sunflower genotypes.

Parameters	DF	DM	PH	HW	Ldg	SWPH	NSPH	SW/HW	TSW	Yld
LRTg	8.8***	15.4***	10.4**	88.6***	82.8***	31.1***	14.3***	34.9***	10.6**	12.7***
LRTge	236.2***	291.1***	2.1ns	0.0ns	0.0ns	173.7***	1.5ns	65.2***	146.5***	176.9***
σ^2 g	2.84	2.81	489.5	1587	31.7	165.5	73520	0	11.38	20250
σ^2 g(%)	23.23	32.79	13.2	46.55	38.23	46.33	16	44.16	24.29	27.81
σ^2 ge	8.07	5.2	323.5	0	0	151.8	32082	0	26.57	41844
σ^2 ge(%)	66.11	60.61	8.72	0	0	42.48	6.98	30.49	56.74	57.46
$\sigma^2\varepsilon$	1.3	0.57	2897	1823	51.23	39.99	353908	0	8.88	10724
$\sigma^2\varepsilon$ (%)	10.66	6.6	78.08	53.45	61.77	11.19	77.02	25.35	18.96	14.73
σ^2 p	12.21	8.58	3710	3410	82.93	357.29		0	46.83	72818
H^2	0.1	0.07	0.14	0.41	0.4	0.39	0.17	0.38	0.15	0.14
h^2mg	0.24	0.18	0.32	0.67	0.67	0.65	0.37	0.65	0.35	0.33
As	0.49	0.43	0.57	0.82	0.82	0.81	0.61	0.81	0.59	0.57
CVg	3.04	1.46	12.1	9.32	50.4	17.9	21.4	21	5.99	13.9
CVr	9.28	5.39	30.5	11.3	62	22.7	47.8	26.9	14.1	34.6
CVg/CVr	0.33	0.27	0.4	0.83	0.81	0.79	0.45	0.78	0.42	0.4

Table 6

Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities obtained in the factor analysis.

Variable	FA1	FA2	FA3	Commu nality	Unique nesses	Sense	Goal	SG (%)
DF	−0.22	**−0.82**	0.01	0.72	0.28	decrease	100	−0.372
DM	−0.11	−0.33	**−0.78**	0.73	0.27	decrease	100	−1.23
PH	−0.14	**−0.91**	−0.11	0.85	0.15	decrease	100	−2.98
HW	0.04	**−0.71**	−0.25	0.57	0.43	decrease	100	−8.35
SWPH	**0.96**	−0.02	0.22	0.97	0.03	increase	0	26.9
NSPH	**−0.92**	−0.14	−0.02	0.87	0.13	increase	100	22.8
SW/HW	**−0.84**	−0.28	−0.3	0.89	0.11	increase	100	38.9
TSW	−0.05	**0.59**	−0.32	0.46	0.54	increase	0	−1.73
Yld	−0.31	0.25	**−0.83**	0.84	0.16	increase	100	16.5
Ldg	−0.4	**−0.68**	0	0.62	0.38	decrease	100	25.2
Average	0.752	0.248						
Total decrease							−14.662	
Total Increase							130.3	
Eigenvalues	4.02	2.35	1.15					
Variance (%)	40.2	23.4	11.6					
Cum. variance (%)	40.2	63.6	75.2					

Bold values indicate the variables grouped within the respective factor and the abbreviations are described in Table 5.

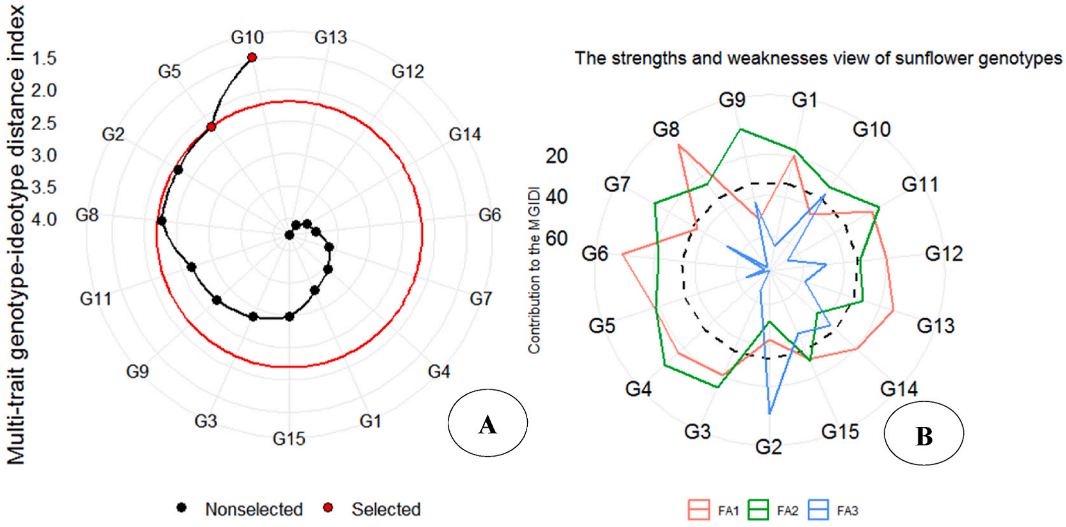


Fig. 4. Genotype ranking in ascending order for the MGIDI index (A); The strengths and weaknesses view of the sunflower genotypes (B). The genotypes are described inSupplementary Table S1.

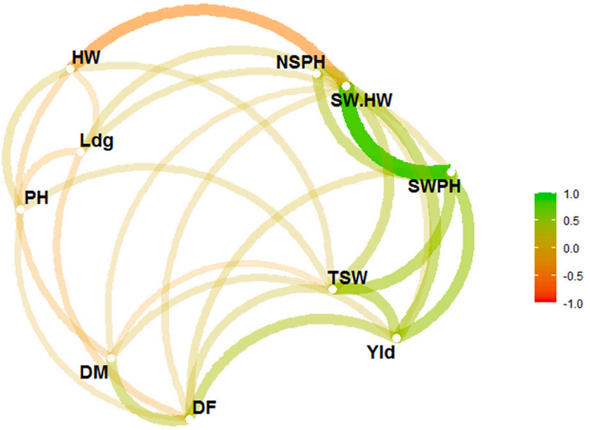


Fig. 5. Correlation network plots of sunflower agronomic traits where highly associated agronomic traits appear to cluster together and connected by stronger paths. The red colored paths indicated negative correlations while green colored paths indicated positive correlations. The abbreviations of the agronomic traits are described in Table 5. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

undesirable ones based on these stability measures (Table 3). Based on the R2, G15 and G9 with highest values of this stability measure, are the most stable while G7 and G6, with lowest values, as unstable genotypes, which is more or less similar to the stability measures of AMMI related indexes.

Based on the Kang rank sum parameter [48], one of the non-parametric statistics, the rank sum of a given genotype for grain yield and stability variance was used as stability and that respective genotype with a lower value is superior. Accordingly, G10, G15 and G9 are the top three most stable genotypes respectively and these genotypes are among the high yielding genotypes. On the other hand, G7 and G6 are the least stable genotypes correspondingly and these genotypes are the low yielding genotypes (Table 3). Non parametric stability measures of [49,50] stability statistics of S(1), S(2), S(3) and S(6) computed based on the genotype rankings in the different environments (Table 3) distinguishing genotypes with minimum change of rank across environments are known as stable genotypes. Based on S(1) stability statistics, G5, G8, G10, G15, G12 and G14 are the most stable genotypes and the former four genotypes are high yielding with mean yield of above the grand mean. S(2) identified that G1, G2 and G15 as the top three stable genotypes and G5 as the least stable one. S(3) and S(6) identified similar genotypes as top two stable (G10 and G9) and least two unstable genotypes (G7 and G12). These S(3) and S(6) are also similar with KRS, GAI, Pi, CV and the BLUP related stability indexes which recognized G10 as the top stable genotypes. The other widely used non-parametric stability measures of Thennarasu stability having four stability parameters viz. N(1), N(2), N(3) and N(4) were also computed [50]. Accordingly, N(1), N(2) selected a common genotype G3 as the most stable genotype and N(1), selected as unstable genotypes respectively. On the other hand, N(3) identified G4, G3 and G7 as the top three stable genotypes. Furthermore, N(4) recognized G12 and G2 as the most stable and unstable genotypes respectively.

3.4. Adapted genotype selection and Principal Component Analysis

An average rank sum (ARS) of the stability statistics groups is taken in to consideration (Table 4). Based on the AMMI based stability statistics G15, G1 and G11 are selected as the top three stable and high yielding genotypes while the WAAS selected G9, G11 and G15 as the most stable genotypes. The BLUP based (G10, G2 and G8) the parametric stability measures (G10, G9 and G15) and the non-parametric stability measures (G1, G15 and G9) selected as the top three stable and high yielding genotypes.

Principal Component Analysis was executed based on the rank of correlation matrix. PC1 and PC2 that revealed the highest (80.4 %) of the total variance and hence, these two PCs were used to create a PCA-based biplot. In the biplot the stability statistics and the yield clustered in to four clusters: cluster-I comprised of S^2, W_i, S^2d_i, R^2, ASV, SIPC, EV, ZA, WAAS, S2, bi and N1; cluster-II encompasses Yld, RPGV, GAI, HMGV, HMRPGV, CV, KRS, S3 and S6; Cluster-III consisted of S1 and N4 while Cluster-IV includes only N2 and N3 (Fig. 3 A). PC1 (53.3 %) was significantly correlated with Yld, S^2, W_i, S^2d_i, R^2, ASV, SIPC, EV, ZA, WAAS, HMGV, HMRPGV, Pi, GAI, KRS, S2, S3 and S6. PC2 (27.1 %) was mainly influenced by RPGV, N1, N2 and N3. PC3 (7.7 %) was associated with S1 and N4 while PC4 (4.4 %) was correlated only with bi (Fig. 3 B).

3.5. Multi-trait mean performance and stability

The genotypic LRT revealed significant ($P < 0.001$) difference for HW, Ldg, SWPH, NSPH, SW/HW, Yld and ($P < 0.01$) for TSW and PH. The interaction effect was significant ($P < 0.001$) for DF, DM, SWPH, SW/HW, TSW and Yld while it was not significant ($P < 0.05$) for PH, HW, Ldg and NSPH. Regarding the proportion of the phenotypic variance (Supplementary Fig. S1), GEI was higher for DF, DM, TSW and Yld while the error variance was higher for NSPH and PH. In the HW and Ldg the GEI was not explained and the error variance was higher than the genotypic variance. The highest phenotypic variance for DF (66.11 %), DM (60.61 %), Yld (57.46) and TSW (56.74 %) was because of the genotype-environment interaction effect. On the other hand, the highest phenotypic variance for PH (78.08 %), NSPH (77.02 %), Ldg (61.77 %) and HW (59.3 %) was because of the residual variance. The highest estimates of broad-sense heritability (H^2) was.

Where: σ^2 g: genotypic variance; $\sigma^2\varepsilon$: residual variance; σ^2 p: phenotypic variance; H^2: broad-sense heritability; h^2mg: heritability of the genotypic mean; As: accuracy of genotype selection; CVg: genotypic coefficient of variation; CVr: residual coefficient of variation; LRTg and LRTge: Likelihood Ratio Tests of the genotype and the interaction respectively. DF: Days to 50 % flowering; DM: Days to 75 % maturity; PH: Plant height; HW: Head weight; SWPH: Seed weight per head; NSPH: Number of seeds per head; SW/HW: The ratio of seed weight to head weight; TSW: Thousand seed weight; Yld: Sunflower yield (Kg/ha)

Explained by Hw (0.41) and Ldg (0.4). The genotypic selection accuracy (As) was higher for HW (0.82) and Ldg (0.82) while it was lower in DM (0.43) (Table 5). Three principal components were retained, and the accumulated variance of these three principal components was 75.2 % and the communality ranged from 0.46 (TSW) to 0.97 (SWPH) (Table 6) with an average communality of 0.752. The weighted average of absolute scores (WAASB) values of the agronomic traits grouped in to three factors: F1 includes SWPH, NSPH and SW/HW; F2 comprises DF, PH, HW and Ldg; while F3 contains DM and Yld. The genotype ranking in the Multi-trait Genotype–Ideotype Distance Index (MGIDI) considering the selection intensity of 15 % is depicted in (Fig. 4A). G10 and G5 are the selected genotypes with MGIDI of 1.45 and 2.19 respectively. In general, the MGIDI index provided higher total gains, i.e. 130.3 % for traits that increased, and −14.66 % for traits that decreased. The strengths and weaknesses of the sunflower genotypes revealed that the FA1 had the highest contribution for genotypes G2, G7, G9 and G10, while FA2 had the highest contribution for genotype G2 and G14. FA3 represented the highest contribution for all of the genotypes except G2 and G10 (Fig. 4B). Moreover, grain yield was highly and positively correlated with TSW, SW, SW/HW while SW was highly and negatively correlated with SW/HW (Fig. 5).

4. Discussion

4.1. Deciphering genotype-by-environment interaction

Any given plant can be evaluated across environments to examine the adaptability and stability of a desirable trait or quality [56] and such interactions may be either quantitative interaction or qualitative interaction and might be also with no interaction [57]. However, it is possible to develop genotypes with low GE interactions via sub-division of heterogeneous area into smaller, more homogeneous sub-regions; and by selecting genotypes with a better stability across a wide range of environments [58,59]. In the present study the combined ANOVA showed that, E, G and GEI explained 54.18, 16.9 and 23.50 % of the total sum of squares correspondingly which is in line to the findings of Matta et al., 2020 and Shojaei et al., 2023 [30,60]. This highest contribution of the environment confirms that sunflower genotypes might be sensitive to environmental factors and this corroborates to the findings of Matta et al., and Van Der Merwe et al. [30,61], who reported that environment is the highest contributors of the total variation in multi environment trials of sunflower. G10 with the highest yield (1457.9 kg/ha) out performs both the evaluated genotypes, the improved variety (G15) and the farmers' seed (G14). This confirms the genotype might be genetically high yielder because of its vigorous agronomic traits and/or the growing environments are suitable for this genotype. However, sunflower productivity can reach up to 2926 kg/ha in some high rainfall receiving areas of Ethiopia [62].

4.2. Yield stability of sunflower genotypes

The additive main effect and multiplicative interaction (AMMI) [63] has been extensively employed in the MET analysis since it provides interesting graphics for easiness of interpretation and it presents more accurate assessments vis-à-vis the traditional ANOVA. On the other hand, Olivoto et al., and Piepho et al. [39,64], stated that the estimates of genotypic responses found by best linear unbiased prediction (BLUP) are more reliable than those obtained from AMMI and for these reasons both AMMI and BLUP related stability measures are included in this study. In this study, the AMMI1 used to clearly describe the performance of the genotypes and informed that the genotypes in the right side of the abscissa produced higher yield than those of in the left side which produced lower than the average yield, and the AMMI2 bi-plot declared six genotypes (G3, G5, G6, G7, G8 and G13) as the highly contributors for the interaction, which concurs with the findings of Abdesatar et al., and Duma et al., [65,66]. Yan, W., and Tinker, N.A [51]. described the importance of the GGE bi-plots for easily interpretation and evaluating the genotypes and the testing sites as well. The bi-plots in (Fig. 2A–C) declared G10 and G2 as the most desirable genotypes and Fig. 2 (D) declared E5 (Humera) as the ideal environment.

Usually, single method cannot adequately identify the desirable genotype. For this reason, Shahbazi, E. and Vaezi et al. [16,67], integrated different parametric and non-parametric stability measures; different scholars [68–71] used BLUP-based indexes while other researchers [10,38,72] implemented stability statistics derived from AMMI to select stable and high yielding genotypes. In evaluating METs some studies were successful in estimating genotypic values using AMMI model [73] while others were successful in using the BLUP model [39]. HMGV, RPGV and HMRPGV selected G10 and G2 as the most stable genotypes and these genotypes are the top two genotypes in the yield rank. Hence, these BLUP based stability indexes, which are also positively and significantly correlated ($P < 0.001$) (Supplementary Table S4) with the yield rank, are best stability measures to identify high yielding and stable genotypes and this result concurs with the studies of many authors [69,74,75].

Both S(3) and S(6) selected similar genotypes as the top two stable and least two unstable confirming that they are similar in selecting stable genotypes. S(2) selected G5 as the most unstable genotypes and this is in contrary to S(1), which declared this genotypes as the most stable one. Exceptionally, S(1) stability statistics selected six genotypes (G5, G8, G10, G15, G12 and G14) as the most stable genotypes with the same rank. S(3) and S(6) identified G10 and G9 as stable and low yielding genotypes; and G7 and G12 as unstable genotypes. N(1), N(2) identified G3 as the most stable genotype while N(3) and N(4) selected G4 and G12 as the most stable genotypes indicating that they are different with the former ones in identifying a desirable genotype. Some of the stability statistics correlates to each other while the others strongly contrasts to each other. These realities makes genotypes selection very difficult and to simplify this difficulty a total rank of the stability measures [76] and an average rank sum (ARS) of the stability statistics groups is taken in to consideration [21]. The AMMI based stability statistics recognized G15, G1 and G11 whereas the WAAS selected G9, G11 and G15 as the top three stable genotypes. The BLUP based statistics identified G10, G2 and G8 as the top three stable genotypes. On the other hand, the parametric stability measures selected G10, G9 and G15 genotype while the non-parametric ones selected G1, G15 and G9 as the stable genotypes. Based on the average rank sum of the stability groups G10, G15 and G9 are the top three selected genotypes (Table 4).

In order to detect the association between the stability statistics and sunflower grain yield a PCA biplot using the rank correlation matrix of 25 stability measures was executed. PC1 (53.3 %) and PC2 (27.1 %) accounted (80.4 %) of the total variance and therefore, these two PCs were used to sketch the biplot. The different stability statistics and the yield grouped in to four clusters: cluster-I comprised of 12 statistics viz. S2, Wi, S2di, R2, ASV, SIPC, EV, ZA, WAAS, S2, bi and N1; Whereas cluster-II encompasses the grain yield and 9 statistics namely, RPGV, GAI, HMGV, HMRPGV, CV, KRS, Pi, S3 and S6 where all of the BLUP based stability measures are grouped in the same cluster [67]. Cluster-III (S1 and N4) and Cluster-IV (N2 and N3) comprised of two statistics each (Fig. 3 A). In the biplot, a narrow cosine angle and large cosine angle between two statistics vectors shows a strong positive correlation weak correlation among the statistics respectively. In contrast, no correlations and strong negative correlations were displayed at cosine 90° and 180° respectively. Accordingly, sunflower seed yield showed strong positive correlation with the stability statistics in cluster II. Sunflower grain yield also showed significant ($P < 0.001$) with most of these stability measures in this cluster (Supplementary Table S4). PC1 (53.3 %) was significantly correlated with Yld, S2, Wi, S2di, R2, ASV, SIPC, EV, ZA, WAAS, HMGV, HMRPGV, Pi, GAI, KRS, S2, S3 and S6. Usually, most of the stability statistics are explained in the first six PCs [21]. PC2 (27.1 %) was mainly influenced by RPGV, N1, N2 and N3. PC3 (7.7 %) was associated with S1 and N4 while PC4 (4.4 %) was correlated only with bi (Fig. 3 B).

4.3. Multi-trait stability of sunflower genotypes

The LRT revealed a significant effect of genotypes for all of the sunflower genotypes indicating that the performance of these traits was highly affected by the genetic pattern of the genotypes. Moreover, the LRT revealed a significant GEI effect for DF, DM, SWPH, SW/HW, TSW and grain yield (Table 5) indicating the performance of these traits was highly influenced by different environmental factors [77]. The GEI variance was higher than the genotypic and residual variance for grain yield, DF, DM and TSW indicating this is the most important component of the phenotypic variance (Table 5 and Supplementary Fig. S1), which is in accordance to the findings of [19]. The residual variance for these traits was lower and as result, moderately higher heritability was observed for these traits. The genotypic selection accuracy (As) was higher for HW and Ldg (0.82) confirming the highest correlation between the predicted and observed values of these traits. Three significant principal components were retained (Table 6). PC1 (40.2 %), PC2 (23.4 %) and PC3 (11.6 %) accounted 75.2 % of the total variance. The communality ranged from 0.46 (TSW) to 0.97 (SWPH) with an average communality of 0.752 showing that a high proportion of each variable's variance was explained by the factors. The WAASB values of the sunflower agronomic traits grouped in to three factors: F1 includes SWPH, NSPH and SW/HW; F2 comprises DF, PH, HW and Ldg; while F3 contains DM and Yld.

Grain yield was highly and positively correlated with TSW, SW, SW/HW, and SWPH was highly and positively correlated with SW/HW while SW was highly and negatively correlated with SW/HW (Supplementary Table S4). Hence, to boost productivity of sunflower it is vital to focus on TSW, SW, SW/HW. Multi-trait genotype–ideotype distance index (MGIDI) integrates the stability of multiple traits [27] and the genotype ranking in the MGIDI is depicted in (Fig. 4A). G10 and G5 are the selected genotypes with MGIDI of 1.45 and 2.19 respectively. Moreover, G2 (MGIDI = 2.256) is also near to the cut point (the red circle) indicating this genotype may contain some important traits and hence, this genotype should be considered for further breeding program [53]. Genotypes G13, G12 and G14 with higher values of MGIDI (4.25, 4.07 and 3.93 respectively) are the most undesirable genotypes according to the different agronomic traits (Supplementary Table S1). The theory of the MGIDI index is centered on rescaling the traits, using factor analysis, planning an ideotype based on known/desired values of traits and computing the distance between each genotype to the planned ideotype [27]. The strengths and weaknesses of the sunflower genotypes revealed that the FA1 highly contributed for genotypes G2, G7, G9 and G10, while FA2 had the highest contribution for genotype G2 and G14. On the other hand, FA3 represented the highest contribution for all of the genotypes except G2 and G10. The minimum the proportion explained by a factor or the closer to the external edge, the more approached the traits within that factor are to the ideotype. The dashed line indicates that the theoretical value if all the factors had contributed equally [77]. The selected genotypes (G10 and G5) associated with FA1 indicating these genotypes were selected for their superiority in SWPH, NSPH and SW/HW of the traits.

5. Conclusion

METs are crucial to select high yielding and stable genotypes especially in rain fed growing areas where there is unpredictable climatic variability. Most of the stability statistics and graphical methods declared G10 and G5 as the most desirable sunflower genotypes in terms of stability and performance of yield and yield components across the environments. These genotypes outperforms the standard check (G15) and local check (G14) in terms of productivity and stability. Hence, these genotypes should be recognized by the Ministry of Agriculture of Ethiopia and thereby to be registered as an open pollinated varieties in the lowlands of Tigray, Northern Ethiopia for further cultivation in these areas and other similar agro-ecologies.

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Data availability

Data are available upon request from the corresponding authors.

CRediT authorship contribution statement

Fiseha Baraki: Writing – original draft, Formal analysis, Conceptualization. **Zenawi Gebregergis:** Conceptualization. **Yirga Belay:** Data curation. **Goitom Teame:** Data curation. **Zerabruk Gebremedhin:** Data curation. **Muez Berhe:** Methodology, Conceptualization. **Dawit Fisseha:** Data curation. **Goitom Araya:** Data curation. **Gebremedhn Gebregergs:** Data curation.

Declaration of competing interest

The authors are composition of researchers and instructor in different disciplines like crop production and protection. These authors contributed in different parts of the research planning, implementation, data collection, data analysis, manuscript drafting and editing. Every member contributed in the research is included in this manuscript. Hence, the authors declare that there are no conflicts of interest. Furthermore, t*his investigation received no specific* fund *from any* funding *agency, commercial or not-for-profit sectors*.

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Appendix A. Supplementary data

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