

*Full Length Research Paper*

# **Performance evaluation and selection of new maize hybrids under sole and inter crop production systems**

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Screening of maize genotypes under different cropping systems (sole and inter cropping) is very important to understand the genotypes response for different abiotic and a biotic stress. Nine maize genotypes including the standard check (BH-543) were planted and evaluated at research and farmers' fields in the 2011 and 2012 cropping seasons. Farmers were invited to evaluate the genotypes based on their criteria of selection. Hawassa-Dume common bean variety was used for intercropping purpose in 2012. The genotypes substantially varied for yield and other traits both under sole and intercropping systems. When combined across seasons, the high yielding genotypes, genotype-1 and genotype-5 showed 38 and 37% yield advantage over the standard check. Besides, genotypes markedly varied for their compatibility for intercropping system with land equivalent ratio (LER) <1 for most of genotypes. However, genotype-4 and genotype-8 had LER >1 highlighting the need to evaluate genotypes for intercropping system at early stage of breeding.

**Key words:** Hawassa-dume, inter-cropping, sole-cropping, *Zea mays*.

## **INTRODUCTION**

Maize (*Zea mays* L.) is the second most widely cultivated crop grown by smallholder farmers under rainfed condition in Ethiopia. Maize yield in Ethiopia vary considerably across seasons and locations making smallholders livelihoods vulnerable to climate variability. Maize and common bean are two of the leading crops in their respective category of cereals and pulses in southern Ethiopia. Accordingly, maize and common bean occupy 36 and 44% of the area devoted to cereals and pulses, respectively (CSA, 2017).

Intercropping systems play an important role in subsistence and food production in developing countries (Tsubo and Walker, 2002). It is most widely practiced in

countries where arable land is scarce where it contributes to biodiversity and food security (Mushagalusa et al., 2008). Land scarcity is one of the constraints facing small farmers in Ethiopia. In the southern Ethiopia, 40% of farmers have an average land holding of 0.1 to 0.5 ha with a further 30% having 0.51 to 1 ha (CSA, 2017). This led farmers to use multiple cropping mainly intercropping to increase yield per unit area and reduce the risk from crop failure due to climate change.

Maize-common bean intercropping is an integral part of the cropping system in small-holder farmers expecting better yield and weed suppression (Getahun and Tenaw, 1990), and provides balanced diet compared to the

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predominant cereal monoculture and gives high total productivity compared to sole crops of bean and maize (Walegn, 2014; Workayehu, 2014). However, all varieties released so far in the country were evaluated under monocropping system and has not been tested for intercropping system at early stage of breeding. Selection of genotypes both under sole and intercropping systems is of paramount importance to enhance yield and varietal adoption in the region. Therefore, the objective of this study was to identify best performed genotypes under sole and intercropping systems.

## MATERIALS AND METHODS

The experiment was conducted under rain-fed condition at Hawassa research station (07°03'71" N, 38°30'88" E, 1689 masl elevation) and on-farms (farm1; 07° 79'43" N, 37° 04' 31" E, 1696 masl elevation and farm2; 07° 78' 28" N, 37° 04' 31" E, 1692 masl ) in 2011 and 2012 main rainy seasons in Ethiopia. This area is characterized by bimodal rainfall between March and September with mean annual maximum and minimum temperatures of 27.3 and 12.6°C, respectively. Nine hybrid maize genotypes were planted in 2011 and 2012 cropping seasons. The hybrids were planted both under sole and inter cropping systems at research station in 2012. These genotypes were also planted only under sole-cropping on two farmers' field in 2011 and 2012 without replication at each farmer's field but for analysis farmers were used as replication. Similarly, in 2011, these genotypes were planted at research field without replication. For analysis of the data collected in 2011, farmers and research station were used as replication because the trial was not replicated both at farmers' and research field. The recently released hybrid variety (BH-543) was included as check in 2011 and 2012 cropping seasons. The genotypes were planted using randomized complete block design with three replications at research field in 2012. Each genotype was planted on two rows 7.65 m<sup>2</sup> area at research station and three rows 11.48 m<sup>2</sup> area at farmers' field. Maize genotypes were planted in 75 and 30 cm spacing between consecutive maize rows and plant, respectively. Common bean genotype named Hawassa-Dume was planted between two rows of maize in one to one ratio for intercropping. At research field, sole common bean was also planted for land equivalent ratio determination. Common bean was planted at the spacing of 40 cm between rows and 10 cm between seeds within a row. Grain yield and other important agronomic traits of component crops were recorded to evaluate the genotypes grown under the sole and inter-cropping systems. Plants from the whole plot were hand harvested at physiological maturity. Ears were shelled, grain weight and grain moisture content measured, and yield was adjusted for 12.5% grain moisture content. However, for common bean yield was adjusted to 10% grain moisture content. In both seasons, farmers were participated to set selection criteria and evaluate maize genotypes. Yield deviation due to inter cropping from the sole maize yield was calculated using the formula

$$\text{Deviation (\%)} = ((\text{inter crop maize yield} / \text{sole maize yield}) \times 100) - 100 \quad (1)$$

Land equivalent ratio calculated was computed as in Adu-Gyamfi et al. (1997).

$$\text{LER} = ((Y_m/Y_{sm}) + (Y_b/Y_{sb})) \quad (2)$$

where  $Y_m$  and  $Y_b$  were grain yields of intercropped maize and bean;  $Y_{sm}$  and  $Y_{sb}$  were grain yields of sole cropped maize and bean.

Grain yield, number of ears (NE), plant height (PH), ear height (EH), gray leaf spot (GLS), turcicum leaf blight (TLB) and common leaf rust (CLR) were analyzed as randomized complete block design in SAS statistical package (SAS, 2002) version 9.0. Performance and stability of genotypes were visualized graphically through an average environment coordination (AEC) view of GGE biplot based on genotype-focused SVP (that is, "SVP=1") (Yan and Rajcan, 2002). Graphs were developed using R software (Table 1).

## RESULTS AND DISCUSSION

### Analysis of variance

Highly significant grain yield (GY) variation was observed among genotypes for sole cropping system in 2011 ( $p < 0.01$ ) (Table 2). Similarly, Mossisa et al. (2019) reported significant difference between 12 early to intermediate maturing and the other with 13 intermediate to late maturing hybrids tested at farmers' for participatory assessment of new stress tolerant maize hybrids in Eastern Africa but in contrast to the finding under this study, Daniel et al. (2014) reported non-significant difference between six released varieties tested at farmers field in Chilga District of North Western Ethiopia. No significant difference was observed among genotypes for yield for both sole and intercropping systems in 2012 cropping (Table 3). This could be due to high drought stress in 2012 cropping season resulting into low genotype variation. This is because variation among genotypes in the optimum condition is high than under stress environments leading to lower chance of genotypes to express their genetic potential under stressful conditions (Mohammadai et al., 2012). In 2011, significantly high variation ( $p < 0.01$ ) was observed among genotypes for plant height (PH), ear height (EH), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR) and number of ears (NE). Genotype-6 was more tolerant to across the three major foliar diseases (GLS, CLR and TLB) compared with the other genotypes (Table 4). Genotype-5 was also showed relative tolerance to these major foliar diseases. Similarly, in 2012 cropping season, significant variation was observed among genotypes tested under sole system for EH and GLS (Table 5). Genotype variation for PH, EH, GLS and CLR under sole cropping system has been previously reported (Berhanu, 2009). However, in this study, genotypes tested under both cropping systems responded consistently excepting small variation. For instance, high GLS score was recorded for genotype 2 and 3 under sole cropping compared with under intercropping system (Tables 5 and 6). However, our study highlights for PH, EH and GLS, Kariuki et al. (2016) reported significant difference between single crosses treatments tested in Kalro experimental stations in Kiambu and Embu counties in 2012. In 2012 under sole crop, significant variation among genotypes was observed for EH and GLS. Genotype variation for GLS, TLB and CLR has been previously reported for this area

**Table 1.** Pedigree of hybrid maize genotypes used for on-station and on-farm experiments in the 2011 and 2012 cropping seasons.

Pedigree	Code	Type	Seed color
CML395int/CML202//30H83-5-1-3-2-1-1	Genotype-1	CN	White
CML395/CML202//Gibe1-91-1-1-1-1	Genotype-2	CN	White
SC 22/124-b (109)//Gibe1-91-1-1-1-1	Genotype-3	CN	White
SC/22CML395//CML197	Genotype-4	CN	White
CML 197/ BH660 (F2)-10-2-1-2-1//CML395 int	Genotype-5	CN	White
CML 197/BH-660(F2))-10-2-1-2-1//CML312	Genotype-6	CN	White
30H83-7-3-4-1-1-1-1//Gutto LMS5	Genotype-7	CN	White
DE-78-Z-126-3-2-2-1(g) CML312//Gibe1-91-1-1-1-1	Genotype-8	CN	White
BH-543	Genotype-9 (Check)	CN	White

Where CN = Conventional normal maize.

**Table 2.** ANOVA for maize yield tested under sole and intercropping systems in the 2011 and 2012 cropping seasons.

ANOVA for genotypes tested under sole cropping in 2011			
Source of variation	Degree of freedom	Mean square	Computed F
Rep	2	13.15***	13.78
Genotype	8	3.64**	3.81
Error	16	0.95	
ANOVA for genotypes tested under sole cropping in 2012			
Rep	2	0.95ns	0.26
Genotype	8	2.85ns	0.77
Error	16	3.69	
ANOVA for genotypes tested under inter-cropping in 2012			
Rep	2	3.80ns	2.31
Genotype	8	1.09ns	0.66
Error	16	1.65	
ANOVA combined for genotypes tested across seasons and cropping systems			
Rep	2	8.25*	3.79
Genotype (G)	8	3.66ns	1.68
Cropping Systems (CS)	2	2.15ns	0.91
CS*G	15	1.25ns	0.58
Error	50	2.17	

ns, \*, \*\* indicate non-significant and significant at  $P < 0.05$  and  $0.01$ , respectively.

(Berhanu, 2009). Similarly, Daniel et al. (2014) and Goshime (2019) also reported significant difference between treatments for PH and EH. In the combined analysis, the difference was significant for PH, EH, CLR and NE whereas the variance was non-significant for GLS, TLB and GY (Table 7). For yield, in contrast to the current finding for grain yield, O'Leary and Smith (1999) reported highly significant variation between three cropping systems (monoculture, maize-bean inter cropping and maize-clover inter cropping). For PH of maize, Zaeem et al. (2019) reported significant variance

between cropping system with the overall higher value obtained for inter cropping with soybean in their study. The highest PH and EH was showed by genotype-6 and by genotype-5, respectively (Table 7).

### Mean performance of the genotypes

Combined over seasons and cropping systems, mean maize grain yield performance of genotypes showed that the highest grain yield advantage was obtained from

**Table 3.** Mean grain yield (GY) (t ha<sup>-1</sup>) and percent yield advantage of genotypes over the check (BH-543) for intercropping and sole cropping for participatory on-farm and on- station trials in the 2011 and 2012 cropping seasons.

Genotype	Mean GY					% GY advantage over the check			
	IC 2012	SC 2012	SC 2011	Combined	Bean	IC 2012	SC 2012	SC2011	Combined
Genotype-1	8.23 <sup>a</sup>	9.05 <sup>a</sup>	10.10 <sup>a</sup>	9.13 <sup>a</sup>	0.30 <sup>a</sup>	23	33	60	38
Genotype-2	8.47 <sup>b</sup>	8.56 <sup>a</sup>	8.10 <sup>bc</sup>	8.38 <sup>ab</sup>	0.14 <sup>c</sup>	27	26	29	27
Genotype-3	7.63 <sup>a</sup>	8.27 <sup>a</sup>	8.40 <sup>bc</sup>	8.10 <sup>ab</sup>	0.14 <sup>c</sup>	14	21	33	23
Genotype-4	8.24 <sup>a</sup>	7.10 <sup>a</sup>	8.40 <sup>bc</sup>	7.91 <sup>ab</sup>	0.19 <sup>bc</sup>	24	4	33	20
Genotype-5	8.07 <sup>a</sup>	10.05 <sup>a</sup>	9.10 <sup>ab</sup>	9.07 <sup>a</sup>	0.32 <sup>a</sup>	21	47	44	37
Genotype-6	7.67 <sup>a</sup>	8.07 <sup>a</sup>	8.20 <sup>bc</sup>	7.98 <sup>ab</sup>	0.26 <sup>ab</sup>	15	18	30	21
Genotype-7	7.67 <sup>a</sup>	8.25 <sup>a</sup>	6.90 <sup>cd</sup>	7.61 <sup>ab</sup>	0.27 <sup>ab</sup>	15	21	10	15
Genotype-8	6.97 <sup>a</sup>	6.75 <sup>a</sup>	8.20 <sup>bc</sup>	7.31 <sup>b</sup>	0.14 <sup>c</sup>	4	-1	30	11
BH-543	6.67 <sup>a</sup>	6.82	6.30 <sup>d</sup>	6.60 <sup>ab</sup>	0.32 <sup>a</sup>	-	-	-	-
Mean	7.74	8.26	8.21	8.01	0.23	-	-	-	-
CV (%)	16.58	10.98	11.99	18.31	25.99	-	-	-	-
LSD	2.22	1.57	0.78	1.57	0.1	-	-	-	-
SE	17.38	5.86	9.9	1.92	0.02	-	-	-	-

Columns with the same letter are not significantly different at P<0.05. IC = intercrop; SC = sole crop.

**Table 4.** Mean grain yield (t ha<sup>-1</sup>), plant height (cm), ear height (cm), gray leaf spot (GLS), turicum leaf blight (TLB), common leaf rust (CLR) and number of ears harvested (NE) of maize genotypes tested under sole cropping in 2011 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	NE	GY
Genotype-1	240 <sup>bc</sup>	136 <sup>bcd</sup>	1.7 <sup>bc</sup>	2.0 <sup>b</sup>	2.0 <sup>c</sup>	89.3 <sup>a</sup>	10.1 <sup>a</sup>
Genotype-2	244 <sup>ab</sup>	148 <sup>ab</sup>	1.8 <sup>bc</sup>	2.0 <sup>b</sup>	2.5 <sup>c</sup>	69.3 <sup>b</sup>	8.1 <sup>bc</sup>
Genotype-3	246 <sup>ab</sup>	143 <sup>abc</sup>	1.7 <sup>bc</sup>	1.7 <sup>b</sup>	2.0 <sup>b</sup>	71.7 <sup>b</sup>	8.4 <sup>bc</sup>
Genotype-4	251 <sup>ab</sup>	153 <sup>ab</sup>	2.0 <sup>ab</sup>	2.0 <sup>b</sup>	2.0 <sup>c</sup>	71.0 <sup>b</sup>	8.4 <sup>bc</sup>
Genotype-5	262 <sup>a</sup>	159 <sup>a</sup>	1.5 <sup>c</sup>	1.7 <sup>cd</sup>	2.0 <sup>c</sup>	64.7 <sup>b</sup>	9.1 <sup>ab</sup>
Genotype-6	261 <sup>a</sup>	156 <sup>ab</sup>	1.7 <sup>ab</sup>	1.5 <sup>d</sup>	1.5 <sup>d</sup>	68.0 <sup>b</sup>	8.2 <sup>bc</sup>
Genotype-7	223 <sup>bc</sup>	111 <sup>e</sup>	2.0 <sup>ab</sup>	1.8 <sup>bc</sup>	2.7 <sup>ab</sup>	68.3 <sup>b</sup>	6.9 <sup>cd</sup>
Genotype-8	235 <sup>bc</sup>	122 <sup>cd</sup> e	2.3 <sup>a</sup>	2.3 <sup>a</sup>	2.8 <sup>a</sup>	69.3 <sup>b</sup>	8.2 <sup>bc</sup>
BH-543	212 <sup>d</sup>	115 <sup>d</sup> e	-	-	-	63.7 <sup>b</sup>	6.3 <sup>d</sup>
Mean	241	138	1.83	1.88	2.19	70.6	8.21
Genotype	***	***	**	**	**	**	**
CV (%)	4.99	9.03	10.93	9.20	6.36	7.40	11.99
R <sup>2</sup>	0.77	0.79	0.80	0.80	0.94	0.77	0.78
LSD	21	21.58	0.35	0.30	0.24	9.1	1.69

Columns with the same letter are not significantly different at P < 0.05.

genotype-1 followed by genotype-5 with 38 and 37% yield over the check, respectively. However, in 2011 under sole cropping, all new genotypes had higher grain yield advantage over the check (Table 3). In 2011, the highest yield (10.1 t/ha) and the lowest (6.3 t/ha) were observed for genotype-1 and genotype-9, respectively. Similarly, in 2012, under inter cropping, the highest grain yield advantage was obtained from genotype-2 with 27% over the check. The second and the third yield advantage was obtained from genotype-4 and genotype-1, respectively. Under sole cropping in 2012, except for

genotype 8, all genotypes showed yield advantage over the check with the highest grain yield advantage observed for genotype-5. The maize yield of genotype-1, genotype-2, and genotype-5 were consistent under both cropping systems in 2012 (Tables 4 to 6). Generally, in 2012 under both sole and intercropping and combined analysis genotypes had higher grain yield advantage over the check (BH-543) except for genotype-8 (Table 3). The overall mean performance was higher from sole cropping compared with the yield harvested from inter cropping with yield penalty of 0.45 t ha<sup>-1</sup> due to inter cropping

**Table 5.** Mean grain yield (t ha<sup>-1</sup>), plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR) and number of ears harvested (NE) of maize genotypes tested under sole crop at Hawassa Research Station in the 2012 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	NE	GY
Genotype-1	177 <sup>ab</sup>	89 <sup>bc</sup>	1.8 <sup>abc</sup>	2.7 <sup>a</sup>	1.8 <sup>c</sup>	11.0 <sup>a</sup>	9.05 <sup>a</sup>
Genotype-2	194 <sup>a</sup>	100 <sup>ab</sup>	2.2 <sup>a</sup>	2.7 <sup>a</sup>	2.5 <sup>ab</sup>	13.6 <sup>a</sup>	8.56 <sup>a</sup>
Genotype-3	188 <sup>ab</sup>	92 <sup>ab</sup>	2.2 <sup>a</sup>	2.7 <sup>a</sup>	2.3 <sup>abc</sup>	10.3 <sup>a</sup>	8.27 <sup>a</sup>
Genotype-4	181 <sup>ab</sup>	91 <sup>abc</sup>	1.8 <sup>abc</sup>	2.5 <sup>a</sup>	2.3 <sup>abc</sup>	6.1 <sup>a</sup>	7.10 <sup>a</sup>
Genotype-5	190 <sup>ab</sup>	105 <sup>a</sup>	1.7 <sup>bc</sup>	2.5 <sup>a</sup>	1.8 <sup>c</sup>	8.7 <sup>a</sup>	10.05 <sup>a</sup>
Genotype-6	191 <sup>ab</sup>	99 <sup>ab</sup>	1.5 <sup>c</sup>	2.5 <sup>a</sup>	2.0 <sup>bc</sup>	10.7 <sup>a</sup>	8.07 <sup>a</sup>
Genotype-7	177 <sup>ab</sup>	76 <sup>c</sup>	2.0 <sup>ab</sup>	2.8 <sup>a</sup>	2.8 <sup>a</sup>	8.3 <sup>a</sup>	8.25 <sup>a</sup>
Genotype-8	163 <sup>b</sup>	97 <sup>ab</sup>	1.7 <sup>bc</sup>	2.3 <sup>a</sup>	2.5 <sup>ab</sup>	9.7 <sup>a</sup>	6.75 <sup>a</sup>
BH-543	196 <sup>a</sup>	92 <sup>ab</sup>	1.8 <sup>abc</sup>	2.7 <sup>a</sup>	2.0 <sup>bc</sup>	10.7 <sup>a</sup>	6.82 <sup>a</sup>
Mean	184	93	1.85	2.59	2.24	9.9	8.26
Genotype	ns	*	*	ns	ns	ns	ns
CV (%)	9.53	9.43	13.37	12.79	15.71	44.81	1.92
R <sup>2</sup>	0.39	0.58	0.66	0.3	0.62	0.42	0.29
LSD	30	15	0.43	0.57	0.61	7.6	3.33

Columns with the same letter are not significantly different at P < 0.05.

**Table 6.** Mean grain yield (t ha<sup>-1</sup>), plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR) and number of ears harvested (NE) of maize genotypes tested under intercropping at Hawassa Research Station in the 2012 cropping season.

Genotypes	PH	EH	GLS	TLB	CLR	NE	GY
Genotype-1	193 <sup>a</sup>	98 <sup>a</sup>	2.2 <sup>a</sup>	2.5 <sup>a</sup>	1.5 <sup>a</sup>	13.0 <sup>a</sup>	8.23 <sup>a</sup>
Genotype-2	197 <sup>a</sup>	102 <sup>a</sup>	1.8 <sup>abc</sup>	2.5 <sup>a</sup>	2.2 <sup>a</sup>	13.0 <sup>a</sup>	8.47 <sup>a</sup>
Genotype-3	190 <sup>a</sup>	98 <sup>a</sup>	1.7 <sup>bc</sup>	2.3 <sup>a</sup>	2.0 <sup>ab</sup>	12.7 <sup>a</sup>	7.63 <sup>a</sup>
Genotype-4	189 <sup>a</sup>	105 <sup>a</sup>	1.7 <sup>bc</sup>	2.7 <sup>a</sup>	2.0 <sup>ab</sup>	15.3 <sup>a</sup>	8.24 <sup>a</sup>
Genotype-5	184 <sup>ab</sup>	97 <sup>a</sup>	1.5 <sup>c</sup>	2.3 <sup>a</sup>	1.7 <sup>bc</sup>	9.7 <sup>a</sup>	8.06 <sup>a</sup>
Genotype-6	193 <sup>a</sup>	102 <sup>a</sup>	1.8 <sup>abc</sup>	2.3 <sup>a</sup>	2.0 <sup>ab</sup>	12.7 <sup>a</sup>	7.67 <sup>a</sup>
Genotype-7	173 <sup>ab</sup>	77 <sup>a</sup>	1.7 <sup>bc</sup>	2.7 <sup>a</sup>	2.2 <sup>a</sup>	11.3 <sup>a</sup>	7.67 <sup>a</sup>
Genotype-8	192 <sup>a</sup>	95 <sup>a</sup>	2.0 <sup>ab</sup>	2.7 <sup>a</sup>	2.0 <sup>ab</sup>	11.3 <sup>a</sup>	6.97 <sup>a</sup>
BH-543	155 <sup>b</sup>	91 <sup>a</sup>	1.8 <sup>abc</sup>	2.7 <sup>a</sup>	1.8 <sup>abc</sup>	9.0 <sup>a</sup>	6.67 <sup>a</sup>
Mean	185	96	1.80	2.52	1.93	12.00	7.74
Genotype	ns	ns	ns	ns	ns	ns	ns
CV (%)	9.38	17.04	14.17	12.74	14.88	36.04	16.58
R <sup>2</sup>	0.48	0.29	0.51	0.40	0.54	0.34	0.38
LSD	30	28	0.44	0.56	0.50	7.49	2.22

Columns with the same letter are not significantly different at P < 0.05.

without considering the bean harvest in 2012 (Table 2). Similar to this, O'Leary and Smith (1999) obtained higher maize grain yield from sole cropping than maize intercropped with bean and clover. The result showed the existence yield penalty due to intercropping when we see the overall effect but individual there were some genotypes which had higher yield under intercropping compared with performance under sole cropping and in line with this finding, Rusinamhodzi et al. (2020) reported as intercropping had maize yields reduction effect due to

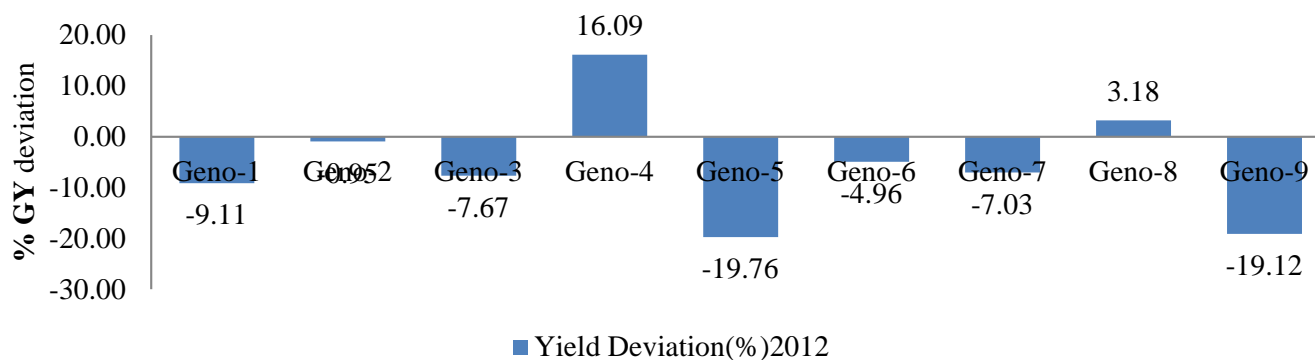
increased competition.

When genotypes were compared in terms of yield reduction/deviation due to intercropping, most the genotypes showed reduction/negative deviation except for genotype-4 and genotype-8 (Figure 1). The highest deviation to the negative side was observed for genotype-5 (-20%) and genotype-9 (-19%) while the least negative deviation was observed for genotype-2 (-1%). The highest deviation to the positive side was observed for genotype-4 (16%) followed by genotype-8 (3%). The

**Table 7.** Mean grain yield (t ha<sup>-1</sup>), plant height (cm), ear height (cm), gray leaf spot (GLS), turicum leaf blight (TLB), common leaf rust (CLR) and number of ears harvested (NE) of maize genotypes combined data across seasons (2011 and 2012) and cropping systems (sole and inter-cropping).

Genotype	PH	EH	GLS	TLB	CLR	NE	GY
Genotype-1	203 <sup>abc</sup>	107 <sup>ab</sup>	1.8 <sup>ab</sup>	2.4 <sup>ab</sup>	1.8 <sup>e</sup>	37.7 <sup>a</sup>	9.13 <sup>a</sup>
Genotype-2	212 <sup>ab</sup>	115 <sup>ab</sup>	1.8 <sup>ab</sup>	2.3 <sup>b</sup>	2.2 <sup>bc</sup>	33.2 <sup>b</sup>	8.38 <sup>ab</sup>
Genotype-3	207 <sup>abc</sup>	112 <sup>ab</sup>	1.8 <sup>ab</sup>	2.3 <sup>ab</sup>	2.3 <sup>abc</sup>	30.7 <sup>b</sup>	8.10 <sup>ab</sup>
Genotype-4	207 <sup>abc</sup>	116 <sup>ab</sup>	1.8 <sup>ab</sup>	2.4 <sup>ab</sup>	2.1 <sup>cd</sup>	31.7 <sup>b</sup>	7.91 <sup>ab</sup>
Genotype-5	212 <sup>ab</sup>	120 <sup>a</sup>	1.56 <sup>c</sup>	2.2 <sup>b</sup>	1.8 <sup>de</sup>	29.1 <sup>b</sup>	9.07 <sup>a</sup>
Genotype-6	215 <sup>a</sup>	119 <sup>ab</sup>	1.6 <sup>bc</sup>	2.1 <sup>b</sup>	1.8 <sup>de</sup>	29.2 <sup>b</sup>	7.98 <sup>ab</sup>
Genotype-7	191 <sup>c</sup>	88 <sup>c</sup>	1.8 <sup>ab</sup>	2.4 <sup>ab</sup>	2.6 <sup>a</sup>	29.3 <sup>b</sup>	7.61 <sup>ab</sup>
Genotype-8	196 <sup>bc</sup>	104 <sup>b</sup>	2.0 <sup>a</sup>	2.4 <sup>ab</sup>	2.4 <sup>ab</sup>	29.2 <sup>b</sup>	7.31 <sup>b</sup>
BH-543	175 <sup>d</sup>	92 <sup>c</sup>	1.8 <sup>ab</sup>	2.7 <sup>a</sup>	1.9 <sup>de</sup>	9.2 <sup>c</sup>	6.60 <sup>ab</sup>
Mean	203	109	1.8	2.4	2.1	29.6	8.01
Genotype	*	**	ns	ns	**	**	ns
CS	**	**	ns	**	**	**	ns
CS*genotype	ns	ns	*	ns	*	**	ns
R <sup>2</sup>	0.86	0.85	0.49	0.68	0.69	0.98	0.38
CV (%)	7.54	11.57	15.5	13.1	13.88	15.56	18.31

Columns with the same letter are not significantly different at  $P < 0.05$ .

**Figure 1.** Percent grain yield deviation of genotypes for sole cropping system over the corresponding yield under intercropping system at Hawassa research field in the 2012 cropping season.

higher deviation to the negative side indicated that the genotypes were affected by common bean in intercropping whereas the genotypes which had yield deviation to the positive side indicated that the maize genotypes are suitable for inter cropping or not affected by intercropping (Figure 1). However, the common bean yields obtained from intercropped with genotype-4 and 8 were the least compared with common bean yields obtained from intercropping with other genotypes (Table 3). Higher common bean yield obtained from intercropped with genotype-1, genotype-5 and BH-543 could in part be due to good leaf structure/architecture of maize genotypes resulting to high radiation interception and hence higher common bean yields or common bean had a better competitive advantage over the genotypes

(Table 3).

#### Land equivalent ratio

The overall LER was evaluated to derive land benefits associated with intercropping of maize genotypes and the bean variety Hawassa-Dume. The LER in intercrops ranged from 0.86 to 1.19. Only three genotypes, genotype-2, genotype-4, BH-543, and genotype-8 had LER of 1.02, 1.19, 1.04 and 1.06, respectively, which is greater than 1 (Table 8). The LER greater than 1 suggests that there is greater land area requirement for the monoculture system or greater relative yield for intercropping of maize genotypes with common bean

**Table 8.** Land equivalent ratio (LER) of maize common bean intercropping systems for maize genotypes tested at Hawassa research field in the 2012 cropping season.

Genotype	Maize		Common bean		LER
	Sole	Inter-crop	Sole	Inter-crop	
Genotype-1	9.05	8.23	5.63	0.30	0.96
Genotype-2	8.56	8.47	5.63	0.14	1.02
Genotype-3	8.27	7.63	5.63	0.14	0.95
Genotype-4	7.10	8.24	5.63	0.19	1.19
Genotype-5	10.05	8.07	5.63	0.32	0.86
Genotype-6	8.07	7.67	5.63	0.26	1.00
Genotype-7	8.25	7.67	5.63	0.27	0.98
Genotype-8	6.75	6.97	5.63	0.14	1.06
BH-543	6.82	6.67	5.63	0.32	1.04

**Table 9.** Genotypes selected by farmers and selection criteria during participatory maize genotypes selection.

Genotype	Desirable characters by which genotypes selected
Genotype -1	Earliness, Stay green, tolerant to diseases, Narrow leaf, Good grain filling, uniformity
Genotype -2	Cob size, tolerant to diseases, uniformity,
Genotype -3	Stay green, tolerant to diseases, Good grain filling
Genotype -8	Earliness, cob size

variety Hawassa-Dume. For instance, LER of 1.19 observed for genotype-4 indicates that there is 19% requirement for the monocropping system or 19% greater relative yield for the intercropping of genotype-4 and Hawassa-Dume. Previous studies on maize common bean intercropping in Ethiopia reported high LER of intercropping system (Walelign, 2014; Tolera et al., 2005; Assefa et al., 2016) and with maize-soybean in Indonesia (Yuwariah et al., 2018). The LERs of intercrops between maize and common bean can save lands up to 48 and 55%, which would have required as additional land for monoculture of each crop (maize or common bean) if not intercropped (Nassary et al., 2019). However, most genotypes in this study had <1 LER indicating that the land productivity will be greater when genotypes are planted in monocropping than intercropping even if the difference was not that much high (Table 9). This is consistent with non-significant difference for cropping system x genotype interaction indicating that maize genotypes responded similarly for cropping systems (Table 7). This study highlights that varieties selected based on monocropping performance may not necessarily do well under intercropping system.

Genotypes are grouped into two mega environments. SC2011 and IC2012 grouped together in one mega environment and SC2012 grouped in the other mega environment (Figure 2). Genotype-1 was the ideal genotype followed by genotype-5 (Figure 3). From ranking biplot graph, genotype-1 and genotype-5 showed better performance in yield and were highly responsive to

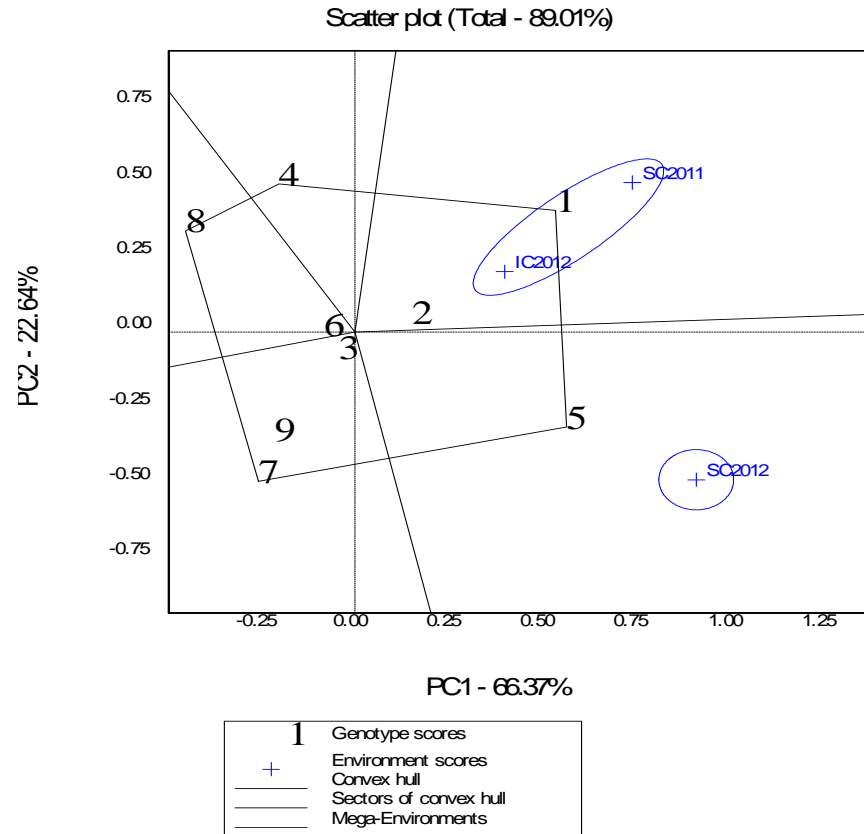
cropping systems. Genotype-2, genotype-3 and genotype-6 were highly stable genotypes compared with other genotypes (Figure 3).

## Conclusion

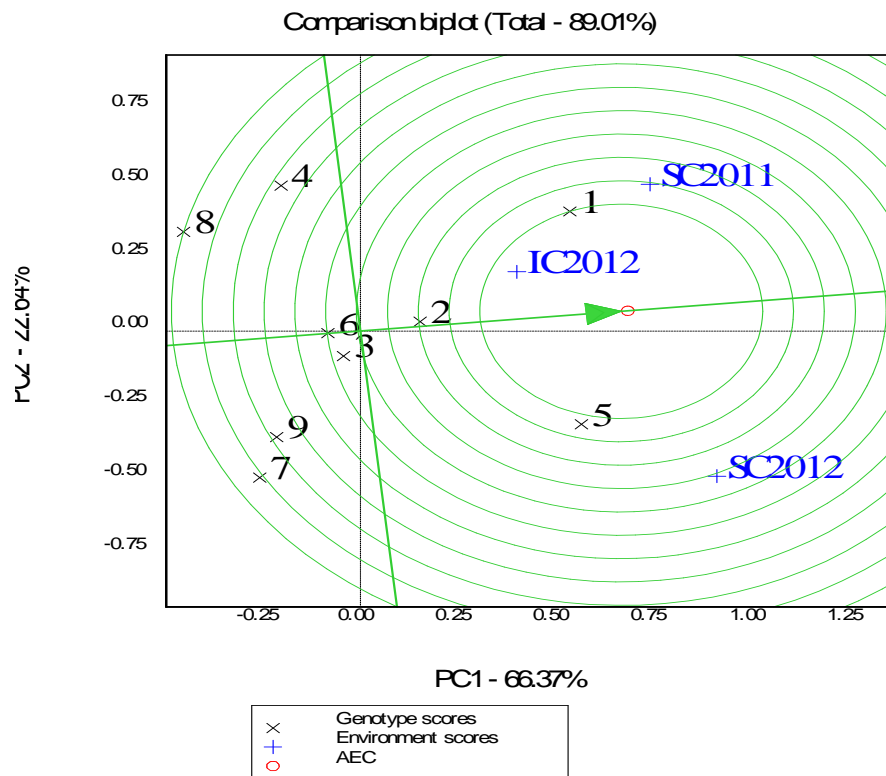
The results of this study showed significant variation among genotypes for yield and other traits. Genotypes used in this study were developed for monocropping system and hence most genotypes had lower LER indicating that they are not compatible to intercropping system. However, genotype-4 and genotype-8 demonstrated higher compatibility to the intercropping system providing an opportunity for farmers to grow under both cropping systems. In regions with maize commonly grown as an intercrop, it is of paramount importance to evaluate maize genotypes for their compatibility to intercropping system at early stage of genotype evaluation. Some morphological traits such as canopy architecture and tolerance to high planting density could be considered for varietal selection. The results of this study highlights the need for participatory varietal selection where farmers criteria could also be met for fast-track release and better adoption of maize varieties.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.



**Figure 2.** Genotypes mega environment classification.



**Figure 3.** Genotypes identification for their performance and stability.



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