Wisdom at the source of the Blue Nile

Volume 7 Number 1
July 2022

Journal of Agriculture and Environmental Sciences (JAES)

Publication of the College of Agriculture and Environmental Sciences
Bahir Dar University, Ethiopia
http://www.bdu.edu.et/caes
ISSN: 2616-3721 (Online); 2616-3713 (Print)

About the Journal

Journal of Agriculture and Environmental Sciences (JAES) is a publication of the College of Agriculture and Environmental Sciences, Bahir Dar University. JAES is a multidisciplinary open access journal, publishing scientifically sound peer-reviewed research results as well as literature review in all aspects of agriculture and environmental sciences and related fields. This journal is issued two times per year.

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Diversity, Abundance and Distribution of Birds in Guna Mountains Community Conservation Area, South Gondar, Ethiopia

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Received: March 3, 2022 Accepted: May 11, 2022

Abstract: *Ethiopian highlands are the center of endemism for fauna including birds. However, due to poor management practice, the habitats of animals have been encroached on from time to time. The main objective of this study was to assess the diversity, abundance and distribution of birds in the Guna Mountain Community Conservation Area. The study was conducted from August 2019 to April 2020, in wet and dry seasons. A stratified random sampling design was used to classify habitats based on vegetation type. The habitat types were: Erica moorland, Guassa grassland, and Rocky with lobelia. Point transects count method for Erica moorland, but line transects method for both Guassa grasslands and Rocky with lobelia habitats were employed. Data were collected in the morning (6:00-10:00 A.M.) and late afternoon (4:00-6:00 P.M.). A Chi-square test was used to test the distribution of birds among the three habitats and difference on the abundance of birds between wet and dry seasons. A total of 76 bird species that belong to 12 orders and 35 families were identified. Four species are endemic to Ethiopia, and nine were endemic both to Ethiopia and Eritrea. Five species were Inter African migrants, 18 highland biome species, and two Palearctic migrant bird species were identified. The Passeriformes were the most dominant order with 44 species and account for 58%, whereas Galliformes, Cuculiformes, Apodiformes and Strigiformes were the least represented orders that have only one species each. Relatively, high diversity of bird species was observed in the grassland habitat (H' =3.67) but the lowest species diversity was observed in the Rocky with lobelia habitat (H'=2.6). The highest evenness was recorded in the rocky with lobelia habitat (E = 0.88), whereas the lowest evenness was recorded in Erica moorland (E = 0.79). The species abundance of birds during the wet and dry seasons was significantly different ($\chi 2$ = 904.541, DF =1, $p<0.001$). There were also significant differences in the distribution of birds among the three habitats ($\chi 2$ = 3315.965, DF =75, $p<0.001$). Food availability, vegetation composition and breeding sites have affected the variety of birds' abundance in different habitats. It has been seen that habitat size, foraging modes and floristic composition influenced the distribution of birds. Grassland and highland biome restricted birds may be affected as they do not have any alternative foraging or breeding sites if the Guna Mountains Conservation Area habitat fragmentation continues. The area supports a variety of avian species with high endemics and habitat specifics. Conservation of the area is vital for habitat restricted and endemic birds.*

Keywords: Afro-alpine, Bird species diversity, Endemic birds, Guna Community Conservation Area

1. Introduction

Ethiopia is one of the top 25 biodiversity-rich countries in the world. It has the largest extent of Afro-alpine and Sub afro-alpine habitats in Africa (Yalden, 1983). The Ethiopian highlands are rich in endemic species (Yalden and Largen, 1992). The Ethiopian highlands are the home of 5200 species of plants of which 555 are endemic. They also host more than 860 species of birds among which 31 are endemic to both Ethiopia and Eretria. Moreover, about 55 of the nearly 311 mammals found in Ethiopian are found nowhere else (Lavrenchenko and Bekele, 2017). Endemic, rare and threatened mammals and birds are the unique features of this ecosystem. These ecosystems are characterized by eye-catching giant herb, known as *lobelia* (*Lobelia*

rhynchopetalum), the evergreen tree heather (*Erica arborea*) and shrubby and herbaceous everlasting flowers *(Helichrysum* species). The vegetation type is the major element to categorize the Ethiopian ecosystem. The Ethiopian Afro-alpine and Sub-afro-alpine ecosystem is described by marked altitudinal variations that create wide a range of climates affecting both flora and fauna distribution (Yalden and Largen 1992).

The temporal and spatial species diversity and abundance of birds are determined by vegetation structures that provide a food source, breeding sites and shelter. This could have resulted from climatic variations such as rainfall, temperature and the topographical nature of the area (Desalgn and Subramanian, 2015). Physical factors such as altitude, slope and others aspects control the diversity, structure and productivity of vegetation which again could also influence the diversity, abundance, distribution, and habitat use of birds (Girma *et al*., 2017).

There are about 10,000 avian species in the world grouped into 29 orders and 181 families (BirdLife International, 2004). More than 50% of the existing species of avian belong to the order Passeriformes (Avibase, 2010). Over 1850 bird species were recorded in Africa (Redman *et al*., 2009). The total number of birds in Ethiopia is estimated at 882, the number of endemics 16 (+2 near endemic), the number of globally threatened species is 42, and the number of introduced species is one (Lepage, 2022).

Guna Mountains Community Conservation Area (GMCCA) was proposed in 2016. The area is mostly covered with grass that uses for grazing. Grazing is one major factor that leads to habitat alteration in different ecosystems (Mamo *et al.,* 2014). This might increase the threat to avian species. It causes changes in the vertical and horizontal structural composition of vegetation through a combination of trampling and grazing (McIntyre *et al*., 2003). Similarly, the diversity of the species might be affected as a result of anthropogenic threats (Mengesha *et al*., 2014).

The Afroalpine ecosystem resources of Ethiopia have been used for millennia Ashenafi *et al.* (2012) but challenged the rapidly growing human population. The fauna and flora resources are threatened due to human pressure. The Afroalpine and Sub-afro alpine ecosystem of Ethiopia is not as such protected due to poor management practices. The natural vegetation is being changed into farmland, settlement, and grazing lands (Andreassen, *et al.,* 2007). The Guna Mountain Conservation Area provides fodder, water, and firewood for the community that lives around it. However, the natural vegetation has become patchy; for instance the *Erica* in Gedeba, Mokish, Amigno and Soras Kebele. This habitat patchiness could have a direct impact on the flora and fauna of the area. Birds are one of the taxonomic entities in which the land use cover change could have affected their ecology at large though some might have adapted to human-modified habitats (Sreekar *et al.,* 2016). The bird assemblage of the Guna Mountain Community Conservation Area is not known yet. Therefore, the present study aimed to study the existing species diversity, relative abundance and distribution of birds in the Guna Mountain Conservation Area for future follow up.

2. Materials and Methods

2.1. Description of the study area

Mount Guna is located in South Gondar Zone, 20 km away from Debre Tabor town. The altitude ranges from 3200 to 4113 m a.s.l; geographically, it is located $11^0 36' 06.07''$ to $11^0 49' 48.59''$ N Latitude, and $38^0 03' 13.81''$ to $38^0 24' 18.79''$ E Longitude (Figure.1). It is characterized by moist agro-climatic zones "Dega" and "Wurch". The highest average maximum monthly temperature was recorded from February to April and the lowest was during January and December (Amhara National Meteorological Services Agency, 2019). It has a bimodal rainfall distribution, described by an extended wet season from June to November. Low rainfall was also recorded in February and May. The dry season ranges from December to April.

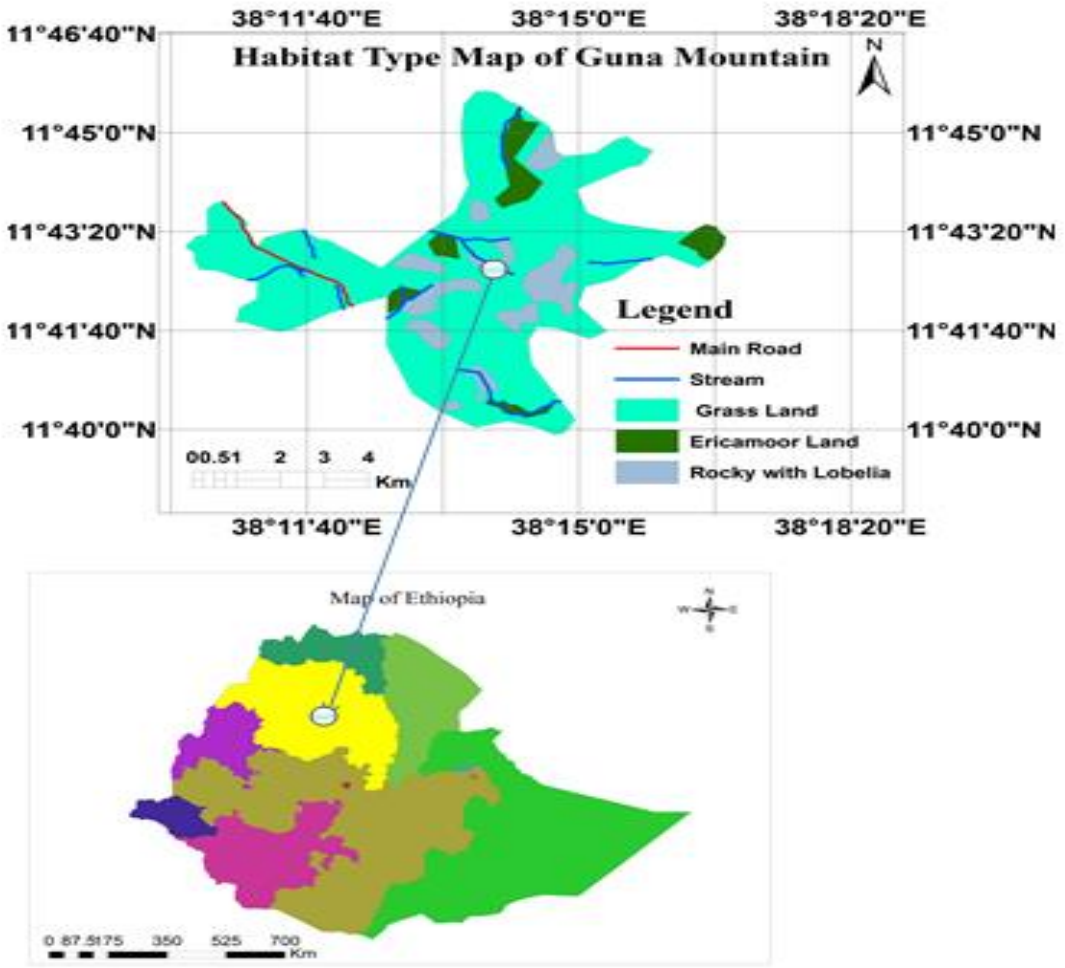

Figure 1: Map of the study area

2.2. Fauna, flora and human population

In the Guna Community Conservation Area 30 mammals are found; however, the most commonly occurring species are rock hyrax (*Heterohyrax brucei*), Common mole-rat (*Tachyoryctes splendens*), Unstriped grass rat (*Arvicanthis abyssinicus*), African wolf (*Canis aureus lupaster*), and Gelada monkey (*Theropithecus gelada*). About 89 bird species have also been reported for the diversity of this area (BoCTPD, 2012).

The area is characterized by Afroalpine and Sub-afro-alpine flora ecosystems. More than 96 species of plants are recorded in the area, out of which *Acanthu seminens*, *Echinopsellen beckii*, *Kniphofia foliosa*, *Lobelia rhynchopetalum* and *Helichrysum hochstetteri* are endemic once. The Afro-alpine zone is mainly covered with Erica moorland dominated by Guassa and rocky with lobelia habitats. In the Sub-afroalpine ecosystem zone, the evergreen tree heather (*Erica arborea*) mixed with *Hypericum revolutum* and *Echinops ellenbeckii* are recently rehabilitating in some parts of Kebeles. However, below the sub-afroalpines, *Eucalyptus globules*, *Juniperus procera*, *Erica arborea*, *Myrica salicifolia*, *Cupressus lusitanica*, *Mytenus arbutifolia*, *Hypericum revolutum* are commonly seen. *Dombeya torrida* along with cultivated land settlements and grazing lands are predominant.

The area is inhabited by 114,931 people. Their livelihood is subsistence agriculture; and the average landholding is less than half a hectare (CSA, 2010).

2.3. Sampling design and data collection

A preliminary survey was conducted at the beginning of August 2019. The overall landscape was surveyed to classify the study habitat. The physical features of the study area were observed using a ground survey. Based on this, the actual study was conducted from August 2019 to April 2020 covering both dry and wet seasons.

In this study, a stratified random sampling design was employed, since the study area has no uniform habitat types. Stratification was made following the methods of Jones (1998), and Krebs (1999). This approach was used to classify habitats and select sampling plots based on vegetation types. Based on the vegetation types and area encroachment, the area was stratified into three habitat types (Erica moorland, Rocky with Lobelia and Grassland). Sampling plots were randomly selected for each habitat type. To make sure that the results were generally representative of the total study area, the number of sampling plots was determined based on the size of the study area (Table 1) (Sutherland, 1996; Bibby et al., 1998). The area of each individual plot measures 300 m in length by 180 m in width. The distance between plots was 150 – 200 m to avoid double-counting among counting stations (Sutherland, 2006). From the total area, 20% of the study area was covered in each sample site (Bibby *et al*., 1992).

The point count method was undertaken from a fixed location within the sample unit of a radius of 30 m with a fixed time interval of 15 minutes. The number of individuals of each species was recorded within a 30 m fixed radius and the unlimited radius points at first detection (Bibby *et al.*, 1998).

Transect lines within a plot were 200 m apart from each other to avoid double counting (Aynalem and Bekele, 2008). During the transect survey, all the birds found in a 45-meter belt length in both directions of the observer were recorded and counted. Line transects were laid in the grassland and rocky with lobelia measuring a length of 300 m each.

The fieldwork was carried out from August to November 2019 for the wet season, and from December 2019 to April 2020 for the dry season. The bird count was made for 15 minutes within the counting station. Stations were surveyed for 72 days during both wet and dry seasons; however, the frequency of data collection was every week twice a day in the morning (6:00-10:00 A.M.) and late in the afternoon (4:00-6:00 P.M.) during the active time of birds and when the weather condition was ideal (Centerbury *et al.*, 2000). For bird identification, the plumage pattern, size, shape, colour, songs and calls were considered (Aynalem and Bekele, 2009). Birds were physically observed using a pair of binoculars. Avian species were identified and their taxonomic groups were categorized using field guides of birds (Redman *et al.*, 2011; Zelelew, 2013). The taxonomic order and nomenclature follow Clements, version 2021.

Table 1: Sampled area and transect counts based on habitat types at Guna Mountain conservation area

Habitat types	Rock with Lobelia	*Erica moorland*	Grassland	Total
Total area coverage (ha)	348	299	3968	6415
Sampled area (ha)	69.6	60	793.4	923
No of sample plots	13	11	147	171
Numbers of line transect	26	-	294	320
Numbers of point transect	-	165	-	165

Note: The total area of the site is = 4615 ha; however, 923 ha (20%) of the area was considered for data collection

2.4. Data analysis

Shannon-Wiener diversity index of diversity was used for the analysis of species diversity in the sampled area (Krebs, 1999).

$$\text{Diversity index } (H') = -\sum P_i \ln P_i \quad [1]$$

Where:

pi = the proportion of species i and ln P_i = the natural logarithm of P_i.

The relative abundance of bird species was estimated using encounter rates that give basic ordinal scales of abundance (abundant, common, frequent, uncommon and rare) (Table 2) (Aynalem and Bekele, 2008). Encounter rate for each species was calculated as:

$$ER = \left(\frac{total\ number\ of\ individuals\ \ again\ observed}{\text{Period of observation in hour}}\right) X\ 100 \quad [2]$$

Where ER is encounter rate.

Table 2: Ordinal scale of abundance used to rank species

Abundance Category	Abundance Score	The ordinal rank of Abundance
< 0.1	1	Rare
0.1-2.0	2	Uncommon
2.1-10.0	3	Frequent
10.1-40.0	4	Common
> 40	5	Abundant

To get the evenness (the pattern of distribution) of birds in the study area, Shannon-Wiener Evenness Index (E) was calculated using the equation;

$$E = \frac{H'}{Hmax} \quad [3]$$

Where:
E = Shannon-Wiener Evenness Index
H' = Shannon-Wiener Diversity Index
H max = ln S= natural logarithm of the total number of species (S) in each site (Henderson and South wood, 2000).

The Chi-square test of independence was also used to test whether the distribution of bird species associated with the three habitats, and differences on the abundance of birds between wet and dry seasons.

3. Results and Discussion

3.1. Species composition

A total of 76 species of birds were observed during the study period. They were belonging to 12 orders and 35 families (Table 3). The order Passeriformes holds 44 bird species which accounted for 58% of the total species. However, the number of avian species identified in the present study was lower than what was reported (BoCTPD, 2012). Apodiformes, Galliformes, Cuculiformes, and Strigiformes were the least diverse orders represented by only one species each. These species are Little swift (*Apus affinis)*, Erckel's francolin (*Francolinus erckelii)*, *White*-cheeked turaco (*Tauraco leucotis),* and Barn owl (*Tyto alba*), respectively. At the family level, the family Accipitridae was the large family which is represented by nine species and accounts for 11.7 %.

It is clear that as altitude increases biodiversity decreases, but the endemicity of species increases. In this study, relatively the number of endemic species was higher as compared to Entoto protected area (Esayas and Bekele, 2011). And hence in this study four species, which account for 5% were endemic to Ethiopia and nine (11.7%) were endemic to Ethiopia and Eritrea. Four species of Inter African Migrate, 16 species of highland biome species and two Palearctic migrant species were also recorded.

Table 3: Bird species identified at Guna Mountain conservation area

Order	Family name	Common name	Scientific name
Apodiformes	Apodidae	Little swift	*Apus affinis*
Anseriformes	Anatidae	Blue-winged goose [E]	*Cyanochen cyanopterus*
		Egyptian goose	*Alopchen aegyptiaca*
Strigiformes	Tytonidae	Barn owl	*Tyto alba*
Pelecaniformes	Ardeidae	Grey heron	*Ardea cinerea*
		Cattle egret	*Ardeola ibis*
		Black-headed heron	*Ardea melanocephala*
	Threskiornithidae	Wattled ibis [E] ♠♦	*Bostrychia carunculata*
		Hamerkop	*Scopus umbretta*
	Scopidae	Spur-winged plover	*Vanellus spinosus*
Charadriiformes	Charadriidae	Spot-breasted plover [E]♦	*Vanellus melanocephalus*
	Recurvirostridae	Black-winged stilt	*Himantopus himantopus*
Columbiformes	Columbidae	White-collared pigeon[E] ♦	*Columba albitorques*
		Speckled pigeon	*Columba guinea*
		Red-eyed dove	*Streptopelia semitoquata*
		Dusky turtle dove♦	*Streptopelia lugens*
Accipitriformes	Accipitridae	Tawny eagle	*Aquila rapox*
		Black kite ♠	*Milvus migrans*
		Common buzzard	*Buteo buteo*
		Augur buzzard	*Bueto augur*
		Lammergeier	*Gypaetus barbatus*
		Rüppell's vulture	*Gyps rueppellii*
		Egyptian vulture	*Neophron percnopterus*
		Hooded vulture	*Necrosyrtes monachus*
		White backed vulture	*Gyps africanus*
Coraciiformes	Bucerotidae	Hemprich´s hornbill	*Tockus hemprichii*
	Upupidae	Eurasian hoopoe	*Upupa epops*
	Phoeniculidae	Black-billed hoopoe	*Phoeniculus somaliensis*
	Buphagidae	Red-billed oxpecker	*Buphagus erythrorhynchus*
Passeriformes	Cisticolidae	Tawny-flanked prinia	*Prinia subflava*
	Corvidae	Pied crow	*Corvus albus*
		Thick-billed raven [E] ♦	*Corvus crassirostris*
		Cape rock	*Corvus capensis*
		Fan-tailed raven	*Corvus rhipidurus*
	Hirundinidae	Red-rumped swallow	*Cecropis daurica*
	Monarchidae	African paradise-flycather	*Terpsiphone viridis*
	Fringillidae	Streaky seedeater♦	*Serinus striolatus*
		White-throated seedeater♦	*Serinus xanthopygius*
		Black-headed siskin (E)♦	*Serinus nigriceps*
	Paridae	White-backed Black Tit	*Parus leuconontus*

Order	Family name	Common name	Scientific name
	Laniidae	Common fiscal	*Lanius collaris*
	Turdidae	Alpine /moorland chat♦	*Cercomela sordida*
		Rüppell´s black chat [E]	*Myrmecocichla melaena*
		Rüppell´s robin chat♦	*Cossypha semirufa*
		Abyssinian Slaty-flycatcher	*Melaenornis chocolatinus*
		Northern black-flycatcher	*Melaenornis edolioides*
		White-winged cliff-chat [E] ♦	*Myrmecocichla semirufa*
		Black-eared wheatear	*Oenanthe hispanica*
	Passeridae	Swainson's sparrow	*Passer swainsonii*
	Motacillidae	Abyssinian long claw E♠♦	*Macronyx flavicollis*
		Mountain wagtail	*Motacilla clara*
		Grey wagtail	*Motacilla cinerea*
		Yellow wagtail ♥	*Motacilla flava*
		Tree pipit	*Anthus trivialis*
	Nectariniidae	Variable Sunbird	*Cinnyris venustus*
		Tacazze sunbird♦	*Nectarinia tacazze*
	Ploceidae	Red collard widowbird	*Euplectes ardens*
		Yellow bishop	*Euplectes capensis*
	Pycnonotidae	Baglafecht weaver♦	*Ploceus baglafecht*
		Common bulbul	*Pycnonotus barbatus*
	Sturnidae	White-billed starling [E] ♦	*Onychognathus albirostris*
	Vidudae	Village indigobird	*Vidua chalybeate*
	Turdidae	Abyssinian ground thrush	*Zoothera piaggiae*
		African thrush	*Turdus pelios*
		Mountain thrush	*Turdus olivaceus*
		Ground scraper thrush	*Psophocichla litsitsirupa*
	Sylviidae	Pectoral patch cisticola	*Cisticola brunnescens*
		Common chiffchaff	*Phylloscopus collybita*
		Blackcap	*Sylvia atricapilla*
		Ethiopian cisticola	*Cisticola lugubris*
	Muscicapidae	Rea breasted wheatear	*Oenanthe bottae*
		Pied wheatear ♥	*Oenanthe pleschanka*
Psittaciformes	Psittacidae	Black-winged lovebird [E]	*Agapornis taranta*
		Yellow-fronted parrot E ♠	*Poicephalus gulielmi*
Galliformes	Phasianidae	Erckel's francolin♦	*Francolinus erckelii*
Cuculiformes	Musophagidae	White-cheeked turaco[E]	*Tauraco leucotis*

Note: E = Endemic to Ethiopia, [E] = Endemic to Ethiopian and Eretria, ♥ = Palearctic Migrant, ♠ = Inter African Migrant, ♦ = Highland biome bird species

3.2. Relative abundance of birds

During the wet and dry season in each study habitat, the relative abundance of birds was different. A total of 86 birds were uncommon species, 83 were frequent, 12 were common, and only six were rare in the area (Table 4).

The seasonal abundance of bird species was compared. The comparison was made on the bases of sightings and hence only the first seven bird species were considered. These species were: Wattled ibis (*B. carunculata*), Brown rumped seedeat er (*S. tristraitus*), Black headed siskin (*S. nigriceps*), White-collared pigeon (*C. albitorques*), Dusky turtle dove (*S. turtus*). The number of counts for the above species was 167, 141, 133 and 126, respectively. The other two species were the Pied crow (*C. capensis*) and Thick-billed raven (C. *crassirostris)*. The abundance difference between the two seasons was statistically significant ($\chi 2 = 7.100$, DF =1, $p < 0.001$).

The variation in abundance of bird species was observed between different habitats. The variation in the abundance of birds could be determined by food availability and breeding sites (Moges *et al.,* 2018).

The last seven bird species with the lowest number of sightings were Variable sunbird (*C. Vanuatu)*, Barn owl (*T. alba*), Tacazze sunbird (*N. tacazze)*, and Abyssinian long claw (*M. flavicollis*). These species were observed only once in the study period, whereas Erckel's francolin (*F. erckelii)*, Blue-winged goose *(C. cyanopterus)*, and Hemprich´s hornbill (*T. hemprichii)* were observed twice. The abundance of these seven listed species were also statistically significantly different between seasons ($\chi 2 = 3.600$, DF=1, $p<0.001$). The distinct seasonality of rainfall and seasonal variation in the abundance of food resources could account for seasonal changes in the species abundance of birds (Gaston *et al*. 2000; Karr and Roth, 1971).

Table 4: Relative abundance of bird species in the dry and wet seasons at Guna Mountain conservation area

Habitat	Season	Uncommon	Frequent	Rare	Common
Grassland	Dry	21	17	3	4
	Wet	22	13		1
Erica moorland	Dry	20	14		
	Wet	16	19		2
Rocky with *lobelia*	Dry	4	16		2
	Wet	3	4	3	3

3.3. Distribution of birds in Guna Mountains Community Conservation Area

Of the total species of bird identified during the study period, the highest species (53 species) were recorded from the grassland and the least (22 species) were recorded from rocky with lobelia habitat. Of these avian species, 64 and 59 species were recorded during the wet and dry seasons, respectively (Table 5). Birds showed differences in the distribution among the three habitats ($\chi 2 = 3315.965$, DF =75, $p<0.001$). The difference could be due to the variation in the size and vegetation composition of the study areas. Antos *et al.* (2006) justified that as the size of survey areas increases, the richness and diversity of bird species also increase. Davidar *et al*. (2001) have also reported that size could be a factor in this variation. Passeriformes and Accipitriformes were the most abundant families and they were commonly distributed. Strigiformes families were the least abundant in the study area and their distributions were not common in the study area.

The highest number of avian species was encountered in moorland **(**Blackwell *et al*., 2013**)**. But, the present study showed that the number of avian species in grassland habitats was highest than in *Erica* moorland. The *Erica* moorland habitat is dominated by few plant species and has little flowers and fruits that could account for the presence of less number of species than the grassland. Therefore, birds that are dependent on fruit such as frugivores birds could not be attracted to the area (Yirdew *et al*,, 2013). Moreover, low species abundance in the *Erica* moorland might be related to the absence of a different variety of plant species, which might be selected only by a few bird species. According to Girma *et al.* (2017); Mengesha and Bekele (2008), a natural forest which is dominated by a few tree species are not suitable for different bird species.

There was also a difference in the number of avian species between the dry and wet seasons. This result agrees with Asmare (2009). The availability of food increases during the wet season as the species richness might increase. Tellaria (1992) pointed out that habitat structure tends to affect the distribution of individual avian species. Similarly, habitat size, foraging modes and floristic composition are also among the other driving factors that tend also to influence the distribution of bird species (Aynalem and Bekele, 2008; Girma *et al.*, 2017).

Table 5: Distribution of bird species in different habitat types and seasons in the study area (+ indicates presence and (-) indicates an absence of species at GMCA

Common name	Scientific name	Habitat types			Season	
		Erica moorland	Grassland	Rocky with Lobelia	Wet	Dry
Abyssinian ground thrush	*Z. piaggiae*	+	+	-	+	+
Abyssinian long claw	*M. flavicollis*	+	+	-	+	-
Abyssinian slaty-flycatcher	*M. chocolatinus*	+	-	+	+	+
African thrush	*T. pelios*	+	+	+	+	+
African paradise-flycatcher	*T. viridis*	+	-	-	+	-
Alpine/moorland chat	*C. sordida*	-	+	+	+	+
Augur buzzard	*B. rufofuscus*	+	+	+	+	+
Baglafecht weaver	*P. baglafecht*	+	+	-	+	+
Barn owl	*T. alba*	+	-	-	-	+
Black kite	*M. migrans*	+	+	-	+	+
Black-billed hoopoe	*P. somaliensis*	-	+	-	+	-
Blackcap	*S. atricapilla*	-	+	-	+	-
Black-eared wheatear	*O. hispanica*	+	-	-	+	+
Black-headed heron	*A. melanocephala*	-	+	-	+	-
Black-headed siskin	*S. nigriceps*	+	+	-	+	+
Black-winged lovebird	*A. taranta*	+	+	-	+	+
Black-winged stilt	*H. himantopus*	+	+	-	+	-
Blue-winged goose	*Cyanochen cyanopterus*	-	+	-	+	-
Cape rock	*C. capensis*	-	+	-	+	+
Cattle egret	*A. ibis*	-	+	-	+	-
Common bulbul	*P. barbatus*	+	-	-	+	+
Common buzzard	*B. buteo*	+	+	+	+	+
Common chiffchaff	*P. collybita*	+	-	-	+	+
Common fiscal	*L. collaris*	+	-	-	-	+
Dusky turtle dove	*S. logins*	+	+	+	+	+
Egyptian goose	*A. aegyptiaca*	-	+	-	+	-
Egyptian vulture	*N. percnopterus*	-	+	-	-	+
Erckel's francolin	*F. erckelii*	+	+	-	+	+
Ethiopian cisticola	*C. lugubris*	+	+	-	+	+
Eurasian hoopoe	*U. epops*	-	+	-	+	-
Fan-tailed raven	*C. rhipidurus*	-	+	-	+	+
Fan-tailed raven	*C. rhipidurus*	-	+	-	+	+
Grey heron	*A. cinerea*	-	+	-	+	-

3.4. Diversity of birds

The highest species diversity was obtained in grassland habitat (H'=3.67), whereas low diversity was recorded in rocky with *lobelia* habitat (H´=2.6). The highest species evenness was recorded in grassland and rocky with lobelia habitat (E=0.88) and the lowest species evenness was recorded in *Erica* moorland habitat and rocky with lobelia (E=0.79). The diversity and evenness of bird species among habitat types between wet and dry seasons are presented in (Table 6). The lowest species diversity was obtained in the rocky with *lobelia* habitat in wet seasons (H´=1.84), whereas grassland had the highest bird species diversity (H´= 3.86). Similarly, during the dry season, the lowest species diversity was obtained in the rocky with lobelia habitat (H´=2.34) and the highest species diversity was obtained in the grassland habitat (H´=3.48). The floristic composition might have a great influence on the distribution of the avian species in the grassland than others (Aynalem and Bekele, 2008; Girma *et al.*, 2017). According to Nancy (1995), larger covered habitats support more species of birds and individuals than smaller ones as they possess diversified microhabitats. This result could be due to the adaptable nature of birds in the grassland habitats (Smith, 1992). The results of the present study, in agreement with the findings of Mengesha and Bekele (2008) and Genet and Ejigu (2017), showed that grassland interspersed patchy habitats have contribution to high diversity, richness, and evenness of birds. The openness of sites compared to *Erica* moorland might have also contributed to the easy identification of species (Hailu, 2008). The overall bird species diversity in the wet season (H'=2.50) was slightly higher than that of the dry season in the study area (H´=1.83). The distinct seasonality of rainfall and seasonal variation in the abundance of food resources could account for seasonal changes in the species abundance of birds (Gaston *et al*., 2000; Karr and Roth, 1971).

Guna Mountains Conservation Area is highly fragmented and exposed to different threats caused by anthropogenic activities. Habitat loss and degradation as a result of anthropogenic activities have caused a significant decline in avian diversity around the world (Taylor and Pollard, 2008). This might lead to a change in the diversity, abundance and distribution of birds (Mengesha *et al.*, 2011). Especially grassland and highland biome restricted birds may be affected as they do not have any alternative foraging or breeding sites.

Table 6: Diversity and evenness indexes of birds at GMCA study habitats

Habitat Types	Season	Individuals	Taxa- S	H'	H'max	Evenness
Rocky with *Lobelia*	Wet	215	15	1.84	2.7	0.68
	Dry	170	19	2.34	2.94	0.8
	Both	323	26	2.6	3.29	0.79
Guassa grassland	Wet	482	49	3.86	3.89	0.99
	Dry	601	43	3.48	3.76	0.93
	Both	1092	64	3.67	4.15	0.88
Erica moorland	Wet	302	33	2.63	3.49	0.75
	Dry	543	42	2.47	3.74	0.66
	Both	969	59	3.22	4.08	0.79

4. Conclusions and Recommendations

he results of this study demonstrate that Guna Mountains Community Conservation Area has a total of 76 species, 12 orders, and 35 families. It is an important area for highland biome restricted species and home of endemic, and nearly threatened species. At this site, four endemic species, and nine species that are endemic both to Ethiopia and Eritrea, four inter African migrants, 16 highland biome species and two Palearctic migrant species were recorded.

The study showed that season and habitat types are the important determining factor for both Palearctic

migrant and resident bird species. Most of the species were uncommon. The highest diversity and distribution of bird species were observed in the grassland and relatively, the lowest diversity and distribution were observed in the rocky with lobelia.

Human activities such as overgrazing, deforestation, agricultural expansion, human settlements and eucalyptus plantation expansions were observed in Guna Mountains Community Conservation Area. Unless appropriate community conservation measures are taken, the entire habitat and the bird species will be affected in the area. This study, recommends that the conservation of the area must be strengthened in order to safeguard the birds and their habitats. The grazing and agricultural land encroachment into the area would affect the fauna and flora of the area at large. Sustainable utilization of the natural resource could maintain the ecological integrity of this afro-alpine habitat.

Conflicts of interest

The authors declare that there is no conflict of interest in publishing the manuscript in this journal.

Acknowledgement

The project finance was partially supported by Bahir Dar University. We are grateful to Guna Mountain Community Based Conservation Area office, especially to Ato Amsalu Moges, for providing us with the necessary information for our work. The support from the scouts of the conservation area is also appreciated.

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Response of dual-purpose sorghum (*Sorghum bicolour* L.) varieties to anthracnose disease, growth and yield performances under dry land crop-livestock farming systems of southern Ethiopia

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Received: March 8, 2022 **Accepted:** May 21, 2022

Abstract: *Integration of food crop production with feed supply in quantity and quality by considering some important foliar diseases could be an ideal approach in the crop-livestock farming system of tropical agriculture. Evaluating the responses of dual-purpose sorghum varieties to anthracnose diseases, growth and yield performances under the dry land farming system was undertaken in Arguba and Chamomile research substation during the 2018 and 2019 major production seasons. Five sorghum varieties (Chelenko, A-2267_2 and NTJ_2, Dishkara, Konoda) and one local check (Rara) were arranged factorial in a randomized complete block design with four replications. The assessment was done on plant height, leaf number, leaf width, leaf length, tiller number, dry biomass and grain yields, as well as on anthracnose disease infection. Variety Chelenko exhibited the tallest main crop plant height while Dishkara was the tallest at ratoon crop harvesting. Rara had a higher tiller number among the varieties. Chelenko had a higher dry biomass yield at the main crop while Dishkara at ratoon harvesting. The total dry biomass yield recorded by Dishkara, Chelenko A-2267_2, Rara, NTJ_2 and Konoda varieties was 45.3, 33.3, 31.8, 29.8 21.7 and 18.5 t/ha, respectively. Dry biomass yield was strongly and positively correlated with plant height. The varieties A-2267_2 and NTJ_2 recorded Anthracnose incidence of 98.90 and 100%, respectively while the severity was about 43.67 and 40.36% in the same order. Similarly, the area under disease progress curves for A-2267_2 and NTJ_2 varieties were 860 and 1085.27%-days, respectively. Dishkara and Chelenko varieties produced 45.3 t/ha and 33.3 t/ha dry biomass yields, which were 33.6% and 9.6%, respectively, higher ($P<0.05$) compared to the overall mean dry biomass yield (30.1 t/ha). On the other hand, the Konoda variety produced about 62.7% (18.5 t/ha) less dry biomass yield than the overall mean dry biomass yield. Although the anthracnose infection was highest in the varieties Konoda and NTJ_2, they produced significantly ($P<0.001$) higher grain yield (3.89 t/ha) than others. Under anthracnose pressure, Chelenko and Dishkara varieties are suggested for dry biomass yield while NTJ_2 for grain yield production in the study area and areas with similar agro-ecologies. Further research on the performance of the varieties under irrigation conditions and the inclusion of their feed quality is also recommended.*

Keywords: Animal feed, AUDPC, biomass yield, disease incidence, disease severity

1. Introduction

Regenerating perennial pastures which could survive for years are a major element in successful livestock enterprises (Collet, 2004). Sorghum (*Sorghum bicolour*) is inherently producing high biomass accumulation, high productivity per unit of water utilized and ratoon crop after harvesting of the plant (Vinutha *et al*., 2017). The crop is truly grown for dual purposes for both feed Stover and grain that are highly valued infrequent drought areas (Balmuri *et al*., 2018). Sorghum is the third most important crop in the study area next to tef and maize and is the fourth important crop in terms of area coverage and volume of production in Ethiopia (MOA, 2016)

which has been produced by 5 million smallholder farmers in 2 million hectares with a production of 4.3 million tons and grain productivity of 2 t/ha (CSA, 2018).

The importance of sorghum as a feed crop in the semi-arid tropics and drier parts of the world has been proven where livestock rearing takes a part in the agricultural production system (Mohammed, 2010). Forage sorghum has been characterized as a sweet tall plant from 1.9 to 2.7 meters (Vinutha *et al*., 2017) and adapted to a ratoon production system. It is best utilized as a silage crop, although it can be grazed or cut for hay if managed appropriately and improve fiber supplement for digestion in milking cows (Hassan *et al*., 2015). According to Vinutha *et al*. (2017), the quality of forage sorghum in terms of nitrogen content for 36 lines was ranging from 2.06% to 2.89% with the production of above-ground dry biomass up to 33.8 t/ha. Structural carbohydrates and starch are the main energy resources that are accumulated in the grain and dry biomass of cereal crops, and they are important for dairy cows (Mohammed, 2010). However, anthracnose (*Colletotrichum graminicola*) (Madhusudhana, 2019) and turcicum (*Exserohilum turcicum*) leaf blight (TLB) (Kiran and Patil, 2019) diseases are the most destructive and affect all aerial tissues of the plant and can cause dry matter and seed yield losses of up to 50% in severely affected fields of sorghum.

In Ethiopia, the feed balance has been reported negative in terms of dry matter at 21.2%, feed metabolizable energy at 51.7% and crude protein at 9.5% whereas in southern Ethiopia including the experimental locations dry matter is 40.3%, metabolizable energy at 62.6% and crude protein 57.9% (Shapiro *et al*., 2015). Negative feed balance in terms of dry matter and forage quality has been affecting animal production in the Ethiopian livestock system (Atumo *et al*., 2022).

Therefore, the objectives of the present study were to assess forage dry biomass yield, grain yield, agro-morphological traits, and leaf to stem ratio of main and ratoon sorghum varieties under the pressure of anthracnose disease, as well as to determine the intensity of anthracnose on the tested six sorghum varieties associated with their growth and yield performances under field conditions in Chamomile and Arguba trial locations, southern Ethiopia. This is particularly to help smallholder farmers in using the most productive dual-purpose sorghum varieties in terms of forage and grain yield under the pressure of major foliar diseases to be resistant to alternative varieties for food production and supplying feed to their livestock in particular circumstances and to provide background data for planning future breeding programs.

2. Materials and Methods

2.1. Description of study areas

Evaluation of sorghum varieties for dry biomass yield under the pressure of anthracnose disease was conducted at Chamomile and Arguba in Arba Minch Zuriya and Derashe special districts, respectively, of southern Ethiopia during the 2018 and 2019 main cropping seasons. The two study sites are situated in the semi-arid tropical belt of southern Ethiopia. Geographically, the Chamomile site is located at 06°06´ N latitude and 37°35´ E longitude, while the Arguba site is located at 05°30´ N latitude and 37°12´ E longitude. Chamomile and Arguba sites are laid at an altitude of 1206 and 1260 meters above sea levels, respectively.

The two experimental sites have a bimodal rainfall pattern. The short rainy season falls from March to May and the long rainy season extends from June to November. Chamomile and Arguba receive mean annual precipitation of 937.9 and 1009.2 mm with average maximum and minimum temperatures of 30.3 and 17.3 ^{0}C, and 27.31 and 18.93 ^{0}C, respectively (NMA, 2021). Monthly distributions of mean rainfall and average maximum and minimum temperatures of Arguba and Chamomile experimental sites for 30 years (1989 to 2019) are presented in Figures 1 and 2, respectively.

According to the analysis results of the collected composite (0–30 cm) sample, soil of Chanomile site was categorized as sandy loam and had 14.47 mg/kg, 0.29%, 1.19% and 1.63% available phosphorus, total nitrogen organic carbon and organic matter, respectively, with the pH of 6.2 (Atumo *et al*., 2021). Similarly the soil of Arguba site was categorized to textural classification of sandy loam and had available phosphorus, total nitrogen, organic carbon

and organic matter of 14.5 mg/kg, 0.31%, 1.22% and 1.72%, respectively, with the pH of 6.15.

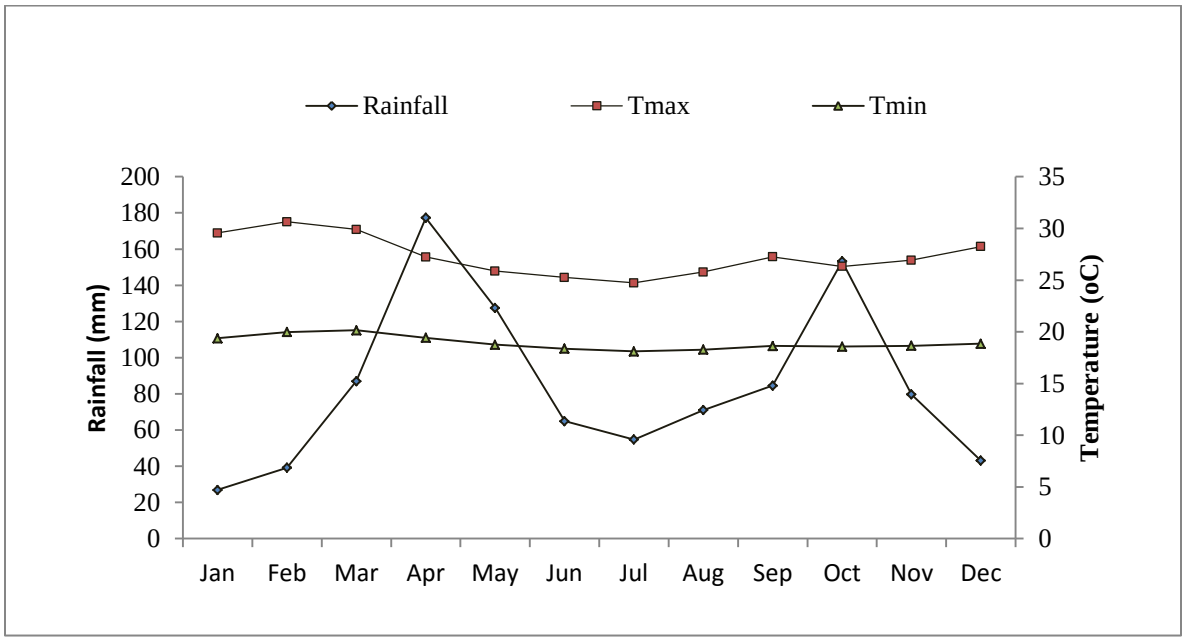

Figure 1: Rainfall, minimum and maximum temperatures of Arguba site during the last 30 years (1989-2019)

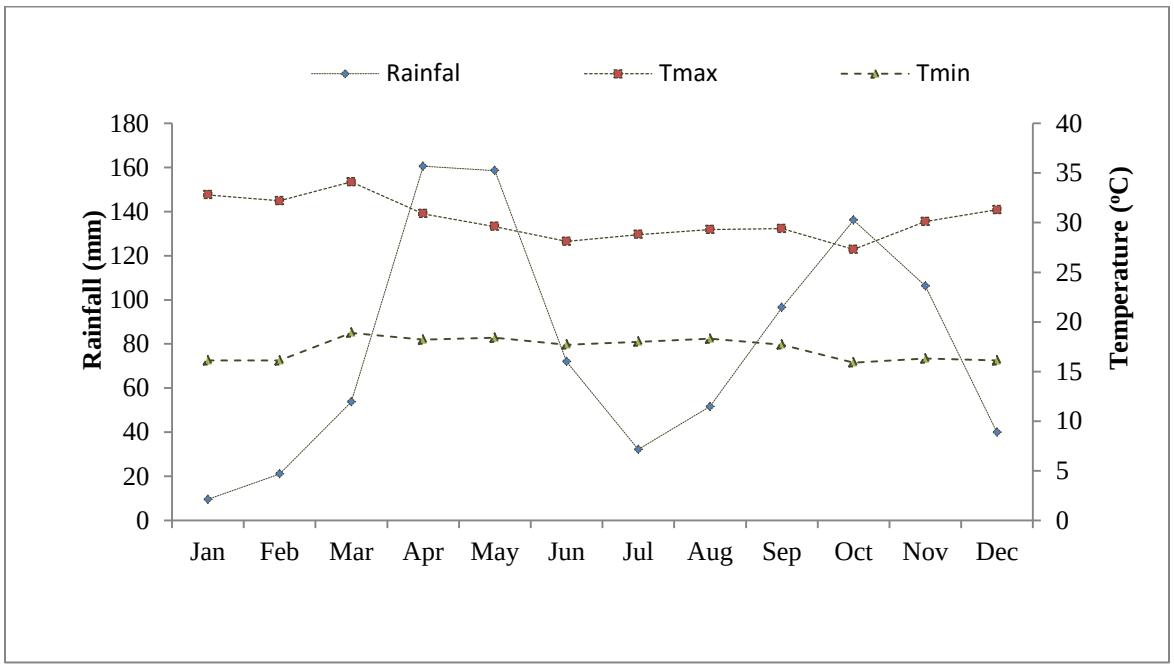

Figure 2: Rainfall, minimum and maximum temperatures of Chamomile site during the last 30 years (1989-2019)

2.2. Description of experimental materials

A total of six dual-purpose sorghum genotypes were used for the study. While the seeds of Chelenko, A-2267_2 and NTJ_2 varieties were collected from Melkasa Agricultural Research Center (MARC), seeds of the remaining Dishkara and Konoda varieties and one local check (Rara) were collected from farmers in Derashe special district (Table 1).

Table 1: Sorghum varieties used in the study

Variety	Adaptation area	Release year	Remark
A_2276_2	<1600	-	
Chelenko	<1600	2005	(MOA, 2016)
Dishkara	1200-1700	-	Farmer cultivar
Konoda	1200-1700	-	Farmer cultivar
NTJ_2	<1600	-	
Rara	1200-1700	-	Farmer cultivar

2.3. Experimental design and procedures

At both experimental sites, the six varieties were laid out in a randomized complete block design with four replications. The Gross and net sizes of experimental plots were 2.4 m*3 m (7.2 m^2) and 1.2 m* 3m (3.6 m^2), respectively. Spacing between experimental plots and replications were 1m and 1.5m, respectively.

After ploughing the selected experimental plots with oxen, the plots were prepared and leveled manually with the help of necessary farm tools. The six sorghum varieties were allocated to the experimental plots randomly using a randomized complete block design method.

Seed sowing was carried out from late March to early April 2018 and 2019. Seeds were sown in a row at inter-and intra-spacing of 60 cm by 25 cm, respectively. To avoid the risk of failing seedling emergence, two seeds were planted per hill and the weak seedlings were thinned out after 40 days of planting to maintain only a single plant per hill.

Experimental plots were fertilized with NPS (19% N, 37% P_2O_5, 7% S) at the rate of 100 kg/ha during planting time, and with Urea (46% N) at the rate of 100 kg/ha in two splits as the first half top-dressed on the 45th days of planting and the remaining half applied after initial harvest for ratoon initiation (MOA, 2016). Experimental plots were kept weed-free with frequent hand weeding.

2.4. Data collection

2.4.1. Growth and *yield parameters*

Data collection for forage and grain yields from the main crop was performed by cutting plants at ground level in the net plot area after physiological maturity. The second harvesting from the ratoon crop was done after 105 days of the first harvest of the main crop. Both fresh and dry biomass yields, as well as grain yield obtained from the net plot area, were converted into a hectare basis. Apart from the collection of forage and grain yields, data on vegetative growth parameters were collected timely. Plant height was measured at a date of 50% flowering from ground level to the tip of the plant with the linear meter. The number of leaves per plant was counted, as well as length and width of leaves in the middle of the plants were measured with linear meters at the forage harvesting time of both ratoon and main crops. Tillers per plant were also counted from both main and ratoon crops just before harvesting. However, growth performance parameters of Dishakara and Konoda varieties at Chanomile site during the 2019 growing season couldn't be collected due seed emergence problems.

Green forage yield per net plot area was measured using a spring balance and expressed as fresh biomass yield per hectare. The sample was taken to the laboratory and subjected to oven drying at 65°C for 24 hours to get constant dry weight. After cooling, the samples were weighed with sensitive balance and expressed as dry biomass yield. Dry biomass yields were estimated by multiplying fresh biomass yields with the dry matter percentage of respective samples. Dry matter of the samples and dry biomass yield of both main crop and ratoon crops were determined using the formulas below as indicated by Tarawali *et al.* (1995):

$$DM\ (\%) = \left(\frac{ODW\ (g)}{FW(g)}\right) * 100 \quad [1]$$

Where
DM = dry matter percent, ODW = oven dry weight, FW = fresh weight of a sample (500 g)

$$DBY\ (t/ha)\ = FBY\ (t/ha) * DM(\%) \quad [2]$$

Where
DBY = dry biomass yield, FBY = fresh biomass yield, DM% = dry matter content in percent

2.4.2. Disease monitoring

Anthracnose incidence and severity assessments were started 40 and 45 days after planting at Arguba and Chamomile sites in the 2018 and 2019 cropping seasons, respectively, when the first symptom of anthracnose appeared on plant leaves within the plot.

Twelve randomly selected and tagged sorghum plants from the central rows of each plot were used for disease assessment and a total of six assessments were made per location per season.

Disease incidence (%) was determined by the rating of diseased plants per total number of plants assessed within the plot. Anthracnose severity was visually assessed from 15 pre-tagged plants per plot following the scale devised by Thakur *et al*. (2007), where, 1 = no visible symptoms or presence of chlorotic flecks, 2 = 1 - 10% leaf area covered with hypersensitive lesions without acervuli, 3 = 11 - 25% leaf area covered with hypersensitive and restricted lesions with acervuli in the center, 4 = 26 - 50% leaf area covered with coalescing necrotic lesions with acervuli and 5 = $\geq$ 50% leaf area covered with coalescing necrotic lesions with acervuli. Severity scores were transformed into percentage severity index (PSI) for analysis using the formula stated below (Wheeler, 1969).

$$\text{PSI} = \left(\frac{\text{Sum of numerical ratings}}{\text{No. of plants scored x maximum score on scale}}\right) * 100$$

The area under the disease progress curve (AUDPC) (the development of disease on a whole plant or part of the plant during the epidemic periods) was estimated from PSI (anthracnose) and mean (turcicum leaf blight) values assessed on different days after planting for each sorghum varieties within the plot using the formula mentioned by Campbell and Madden (1990) and indicated as below.

$$\text{AUDPC} = \sum_{i=1}^{n-1} 0.5\ (X_i + X_{i+1})\ (t_{i-1} - t_i) \qquad [4]$$

Where
n is the total number of disease assessments, t_i is the time of the i^{th} assessment in days from the first assessment date and x_i is the PSI of disease at the i^{th} assessment.

AUDPC was articulated in %-days since severity (X) is expressed in percent and time (t) in days.

2.5. Data analysis

Genstat software (Payne *et al*., 2015) package was used to compute the analysis of variance (ANOVA) of all parameters considered in the study. Whenever the ANOVA results were significant, the means of the parameters were separated using Least Significance Difference (LSD) at a 5% level of error. The two seasons and locations were recorded as distinct environments due to heterogeneity of error variances in Bartlett's test as indicated by Gomez and Gomez (1984). Due to this, data were separately analyzed as location and season effects. Associations of anthracnose incidence, severity and AUDPC with growth and yield-related traits of sorghum varieties were examined using simple correlation analysis. Spearman correlation coefficients (r) were used to indicate the strength of the relationships among the parameters.

3. Results and Discussion

3.1. Growth performance

3.1.1. Plant height

The plant height of sorghum varieties for the main plant was significantly ($P<0.001$) varied for the interaction of variety*location*year (Table 2). The tallest plant height of 430 cm followed by 410.8 cm was recorded at the Chanomile sub research substation during the 2018 and 2019 planting season for the variety Chelenko while the lowest plant height of 174.3 cm was at Aruba in 2019 for the variety NTJ_2. Ratoon crops' plant height was also significantly ($P<0.001$) varied among sorghum varieties. Dishkara (227.7 cm) recorded the highest plant height at Chanomile followed by A-2267_2 (203.9 cm) among other varieties while the lowest plant height was at Arguba for Rara (68.0 cm).

The plant height of the ratoon crops is presented in Table 3. Dhishakara variety recorded significantly ($P<0.05$) as the tallest ratoon crop (196.65 cm) among the sorghum varieties while the variety Rara recorded the shortest (110.45 cm). Moreover, the average plant height of main crops (264.3 cm) was greater than the ratoon crops (159.61 cm).

The plant height recorded in the present study is generally greater than the plant heights of sorghum varieties reported by other researchers where the plant heights of the main and ratoon crops were 147 and 129 cm, respectively (Hassan *et al*., 2015). Plant height contributes to and plays a great role in aboveground biomass accumulation (Halim *et al*., 2013). This may be due to the taller a plant, the higher the amount of light energy absorbed and the higher the rate of photosynthesis and consequently

the amount of assimilation produced by the leaves (Ngo, 2017). Some scholars reported a higher average plant height of ratoon crops (259 cm) than main crops (228 cm) (Vinutha *et al*., 2017) for 36 sorghum lines. That may be due to the variation among genotypes and other management options.

3.1.2. Leaf number

Chelenko variety at Chanomile site produced significantly (P<0.001) higher (17.13) main crop leaf number than others during 2019 followed by 14.8 leaves during 2018 (Table 2). NTJ_2 produced the lowest number (5.73) of main crop leaves at Arguba in 2018. The variety Chelenko at the Aruba site produced a higher (P<0.001) ratoon leaf number (10.73) compared to other varieties at both locations while variety NTJ_2 recorded the lowest ratoon leaf number (6.5) (Table 3). NTJ_2 produced the lower leaf number in both main and ratoon crops in the present study. Generally, the main crop produced a higher average leaf number than the ratoon crop. In agreement with our findings, a significant variation in leaf number per plant of 8.4 to 10.3 was reported by Afzal *et al*. (2013). The increment of leaf number after two consecutive cuttings reported by Afzal *et al*. (2013) disagrees with the findings of the present study. Environmental conditions determine the number of leaves ranging from 8 to 22 per plant (Plessis, 2008) and the results of our findings is included in this range.

3.1.3. Length and *width of a leaf*

The results of leaf length and width of sorghum varieties at the main and ratoon cropping system are presented in Tables 2 and 3, respectively. Variety NTJ_2 produced significantly (P<0.001) wider (11.03 cm) the main crop leaves at Chanomile site in 2018 while the similar variety gave narrower plant leaves of 6.2 cm at Arguba site in 2018. Dishkara variety demonstrated the longest (98.2 cm) leaves at Chamomile in 2018 among other experimental units. A lower leaf length of 50.87 cm was observed for the variety Konada at the Arguba site in 2019. Rara variety demonstrated wider ratoon crop leaf followed by Dishkara variety at Chamomile and Konoda variety at Chamomile and Arguba sites.

The leaf length and width of a given plant are important parameters that influence leaf area index and thus the productivity of the given plant (Krishnamurthy *et al*., 1974, Koester *et al*., 2014, Schrader *et al*., 2021). Some varieties like NTJ_2 in the present study demonstrating lower biomass yield with wider leaf concurs with the results of other researchers who stated crops having higher leaf area demonstrate higher quality while the biomass yield depends on the other factors (Weraduwage *et al*., 2015).

3.1.4. Number of tillers per plant

The results of tiller number are presented in Table 2 for main crops and in Table 3 for ratoon crops. The main crop tiller number per plant was significantly (P<0.001) higher (6.73) for variety Rara at Arguba site during the 2019 cropping season while the lower tiller number (1.53) was recorded from variety NTJ_2 at Chanomile site during the 2018 and 2019 production seasons. A higher ratoon tiller number was recorded from variety NTJ_2 (11.33) followed by the Rara variety (9.73) at the Aruba site while the lowest tiller number was recorded from the Konoda variety (2.07) at the Chamomile site.

In the present study, the tiller number was much higher in the ratoon crop (4.6) compared to the main crop (2.79), which is in line with the previous findings of (Vinutha *et al*., 2017) which the tiller number of the ratoon crop was about 5 while the main crop recorded tiller number of 3.

3.1.5. Internode length

The results of internodes of sorghum varieties are presented in Figure 3. There was a significant (P<0.01) variation of internode length among sorghum varieties in the main crop. Chelenko had wider internodes (16.73 cm) while Dishkara (8.4 cm), Konoda (8.4 cm) and NTJ_2 (9.53 cm) had the shortest internodes.

Internode length contributes to the dry biomass yield whereas varieties with the longer internodes gave higher dry biomass yield. The varieties with taller juicy stems with longer internodes are characterized as forage sorghum (Havilah, 2017). Generally, the internode lengths observed in the present study were relatively high compared to the previous reports where an internode length of 5 cm was reported (Kebrom *et al*., 2017).

Table 2: Growth performance of the main crop sorghum as influenced by variety, experimental years and locations

Year	Location	Variety	PH (cm)	LNPP	LW (cm)	LL (cm)	TNPP
2018	Chanomile	A_2267_2	335.3^{bcd}	12.87^{b-e}	8.68^{b-f}	89.1^{abc}	1.93^{cde}
		Chelenko	430.0^{a}	14.8^{ab}	9.66^{abc}	86.1^{a-d}	1.87^{cde}
		Dishkara	335.7^{bcd}	11.47^{d-h}	9.93^{abc}	98.2^{a}	2.2^{cde}
		Konada	398.6^{gh}	14.6^{abc}	9.95^{abc}	86.3^{a-d}	1.73^{de}
		NTJ_2	254.7^{ef}	10^{f-j}	11.03^{a}	93.0^{ab}	1.53^{e}
		Rara	255.4^{ef}	11.8^{c-g}	9.78^{abc}	85.47^{a-d}	2.47^{cde}
	Arguba	A_2267_2	259.3^{ef}	7.53^{jkl}	6.70^{fg}	62.93^{fgh}	2.33^{cde}
		Chelenko	386.1^{ab}	12.6^{b-f}	8.60^{b-f}	86.93^{a-d}	2.00^{cde}
		Dishkara	307.9^{cde}	9.27^{g-k}	8.02^{b-g}	88.47^{abc}	2.87^{cde}
		Konada	369.0^{abc}	10.27^{e-j}	9.13^{a-e}	87.67^{a-d}	2.27^{cde}
		NTJ_2	177.3^{gh}	5.73^{l}	6.20^{g}	63.2^{fgh}	2.33^{cde}
		Rara	227.9^{fgh}	8.53^{i-l}	8.45^{b-g}	84.13^{a-e}	2.6^{cde}
2019	Chanomile	A_2267_2	304.7^{de}	12.13^{b-f}	6.90^{efg}	71.53^{d-g}	2.47^{cde}
		Chelenko	410.8^{a}	17.13^{a}	9.40^{a-d}	84.47^{a-e}	2.80^{cde}
		NTJ_2	265.7^{ef}	10.13^{e-j}	9.13^{a-e}	79.4^{b-f}	1.53^{e}
		Rara	259.7^{ef}	13.47^{bcd}	10.07^{ab}	92.67^{ab}	2.67^{cde}
	Arguba	A_2267_2	239.2^{fg}	8.87^{h-k}	7.30^{d-g}	68.93^{efg}	2.47^{cde}
		Chelenko	306.2^{cde}	13.13^{bcd}	8.39^{b-g}	83.13^{a-e}	2.93^{cd}
		Dishkara	283^{def}	11.27^{d-i}	7.88^{b-g}	74.27^{c-g}	4.87^{b}
		Konada	182.6^{gh}	8.37^{jkl}	6.43^{fg}	50.87^{h}	2.08^{cde}
		NTJ_2	174.3^{h}	6.47^{kl}	6.93^{efg}	62.8^{gh}	3.20^{c}
		Rara	180^{gh}	8.07^{jkl}	7.71^{c-g}	74.13^{c-g}	6.73^{a}
Mean			264.3	9.94	7.76	73.1	2.79
P-value			<0.001	<0.001	<0.001	<0.001	0.019
$LSD_{0.05}$			62.84	2.84	2.27	16.5	1.36
CV%			14.5	17.4	17.8	13.7	30.1

PH = plant height, LNPP = leaf number per plant, LW = leaf width, LL = leaf length, TNPP = tiller number per plant, $LSD_{0.05:}$= least significant difference at $P < 0.05$, CV% = coefficient of variation

Table 3: Dry biomass yield and growth performance of ratoon crop as influenced by sorghum variety and location

Location	Variety	DMY t/ha	PH cm	TNPP	LL cm	LW cm	LNPP
Chanomile	A-2267_2	25.77^{b}	203.9^{ab}	2.8^{cd}	69.60	6.78^{bc}	9.8^{b}
	Chelenko	4.44^{de}	186.8^{bc}	2.27^{d}	71.70	7.35^{b}	9.93^{b}
	Dishkara	41.67^{a}	227.7^{a}	3.53^{cd}	80.70	7.52^{ab}	9.2^{b}
	Konada	3.56^{de}	156.1^{cd}	2.07^{d}	72.20	7.52^{ab}	9.0^{b}
	NTJ_2	15.06^{c}	155.5^{cd}	3.2^{cd}	61.90	6.97^{bc}	6.73^{c}
	Rara	16.47^{c}	152.9^{cd}	3.27^{cd}	69.30	8.19^{a}	9.13^{b}
Arguba	A-2267_2	3.53^{de}	145.5^{de}	5.2^{bc}	63.00	6.0^{d}	9.33^{b}
	Chelenko	5.39^{d}	186.6^{bc}	3.2^{cd}	61.50	6.3^{cd}	11.53^{a}
	Dishkara	5.7^{d}	165.6^{cd}	6.53^{b}	65.10	7.33^{b}	9.73^{b}
	Konada	3.56^{de}	156.1^{cd}	2.07^{d}	72.20	7.52^{ab}	9.00^{b}
	NTJ_2	2.34^{e}	110.6^{e}	11.33^{a}	45.10	4.95^{e}	6.27^{c}
	Rara	2.5^{e}	68.0^{f}	9.73^{a}	58.90	5.97^{d}	6.60^{c}
LSD0.05		2.42	37.82	2.596	NS	0.76	1.54
Main effect variety	A-2267_2	14.65^{b}	174.7^{ab}	4.00^{cd}	66.3^{ab}	6.39^{cd}	9.57^{b}
	Chelenko	4.92^{d}	186.7^{a}	2.74^{de}	66.6^{ab}	6.83^{bc}	10.73^{a}
	Dishkara	23.68^{a}	196.65^{a}	5.03^{bc}	72.9^{a}	7.43^{a}	9.47^{b}
	Konada	3.56^{d}	156.1^{bc}	2.07^{e}	72.2^{a}	7.52^{a}	9.0^{b}
	NTJ_2	8.7^{c}	133.05^{cd}	7.27^{a}	53.5^{c}	5.96^{d}	6.5^{d}
	Rara	9.48^{c}	110.45^{d}	6.5^{ab}	64.1^{b}	7.08^{ab}	7.87^{c}
LSD0.05		1.17	26.74	1.84	7.61	0.54	1.09
CV%		13.2	14	31.3	9.6	6.5	10.3

DMY= dry biomass yield, PH = plant height, TNPP = tiller number per plant, LL = leaf length, LW = leaf width, LNPP = leaf number per plant, $LSD_{0.05}$ =: least significant difference at P<0.05, CV% = coefficient of variation

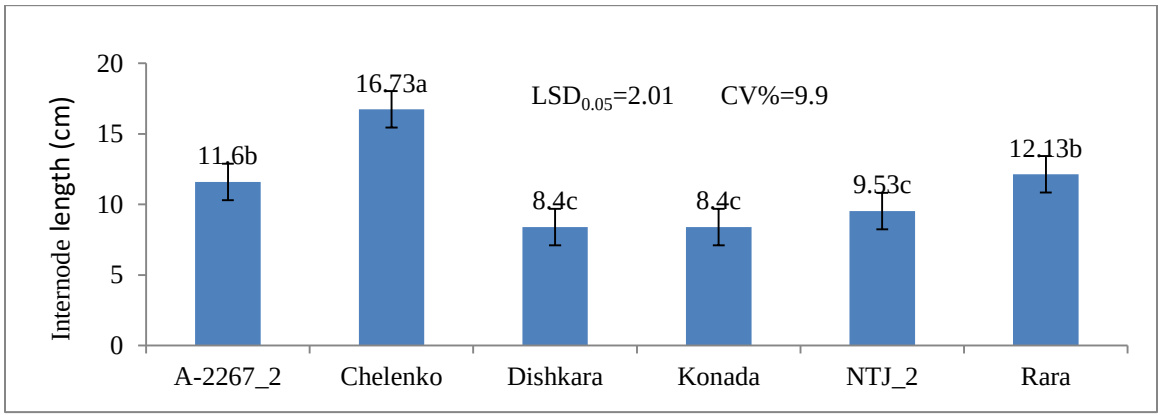

Figure 3: Internode length of the main crop as influenced by sorghum varieties

3.2. Grain yields

The mean values of grain yields for sorghum varieties are presented in Figure 4. Grain yield was significantly (P<0.01) varied among sorghum varieties. Variety NTJ_2 (3.89 t/ha) followed by Konada (3.77 t/ha) demonstrated the highest grain yield than other varieties while variety Chelenko (1.74 t/ha) gave the lowest yield. Grain yields of A-

2267_2, Chelenko, Dishkara and Rara were not varied significantly. Varieties in the present study producing higher dry biomass yield gave lower grain yield and vice versa. For example Konoda and NTJ_2 demonstrated higher grain yield with lower dry biomass yield than other varieties in the test. This result is in agreement with the findings of Borghi *et al*. (2013) where sorghum dry biomass yield was reduced by increased grain yield. The extent of grain yields of dual purpose sorghum varieties recorded in the present study was in line with findings of other researchers (Mahfouz *et al*., 2015). Sorghum varieties used in the present study generally gave relatively higher mean grain yield (2.58 t/ha) compared to reports for dual purpose sorghum genotypes, which recorded grain yield of 0.62 t/ha in winter and 0.55 t/ha in summer production (Hassan *et al*., 2015).

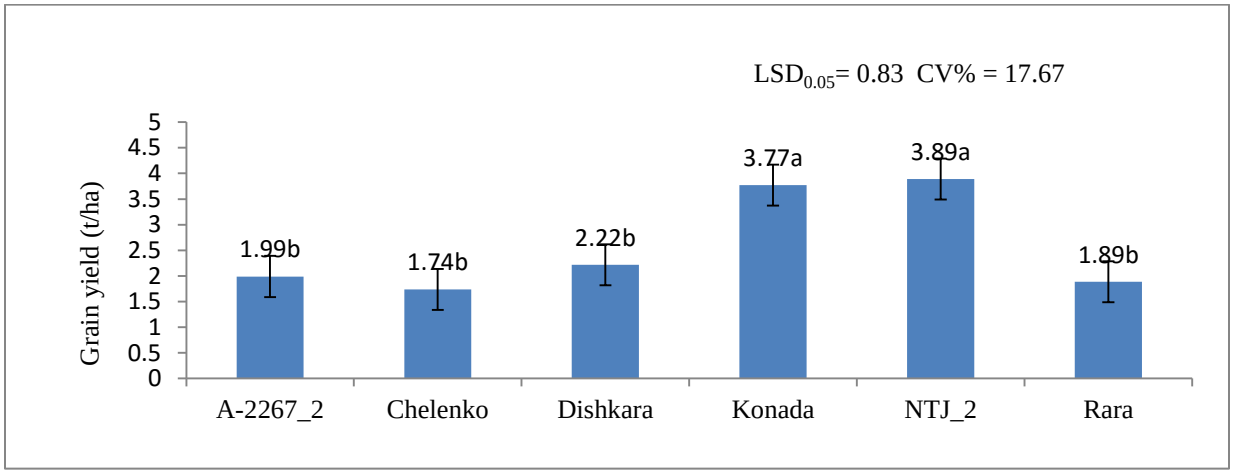

Figure 4: Grain yield of sorghum main crop as influenced by different varieties

3.3. Dry biomass yield

The results of dry biomass yield of ratoon and main crops of sorghum varieties are presented in Table 3 and 4, respectively. Dry biomass yield of the main crop was significantly (P<0.001) different among sorghum varieties, location and years. The highest main crop dry biomass yields were recorded by Chelenko variety at Arguba site during the 2018 growing season (42.2 t/ha) and at Chanomile site during the 2019 (38.41 t/ha) and Rara variety at Chanomile site during the 2019 (37.33 t/ha), which were statistically similar. The lowest dry biomass yield the main crop was recorded by variety Konoda grown at Arguba site during the 2019 growing season (Table 4).

Dry biomass yields of ratoon crop harvested at 105 days after main crop were significantly (P<0.001) varied among varieties and locations. Variety Dishkara demonstrated the highest total (dry biomass yield of main crop + ratoon crop) dry biomass yield (41.67 t/ha) at Chanomile site while Rara (2.5 t/ha) and NTJ_2 (2.34 t/ha) varieties recorded the lowest dry biomass yields at Arguba site (Table 3).

As indicated in Figure 5, Dishkara variety produced significantly (P<0.05) higher total (yield of main crop + ratoon crop) dry biomass yield (45.3 t/ha) followed by Chelenko variety (33.3 t/ha) while the lowest dry biomass yield was obtained from Konada variety (18.5 t/ha).

Ratoon crops are very important for contribution of dry lowland forage production system where dual purpose sorghum varieties could generate both grain and forage production. Forage dry biomass yield parameter is important agronomic trait in forage crops production (Lauer, 2006), especially for the production of dual purpose sorghum varieties (Chen *et al*., 2020). The higher dry biomass yields in the main crop than in the ratoon could be associated to the change in seasonal conditions for growth of the crops and probably depletion of nutrient levels in the soil (Vinutha *et al*., 2017). To boost the production it needs the amendment of the nutrient depletion during

the harvesting of main crops and ratoon crops (Afzal *et al*., 2013).

Table 4: Dry biomass yield of sorghum main crop as influenced by variety, experimental year and location

Sorghum varieties	Chanomile site		Arguba site	
	2018	2019	2018	2019
A-2267_2	12.42g	24.51cd	24.00cde	7.59ghi
Chelenko	22.55c-f	38.41ab	42.20a	10.29gh
Dishkara	18.87f	-	35.94b	10.04ghi
Konada	19.12ef	-	20.57def	5.08i
NTJ_2	9.13ghi	26.00c	10.37gh	6.57hi
Rara	12.03g	37.33ab	24.12cde	7.66ghi
Mean	15.69	21.04	26.2	8.26
$LSD_{0.05}$	5.04			
CV%	17.30			

Means with common letter (s) are not statistically different (P.0.05), $LSD_{0.05}$ = Least Significant Difference at P < 0.05, CV% = coefficient of variation

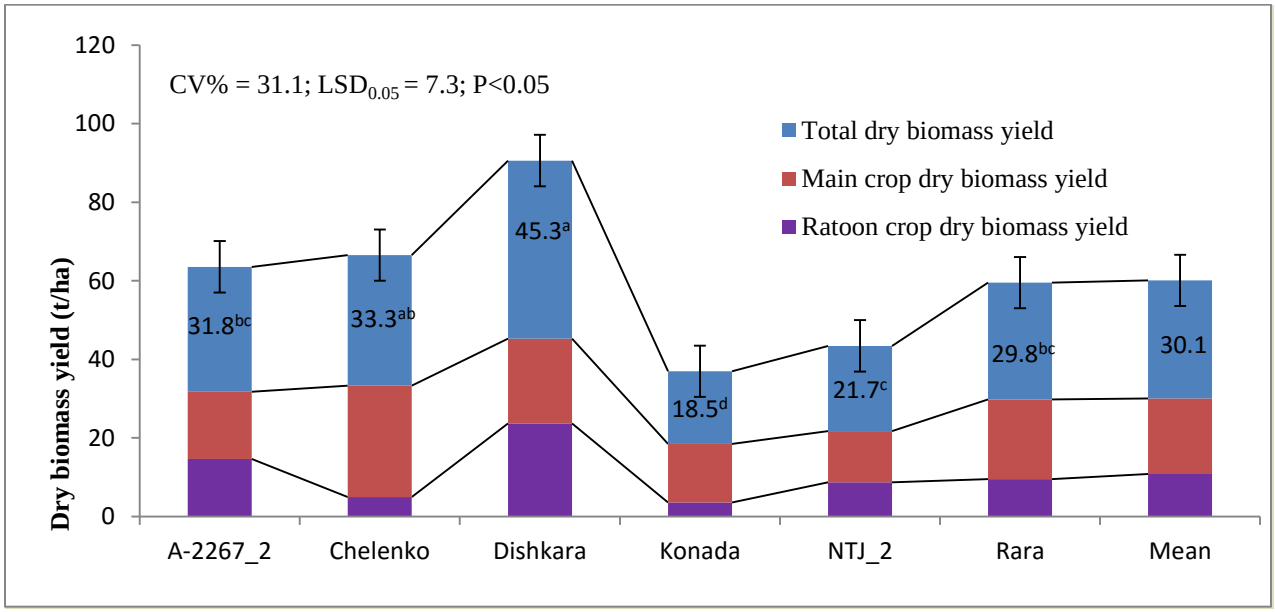

Figure 5: Dry biomass yields of sorghum varieties used in the present study

3.4. Incidence, severity and AUDPC of Anthracnose

The incidence, severity and AUDPC were significantly (P < 0.05) varied among the tested sorghum varieties at Chanomile and Arguba districts in the 2018 and 2019 cropping season (Table 5). In Chanomile site, the highest mean anthracnose incidences of 98.90 and 100% were recorded from A-2267_2 variety grown during the 2018 and 2019 cropping seasons, respectively. Similarly, highest anthracnose severity of 43.67 and 40.36% and AUDPC of 860 and 1085.27%-days) were recorded from the same variety grown at Chanomile site during the 2018 and 2019 cropping seasons, respectively. The lowest mean anthracnose incidence, severity and AUDPC were recorded from Konada variety during the 2018 growing season. Similarly, the lowest incidence, severity and AUDPC were recorded from variety Rara grown at Chanomile site in 2019.

At Arguba site, the highest mean anthracnose incidence (100%) was noticed from genotype A-2267_2 in 2018, while in 2019 the highest mean anthracnose incidence (100%) was recorded from A-2267_2 and NTJ_2 varieties. The lowest mean anthracnose incidence was noted from Rara (61.15%). The highest mean anthracnose severity was recorded from the varieties A-2267_2 (32.02%), NTJ_2 (31.98%) and Dishkara (26.81%) in 2018, while in 2019 the highest mean anthracnose severity was noted from all varieties except for Konada and Rara varieties. The highest value of AUDPC at Arguba site was recorded from the variety A-2267_2 (829.92%-days) followed by NTJ_2 (741.55%-days) and (Dishkara 703.13%-days) during the 2018 growing season, while the highest mean AUDPC values were observed from the varieties A-2267_2 (734.23%-days), Dishkara (696.22%-days) and NTJ_2 (724.15%-days) during the 2019 growing season.

Anthracnose is the most severe and distressing sorghum disease in terms of dry biomass and grain yields in the study areas (Getachew *et al*., 2021). The plant disease epidemic development is highly affected by availability of optimum temperature, relative humidity, host tissue, levels of host resistance, and other factors during the growing periods of the crop (Campbell and Madden, 1990).

Table 5: Incidence, severity and AUDPC of sorghum varieties to Anthracnose at different sites during the 2018 and 2019 main cropping seasons

Sorghum varieties	Chanomile						Arguba					
	2018 cropping season			2019 cropping season			2018 cropping season			2019 cropping season		
	PDI_f (%)	PSI_f (%)	AUDPC (%-days)	PDI_f (%)	PSI_f (%)	AUDPC (%-days)	PDI_f (%)	PSI_f (%)	AUDPC (%-days)	PDI_f (%)	PSI_f (%)	AUDPC (%-days)
A-2267_2	98.90a	43.67a	840.00a	100a	40.36a	1085.27a	100a	32.02a	829.92a	100a	31.22a	734.23a
Chelenko	83.08b	26.67bc	583.33bc	91.88ab	31.33a-c	671.49bc	67.28bc	24.60b	576.33d	90.78a	25.29ab	537.44b
Dishkara	83.08b	27.22bc	711.67a-c	-	-	-	76.28bc	26.81ab	703.13bc	95.18ab	28.84a	696.22a
Konada	77.14b	20.00c	560.00c	-	-	-	75.05bc	19.70b	553.28d	78.85c	19.20b	507.77b
NTJ_2	82.67b	31.11b	750.56ab	93.50ab	34.77ab	863.80b	81.13ab	31.98a	741.55ab	100a	30.88a	724.15a
Rara	79.78b	30.56b	617.83bc	75.34c	29.13bc	592.87c	61.15c	23.43b	599.86d	86.64bc	26.43b	575.60b
P-value	< 0.05	< 0.001	< 0.05	< 0.05	< 0.05	< 0.05	< 0.05	< 0.05	< 0.001	< 0.05	< 0.05	< 0.001
Grand mean	84.11	29.87	703.56	90.18	33.89	803.36	76.81	26.42	667.34	91.91	26.98	629.23
LSD (0.05)	13.09	10.35	172.42	13.87	10.01	208.48	19.48	7.23	115.58	11.41	7.00	117.69
CV (%)	8.75	19.49	13.78	8.80	17.76	15.25	14.26	15.40	9.73	6.98	14.59	10.51

Means following with the same letter(s) in a column are not significantly different ($P \leq 0.05$) PDI_f = Percent disease incidence at final date; PSI_f = Percent severity index at final date; AUDPC = area under disease progress curve; LSD = least significant difference at a 5% probability level; and CV = coefficient of variation

3.5. Correlation analysis of growth and yield parameters as influenced by sorghum variety, location and years

The correlation of yields (dry biomass and grain) with growth and disease assessment parameters for main and ratoon crops are presented in Tables 6 and 7, respectively. Dry biomass yield of main crops was positively correlated with plant height, tiller number leaf length, leaf number, and internodes. The correlation of dry biomass yield was significantly ($P<0.001$) strong with internodes (0.946) of main crops. Tiller number and leaf length of the main crop had weak relationship with dry biomass yield of sorghum varieties. Day biomass yield of the main cropping season was negatively correlated (-0.785) with grain yield. Dry biomass yield of main crop was the function of internodes of the stem in the present study.

Dry biomass yield of ratoon crops was positively correlated with plant height (0.426), tiller number (0.32), leaf length (0.271), leaf width (0.113), and leaf number (0.088). The positive correlation of biomass yield of ratoon crop with area under disease progress curve showed anthracnose disease not affected the growth and development of ratoon crops in this study. Positive correlation of parameters either for main or ratoon crops of sorghum varieties indicates that, selection on any one of the traits will increase in the other traits, thereby improving biomass yield in sorghum. Similar finding with the present result was reported by other scholar for fifteen genotypes of sorghum (Naharudin *et al*., 2021). The phenotypic correlation of plant height of sorghum varieties with biomass yield was reported as 0.349 (Narkhede and Seeds, 2020) while the correlation of plant height for the present study was as higher as 0.804 for main crop and 0.426 for ratoon crop.

Positive association of dry biomass yield with plant height and tiller number for main and ratoon crops was reported previously as plant height and tillering were contributing to forage yield (Bhat, 2019). The association of dry biomass and grain yields with growth parameters was also supported by another findings on sorghum production (Madhusudhana, 2019).

Table 6: Relationships of growth, yield and disease parameters of main crop of sorghum as influenced by variety, location and year

	DMY	PH	TNPP	LL	LNPP	Internodes	GY	AUDPC
DMY	1							
PH	0.804	1						
TNPP	0.019	-0.419	1					
LL	0.387	0.175	-0.394	1				
LNPP	0.67	0.839*	-0.695	0.591	1			
Internodes	0.946**	0.851*	0.077	0.128	0.616	1		
GY	-0.785	-0.491	-0.069	-0.332	-0.426	-0.648	1	
AUDPC	-0.223	-0.141	0.3	-0.733	-0.542	-0.156	-0.093	1

Table 7: Relationships of growth, yield and disease parameters of ratoon crop of sorghum as influenced by variety, location and year

	DMY	PH	TNPP	LL	LW	LNPP	AUDPC
DMY	1						
PH	0.426	1					
TNPP	0.32	-0.585	1				
LL	0.271	0.586	-0.707	1			
LW	0.113	0.239	-0.492	0.878*	1		
LNPP	0.088	0.796	-0.801	0.728	0.436	1	
AUDPC	0.562	0.269	0.287	-0.28	-0.633	-0.078	1

PH = plant height, TNPP = tiller number per plant, LL= leaf length, LNPP = leaf number per plant, GY = grain yield, AUDPC = area under disease progress curve, DMY = dry biomass yield

4. Conclusion and Recommendations

Plant height, leaf number, tiller number, and dry biomass and grain yield variations for main and ratoon crop sorghum varieties under anthracnose stress at Arguba and Chanomile sites were observed during the 2018 and 2019 cropping season. Chelenko variety exhibited higher plant height for main crops while Dishkara for ratoon crops. Anthracnose disease affected more the grain yield than dry biomass yield. Dishkara variety recorded 45.3 t/ha total biomass yield, which is about 33.6% more yield compared to the overall mean value (30.1 t/ha) followed by Chelenko variety which gave about 9.6% more total biomass yield. The variety Konoda recorded the lowest total dry biomass yield (18.5 t/ha), which was reduced by 40% compared to the mean value. Dry biomass yield of main crop had positive association with plant height, leaf number per plant, leaf length and tiller number per plant and negative association with grain yield. While the dry biomass yield of ratoon crop had positive association with all parameters. The correlation analysis result indicated that anthracnose disease didn't affect the ratoon yield. Under anthracnose stressed areas of Arba Minch, Dhirashe and areas with similar agro-ecologies, the varieties Dishkara and Chelenko for dry biomass yield production and variety NTJ_2 for grain production could be recommended.

Acknowledgement

Highly acknowledge Southern Agricultural Research Institute (SARI) and Arba Minch Agricultural Research Center for technical and financial support. Getinet Kebede is duly thanked for data collection and field management.

Conflict of interest

Authors declare no conflict of interest.

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Yield Response and Nutrient use Efficiencies of Maize (*Zea mays* L.) As Determined through Nutrient Omission trial in Jimma Zone, Southwestern Ethiopia

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Received: March 22, 2022 Accepted: June 2, 2022

Abstract: *Appropriate fertilization based on actual limiting nutrients and crop requirements is economic and judicious for sustainable crop production. A field experiment was conducted to identify yield-limiting nutrients, to determine yield response, nutrient uptake and use efficiencies of maize (Zea mays L.) through nutrient omission technique in the Nitisols of Omo Nada District Southwestern Ethiopia for one cropping season (2019/20). The experiment was laid out in Randomized Complete Block Design with four replications. The treatments were control, NP, PKS (-N), NKS (-P), NPS (-K), NPK (-S), NPKS, NPKSZn (-B), NPKSB (-Zn) and NPKSZnB. One composite soil sample was collected from an experimental plot at a depth of 0-20cm before treatment application and analyzed to estimate the inherent N, P, K, S, Zn and B supplying capacity of the soil. Grain and straw samples were collected to determine N, P, K, S, Zn and B contents. Maize yield and yield components, nutrient uptake and agronomic efficiencies of maize were subjected to ANOVA using SAS 9.3 software. The LSD test was used to separate means at a 5% level of significance. The results of soil showed moderately acidic, sandy clay loam texture, low total N, available P and medium in K, S, Zn, B, OC, OM and CEC. Grain yield and yield components, nutrient uptake and agronomic efficiency of each nutrient were significantly affected due to nutrient omitting. Accordingly, the highest grain yield response of maize (5909.1kg ha^{-1}) was obtained from N fertilized plots indicating N was the most yield-limiting nutrient. Owing to the magnificent yield response to N fertilizer in the current study, proper management of N is very essential for the intensification of maize productivity. The maximum total nutrient uptake of N (87.38), P (40.40), K (114.95), S (22.22), Zn (2.67), B (0.28) and agronomic efficiencies of N (55.6), P (166.9), K (166.9), S (333.7), and Zn (1359.8) was obtained from integrated use of macronutrients (NPKS) with Zn.*

Keywords: Agronomic efficiency, Nutrient combination, Nutrient recovery, Nutrient uptake

5. Introduction

Soil nutrient depletion and inadequacy of current fertilizer recommendations due to ignoring soil fertility status and excluding major nutrients other than nitrogen (N) and phosphorus (P) from the recommended dose continuously decreased soil quality and crop production. In most areas, nutrients available in soil are rarely present in adequate amounts and are most probably of unbalanced proportion to meet the nutrient requirements of crops. To increase productivity and subsequently improve food security in Ethiopia, it is imperative to identify soil nutrients limiting maize growth and production. The national soil inventory data (EthioSIS, 2013) also revealed that in addition to N and P, sulfur (S), boron (B) and zinc (Zn) deficiencies are widespread in Ethiopian soils in general and in Southwestern parts of Ethiopia in particular. Therefore, future gains in food grain production will be more difficult and expensive considering the increasing problem of multi-nutrient deficiencies unless immediate action is taken.

Maize (*Zea mays* L.) is one of the most important staple food crop in Ethiopia and its production and consumption have grown widely across regions. However, current average yield is 3944 kgha^{-1} (CSA, 2017), which is much lower than its yield potential. The deficiency of essential elements has been implicated to limit the uptake of the nutrients, growth and yields of crops. In Ethiopia, regional

fertilizer recommendations have been developed for maize which is slightly region-specific excluding the nutrient status of the soil Wakene *et al.* (2011). Yet cropping systems, management practices, soil type, fertility status, climatic conditions and other factors governing yield response to nutrients vary considerably in space and time Kiara *et al.* (2016). Due to such localized differences in crop growing conditions and the soils' indigenous nutrient supply capacity, grain yield and nutrient use efficiencies vary across maize producing regions of the country Tesfaye *et al.* (2019).

Recognition of this variability has prompted many researchers to consider managing this variability. Research that aims to improve soil fertility management and productivity of small-scale farmers has to reckon with soil variation by identifying the most limiting nutrient elements and coming up with flexible recommendations rather than blanket recommendations. Flexible recommendations could be based on variations in soil characteristics that affect productivity and yield responses. Thus, the nutrient omission technique (all the other nutrients are supplied other than the nutrient in question) is a useful tool to quantify soil nutrient supply capacity and to identify yield-limiting nutrients in a given area. Therefore, this experiment was conducted (i) to identify the most yields limiting nutrient for maize (ii) to determine the yield response of maize through the nutrient combination (iii) to determine maize nutrient uptake and agronomic efficiencies of N, P, K, S and Zn in Omo Nada District, Jimma Zone.

6. Materials and Methods

6.1. Description of the study areas

The experiment was conducted on farmers' fields in Nitisols of Goroseden Kebele, Omo Nada District South-western Ethiopia during the main cropping season (2019/20). The experimental site was selected systematically to cover a wide range of major maize growing areas in the district. Geographically, the experimental site was located between 070 40' 09 3" N latitude, 0370 14' 41.5" E longitudes and an altitude of 1750 meters above sea level. According to the data from Jimma Meteorological Station (2019), the average minimum and maximum temperature and mean annual rainfall of the experimental sites were 12.64 °C, 28.36 °C and 1198 mm, respectively. The predominant soil type of the study area, in particular, is Nitisols which have a reddish colour with moderately acidic in reaction. On average, the soil is deep and highly weathered well-drained, sandy clay in texture and strong to moderately acidic in a reaction as reported by Wispelaere *et al.* (2015).

6.2. Soil sampling and laboratory analysis procedures

One representative composite soil sample (0-20cm depth) was collected using an auger before treatment application. The collected sample was analyzed for soil pH, organic carbon (OC), total nitrogen (TN), available phosphorus (Av. P), available potassium (K), available sulfur (S), cation exchange capacity (CEC), and micronutrients (B and Zn) at Jimma Soil and Tissue Analysis Laboratory based on procedures described in Van Reeuwijk (2006). The pH-H_2O was measured at 1:2.5 soils to solution suspension using a pH meter. The Walkley and Black method functioned to determine the OC content while the Kjeldahl method was employed to determine total nitrogen Bremner and Mulvaney (1982). Available P was determined using the Bray II method by Bray and Kurtz (1945). Available S, B, and Zn and exchangeable K of the soil were extracted by the Mehlich-III multi-nutrient extraction method Mehlich (1984) and measured with their respective wavelength range by Inductively Coupled Plasma Optical Emission Spectrometer.

6.3. Treatments and experimental design

Ten treatments of different rates of six single nutrients ($N_{120,}$ $P_{40,}$ $K_{40,}$ $S_{20,}$ Zn_5 and $B_{2.5}$ kg ha^{-1}) were used in the present study. Each fertilizer rate was set based on the recommendation given by Tesfaye *et al. (*2019) and the rate of each nutrient indicated in Table 2. Even though farmers are not growing maize without fertilizer, control treatment was included for comparison among the rest of the treatments. The treatments were laid out in a randomized complete block design in four replications. The gross plot area was 18 m^2 (6 m x 3 m), which accommodated 8 rows and 10 plants per row while the net plot area was 10.8 m^2 (4.5 m x 2.4 m).

Table 1: Soil Physicochemical properties of experimental site before treatment application

Soil Properties	Value	Rating	Reference
pH (1:2.5 H_2O)	5.40	Moderately acidic	Tekalign, 1991
Soil BD (g cm^{-3})	1.23	Optimum	Hunt and Gilkes,1992
CEC (cmol(+)Kg^{-1})	16.06	Medium	Hazelton and Murphy, 2007
Total N (%)	0.18	Medium	Tekalign, 1991
Available P (mg kg^{-1})	8.18	Low	FAO, 2008
Available K (mg kg^{-1})	249.62	High	Horneck *et al.* (2011)
Available S (mg kg^{-1})	6.10	Medium	Horneck *et al.* (2011)
B (mg kg^{-1})	0.61	Medium	Horneck *et al.* (2011)
Zn (mg kg^{-1})	1.47	Marginal	Jones, 2003
OC (%)	2.83	Medium	Tekalign, 1991
OM (%)	4.88	Medium	Tekalign, 1991
Sand (%)	60	Soil Textural Class: Sandy clay loam, which is ideal	Onwueme and Sinha, 1991
Silt (%)	5		
Clay (%)	35		

Table 2: Treatments used in the present study

Treatments	N (kg ha^{-1})	P (kg ha^{-1})	K (kg ha^{-1})	S (kg ha^{-1})	Zn (kg ha^{-1})	B (kg ha^{-1})
T_1 = Control	0	0	0	0	0	0
T_2 = NP	120	40	0	0	0	0
T_3 = PKS (-N)	0	40	40	20	0	0
T_4 = NKS (-P)	120	0	40	20	0	0
T_5 = NPS (-K)	120	40	0	20	0	0
T_6 = NPK (-S)	120	40	40	0	0	0
T_7 = NPKS	120	40	40	20	0	0
T_8 = NPKSZn (-B)	120	40	40	17.6	5	0
T_9 = NPKSB (-Zn)	120	40	40	20	0	2.5
T_{10} = NPKSZnB	120	40	40	17.6	5	2.5

6.4. Experimental materials and planting procedures

High yielding (BH-661) maize variety was used as a test crop in the study, which was released from Bako Agricultural Research Center. The variety is popularly accepted and grown by farmers. The full doses of all fertilizers in the respective treatments except the nutrient to be omitted were applied at planting. Urea was applied in splits where the half rate at planting and the remaining half rate was applied (3-4 weeks after planting) when the plant attains at knee height stage. Urea, Triple Super Phosphate (TSP), Murata of Potash (KCl), Calcium Sulfate ($CaSO_4.2H_2O$), Zinc Sulfate ($ZnSO_4.7H_2O$) and Borax ($Na_2B_4O_7.5H_2O$) were used as sources of N, P, K, S, Zn and B, respectively. All cultural practices were done uniformly for all treatments, as per the recommendation for maize production in the area. Harvesting was done manually from the net plot area when the crop physiologically matured.

6.5. Data collection

6.5.1. Maize yield and yield components

Data on a plant basis was recorded from the six central harvestable rows (3.75mx2.4m=9m^2). The collected data include leaf area index (LAI), grain yield, ear length, number of kernel rows cob^{-1}, number of kernels cob^{-1} and biomass yield. The LAI was calculated as the ratio of the total leaf area of ten plants (cm^2) per area of land occupied by these plants. Cob length was measured from ten randomly selected cobs per plot at harvesting and the average value was recorded for each plot. The number of kernel rows cob^{-1} was counted from ten randomly selected ears and the average value was recorded for each plot. The number of kernels cob^{-1} was determined by counting the number of kernels cob^{-1} from ten randomly taken cobs and the average value was registered. Grain yield (economic yield) was determined from the entire net plot and converted into kilogram per hectare where the actual grain yield was adjusted to 12.5% moisture level, which is the standard moisture content of cereal crops. Above-ground biomass (Biological

yield) was measured from the weight of above-ground biomass for plants in a net plot area and converted to kilogram per hectare. Harvest Index (%) was determined as a ratio of grain yield to above-ground biological yield on a dry weight basis in percentage Singh and Stoskopf (1971) as described in the following formula.

$$\text{HI} = \left(\frac{Grain\ yield}{Above\ ground\ biomass}\right) * 100 \quad [1]$$

6.5.2. Determination of agronomic efficiency

Agronomic efficiency (AE) refers to the additional produce obtained in kg kg^{-1} of an applied nutrient which was calculated using the formula of Fageria *et al.* (2010) as follows:

$$\text{AE} = \frac{Grain\ yield\ (fertilized\ plot) - Grain\ yield\ (no\ fertilizer)}{Fertilizer\ applied\ kg/ha} \quad [2]$$

6.5.3. Apparent nutrient recovery efficiency

The apparent nutrient recovery efficiency of nutrients was determined as the quantity of nutrient uptake per unit of nutrient applied then finally changed to a percentage using the formula indicated below [3]. Grain and straw samples were collected randomly from the net plot area during harvesting from each plot and bulked over replication to determine N, P, K, S, and Zn contents.

$$ARE\ (\%) = \frac{(Nf - Nu)}{Na} x100 \quad [3]$$

Where

ARE = Apparent nutrient recovery efficiency

Nf = total nutrient uptake (grain plus straw) of the fertilized plot (kg ha^{-1})

Nu = total nutrient uptake (grain plus straw) of the unfertilized plot (kg^{-1})

Na = quantity of nutrient applied (kg ha^{-1})

6.6. Data Analysis

The collected data were subjected to analysis of variance (ANOVA) appropriate to RCBD using SAS Institute (2012) 9.3 version software and the interpretations were made following the procedure described by Gomez and Gomez (1984). The least significant difference (LSD) test at a 5% probability level was used for treatment mean comparison when the ANOVA showed significant differences among treatments.

7. Results and Discussion

7.1. Grain yield response of maize to different nutrients

7.1.1. Nitrogen

Compared with tested nutrients highest grain yield response was obtained from the application of 120 kg ha^{-1}N indicating N is the most yield-limiting essential plant nutrient for maize production hence it needs special attention. This condition happened whenever the soil contains appropriate moisture because soil moisture is the solvent and medium of nutrient transport to the absorbing root zoon and plays a key role in influencing crop response to fertilizer application. This might be attributed due to the availability of N forms in the soil solution owing to sufficient soil moisture. When the soil contains optimum moisture there is high water flux both of which increase the mass flow of N ions to the root surface enhancing N uptake since mass flow rate is a function of both water flux in the root rhizosphere and nutrient concentration in the soil solution. The current result was in agreement with the findings of Tesfaye *et al.* (2019), who reported that the maximum yield response was recorded from plots treated with 120 kg ha^{-1} nitrogen.

7.1.2. Phosphorous

Yield response to P was significantly higher at a rate of 40 kg ha^{-1} however, not as high as the yield response to N application and such a lesser yield response to P application can be attributed due to the P fixing nature of the weathered Nitisols and calcareous soils of the high rainfall areas. In areas having appropriate moisture conditions, a higher fraction of available P goes to the soil solution and is hence transported to the root surface via diffusion since the rate of diffusion depends on both water availability in the root rhizosphere and the concentration of the nutrient ions in the soil solution. The current result was in line with the finding of Tesfaye *et al.* (2019) who reported that the maximum yield response was obtained from plots treated with 40 kg ha^{-1} P.

7.1.3. Potassium

Concerning K, 1470.8 kg ha^{-1}maize grain yield response was recorded when supplying 40kg ha^{-1}K even though the response was not as higher as compared to NP. The result showed that to increase the production of cereal crops including maize, increasing the appropriate use of all essential nutrients containing K is an option. Since plant growth and crop production require an adequate

supply and balanced amounts of all nutrients to maximize productivity by optimizing the plant nutrient uptake, adding K fertilizer can increase fertilizer use efficiency and grain yield for different cereal crops. Therefore, improving the nutrient content of the fertilizer that fits the needs of the crops is required to improve the productivity of maize due to the presence of synergetic interaction of K with macronutrients (N and P) and micronutrients (Zn) but it has antagonistic interaction with B which was in confirmed with the finding of Malakouti (2008).

7.1.4. Sulfur

The remarkable grain yield response to the application of S cannot attribute compared to other major macronutrients. This might be due to the presence of magnesium and calcium that hides the effects of sulfur as supported by Sumner (1981). However, the result of pre-planting soil samples showed that soil S content as medium critical soil sulfur level of 6.10 mg kg^{-1}, which may confirm that the grain yield response is less likely due to S application compared to other major macronutrients.

7.1.5. Micronutrients (Zn, B)

The grain yield response due to micronutrients especially (Zn) was observed even if it is not as remarkable as compared with macronutrients. However, the application of B does not give a yield response, which might be the presence of an optimum level of B in the soil. Thus, the grain yield response could be due to Zn application since the Zn content of all fields was below the critical level (1.5 mg kg^{-1}) soil as suggested by Horneck *et al*. (2011) for maize. However, there is need for a further study to understand the impact of each of the secondary macronutrients and micronutrients on maize production.

7.2. Effects of nutrient omitting on yield and yield components of maize

7.2.1. Growth parameters

Leaf area index values ranged from 2.3 to 4.6, recording the lowest value from control while the maximum from the application of (NPKSZn). The reason for an increase in LAI might be due to the development of more expanded leaves produced in response to the balanced application of nutrients that enhanced vegetative growth. This showed that the balanced application of mineral nutrients on maize increased leaf size (to maximize light interception) and maximize the overall plant economy of the crop. Fertilization of balanced nutrients to crops up to optimum level helps efficient utilization of nutrients that leads to high photosynthetic productivity and accumulation of high dry matter. This ultimately increases plant growth and development, which may result in improved yield attributes like leaf length and leaf size, thereby increasing production as supported by (Mikos-Szymańska, 2018). The result was in line with the finding of Kumar *et al.* (2005).

The ANOVA result showed that fertilizer treatments had a highly significant effect ($P < 0.01$) on the number of rows cob^{-1}. The highest number of rows cob^{-1} (14.0) was recorded from the application of NPKSZn while, the lowest (12.9) was obtained from the control, N and P-omitted plots (Table 3). Application of major macronutrients (NPKS) in combination with micronutrients (Zn) increased the number of rows cob^{-1} by 8.5% compared to control, N and P-omitted plots. In agreement with this result, Adediran and Kogbe (2003) reported that maize production depends mainly on the availability of essential nutrients. On the other hand, there was no significant difference observed between numbers of rows cob^{-1} due to the application of B indicating B did not bring a significant difference, which might due to the presence of a medium quantity of B in the soil of study sites.

The maximum cob length (20.0cm) was obtained from the application of NPKSZn, which is statistically at par with plots treated with NPK (19.3cm), and NPKS (19.98cm), NPKSB (19.6cm) and NPKSZnB (19.6cm). The minimum cob length (12.5cm and 12.8cm) was obtained from control and N-omitted plots respectively. The highest ear length development might be due to an increase in photosynthetic activities on the account of an adequate supply of N and P. The current result was in agreement with the finding of Ahmad *et al.* (2018) who reported that a significant increase in cob length with increased rates of N and P. Nitrogen is required for ear growth if the soil is nourished through mineral fertilizer which had an impact on yield. To do so the maximum assimilates supply should be available during maize grain filling with a split application of N Arif *et al.* (2010). Moreover, when the environmental condition allows for optimum utilization of solar

radiation, there is higher assimilation production and its conversion to starches results in higher cob length as reported by Derby *et al.* (2004).

The highest number of grains of cob-1 (589.8) was recorded from the application of NPKSZn, while the lowest number (355.5) was obtained from the control (Table 3). Application of NPKSZn increased the number of grains per row by65.9%, 58.8% and 16.8%, over control, N-omitted and NP, respectively. This might be due to an increase in the number of grains row^{-1}, ear length and a number of rows cob^{-1} with higher and balanced fertilization. The optimum availability of synthetic fertilizers, which might boost growth indices and consequently increase ear length as reported by Chapagain and Gurung (2010) which produced more grains cob^{-1}. The current result confirmed the findings of Redai *et al.* (2018) who reported that the maximum grain was recorded from the application of macronutrients (NPK) in combination with Zn.

The highest ear diameter (4.7cm) was recorded from the application of NPKS, which was statistically at par with NPK, NPKSZn and NPKSZnB treated plots (Table 3). On the other hand, the lowest cob diameter (4.1cm) was recorded from the control. The availability of essential nutrients from NPKS leads to improved cell activities, enhanced cell multiplication, enlargement and luxuriant growth. The result was in agreement with the finding of Baharvand *et al.* (2014) who reported that the ear diameter of maize increased due to the increasing rate of chemical fertilizers.

The highest HI (47.2%) was recorded from the application of NPKSZnB which was statistically at par with the value obtained from the application of NPKSB (47%). The lowest HIs (37.3% and 39.7%) were recorded from the control and N-omitted plots. The current result was in the acceptable range of HI (40 to 60%) for maize Hay (1995). Thus, an adequate supply of balanced nutrients including micronutrients is important in optimizing the partitioning of dry matter between grain and other parts of a maize plant. Optimum utilization of solar radiation, higher assimilation production and its conversion to starch results in higher biomass and grain yield leading to a higher harvest index. This finding was supported by Obsa *et al.* (2021) who reported that the highest HI (47.36%) was obtained from the application of NPK + CaMgSZnB while the lowest HIs (33% and 34%) were recorded from the control and N-omitted plots from the same soil type.

Table 3: Effect of nutrient omission on number of rows and grains, ear length, and ear diameter of maize

Treatments	LAI	Rows cob^{-1}	Ear Length (cm)	Grain cob^{-1}	Ear Diameter (cm)	HI (%)
Control	2.28^{f}	12.90^{b}	12.50^{d}	355.50^{d}	4.10^{c}	37.30^{c}
NP	3.83^{cd}	13.50^{ab}	16.80^{c}	505.00^{c}	4.30^{bc}	42.10^{b}
PKS (-N)	2.70^{e}	12.90^{b}	12.80^{d}	371.50^{d}	4.10^{c}	39.70^{bc}
NKS (-P)	3.73^{d}	12.90^{b}	17.90^{b}	502.90^{c}	4.50^{ab}	43.30^{ab}
NPS (-K)	4.13^{bc}	13.40^{ab}	18.00^{b}	515.10^{c}	4.40^{ab}	43.70^{ab}
NPK (-S)	4.48^{ab}	13.40^{ab}	19.30^{a}	567.50^{ab}	4.60^{a}	43.30^{ab}
NPKS	4.38^{ab}	13.70^{ab}	19.98^{a}	576.70^{ab}	4.70^{a}	44.00^{ab}
NPKSZn (-B)	4.63^{a}	14.00^{a}	20.00^{a}	589.80^{a}	4.70^{a}	43.90^{ab}
NPKSB (-Zn)	4.35^{ab}	13.60^{ab}	19.60^{a}	567.20^{ab}	4.50^{ab}	47.10^{a}
NPKSZnB	4.35^{ab}	13.40^{ab}	19.70^{a}	565.80^{b}	4.60^{a}	47.20^{a}
Mean	3.89	13.37	17.66	511.70	4.45	43.16
LSD (0.05)	0.38	0.90	0.90	23.60	0.30	4.56
CV (%)	6.82	4.46	3.68	3.18	4.14	7.28

Means followed by a common superscript letter within a column are not significantly different from each other at P<0.05

7.2.2. Grain Yield

It is evident from the result that the grain yield of maize ranged from 2028.5 to 8702.6 kg ha^{-1}, recording the lowest yield from the control and N-omitted treatment while the highest yield from the application of (NPKSZn) nutrients up to optimum level (Figure 2). There were 329.0% and 29.8% grain yield advantages obtained due to the application of NPKSZn compared to control and existing NP recommendations. Application of NPKSZn produced grain yield advantage 350 kg ha^{-1} compared to the application of NPKS, which is obvious associated with the application of 5 kg ha^{-1} Zn. Thus, one can conclude that adding

micronutrients such as Zn results a significant grain yield difference whereas adding up B on NPKS have no significant grain yield advantages. This might probably be due to the optimum content of boron on the initial soil of the experimental site.

Treatments omitting N, P, K, S or Zn resulted in a marked yield loss compared to the full application of NPKSZn, indicating the significance of replenishment of these nutrients for achieving a high yield target. Compared to the NPKSZn, which recorded the highest yield, yield reductions were 5910, 2540, 1470, 1200 and 500 kg ha^{-1} in the omission of N, P, K, S, and Zn plots, respectively. Although treatments receiving the existing recommended NP dose of fertilizer had higher grain yield over control, it showed 2000 $kgha^{-1}$ yield reduction compared to the NPKSZn treatment. The lowest yield from the control plot indicates that the indigenous soil is unable to supply a sufficient amount of nutrients while the lower yield of N - omitted plots indicates that application cannot be substituted by any other nutrient and has the highest contribution to maize yield. This confirms that N is the most limiting nutrient for maize production. It could be due to the effect of N on chlorophyll formation, photosynthesis and assimilated production because N stress reduces crop photosynthesis by reducing leaf area development and leaf photosynthesis rate by accelerating leaf senescence thereby reducing the final yield Diallo *et al.* (1997). Unlike the current study, Tesfaye *et al.* (2019), however, did not observe any significant positive effect of micronutrients on maize grain yield from the same district and this could probably be due to the soil application, especially of higher boron doses.

The second most yield-limiting nutrient following N was P. Phosphorus omitted treatments gave numerically lower yield compared to other treatments except control and N-omitted plots, meaning that P deficiency also limits maize yield. Its deficiency is a common crop growth and yield-limiting factor in unfertilized soils and affects leaf growth dynamics in maize (Ibrikci *et al.*, 2005; Rehman *et al.*, 2011). The present result revealed that P-omitted plots showed reduced maize growth characters compared to NPKSZn treated plots and 2540$kgha^{-1}$ yield reduction was recorded indicating that the soil might be unable to supply sufficient amount of P that is required for proper growth and development of plants.

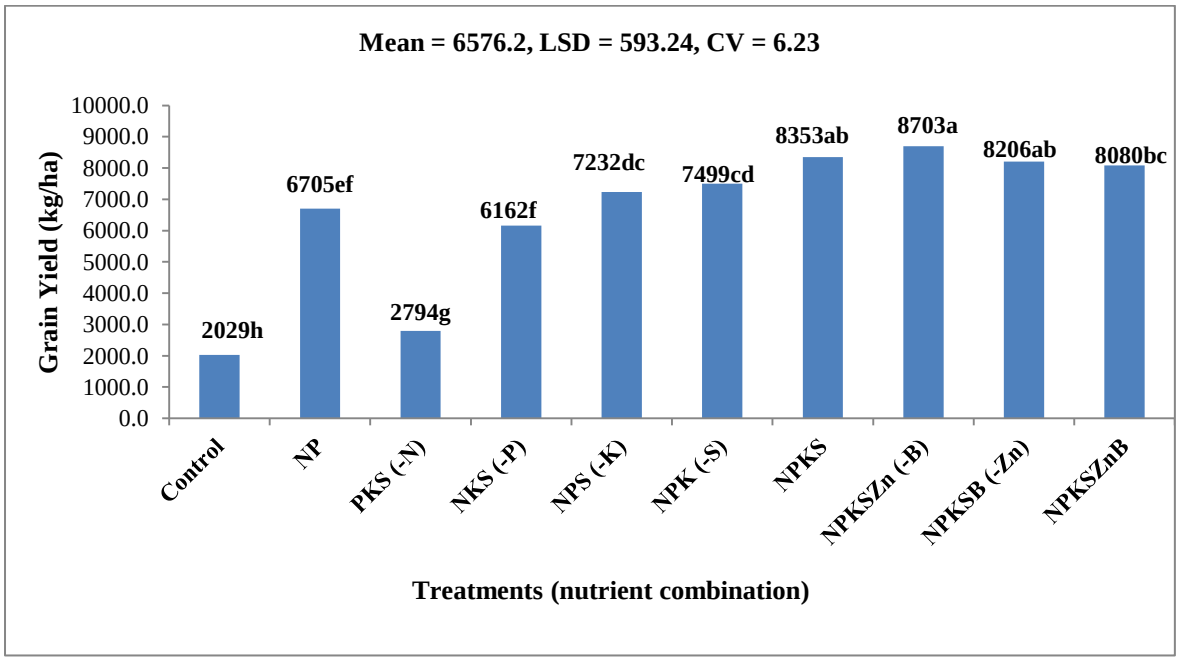

Figure 2: Effect of nutrient combination on maize grain yield at Jimma area

Note: Different small letters denote significant differences between treatments at $P<0.05$

7.3. Total nutrient uptake

The highest total N uptake (87.38 kg ha^{-1}) was recorded from the application of NPKSZn, which was statistically at par with the application of NPKSB (83.29). Due to the application of NPKSZn, 659.83% and 374.12% of total N uptake

increments were recorded compared to unfertilized and N-omitted plots. The increment in total uptake might be due to the efficient use of N from fertilizer applied. Total uptake of N supplied from fertilizer can increase by increasing yield and efficient use of N Haney *et al.* (2015). A higher amount of N uptake or accumulation in grain is important because crop yield is directly associated with N accumulated in grain. Higher N uptake in straw is also desirable because if straw has a higher N concentration, during crop growth N is translocate to grain when plant demand increases, thereby improving yield. A similar finding was also obtained by (Lopez-Bellido *et al.* 2003; Dagne 2016) for Nitisols of Western Ethiopia who reported that the application of macronutrients in combination with micronutrients produced the highest N concentration and uptake.

The maximum total P-uptake (40.40 $kgha^{-1}$) was obtained from the application of NPKSZn, while the lowest (8.07 $kgha^{-1}$) was recorded from the control. Application of NPKSZn improved total p uptake by 400.62% and 59.32% compared to control and P-omitted plots, respectively. These results showed that there was a positive effect of P on maize grain and straw yields and the improvement of grain and straw P contents by application of balanced fertilizers including P containing sources. Moreover, the highest nutrient uptake recorded might be due to the positive interaction of P with other nutrients, because the existence of synergetic nutrient interactions is an important factor in improving the yield of field crops where the presence of one element facilitates the uptake of other Wilkinson (2000). Phosphorus has a positive significant interaction with N, K and S. This positive interaction gives rise to improvement in growth and yield of crop plants with P fertilization. Phosphorus also has synergistic interaction with micronutrients. Among micronutrients, P-Zn interaction is widely reported by Wilkinson (2000) where, Zn deficiency in this situation is associated with the rapid growth of plants, and soil-available Zn cannot fulfill the demands of rapidly growing plants, which makes Zn deficiency, induced P toxicity.

Total nutrient uptake of K ranges from 20.43 to 114.95$kgha^{-1}$ recording the lowest uptake from unfertilized plots, while the highest K uptake is from plots treated with NPKSZn. The highest nutrient uptake is based on the concept that the concentration of an essential nutrient in a plant or part of a plant indicates the soil's ability to supply that nutrient and the positive interaction that exists among the nutrients applied Hillel (2005). Maximum total K uptake enhanced under NPKSZn fertilization is an indication of synergetic interaction of K with macronutrients (N and P) and micronutrients (Zn) but it has antagonistic interaction with boron. Kalpana and Krishnarajan (2002) noticed that the application of increasing levels of K up to 50 kg ha^{-1} significantly increased N and K uptake in baby corn. This illustrated that NPKSZn fertilization was better for improving N, P and K accumulation. The lower K uptake and concentrations from the control and K - omitted plots might therefore be due to low K availability in the experimental soil, as was confirmed by soil analysis results before planting.

Concerning S, the maximum total S uptake (22.22 kg ha^{-1}) was obtained from the application of NPKSZn, while the minimum (4.74 $kgha^{-1}$) was obtained from the control. This evidence indicates that the application of macronutrients (NPKS) including Zn improves S uptake by 368.78% and 299.79% advantages compared with control and S omitted plots respectively. An increase in the availability of S in soil and its absorption by the crop due to NPKSZn might be the release of more soil S from the absorption site because of ion exchange synergistically as reported by Gowda *et al.* (2001). Moreover, maximum S uptake in grain and straw was higher at a high N rate compared to the low rate of N, indicating improvement in S use efficiency with the integrated application of N. The efficiency of nutrient absorption is often determined by the ability of the plants to absorb a certain element at a low level of soil stocks or the nutrient medium Dawson *et al.* (2008).

The maximum total Zn uptake (2.67$kgha^{-1}$) was obtained from the application of NPKSZn which was statistically at par with treated NPKS (2.47), while the minimum total Zn uptake (0.67kg ha^{-1}) was obtained from control. The current result was confirmed by the finding of (Jain and Dahama, 2005) who noticed that N, P, K, S and Zn contents and uptake in maize were significantly higher at 9$kgha^{-1}$. Azab (2015) also proved that combined application of Zn and NPK fertilizer significantly improved N, P, K and Zn content and uptake as compared to plots fertilized only NPK.

Boron uptake in grain ranged from 0.04 to 0.28kg ha^{-1}, recording the lowest value from unfertilized crops and N - omitted plots while the highest value from the application of NPKS, NPKSZn and NPKSZnB. Comparing the average B uptake values from the application of NPKS, NPKSZn and NPKSZnB no significant difference was observed, but there is a slight numerical B uptake difference between treatments. From this, it can be concluded that adding up B has a small but non-significant difference observed, which might be an overdose of this nutrient and antagonistic interactions among the applied elements.

Table 4: Total nutrient uptake of maize as affected by nutrient combinations

Treatments	Total nutrient uptake ($kgha^{-1}$ nutrient applied)				
	N	P	K	S	Zn
Control	11.50^{g}	8.07^{e}	20.43^{e}	4.74^{f}	0.67^{f}
NP	48.56^{d}	30.38^{c}	72.55^{d}	17.14^{cd}	2.02^{bc}
PKS	18.43^{f}	11.14^{e}	27.67^{e}	6.80^{e}	0.79^{f}
NKS	43.72^{e}	25.57^{d}	74.06^{d}	15.20^{d}	1.80^{cd}
NPS (-K)	60.68^{c}	29.47^{c}	88.60^{c}	17.37^{c}	1.25^{e}
NPK (-S)	63.44^{c}	32.39^{c}	100.64^{b}	18.95^{bc}	1.84^{cd}
NPKS	74.12^{b}	36.56^{b}	102.70^{b}	19.81^{b}	2.47^{a}
NPKSZn (-B)	87.38^{a}	40.40^{a}	114.95^{a}	22.22^{a}	2.67^{a}
NPKSB (-Zn)	83.29^{a}	36.04^{b}	93.19^{bc}	20.40^{ab}	1.41^{de}
NPKSZnB	70.26^{b}	37.53^{ab}	97.61^{b}	20.55^{ab}	2.35^{ab}
Mean	56.14	28.75	79.39	16.18	1.73
LSD (0.05)	4.52	3.16	8.30	1.97	0.45
CV (%)	5.54	7.57	7.22	8.33	18.02

Means followed by a common letter/s within a column are not significantly different at P<0.05

7.4. Agronomic efficiencies

Agronomic efficiency (AE) of each nutrient was highly significantly ($P < 0.01$) affected due to nutrient combination where the application of NPKSZn resulted in the highest value. Nutrient use efficiency was increased via increasing crop nutrient uptake and use efficiency by decreasing nutrient losses from the soil-plant system. This improvement was attributed due to nutrient uptake increment through the integrated application of macronutrients with micronutrients in nutrient deficient soil as a result enhanced nutrient use efficiency of crops thereby boosting yield and productivity Redai *et al*.(2018).

Accordingly, the highest agronomic efficiency of nitrogen (AEN) (55.6 kg kg^{-1}) was obtained from the application of NPKSZn. The lowest AEN (34.5 kg kg-1) was recorded from the application of NKS (-P) indicating the combined application of N and P is especially very important since the absence of one of these nutrients remarkably reduced the AE of other nutrients (Table 5). Selecting a fertilizer combination that confers the highest AE of each nutrient is quite important, which is in agreement with the findings of Kurwakumire *et al.* (2014). On the other hand, the highest AEN might be attributed due to the synergetic interaction effect of N with P, K, S and Zn. Even though, N interaction with micronutrients depends on the forms of N absorbed and the soil pH changes in the rhizosphere. If N is absorbed in the form of NH_4^+, soil pH may decrease, and uptake of most micronutrients increases. If N is mainly absorbed as NO_3^-, soil pH may increase, and uptake of most micronutrients decreases Wilkinson (2000).

The highest agronomic efficiency of phosphorus (AEP) (166.9 kg kg^{-1}) was obtained from the application of NPKSZn and the least (19.1 kg kg^{-1}) was recorded from N-omitted plots. Application of NPKSZn increased ATP by 42.7% and 772.7% compared with NP and N-omitted plots, respectively. Omitting N (i.e. PKS treatment) extraordinarily reduced AEP, which might be reduced root growth and negatively influences the absorption of water and nutrients. This showed that the application of P in the absence of N cannot improve the AEP which was confirmed by the finding of Tesfaye *et al.* (2019).

The highest agronomic efficiency of potassium (AEK) 166.5$kgkg^{-1}$ was obtained from the application of NPK indicating positive interactions

of K with N and P, while the lowest AEK (19.1 kg kg^{-1}K) was recorded from plots treated with PKS (-N) indicating N-deficiency negatively affects AEK of crops. Similarly, the same trend was observed in the case of S and Zn agronomic efficiencies. Higher AE is generally obtained if the yield increment per unit of nutrient applied is high (Obreza and Rhoads, 1988) which supports the finding of the current study. On the other hand, a lower yield response indicates higher soil indigenous nutrient supply or higher soil fertility, resulting in lower agronomic efficiency.

In general, higher agronomic efficiencies would be obtained if the yield increment per unit of nutrient applied were high, nevertheless what amount can be considered as high AE is not exactly identified Robert (2008). Further increasing nutrient levels beyond crop requirement may decrease agronomic efficiency of a nutrient by the crops, which indicates a higher amount of fertilizer application over optimum dose in luxury nutrient uptake might not contribute to physiological processes and hence yield.

Table 5: Agronomic efficiency of N, P, K, S, Zn and B as affected by omitted nutrients

Treatments	Agronomic Efficiency (kg grain kg^{-1} nutrients applied)				
	N	P	K	S	Zn
Control	-	-	-	-	-
NP	38.97^{f}	116.9^{g}	-	-	-
PKS (-N)	-	19.1^{h}	19.1^{f}	38.3^{g}	-
NKS (-P)	34.50^{g}	-	103.3^{e}	206.7^{f}	-
NPS (-K)	43.40^{e}	130.1^{f}	-	260.2^{e}	-
NPK (-S)	45.60^{d}	136.8^{e}	136.8^{d}	-	-
NPKS	52.70^{b}	158.1^{b}	158.1^{b}	316.2^{b}	-
NPKSZn (-B)	55.60^{a}	166.9^{a}	166.9^{a}	333.7^{a}	1359.8^{a}
NPKSB (-Zn)	51.50^{bc}	154.4^{c}	154.4^{bc}	308.9^{c}	-
NPKSZnB	50.40^{c}	151.3^{d}	151.3^{c}	302.6^{d}	1210.3^{b}
Mean	46.58	129.20	127.13	252.36	1285.06
LSD (0.05)	1.36	2.36	4.12	4.42	42.64
CV (%)	4.25	3.41	4.52	5.36	6.88

Means followed by a common letter/s within a column are not significantly different at $P<0.05$

7.5. Apparent recovery of nutrients

The apparent recovery efficiency of each nutrient showed a positive response due to the inorganic fertilizer combination. The highest recovery fraction of N (0.64), P (80.2), K (236.32), S (87.40) and Zn (40.10) was recorded from the application of NPKSZn. The increment of recovery fraction might due to the integrated use of macronutrients (NPKS) with micronutrients (Zn) in the appropriate form of fertilizer. The result was in line with the finding of Jones *et al.* (2011) who reported that matching appropriate essential macronutrients in combination with micronutrients with crop nutrient uptake could optimize nutrient use efficiency thereby apparent recovery of nutrients.

8. Conclusion and Recommendation

Based on the results, we conclude that rational fertilizer promotions and recommendations based on actual limiting nutrients for a given crop are not only revealed to supply adequate plant nutrients but also helped to understand the long-term ecological and economic benefits of the studied crop. According to the result, it is possible to conclude that the inherent N supplying capacity of soil is very low and highly limits grain yield of maize followed by P in the study area. Therefore, the use of an optimum dose of N and P should take great attention to efficient nutrient uptake, which ultimately increases maize productivity. The wider variability in maize yield response to the application of different nutrient combinations observed in this study, suggests that site-specific nutrient management is fundamental to intensifying maize production and productivity. Therefore, we can conclude that N is the most yield-limiting nutrient followed by P in the study area.

Moreover, the results of this experiment have substantiated the importance of micronutrients (Zn) in combination with macronutrients NPKS for improving nutrient concentration and uptake and have confirmed the significant yield increase in maize. The highest total nutrient uptake, agronomic efficiency and apparent recovery of nutrients were obtained from plots treated with fertilizer containing NPKSZn. Therefore, it can be concluded that the application of macronutrients in combination with micronutrients increased maize yield and concomitantly improved N, P and K uptake and its nutrient use efficiency.

Further researches need across different locations and soil types and nutritional quality analysis are also recommended.

Conflict of Interest

The authors declared that there is no conflict of interest.

Acknowledgements

The authors acknowledge the Ethiopian Institute of Agricultural Research for funding of this study. Staffs of Natural Resource Management of Jimma Agricultural Research Center (JARC) are highly acknowledged for their support during the study. Soil and Plant Tissue Analysis Laboratory of Jimma Agricultural Research Centers is also duly acknowledged for the analysis of experimental samples.

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Genotype by Environment Interaction and Yield Stability of Drought Tolerant Mung Bean [*Vigna radiata* (L.) Wilczek] Genotypes in Ethiopia

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Received: May 4, 2022 Accepted: June 14, 2022

Abstract: *A multi-environment evaluation of mung bean genotypes was conducted in six environments across Ethiopia to select promising genotypes. This study was conducted to estimate the magnitude of genotypes by environment interaction (GEI) and seed yield stability of the selected drought-tolerant mung bean genotypes across different environments. A total of fifteen mung bean genotypes were used. Out of these, two released varieties were used as standard checks. The field experiments were conducted during the 2019 main cropping season at six locations namely Humbo, Gofa, Melkassa, Konso, Jinka, and Kako using a randomized complete block design with three replications. Data were subjected to analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI), and GGE bi-plot analysis. A combined analysis of variance revealed significant variations among the genotype, environments, and GEI for yield and yield-related traits, indicating that seed yield was significantly affected by these factors. Analysis of variance from the AMMI model indicated the contribution of environment, genotype, and GEI was 59.6%, 16.8%, and 14.8% of the total variation in seed yield, respectively. Sum squares of the first and the second interaction principal component axis (IPCA) explained 47.4% and 7.4% of the GEI variation, respectively. The IPCA1 mean square was highly significant ($P \leq 0.01$) and that of IPCA2 was significant ($p \leq 0.05$), indicating the adequacy of the AMMI model with the first two IPCAs for cross-validation of the seed yield variation. The magnitude of the GEI sum squares was 4.4 times that of the genotypes sum squares for seed yield, indicating the presence of substantial differences in genotypic responses across the environments. The results for the AMMI, Yield stability index (YSI), AMMI Stability Value (ASV), and GGE biplot, analyses depicted that the genotypes G6 (NLLP-MGC-24), G13 (Acc006), and G3 (NLLP-MGC-15) were identified as stable and high yielders across the environments and should be considered for variety release. AMMI1 biplot showed Kako was the potential and favorable environment for mung bean production, while Humbo was an unfavorable for mung bean production.*

Keywords: *AMMI Stability Value*, GGE biplot, Kako, Gofa, Yield Stability Index

1. Introduction

Mung bean [*Vigna radiata* (L.) Wilczek] is an important self-pollinated pulse crop of Asia and can be grown in sandy and loam soils, with a pH range of 6.2 to 7.2. Multi-environment trials allow breeders to select the best-performing genotype for their target areas by assessing the relative performance of genotypes under a variety of locations and environmental conditions (Zu, 2010). Genotypes tested in different locations and over years have significant fluctuations in yield due to variations in soil fertility, unpredicted rainfall, and the presence of other biotic and abiotic stresses (Kang, 1993). Differential response of genotypes to different environmental conditions is termed genotype by environment interaction (GEI). In this context, genotypes across environments may be classified as stable when the classification of genotypes remains constant in various environments and there is significant interaction due to the differences in the magnitude of the responses; or complex when the classification of the genotypes is different from one environment to another, which is quite common and has greater importance in plant breeding (Mohammadi and Amri, 2013). The magnitude of an environment, genetics, and their interaction effects are a serious problem for the yield and stability of genotype

across environments because it reduces the efficiency of the genetic gain. Comestock and Moll (1993) suggested that GE interaction reduces the genetic progress in plant breeding programs by minimizing the association between phenotypic and genotypic values. Hence, GE interaction must be either exploited by selecting a superior genotype for each specific target environment or avoided by selecting a widely adapted and stable genotype across a wide range of environments (Ceccarelli, 1996).

Genotypes x environment interactions exist, when the responses of the genotypes to different levels of environmental factors fail to respond similarly (Allard and Bradshaw, 1964). Major constraints in breeding pulses such as mung beans are the high genotype x environment (GxE) interactions and the low genetic diversity in the primary gene pool (Jitendra *et al*., 2011). Researchers working in the area of plant breeding have the trend of evaluating genotypes in multi-environments, representing favorable and unfavorable growing conditions, to estimate and understand the stability of the genotype across environments. Hence, Tiwari *et al*. (2000) and Mehla *et al*. (2000) suggested testing varieties over a large number of environments is necessary to observe GEI effects

Grain yield performance is not the only parameter for selection as a genotype with the highest grain yield and would not be necessarily stable and adaptable across locations and years. The plant breeders need to identify adaptable and stable high-yielding genotypes with other desirable traits under varying environmental conditions as a desirable variety (Showemimo *et al*., 2000; Mustapha *et al*., 2001).

In Ethiopia, G x E interaction studies have been conducted on different food legumes, thus on cowpea (Tariku *et al*., 2018), common bean (Asrat *et al*., 2008; Nigussie *et al*., 2012), soybean (Asrat *et al*., 2009), faba bean (Gemechu *et al*., 2002; Gemechu and Musa, 2002; Musa and Gemechu, 2004; Gemechu *et al*., 2006; Mulusew *et al*., 2008; Tamene *et al*., 2015; Asnakech *et al*., 2017; Tadele *et al*., 2017; Tekalign *et al*., 2019), field pea (Mulusew *et al*., 2009; Mulusew *et al*., 2014), and mung bean (Asrat *et al*., 2012). However, information on the effect of genotype, environment, and GEI on mung bean yield with drought-tolerant traits is limited in Ethiopia. There have been only limited studies on the use of the GGE biplot study for mung bean genotypes evaluation in Ethiopia. In these areas, more studies are needed to help mung bean farmers choose the right genotypes. Therefore, the present study was conducted to estimate the magnitude of genotypes by environment interaction effect and to evaluate the performance and stability of promising drought-tolerant mung bean genotypes for wider and /or specific recommendations for cultivation under farmers' conditions in Ethiopia.

2. Materials and Methods

2.1. Description of the study areas

The field experiments were conducted during the 2019 main cropping season at six locations namely Humbo, Gofa, Melkassa, Konso, Jinka, and Kako. The geographical locations and mean rainfall and temperatures of the study area over several years (2009 to 2019) are presented in Table 1. The weather data were collected from the nearby stations, respective woreda, and zonal Bureau of Agriculture and research centers (Personal Communication).

2.2. Experimental materials

A total of fifteen selected genotypes were used. Out of these, two released varieties were used as standard checks and thirteen genotypes were selected from the drought experiment where 60 genotypes were tested (Table 2). Genotypes were sourced from Melkassa Agricultural Research Center as well as our collections from southern Ethiopia.

2.3. Experimental design and procedures

The experiments were laid out using a randomized complete block design with three replications. During planting, blended NPSB fertilizer at the rate of 100 kg ha^{-1} was applied. Agronomic management practice namely, weeding was carried out uniformly for all experimental units. Experiments were planted from early June to early July of the 2019 cropping season at each location. The plot size was 4 m long, 0.3 m between rows, and 0.05 m between plants. Each experimental plot had an area of 6.0 m^2. It consists of five rows accommodating 80 plants per row. The distance between plots and replications was 1 m and 2 m, respectively. The data were collected from the middle three rows, which have a 3.6 m^2 net plot area.

Table 1: Description of the experimental sites

Experimental sites	Soil Type	Geographical location			Rainfall (mm)	Temperature (°C)	
		Altitude (m.a.s.l)	Latitude (N)	Longitude (E)		MinT (°C)	MaxT (°C)
Humbo	Vertisols	1390	6° 39'	37° 48'	710-1337	18.3	21.0
Gofa	Cambisols	1276	6°19′	36°56′	800-1200	17.5	20.0
Melkassa	Andosols	1550	8°30'	39° 24'	763	15.73	27.31
Konso	Vertisols	1432	5°23'	37°20'	787	18.4	30.70
Jinka	Cambisols	1420	5° 47'	36° 38'	1381	16.61	27.68
Kako	Cambisols	1407	5° 39'	36° 41'	637.3	23.1	38

Table 2: List of genotypes used

Genotypes	Genotypes code
NLLP-MGC-01	G1
NLLP-MGC-12	G2
NLLP-MGC-15	G3
NLLP-MGC-20	G4
NLLP-MGC-22	G5
NLLP-MGC-24	G6
NLLP-MGC-27	G7
VC1973A	G8
NM94 (VC6371-94)	G9
VC6368(46-40-4)	G10
NLLP-MGC-06	G11
Acc002	G12
Acc006	G13
N-26 (Standard check)	G14
NVL-1 (Standard check)	G15

2.4. Data collection

The quantitative data were collected according to the descriptor of the mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980). The data collected on the plot basis were; days to flowering (days), days to maturity (days), hundred seed weight (g), and seed yield per hectare (kg). The data collected on a plant basis were; plant height (cm), number of pods per plant, five plant pod numbers, and number of seeds per pod.

2.5. Data analysis

Different statistical packages were used to analyze the data. GenStat Software 16th edition (GenStat, 2014) was used for the analysis of variance of the individual location and the combined data over locations, AMMI, and GGE biplot analysis. GEA-R (Genotypic by Environment Analysis with R for Windows) Version 4.1 was also used (Angela *et al.*, 2016). The AMMI model was used based on the recommendation of Choukan (2010) who suggested that the additive main effects and multiplicative interaction (AMMI) are an effective alternative method for assessing the suitable genotype. The author also proposed that the GGE biplot is an effective tool for the Mega-environment analysis (which-won-where pattern), genotype evaluation, mean performance and stability, and environment evaluation to discriminate among genotypes in the targeted environment.

2.5.1. *Analysis of variance*

The analysis of variance of each location and combined data over location were performed using a mixed linear model to assess the differences among genotypes as per Gomez and Gomez (1984). The combined analysis of variance across the environment was analyzed by using GenStat Software 16th edition (GenStat, 2014) to determine the differences between genotypes across the environment, among environments, and their interaction. Bartlett's test was used to assess the homogeneity of error variances before combined analysis over the environments (Bartlett, 1947). In the combined analysis of variance, the location was used as random while genotypes were a fixed variable.

2.5.2. *additive main effect and multiplicative interaction model analysis*

The Additive Main effect and Multiplicative Interaction (AMMI) model analysis proposed by Zobel *et al*. (1988) was used for analyzing the magnitudes of GEI. The seed yield data were

analyzed using this model because AMMI partitions the sum of squares into the interaction principal component (IPC) axis. The AMMI analysis of variance summarizes most of the magnitude of GEI into one or a few interaction principal component axes (IPCA). The AMMI model equation is indicated below [1].

$$Yij = \mu + G_i + E_j + (\sum K_n V_{ni} S_{ni}) + Q_{ij} + e_{ij} \quad [1]$$

Where

- *Y*ij = the observed yield of genotype i in environment j
- μ = grand mean
- G_i = additive effect of the ith genotype (genotype means minus the grand mean)
- E_j = additive effect of the jth environment (environment mean deviation)
- K_n = eigenvalue of the interaction principal component (IPCA) axis n
- V_{ni} and S_{ni} = scores for the genotype i and environment j for the PCA axis n
- Q_{ij} = residual for the first n multiplicative components
- e_{ij} = error

2.5.3. ***GGE biplot analysis***

The GGE biplot has many visual interpretations that additive main effects and multiplicative interaction do not have; particularly it allows visualization of any crossover G x E interaction. GGE biplot is close to the best additive main effects and multiplicative interaction model in most cases (Yan and Ma, 2006). Moreover, the GGE biplot is more logical for biological objectives in terms of explaining the first principal component score, which represents the genotypic level rather than the additive level (Yan *et al.,* 2000). The GGE biplot is built on the first two major components of a principal component analysis (PCA) using the Site Regression (SREG) model. When the first component is highly correlated with the main effect of the genotype, the proportion of the yield is considered to be due only to the characteristics of the genotype. The second component represents the part of the yield due to the G×E (Yan, 2011). The model for a GGE biplot (Yan, 2002) is based on singular value decomposition of the first two principal components [2].

$$Yij - ì - âj = ël îil çjl + ë2 îi2 çj2 + εij \quad [2]$$

Where

- Yij = the measured mean of genotype i in environment j
- Ì = grand mean
- Âj = main effect of environment j,
- ì+âj = mean yield across all genotypes in environment j
- ë1 and ë2 = singular values for the first and second principal components, respectively
- îi1 and îi2 = eigenvectors of genotype i for the first and second principal components, respectively
- ç1j and ç2j = eigenvectors of environment j for the first and second principal components, respectively
- åij= residual associated with genotype i in environment j.

2.5.4. ***Stability analysis***

The AMMI stability parameters (Guach and Zobel, 1988; Zobel *et al*., 1988) and GGE biplot by using GenStat Software 16th edition (GenStat, 2014) were computed for grain yield and the GEI analyses of variance. Accordingly, regression coefficient (bi) and deviation from linear regression (S^2di) from Eberhart and Russell‟s (1966) model and interaction principal component axes (IPCA) scores of genotype and environment and AMMI Stability Value from the AMMI model were computed as per the established standard procedures for each model. The pooled deviations mean square was tested against the pooled error mean square by F-test to evaluate the significance of the differences among the deviations of genotypes from their expected performances. Hence, to test whether there is a significant difference among the genotypes concerning their mean grain yields, genotypes mean square and regression mean square were tested against the pooled error mean square using the F-test.

2.5.5. ***AMMI stability value (ASV)***

Since the AMMI model does not make provision for a quantitative stability measure that guides us to rank genotypes in terms of their yield stability. The AMMI stability values (ASV) were calculated to study the stability of genotypes across the environments following the formula of Purchase (1997) expounded by Purchase *et al.* (2000) was applied to quantify and rank genotypes according

to their yield stability. Therefore, AMMI stability value (ASV) was computed to quantify and rank genotypes according to their yield stability by using Microsoft office excel 2007. The larger the absolute value of IPCA, the greater the adaptability of a specific variety for a certain environment. Conversely, lower ASV values indicate greater stability in different environments (Farshadfar *et al.*, 2011).

$$ASV = \sqrt{\left[\left[\frac{\text{IPCA 1 Sum of squares}}{\text{IPCA 2 Sum of squares}}\right](\text{IPCA 1 scores})\right]^2 + [\text{IPCA 2 scores}]^2} \quad [3]$$

Where

- ASV = AMMI's stability value
- SS = sum of squares
- IPCA1 = interaction of principal component analysis one
- IPCA2 = interaction of principal component analysis two.

The ASV is the distance from zero in a two-dimensional scatter graph of IPCA1 (Interaction Principal Component Analysis Axis 1) scores against IPCA2 (Interaction Principal Components Analysis Axis 2) scores. Since the IPCA1 score contributes more to the GEI sum of squares; it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GEI sum of squares.

2.5.6. *Yield stability index (YSI)*

YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Bose *et al*., 2014; Tumuhimbise *et al*., 2014). The yield stability index was calculated using the following formula below [4].

$$YSI = RASV + R \quad [4]$$

Where

- RASV = the ranking of the AMMI stability value
- R = the ranking of mung bean genotypes yields in all environments.

3. Results and Discussion

3.1. Combined analysis of variance across environments

The combined analysis of variance showed significant differences in the environment, genotype, and genotype-by-environment interactions (Table 3). The result revealed that there were significant variations among genotype, environments, and GEI for yield and yield-related traits, indicating that the environment had a great impact on seed yield potentials of the tested genotypes.

As presented in Table 3, days to maturity, five plant pods, seeds per pod, and a hundred seed weights were significantly ($P \leq 0.01$) influenced due to genotype, environments, and genotype x environment interaction. Pods per plant and seed yield per hectare were significantly ($P \leq 0.01$) affected due to genotype. The environment had exerted a significant ($P \leq 0.01$) effect on days to flowering. The results also depicted that GEI for days to flowering, days to maturity, plant height, five plants pod number, number of pods per plant, hundred seed weight and seed yield per hectare were highly significant ($P \leq 0.01$), while it had brought significant ($P \leq 0.05$) effect on plant height, indicating that the environment had a great impact on the seed yield potential of the tested genotypes (Table 3). Generally, the result signifies that the studied phenological and other yield-related traits of mung bean genotypes were influenced by environmental factors and it also indicated the presence of genetic variability among the tested genotypes. This result agreed with the previous findings of Lal *et al*. (2010) on fifteen mung bean genotypes at 10 locations and found that the genotype by environment interaction and both variances due to genotypes and environments were significant, which coincides with the reports of several researchers (Dhillion *et al*., 2009; Tyagi and Khan, 2010) on soybean, Kan *et al*. (2010) on chickpea, Nigussie *et al*. (2015) on common bean, Yeyis *et al*. (2014) on field pea, Akande (2009), and Tariku *et al*. (2018) on cowpea genotypes.

Moreover, this study revealed that the magnitudes of the GEI sum square were about 4.4 times that of the genotypes sum squares for seed yield, indicating that there were considerable differences in genotypic responses across environments thereby differential responses of genotypes across environments were observed. This result agreed with the work of Dyulgerova and Dyulgerov (2019), who reported that the magnitude of the GEI sum of squares was two times larger than that of genotypes, indicating that there was a substantial difference in genotypic response across environments. The larger sum of squares of GEI

compared to the genotype indicated larger differences in genotypic response across environments, indicating that there was a considerable variance in genotypic response across environments. Therefore, GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance and minimizing the association between genotypic and phenotypic values (Crossa, 1990). The GEI in the current analysis was a cross-over type whereby a change in the ranking of genotypes for a target environment because of the difficulty to interpret seed yield based on genotype and environment means alone. This finding is in line with the previous report of Asrat *et al*. (2009) on soybean.

3.2. Comparison of mean seed yield across the environments

The average environmental seed yield across genotypes ranged from 507 kg ha^{-1} at E2 (Humbo) to 2081 kg ha^{-1} at E4 (Kako) with the overall environmental mean yield of 1164 kg ha^{-1}, while the average genotype seed yield across environments ranged from 696 kg ha^{-1} for the genotype (G4) to 1375 and 1580 kg ha^{-1} for G13 and G8, respectively (Table 4). This indicates that the tested genotypes had inconsistent performance across the tested environments. In this study, most of the tested genotypes gave relatively good seed yield performance and could be suggested that there is an opportunity to get high-yielding mung bean genotypes for future variety development. The large variation due to the environments in our study also confirmed the high diversity of weather conditions during growing seasons and also the locations had different soil types, temperatures, and rainfall as well as altitude, directly affecting the performances of the genotypes. Hence, the selection and development of mung bean varieties in the future should follow environment-specific approaches.

The results of the present study are in agreement with the work of Tariku *et al.* (2018) on the cowpea genotype, who reported that the performance of cowpea genotypes was different from location to location, similar to that of Aremu *et al.* (2007) in cowpea. Ranking based on the genotype-focused scaling assumed that stability and mean yield was equally important (Yan, 2002). The best candidate genotypes were expected to have a high mean seed yield with stable performance across all test locations. However, such genotypes are very rare to find in practice. Therefore, high-yielding and relatively stable genotypes can be considered as a reference for genotype evaluation (Yan and Tinker, 2006).

In this study, the mean values of seed yield and yield-related traits are presented in table 5. The highest mean seed yield (1580 kg ha^{-1}) was recorded for the genotype (G8) and the least (696 kg ha^{-1}) was recorded for the genotype (G4), with an overall mean of (1164 kg ha^{-1}). Overall mean values for days to flowering ranged from 40.42 days for the genotype (G5) to 59.77 days for the genotype (G14). Days to maturity ranged from 66.72 to 98.98 days. Genotypes (G6, G13, G14, and G15), respectively took 96.33, 98.98, 97.72, and 98.39 days to attain their physiological maturity. Plant height ranged from 37.57 cm for (G8) to 48.79 cm for (G15). The number of pods per five plants ranged from 38.5 for (G11) to 96.6 for (G3). In this study, the maximum pods per five plants of 96.6, 94.9, and 88.7, respectively were also recorded for the genotypes (G3, G2, and G8) while the minimum number of pods per five plants of 38.5 and 44 were recorded for G11 and G15, respectively. Pods per plant varied from 14.03 for G13 to 25.14 for G5. Seeds per pod ranged from 9.29 for G11 to 12.35 for G1. Hundred seed weight ranged from 3.66 g for the genotype (G5) to 5.94 g for G11.

Table 3: Mean square of combined ANOVA for eight traits of 15 mung bean genotypes

Source	DF	DTF	DTM	PH	FPP	PPP	SPP	HSW	SY
Genotype (G)	14	581.04**	3307.60**	147.34**	6180.2**	232.0*	11.613**	6.3254**	743921*
Environment (E)	5	32.70*	26.993**	751.17**	4840.3**	978.6**	45.428**	2.6136**	15313847**
GEI	70	0.01**	0.004**	151.14*	242.1**	50.9**	1.449**	0.0272**	655105**
Error	178	25.54	3.524	20.95	642.1	118.1	3.163	0.3648	561079

*, ** = significant at 5% and 1% probability level, respectively, SV = source of variation, DF = Degree of freedom, GEI = genotype by environment interaction, DTF= days to flowering, DTM days to maturity, PH= plant height, FPP= five plants pod, PPP= number of pods per plant, HSW= hundred seed weight, SPP= the number of seeds per pod

Table 4: Mean Seed yield (kg ha^{-1}) **of 15 mung bean genotypes at six environments and stability indicators of AMMI analysis**

Genotype	E1	E2	E3	E4	E5	E6	Mean	IPCAg[1]	IPCAg[2]
G1	939	421	1101	3143	421	939	1161	-19.98967	5.99378
G2	1072	572	1237	2922	572	1072	1241	-14.48429	7.06782
G3	1320	791	1289	1509	1325	1320	1259	11.77525	17.02819
G4	944	364	583	979	364	944	696	11.49340	7.04205
G5	1709	446	1584	878	446	1709	1129	21.74822	-8.60742
G6	1437	593	1011	2499	760	1437	1290	-5.21787	1.15422
G7	2037	633	911	1237	633	1704	1192	16.79039	-11.77015
G8	1550	693	1112	3881	693	1550	1580	-25.16245	-3.87765
G9	1301	584	999	1979	584	1301	1125	1.11140	2.62966
G10	1453	557	1484	813	557	1453	1053	21.12314	0.73750
G11	1188	454	1111	904	587	1188	905	16.64242	6.21678
G12	1063	459	1022	2201	459	1063	1044	-4.66412	5.19843
G13	2098	306	1276	2833	306	1432	1375	-9.17042	-21.46960
G14	1071	457	1315	3298	457	1071	1278	-20.64006	3.65807
G15	1612	275	1188	2138	275	1278	1128	-1.35534	-11.00170
Mean	1386	507	1148	2081	563	1297			
IPCAe[1]	13.36480	8.13392	8.80096	-54.21802	10.28095	13.63738			
IPCAe[2]	-25.23624	13.09221	2.23948	-2.14545	20.72911	-8.67911			

E1 = Gofa, E2 = Humbo, E3 =Jinka, E4 = Kako, E5 =Konso, E6 = Melkassa, G1 = NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 = VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1

Table 5: Mean values of seed yield and yield-related traits of 15 mung bean genotypes

Genotypes	DF	DM	PH	FPP	PPP	SPP	HSW	SYLD
G1	42.56	69.39	42.98	53.9	14.86	12.35	4.528	1161
G2	53.22	67.72	42.02	94.9	20.19	11.07	4.028	1241
G3	45.22	67.72	40.06	96.6	22.36	10.24	4.25	1259
G4	40.69	69.39	37.82	63.2	14.81	10.63	4.667	696
G5	40.42	68.39	40.77	59.4	25.14	11.57	3.656	1129
G6	51.38	96.33	43.49	47.4	15.47	10.51	4.089	1290
G7	44.31	66.72	40.28	62	20.36	10.74	4.694	1192
G8	45.22	68.12	37.57	88.7	23.64	10.07	3.683	1580
G9	51.22	68.39	40.08	79.9	20.25	10.96	4.294	1125
G10	45.36	69.39	41.27	74.4	20.86	11.35	4.333	1053
G11	41.56	66.72	38.63	38.5	17.47	9.29	5.944	905
G12	42.69	68.727	38.69	75.4	15.31	9.63	4.52	1044
G13	57.56	98.98	43.74	61.5	14.03	10.24	4.222	1375
G14	59.77	97.72	41.74	47.5	15.36	11.51	4.639	1278
G15	55.56	98.39	48.79	44	20.36	10.18	5.361	1128
Mean	47.78	76.14	41.20	65.82	18.70	10.69	4.46	1164
SD	4.48	1.71	4.18	23.12	9.92	1.62	0.55	8.27
CV (%)	2.3	2.5	11.1	28.5	16.4	16.6	13.6	28.3

CV = Coefficient of variation, SD = standard deviation, G = genotype, DF = days to flowering, DM = days to maturity, PH = plant height, FPP = five plants pod, PPP = number of pods per plant, HSW = hundred seed weight, SPP = seed per pod. G1 = NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 = VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1.

3.3. Stability analysis

3.3.1. *Additive main effects and multiplicative interaction analysis*

The AMMI analysis of variance for seed yield (kg ha-1) of 15 mung bean genotypes tested at six environments is presented in Table 6. Considering the additive component of the analysis, genotype had brought significant (P≤0.01) effects on seed yield, while the environment significantly (P≤0.001) affected seed yield. A similar result was reported by Kocaturk *et al*. (2019) on soybean genotypes, who reported that significant (P≤0.01) effects were observed due to environment, genotype, and G×E interaction for the seed yield and yield components. In this study, the environment accounted for the largest part of the variation in seed yield (59.6%) followed by genotype (16.8%). This finding is supported by the works of (Asrat *et al*., 2009; Kocaturk *et al*., 2019) on soybean, and Tamene *et al*. (2013) on field pea, that demonstrating the environment accounted for the largest part of the variation in seed yield followed by the genotype. Similarly, Yan and Kang (2003) reported the environment was considered as the predominant source of variation. In the current study, the largest variation in seed yield was explained by environments, which indicated the presence of different environments that can be sub-grouped into mega-environments. This result is in agreement with the work of Dessalegn *et al*. (2018) on finger millet, who reported that the difference in seed yield across environments implies that the environments are highly variable. This indicated the presence of different environments that can be sub-grouped into mega-environments, since, the largest variation in seed yield was explained by environments.

Regarding the multiplicative component, genotype by environment interaction significantly (P≤0.01) influenced seed yield. According to the result of AMMI, (14.8%) was explained due to GEI effects on the variation in the total sum of squares (Table 6). This finding conforms to the report of Kocaturk *et al*. (2019) on soybean, who reported that the GE interaction explained (20.84%) of the total variation. The highest share of the total sum squares was contributed by environment and genotype total sums of squares as compared to the GEI, with large differences among environmental means causing most of the variation in seed yield of mung bean. This finding also coincides with the previous works on cowpea (Akande, 2009; Sarvamangala *et al*., 2010; Nunes *et al*., 2014; Tariku *et al*., 2018), Zali *et al*. (2012) in chickpea who reported that the larger contribution of GEI than genotype effect for the observed yield variation was due to large contribution of the environment in GEI.

The AMMI model extracted two significant Interaction Principal Component Axis (IPCAs) from the interaction component (Table 6). The multiplicative component of the AMMI further revealed that the mean squares were highly significant (P≤0.01) for the first interaction principal component axis (IPCA1) and significant (P≤0.05) for the second interaction principal component axis (IPCA2). Hence, these two IPCAs (IPCA1 and IPCA2) captured 47.4% and 7.4% of the interaction of sum squares, respectively accounting for a total of 54.8% of the total GEI sum of squares. Moreover, the IPCA1 mean square was greater than that of IPCA2, indicating the presence of differences in seed yield performance of the genotypes as a result of GEI. This finding is in agreement with the previous reports by Tamene *et al*. (2013) for field pea, Hagos and Fetien (2013) for bread wheat, and Ashraf *et al*. (2016) on flax. The first and the second IPCA together explained 54.8% of the variability in seed yield of mung beans due to GEI. This indicated that the first two IPCAs had exerted a significant contribution to the variations in GEI.

In this study, the two IPCA's accounted for greater than 50% of the interaction of sum square and were significant. Therefore, the AMMI model with the first and second multiplicative terms was adequate for cross-validation of seed yield variation explained by GEI that can easily be visualized with the aid of the biplot whereas, the residual was considered as noise. The results were in agreement with the several authors who took the first two IPCAs for GGE biplot analysis for different crops (Zobel *et al*., 1988; Mohammadi and Mahmoodi 2008; Asrat *et al*., 2009; Hagos and Fetien, 2013; Tamene *et al*., 2013; Kilic, 2014; Pržulj *et al*., 2015; Dyulgerova and Dyulgerov, 2019) which showed a similar magnitude of GEI variance revealed by the first two principal components of GEI and indicated that AMMI with the first two multiplicative terms was the best predictive model.

Table 6: AMMI ANOVA for seed yield (kg ha^{-1}) of 15 mung bean genotypes

Source	DF	SS	MS	Sum of squares explained (%)	GxE Interaction explained (%)	Cumulative explained (%)
Total	269	238218571	885571			
Treatments	89	132841482	1492601***	33.6		
Genotypes	14	10414899	743921**	16.8		
Environments	5	76569237	5313847***	59.6		
Block	12	30842052	2570171ns	5.79		
Interactions	70	45857346	655105**	14.8		
IPCA 1	18	37882199	2104567**		47.4	47.4
IPCA 2	16	5250316	328145*		7.4	54.8
Residuals	36	2724831	75690*	1.7		
Error	168	74535037	443661			

E = Environments, G = Genotypes, SS = Sum of Squares, MS = Mean Squares, DF = Degree of Freedom, IPCA1 = Interaction Principal Component Analysis Axis 1 scores, IPCA2 = Interaction Principal Components Analysis Axis 2 scores.

3.3.2. *GGE biplot analysis*

The GGE biplot displays the genotypic main effect (G) and genotype by environment (G x E) interaction of a genotype by the environment data set (Yan *et al*., 2000). The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 75.22% and 14.06% of the GGE sum of squares, respectively (Figure 1).

3.3.3. *Mean performance and stability of genotypes*

Desirable genotypes are those located close to the ideal genotype. Genotypes G8, G6, and G15 can be thus used as benchmarks for the evaluation of mung bean genotypes since they are placed near the ideal genotype and found near the first concentric circle, and thus are desirable genotypes. This finding is in line with the reports by Muez *et al*. (2015), who found outstanding genotypes near to the ideal genotype in wheat. Based on the average environmental coordination (AEC) method, genotypes (G4, G10, and G11) were the most unstable and undesirable genotypes across the tested environment since these genotypes had a larger distance from the origin of the biplot and were found far distant from the first concentric circle (Figure 1).

The ideal genotype is the one presenting high means and is identified based on the length of the vector; thus, the longer the PC1 and PC2 without projections and the closer to the concentric circle, the better the genotype (Santos *et al*., 2017). Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero GE, as represented by the small circle with an arrow pointing to it (Yan, 2001). Thus, starting from the middle concentric circle pointed with arrow concentric circles were drawn to help visualize the distance between genotypes and the ideal genotype (Yan and Tinker, 2006). Based on this, the genotype (G13) was considered the ideal genotype and was followed by the genotype (G6). Genotypes were classified in the following order according to their performances: Genotype (G13) > (G6) ≅ (G8) > (G15) > (G9) ≅ (G2) ≅ (G14) ≅ (G7) > (G1) ≅ (G12) ≅ (G3) > (G5) > (G10) > (G11) > (G4). A position in either direction away from the biplot origin, on this axis, indicates greater GEI and reduced stability (Yan, 2002). Genotypes (G8, G6, and G15) are located on the next consecutive concentric circles, and these genotypes are considered the most desirable genotypes. On the other hand, undesirable genotypes were those very far distant from the first concentric circle; namely, genotypes (G4, G10, and G11) in Figure 1.

The ranking of fifteen mung bean genotypes based on their mean yield and stability performance is shown in Figure 2. The line passing through the bi-plot origin is called the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang, 2003). The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa indicating a greater G×E interaction effect and reduced stability in either direction away from the biplot origin and separates genotypes with below-average means from those with above-average means (Bhartiya *et al*., 2017). For selection, the ideal genotypes are those with both high mean yield and high stability. The

average yield of a genotype is approximated by the projections of their markers on the AEC x-axis while the stability is determined by the projection onto the AEC ordinate line (y-axis) (Yan and Rajcan, 2002). As shown in Figure 2, the genotypes further along the average tester axis (ATA), away from the biplot origin and in direction of the arrow (to the left), exhibited higher mean performance. Therefore, the genotypes that gave higher yield values were in the order of (G8) > (G13) > (G6) > (G14) > (G15); while the lowest yielding genotype was (G4). Generally, in the bi-plot, as shown in Figure 2, the genotypes G6 (NLLP-MGC-24), G15 (NVL-1), and G8 (VC1973A) can be considered as genotypes with both high yield and stable performance since these genotypes are close to the origin and have the shortest vector from the ATC. The genotypes with the highest yielding performance but relatively low stability were G7 (NLLP-MGC-27), whereas the genotype with low yield and low stability were G5 (NLLP-MGC-22) and G10 (VC6368 (46-40-4)). The other genotypes on the left side of the line with no arrow have yield performance greater than the mean yield and the genotypes on the right side of this line had yields less than the mean yield.

As indicated in the bi-plot (Figure 2) the genotypes, G6 (NLLP-MGC-24), G15 (Acc0013), and G8 (VC1973A) were the most stable genotypes with better mean yield performance. The genotypes G1 (NLLP-MGC-01), G14 (N-26), G10 (VC6368 (46-40-4)), G12 (Acc002), G7 (NLLP-MGC-27), and G5 (NLLP-MGC-22) can be recommended for specific adaptation, whereas genotypes G6 (NLLP-MGC-24), G9 (NLLP-MGC-09), G8 (NLLP-MGC-08), G15 (NVL-1), G11 (NLLP-MGC-06), G4 (NLLP-MGC-20), G13 (Acc006), and G3 (NLLP-MGC-15) can relatively be recommended for wider adaptation.

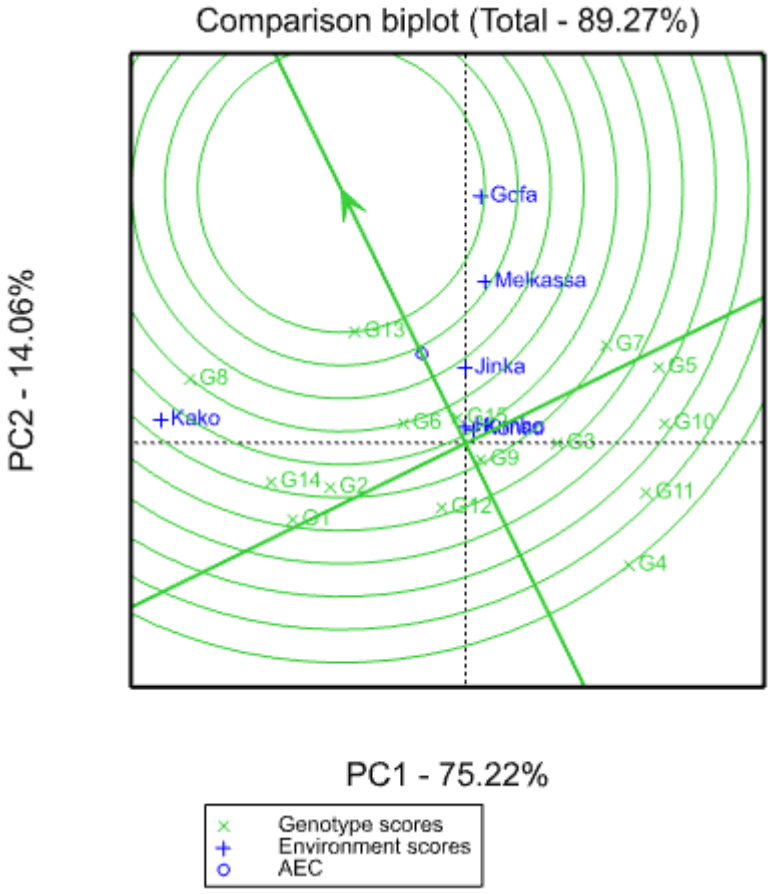

Figure 2: GGE biplot-based genotype-focused scaling for comparison of the genotypes with the stable genotype

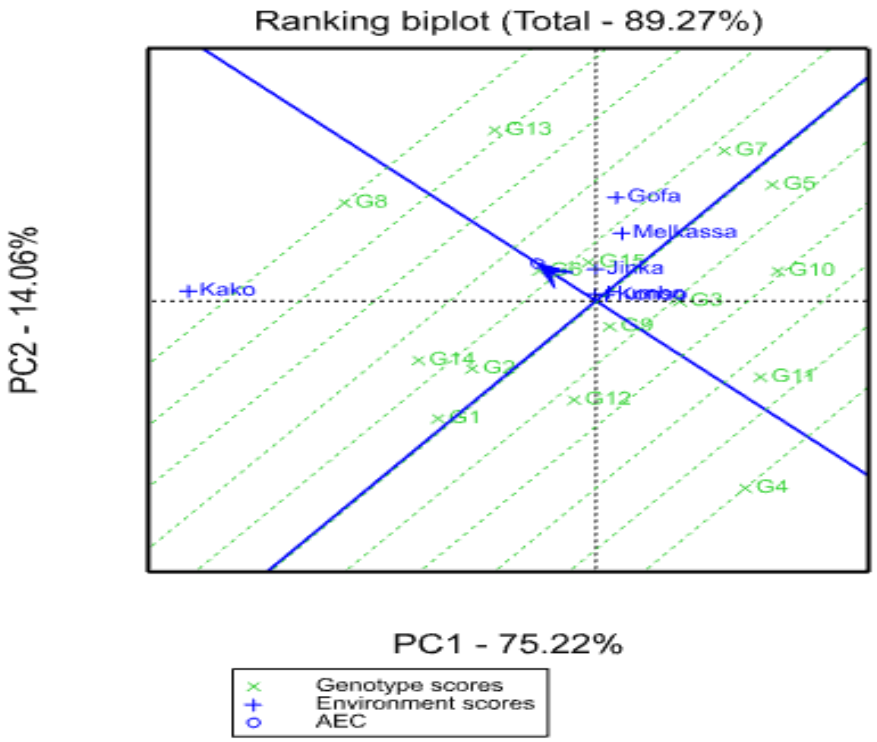

Figure 2: The AEC Views of the GGE Biplot Based on Environment-focused Scaling for the Mean Performance and Stability of Genotypes

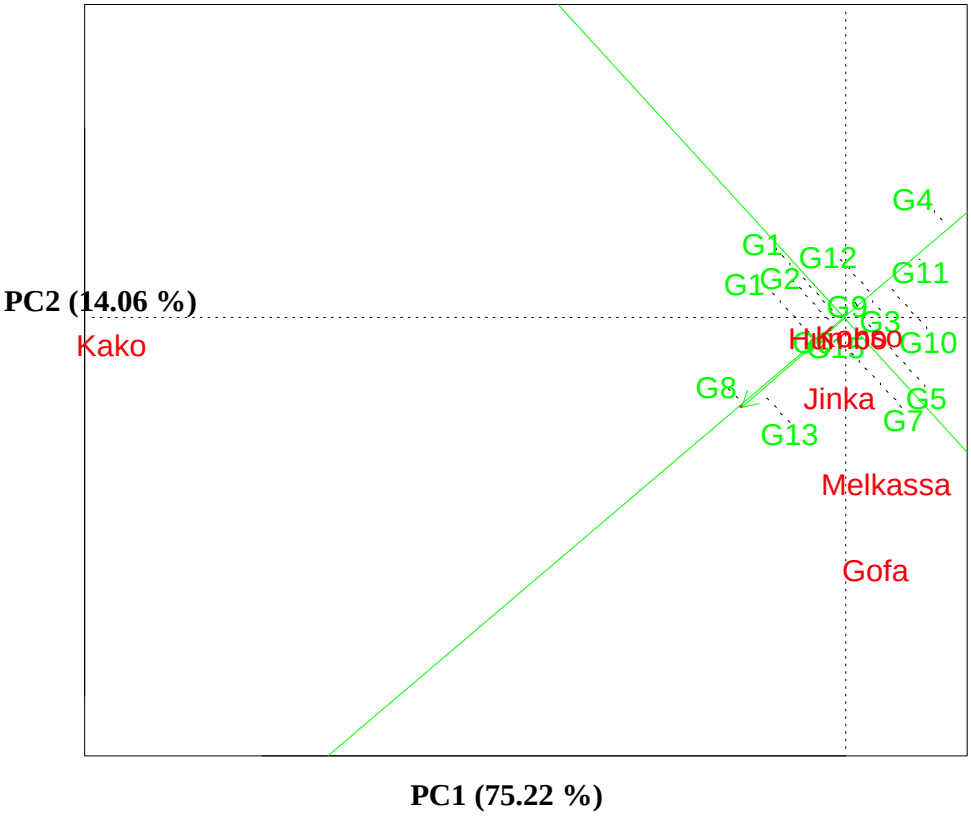

Figure 3: Mean and stability view of the GGE bi-plot for mung bean genotypes evaluated at six environments

3.3.4. *'Which-Won-Where' patterns of genotypes and environments*

As indicated in Table 6, the residual mean square for seed yield was significant (P≤0.05), suggesting that the importance of constructing an AMMI biplot is very low or good for nothing. The polygon view of the GGE biplot is the best way the identification winning genotypes by visualizing the interaction patterns between genotypes and environments (Yan *et al*., 2000; Yan and Kang, 2003). Therefore; the GGE biplot has been used in a variety of trials to identify the best-performing genotype(s) across environments, and categorize the best genotypes for specific environments, whereby specific genotypes can be recommended to specific environments (Yan and Kang, 2003; Yan and Tinker, 2006).

Therefore, it was necessary to construct a GGE biplot for visual observation to understand which genotypes were best performed in which environment or which genotypes were stable and unstable (Figure 4). A polygon view of GGE was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. Genotypes (G8, G13, G7, G5, G4, and G1) were the vertex genotypes, having the largest distance from the origin and were more responsive to environmental changes and gave high yield except G4 were considered as specially adapted genotypes. The genotypes located on vertices of polygon performed either best or poorest in one or more environments. Therefore, these genotypes are best in the environment lying within their respective sector in the polygon view of the GGE-biplot (Yan and Tinker, 2006); thus these genotypes are considered specifically adapted. The vertex genotypes in each sector are the best genotype in environments whose markers fall into the respective sector. If a genotype at an angular vertex of the polygon falls within one sector with an environment marker (or with several markers), that means that the yield capacity of this genotype was the highest in this particular environment. Environments within the same sector share the same winning genotypes and environments in different sectors have different winning genotypes. Genotypes (G8 and G13) performed well at Kako while genotypes (G5 and G7) performed well at Gofa and Melkassa and were moderately adapted to Jinka. Two vertex genotypes, G1, and G4 had the highest yield in none of the environments (Figure 4). Genotypes close to the origin of axes have wider adaptation (Fetein and Bjornstand, 2009). In this study, the genotypes (G3, G9, G2, G12, G15, G6, G11, and G14) were located within the polygon and were less responsive. This finding is supported by the previous works (Yan *et al.,* 2001; Yan and Tinker, 2006), who reported that the genotypes within the polygon and nearer to origin were less responsive than the vertex genotypes.

The polygon view of the GGE-biplot analysis in (Figure 4) helps to detect cross-over and non-crossover genotype-by-environment interaction and to analyze possible mega environments in multi-location yield trials (Yan *et al*., 2007). The perpendicular lines were equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. Line 1 is between G8 and G13 and line 2 is perpendicular to side G13 and G7; line 3 is perpendicular to side G7 and G5; lines 4 and 5 are perpendicular to side G10 and G11; similarly, line 6 is perpendicular to side G4 and G1; while, line 7 is perpendicular to side G1 and G8. The environments fall into two quadrants while the genotypes are into four quadrants. In the GGE biplot, the vectors from the biplot center divided the graph into seven sectors.

The GGE biplot presented in Figure 4, indicating that the best performing genotypes for a specific environment and the group of environments. This finding is following the results of (Yan *et al.,* 2007; Dessalegn *et al.,* 2018) who reported that when different environments fell into different sectors; it shows that they had different high-yielding cultivars for those sectors, and also the presence of a cross-over interaction. The rays of the bi-plot divided the plot into seven sections. The environments appeared in three of them, revealing two mega environments. The vertex families for each quadrant represented the genotypes with the highest yield in the specific environment hence the highest yielding genotypes were identified for each sector. This finding is in agreement with the previous reports on soybean genotypes (Bhartiya *et al*., 2017; Ramos *et al*., 2017; Kocaturk *et al*., 2019), who reported that the GGE biplot created for soybean genotypes in seed yield was divided into six or eight sectors. When using the first two principal components, two clusters of environments (mega-environments) were formed using the GGE biplot methodology, indicating the environmental groupings, which suggests the possible existence of

different mega-environments. The polygon view of the GGE biplot indicated the presence of a crossover G x E interaction as the environments fell in different sectors of the polygon view and had different high-yielding genotypes (Yan and Kang, 2003). The current test locations could be grouped into two different mung bean-growing mega-environments. Thus, in our studies, the first mega-environment consists of environments Jinka, Humbo, Konso, Gofa, and Melkassa whereby genotypes (G5 and G7) in Gofa and Melkassa produce the highest yield (Figure 4), while the genotypes (G8 and G13) are producing the highest yield in Jinka, Humbo, and Konso.

3.3.5. *Discriminating and representativeness of the test environments*

The IPCA scores of the genotype in the AMMI analysis signify the adaptability of the genotypes across environments and the relationship between genotypes and environments. This is supported by the reports of (Zobel *et al*., 1988; Gauch and Zobel, 1996). Therefore, genotypes with small scores close to zero have low interactions and were stable, whereas, genotypes with large scores have high interactions and were unstable. In the present investigation, IPCA1 alone and despite positive or negative signs, genotypes (G6, G9, and G12) had small scores close to zero and were stable, while the genotypes (G10, G3, G5, G7, G8, G11, G1, and G14) had large IPCA1 scores and far from zero were unstable (Figure 5). The genotype (G9) had a small and positive sign of IPCA1 scores and thus this genotype was stable across the environments. Oliveira *et al*. (2014) and Tariku *et al*. (2018) reported that the genotypes with lower IPCA1 scores would produce lower G×E interaction effects than those with higher IPCA1 scores and have less variable yields or more stable across environments. In the present study G3, G13, G8, G5, G7, G1, G14, and G10 had more responsive since they were away from the origin whereas the genotypes G4, G11, and G15 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G6, G9 and G12 were closest to the origin and hence had almost no interaction forces. Genotypes (G9, G11, and G4) had a positive sign of IPCA1 scores and had a shorter vector to the origin. Here the genotype (G9) is adapted to Jinka while genotypes (G4 and G11) are adapted to Humbo, genotypes (G5 and G7) are adapted to Gofa and Melkassa, while genotype (G3) is adapted to Konso. In contrast, the genotype (G8 and G13) was adapted to Kako with a larger and negative IPCA1 score.

As shown in Figure 5, the discriminating ability and representativeness of test environments, Kako, Konso, and Gofa were more discriminating environments with longer vectors and larger angles which provides much information about differences among genotypes. These environments cannot be used for selecting superior mung bean genotypes, but are useful in culling out unstable genotypes. Environments with longer vectors are more discriminating with the genotypes whereas environments with very short vectors are little or not informative on the genotype difference (Yan, 2002; Yan *et al*., 2007). On the other hand, if the marker of a test environment is close to the biplot center, having a short vector, all genotypes in it are similar, and this environment is not informative about their differentiation. Environments with short spokes do not exert strong interactive forces while those with long spokes exert strong interaction.

In this study, Jinka, Humbo, and Melkassa had relatively short vectors and were close to the origin, indicating that all genotypes performed similarly and therefore it might provide little or no information about the genotypes' differences. The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Therefore, it should not be used as a test environment for mung bean genotypes. As suggested by Yan and Tinker (2006), though, identification and removal of non-informative test environments as well as identification of test environments for yield evaluation trials require multiyear data. If budgetary constraints allow only a few test environments, these test environments would be the first choice. The cosine of the angle between environment vectors is used for the assessment of approximation between environments; the smaller the angle between environment vectors; the larger the correlation between them (Yan and Holland, 2010). The smaller the angle, the more representative the environment is (Yan and Tinker, 2006; Yan *et al*., 2007). Representativeness of the test environment is visualized by the angle formed between the environment vector and abscissa of the average environment axis. Correspondingly, there is a strong correlation between environments Humbo

and Konso since the cosine of the angle between these two environment vectors is small. As suggested by Yan (2001), discriminating ability and representativeness are the important properties of test environments. An ideal environment should be highly differentiating for the tested genotypes and is also representative (Yan and Kang, 2003). Thus, environments Kako, Konso, and Gofa with long vectors had high discriminating power, and environments Jinka, Humbo, and Melkassa were characterized by low discriminating power (Figure 5). Hence, environments Kako, Gofa, and Konso exerted strong interaction forces while the rest three (Jinka, Humbo, and Melkassa) did less. Therefore, the tested environments, Kako, Gofa, and Konso were more discriminating environments with longer vectors and larger angles which provides more information about differences among genotypes. Contrastingly, Jinka, Humbo, and Melkassa had relatively short vectors and were close to the origin and all genotypes performed similarly and therefore provide little or no information about the genotypes' differences (Figure 5). On the contrary, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction.

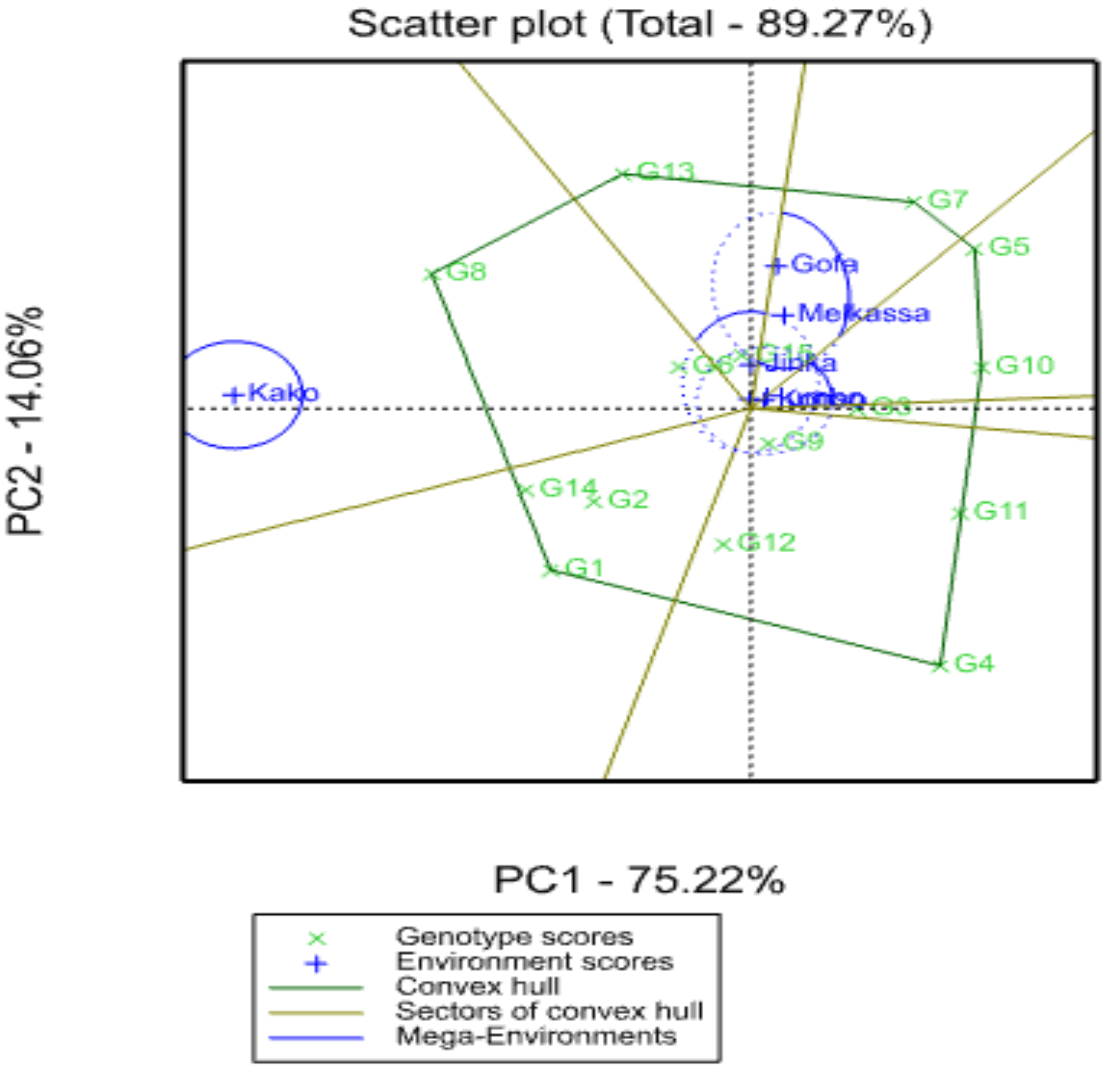

Figure 4: Polygon view of GGE biplot showing the relationship among environments and the specific ideal niches of the tested genotypes

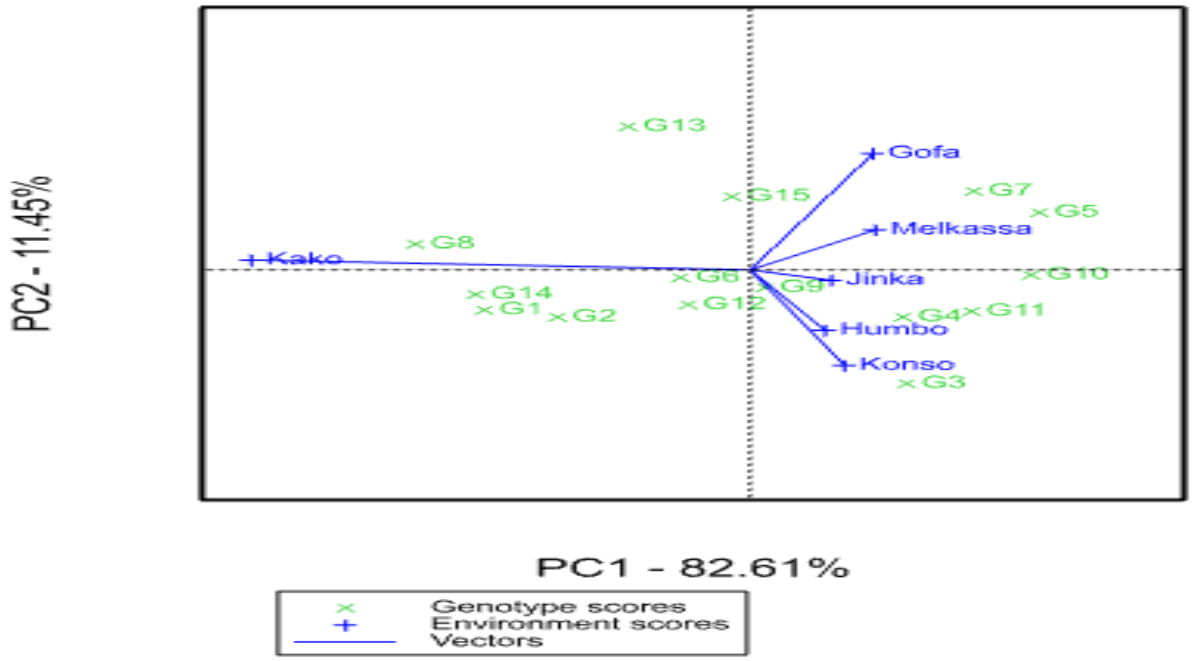

Figure 5: Discriminating power and representativeness of test environments

3.3.6. *AMMI stability value (ASV) and yield stability index (YSI)*

According to the ASV model, genotypes (G9), (G15), and (G12) were stable and high yielders among the tested genotypes, indicating that the yield performance and stability had the same trend in the present study (Table 7). Similarly, Annicchiarico (2002) noted the dynamic of stable genotype and yield response that is always parallel to the mean response of the tested environments. Such findings have been observed by Getachew *et al*. (2015) in chickpea, Nigussie *et al*. (2015) in common bean and Tariku *et al*. (2018) in cowpea. However, genotypes G10, G8, and G14 were the most unstable. These genotypes are adapted to specific and favorable environments. Likewise, Lotan *et al*. (2014) reported genotypes with the higher IPCA score and AMMI stability values were more specifically adapted to a certain environment. The principles of stability alone might not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance. Therefore, as per the suggestion (Hassan *et al*., 2012; Lotan *et al*., 2014), the stability per se should however not be the only parameter for selection because the most stable genotypes would not necessarily give the best yield performance. Therefore, there is a need for approaches that incorporate both mean yield and stability in a single index. To this end; the yield stability index (YSI) method incorporates both yield and stability into a single index, reducing the problem of using only yield stability as the single criteria for the selection of genotypes. Genotypes with the least YSI values are considered the most stable with a high grain yield (Bose *et al*., 2014; Lotan *et al*., 2014). Genotypes G6 and G13 were the most stable with low YSI values and high mean performance. Therefore, the yield stability index (YSI) discriminated genotypes G6 and G13 with high adaptability and high grain yield (Table 7). Thus, according to the YSI method, the most desirable genotypes which can be considered as widely adapted and with seed yield above the grand mean (1164 kg ha^{-1}) among 15 mung bean genotypes are presented in Table 7. Similarly, Hassan *et al*. (2012) indicated that both yield and stability should be considered simultaneously to exploit the useful effect of GE interaction and to make the selection of the genotypes for a diverse environment. Conversely, genotypes like G1, G4, G5, G9, G10, G11, G12, and G15 had high YSI values and below the grand mean (1164 kg ha^{-1}) seed yield performance, which indicates instability of the genotypes across the tested environments.

Table 7: Mean seed yield (kg ha^{-1}) of fifteen mung bean genotypes, AMMI stability values (ASV), Ranks, yield stability index, IPCA1, and IPCA2 scores

Genotypes	IPCA1	IPCA2	ASV	R^a	MSY	R^y	YSI
G1	-19.98967	5.99378	6.89	11	1161	8	19
G2	-14.48429	7.06782	5.55	8	1241	6	14
G3	11.77525	17.02819	4.89	7	1259	5	12
G4	11.49340	7.04205	4.87	6	696	15	21
G5	21.74822	-8.60742	6.95	12	1129	9	21
G6	-5.21787	1.15422	3.68	4	1290	3	7
G7	16.79039	-11.77015	5.84	9	1192	7	16
G8	-25.16245	-3.87765	8.60	14	1580	1	15
G9	1.11140	2.62966	1.56	1	1125	11	12
G10	21.12314	0.73750	10.82	15	1053	12	27
G11	16.64242	6.21678	6.12	10	905	14	24
G12	-4.66412	5.19843	3.06	3	1044	13	16
G13	-9.17042	-21.46960	4.47	5	1375	2	7
G14	-20.64006	3.65807	7.60	13	1278	4	17
G15	-1.35534	-11.00170	2.08	2	1128	10	12
Grand Mean					1164		

ASV = AMMI Stability Value, R^a = rank of ASV, MSY = means of seed yield, R^y = rank of seed yield, YSI = Yield Stability Index, G1= NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 =, VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1

4. Conclusion

Combined analysis of variance shows that genotype, environment, and G x E interaction are highly significant, which indicate the existence of a wide range of variation between the genotypes, environments, and interactions.

According to AMMI and GGE biplot methods, G6, G13, and G3 were identified as stable and high yielder genotypes across the environments. Besides, the results of the yield stability index and AMMI stability values identified genotypes G6, G13 and G3 as high yielding with stable performance across the environments and be recommended for diverse environments. Therefore, genotype G13, which fell into the center of concentric circles, was the ideal genotype in terms of higher yield ability and stability, compared with the rest of the genotypes. Also, genotypes, G6, G8 and G15 can be considered as desirable genotypes. In this study, genotype G13, which fell in the first concentric circle, was the ideal genotype in terms of higher-yielding ability and can be used as a benchmark for evaluation of mung bean variety development in future breeding programs. However, G1, G4, G5, G9, G10, G11, G12, and G15 were identified as least stable with high YSI and ASV values that can be recommended for specific environments.

In general, this study has provided highly valuable information on the yield stability status of the mung bean genotypes and the best environments for future improvement programs in Ethiopia. Therefore, the mung bean improvement strategy in Ethiopia should be based on the performance of the genotypes across environments. Generally, GGE biplot analysis, AMMI, and Eberhart and Russell's model revealed that genotype G13 was stable and high yielding.

Acknowledgment

The authors extend their gratitude to the Southern Agricultural Research Institute for the financial support of this research. Also, the authors' deep gratitude and acknowledgment go to Melkassa Agricultural Research Center for providing the mung bean genotypes for this study. The authors also recognize Jinka Agricultural Research Center for its administrative facilitation during the implementation of this research.

Conflict of interest

The author declares that there is no conflict of interest.

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Genetic Variability of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes under Irrigation Condition in South Omo, Southern Ethiopia

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Received: March 9, 2022 Accepted: June 27, 2022

Abstract: *Bread wheat (Triticum aestivum L), is a self-pollinating annual plant in the true grass family Gramineae (Poaceae), and is the largest cereal crop extensively grown as staple food source in the world. The objective of this study was to assess the genetic variability and genetic diversity among genotypes using a triple lattice design in Bena-Tsemay district in 2020 under irrigation conditions. The analysis of variance revealed highly significant variation (P≤0.01) among the genotypes for yield and yield components. Wide ranges of the mean values were observed for most of the traits like grain yield, plant height, days to maturity, and grain filling period, indicating the existence of variations among the tested genotypes. Moderate Phenotypic coefficient of variability and genotypic coefficient of variability was recorded for days to maturity, grain yield, and harvest index; while high heritability values were observed for plant height and days to heading. Among the studied characters grain yield showed high genetic advance. The D^2 analysis grouped the 36 genotypes into six clusters. The maximum inter-cluster distance was observed between clusters V and VI (D^2=777.99), followed by that between clusters III and V (D^2=525.49) and I and III (D^2=310.81), which showed that the genotypes included in these clusters are genetically more divergent from each other than those in any other clusters. Principal components (PC1 to PC6) having Eigen value greater than one, accounted for 75.6% of the total variation. The first three principal components, i.e., PC1, PC2, and PC3, with values of 22.0, 35.7, and 47.9, respectively, contributed more to the total variation. Generally, the results of this study showed the presence of variations among the studied genotypes for agro-morphology traits that could allow selection and/or hybridization of genotypes.*

Keywords: Genetic advance, GCV, Heritability, PCV

1. Introduction

Bread wheat (Triticum aestivum L), a self-pollinating annual plant in the true grass family Gramineae (Poaceae), is the largest cereal crop extensively grown as staple food source in the world (Mollasadeghi and Shahryari, 2011). It is one of the most important exports and strategic cereal crops in the world and in Ethiopia in terms of production and utilization. Ethiopia is the first largest wheat producer in Sub-Saharan Africa followed by South Africa and fourth in Africa with the harvested area of 1.8 million hectares with a production of 5.3 million tons and an average yield of 2.97 t ha-1 (CSA, 2021). The narrow genetic background has rendered improved varieties less tolerant to biotic and abiotic stresses (Maqbool *et al.*, 2010).

Reduction in genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes (Aremu, 2012). Therefore, precise information on the nature and degree of genetic variability and divergence present in wheat would help to select parents for evolving superior varieties. For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003). From 1974 to 2011, the country's research efforts

resulted in the development of more than 87 bread wheat varieties: thirty varieties from 1974 to 1997 (Degewione and Alamerew, 2013), and fifty-seven varieties from 1998 to 2011, with some of them in production in various agro-ecological zones. Significant genetic variability was reported in bread wheat (Tarekegne *et al*., 1994; Degewione et al., 2013). Previous research has shown that in the study area, little information is generated about the genetic variability of yield and yield component attributes of bread wheat genotypes under irrigation. Thus, the present study was conducted to assess the extent of genetic variability of yield and yield-related traits of bread wheat genotypes under irrigation conditions.

2. Materials and Methods

2.1. Description of the study area

The genotypes were tested at Bena-Tsemay Weyito Nasa Agricultural-Farm in 2019/2020 E.C. The experimental site has an altitude of 550 m a.s.l. with an annual rainfall of 750 mm with an average minimum and maximum temperature of 22 °C and 32°C, respectively. The soil type of the site is classified as vertisol and the textural class of the experimental area is sandy loam soil with a pH of 7.9-8.1 (Haileslassie *et al*., 2015).

2.2. Experimental materials

The experimental materials consisted of 36 bread wheat (*Triticum aestivum*) genotypes including nine standard checks (Fentale, ADEL-2, *Fentale-2*, Atila-7, GAMBO, Amibara, Amibara-2, LUCY, and *Kakaba*). The genotypes were obtained from the National Wheat Research Program, specifically from Werer (WARC) Agricultural Research Center. The genotypes were selected based on adaptation to heat stress and classified under lowland type.

2.3. Experimental design and trial management

The experiment was carried out in a 6 x 6 triple Lattice design comprising six incomplete blocks where each block contains 6 test entries and 4 checks (randomly allocated) with a total of 36 genotypes in each block. The genotypes were grown under irrigation conditions. Each genotype was sown in six rows of 1.8 m long and 30 cm apart, with a seed rate of 7.5g, 120 kg/h. Weeds were controlled manually by hand weeding. Planting was done by hand drilling on July 05, 2011, EC. Recommended fertilizer rate of 100kg/ha NPSB in (19% N, 38%P: 7% S, and 2.5% B) at the rate of 50 kg ha^{-1}in the shallow furrow depths and mixed with soil at the same time during sowing.

2.4. Statistical analysis

2.4.1. Analysis of variance

The analysis of variance (ANOVA) was carried out to dissect total variability of the entries into sources attributable to genotype and error using the SAS software version (9.2) (SAS, 2008). The statistical model for the augmented design was the same as that of the randomized complete block design (Federer, 1956) as indicated below [1].

$$yij = \mu + gi + cj + \beta j + \varepsilon ij \quad [1]$$

Where

- yij = observation of treatment i in jth block
- μ = general mean,
- g = effect of test treatment,
- cj = effect of control treatments in a jth block
- βj = block effects
- ε = error

2.4.2. Estimation of variance components

The phenotypic, genotypic, and environmental variances were calculated as indicated below.

$$\sigma 2\ p = \sigma 2\ g + \sigma 2\ e \quad [2]$$

Where

- σ2 p = phenotype variance
- σ2g = genotypic variance
- σ2 e = environmental variance

$$\sigma 2\ g = \frac{[\mathrm{Msg} - \mathrm{Mse}]}{r} \quad [3]$$

Where

- σ2g = genotypic variance
- MTS = MST mean square treatment
- σ2e = environmental variance
- Msg = mean square of genotype,
- Mse = mean square of error,
- r = number of replications

$$\mathrm{PCV} = \left(\frac{(\sigma 2\mathrm{p})}{\bar{x}}\right) * 100 \quad [4]$$

$$\mathrm{GCV} = \left(\frac{(\sigma 2\mathrm{g})}{\bar{x}}\right) * 100 \quad [5]$$

Where

- $\bar{x}$ = Grand mean of the character studied
- PCV = phenotypic coefficient of variability
- GCV = genotypic coefficient of variability

PCV and GCV values were categorized as low (0-10), moderate (10-20), and high (>20) as indicated by Burton and de vane (1953).

2.5. Broad sense heritability

Broad sense heritability (H^2B) for all characters was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage [6] according to the methods suggested by Falconer *et al*. (1996).

$$H^2B = \left(\frac{\sigma 2g}{\sigma 2p}\right) * 100 \quad [6]$$

Broad sense heritability values were categorized as High (>60%), Moderate (30-60%), and Low (0-30% as described by Johnson et al. (1955).

2.6. Genetic advance under selection

The expected genetic advance expressed under selection (GA) in a broad sense, assuming selection intensity of 5% of the superior progeny was estimated in accordance with the methodology methods illustrated by Johnson *et al*. (1955).

$$\mathrm{GA} = K * SDp * H2 \quad [7]$$

Where

- GA = Genetic advance
- SDp = Phenotypic standard deviation on mean basis
- H2 = Heritability in the broad sense.
- K = the standardized selection differential at 5% selection intensity (K = 2.063).

2.7. Genetic advance as percent of mean

Genetic advance as percent of mean (GAM) was estimated following the formula described by (reference), which is indicated below [8].

$$GAM = \left(\frac{\mathrm{GA}}{\bar{x}}\right) * 100 \quad [8]$$

Where

- GAM = Genetic advance as percent of mean,
- GA = Genetic advance

Genetic advance as percent of mean was categorized as low (0 - 10%), moderate (10 – 20%) and high (>20%) as suggested by Johnson *et al.* (1955).

3. Results and Discussion

3.1. Analysis of variance

Mean squares of the 13 yield and yield-related traits from the analysis of variance (ANOVA) showed highly significant differences among genotypes ($P \leq 0.01$) for days to heading, days to maturity, grain filling period, 1000 kernel weight, kernel number, plant height, spike length, number of spikelet's per spike and grains yield (Table1). Significant differences were observed in the number of productive tillers per plant, biomass yield, and seeds per spike. In line with the present results, many scholars also reported highly significant differences among all the wheat genotypes for all the traits (Mohammed *et al*., 2011; Dergicho *et al*., 2015; Gezahegn *et al*., 2015). Significant differences among genotypes for all traits except for plant height and number of spike lets per plant were reported by Adhiena *et.al.* 2016. Similarly, moderate values for the phenotypic and genotypic coefficients of variation in wheat were reported by Kolakar *et al*. (2012), Mohammed *et al*. (2011), and Berhanu *et al*. (2017) for grain yield, biomass yield, plant height, spike length, number of productive tillers per plant, number of spikelets per spike, number of grains per spike and 1000-grain weight.

Table 1: Mean squares of thirty six bread wheat genotypes evaluated at Bena-Tsemay weyito during the 2020 growing season

Traits	Replication	Block within rep. (Adj.)(d.f=15)	Treatment (df=35) unadj.)	Treatment (Adj.)	Intra block error (DF = 55)	RCBD error	RE (%)	CV (%)
Days to heading	13.12*	0.78**	140.76	109.11***	0.82	0.8	98.9323	2.272
Grain filling period	0.25ns	2.751*	297.14	248.67***	1.42	1.70	108.78	1.727
Days to maturity	2.56ns	1.08ns	1469.03	1098.59***	0.97	0.99	100.22	1.720
Plant height (Ph)	4.014ns	5.21ns	45.69	131.08***	7.11	6.7060	94.26	4.721
No. of fertile tillers/plant	3.45**	0.59ns	1.064	0.96*	0.58	0.5880	100.00	23.658
Spike length (cm)	0.031ns	2.36ns	4.40	4.32 **	2.21	2.2484	100.09	14.676
No. of spikelet/spike	0.703ns	0.55ns	3.02	2.49***	0.38	0.4180	102.91	18.712
No. of kernels/ spike	90.19**	16.34ns	35.85	31.41**	11.66	12.6690	102.32	19.888
Seeds/spike	0.70ns	0.55ns	3.02	60.51*	0.38	0.41	102.00	6.01
1000-kernel weight (g)	46.001*	13.61ns	25.71	20.91**	8.39	9.5129	104.71	14.521
Grain yield (kg/ha)	971899	1202694	32942	1421576***	1165619	1173564	100.02	6.086
Biomass yield (t/ha)	3.91**	0.42ns	1.4995	1.23*	0.49	0.4800	97.20	29.881

Note: ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively, DF = degree freedom, RE = relative efficiency, RCBD = completely randomized block design, CV= coefficient of variations, adj. = adjusted treatment, unadj. = unadjusted treatment

3.2. Phenotypic and genotypic coefficient of variability

The PCV of traits ranged from 15.87% for grain filling period to 92.85% for Plant height whereas GCV ranged from 8.25% for the spike length to 85.76% for plant height (Table 4). In the present study, high PCV coupled with high GCV of traits were observed for days to maturity, grain yield, and biomass yield and harvest index. Considering the GCV estimates, number of fertile tillers per plant, thousand-kernel weight, and kernel number and seeds per spike exhibited moderate values. Moderate GCV with moderate PCV was observed for a number of grain filling periods, thousand-kernel weight, and spike length. Accordingly, the genotypes coefficient of variation (GCV) ranged from 5.67% for the plant height to 14.74% for a number of fertile tillers plant-1, whereas the phenotypic variation (PCV) ranged from 7.06% for days to maturity to 19.08% for a number of fertile tillers plant-1 (Table 4).

Moderate GCV coupled with moderate PCV was observed for the grain filling period and thousand seed weight. Considering the GCV estimates, days to heading, fertile tiller per plant, and seeds per spike exhibited moderate values. The studied characters that had high GCV coupled with high PCV values were days to maturity, plant height, spikelet's number per spike, grain yield, biomass yield, and harvest index.

The high PCV and GCV indicate that selection may be effective based on these traits. In support of such a study, several workers reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight, and plant height in wheat. Medium PCV and GCV values were recorded for the rest of the characters. The high and medium PCV and GCV indicate that selection may be effective based on these traits. In support of this study, Tarekegne et al. (1994) reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight, and plant height in wheat. In addition, the findings of Ali and Shakor (2012) reported medium PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione *et al*. (2013) reported medium PCV and GCV for 1000-grain weight, plant height, and days to heading in twenty-six bread wheat genotypes. Similar to the current finding, Berhanu *et al*. (2004) reported that higher GCV and PCV values were observed for grain yield, thousand-kernel weight, harvest index, tillers per plant, spikes per plant, spike length, kernels per spike, and grain protein yield while lowest GCV and PCV values (<5%) were observed for days to maturity in bread wheat. Similar results of PCV to GCV estimates for most characters were also reported by Dawit et al. (2012) and Adhiena et al. (2016).

Similar observations showed moderate values for the PCV and GCV in wheat were reported by Kolakar et al. (2012), Mohammmed et al. (2011), and Berhanu et al. (2017) for grain yield, biomass yield, plant height, number of productive tillers per plant, spike length, number of spikelets per spike, number of grains per spike and 1000-grain weight. Similar to the current finding, Berhanu et al. (2004) reported that higher GCV and PCV values for grain yield, thousand kernel weight, harvest index, tillers per plant, spikes per plant, spike length, kernels per spike, and grain protein yield while contrary lowest GCV and PCV values (< 5 %) were observed for spike length in bread wheat.

Adhiena (2015) reported high heritability for days to heading which supports this finding. Similarly, Kyosev and Desheva (2015) and Desheva and Cholakov (2014) reported a high heritability value for spike length. Kyosev and Desheva (2015) also reported high estimates of heritability for spike length with awns (74.93%), spike length without awns (80.48%), spikelets per spike (63.96%), grain weight per spike (67.47)% and thousand-grain weight (73.51%) in their study on variability, heritability, genetic advance.

3.3. Estimates of heritability In Broad Sense

In the present study, the heritability in broad sense (H^2B) estimates ranged from 19.56 % for days to heading to 100.2% for grain yield (Table 2). High heritability was noticed for days to maturity (99.87%) followed by grain filling period (98.30%), plant height (85.31), grain yield (97.67%), and the number of spikelet's per spike (64.91). Moderate heritability values were also recorded for No. of kernels/ spike, 1000-kernel weight, and biomass yield. The remaining traits like fertile tiller per plant, spike length, and seeds per spike had low heritability. High

heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from the selection. This may be attributed due to uniform environmental conditions during the conduct of the experiment. The results of the present study were in agreement with the results of El-Mohsen *et al*. (2012) who noticed higher heritability values for plant height, days to 50 percent flowering, number of productive tillers per plant, grain yield per plot, and number of grains per spike. Further, Salem *et al* (2008), and Ali et al. (2008) recorded high heritability estimates for grain yield, the number of kernels per the main spike, plant height, thousand kernel weights, and the number of tillers per plant.

The results obtained in the present study are similar to that of results reported by El-Mohsen *et al*., (2012) and Farshadfar and Mohammed (2012). Rahim *et al*. (2010) noticed higher heritability value for plant height, days to 50% flowering, the number of productive tillers per meter length, grain yield per plot, and the number of grains per spike. Awale *et al*. (2013) also reported high heritability values for plant height, tillers per meter, and spike length. In contrary with the current result, Berhanu *et al*. (2017) reported moderate heritability for grain filling period, kernels per spike, plant height, biomass, thousand-kernel weight in bread wheat genotypes. The present results were also in line with the results of Dergicho *et al*. (2015) who reported high heritability was observed for, days to heading, thousand-grain weight, grain filling period, days to maturity, spike length, and the number of spikelets per spike in 68 bread wheat genotypes. Jericho *et al*. (2015) reported similar findings for high heritability associated with high genetic advance for grain yield per plot and harvest index which supports the present findings. Mohammed *et al*. (2011) and Berhanu *et al*. (2017) also reported similar results, showing relatively high estimates of genetic advance (as a percentage of mean) for grain yield and yield-related traits like the number of fertile tiller per m2, plant height, thousand-kernel weight, kernel number per spike and harvest index.

The contrasting results as compared to the present investigation, Berhanu *et al*. (2017) reported as high heritability is coupled with moderate genetic advance as percent of the mean for days to heading and days to maturity in bread wheat genotypes. This finding is in part similar to those reported by Gezahegn et al. (2015). Rehman *et al*. (2015) report explained that high heritability is coupled with high genetic advance. Contrasting results as compared to the present investigation, high heritability associated with high genetic advance noticed for days to heading, grain filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand-grain weight, and biomass yield per plot respectively by Dergicho *et al*. (2015); moderate heritability coupled with high genetic advance observed for grain yield (41.71%, 63.05%) whereas high heritability coupled with moderate genetic advance as percent of mean was observed for 1000 kernel weight (74.28%, 20.13%), and plant height (69.43%, 10.27%), respectively (Gezahegn *et al*., 2015).

3.4. Estimates of expected genetic advance

Genetic advance (GAM %) as a percentage of the mean was high for grain yield (92.08%) followed by the number of days to maturity (62.50%), the number of spikelets per spike (42.35%), biomass yield (33.92), and grain filling period (32.20%) as indicated in Table 2. plant height, spike length, days to heading, thousand-kernel weight, number of kernels per spike, seeds per spike, and harvest index showed moderate GAM. It was also moderate for seeds per spike (18.79%) and the number of kernels per spike (18.31%), harvest index (14.50%), and seeds per spike (10.12).

Accordingly, high heritability with high genetic advance as a percent of mean shows for grain yield (97.67%, 92.08%), spikelet's number per spike (64.91%, 42.35%), grain filling periods (98.30 %, 32.20%) and days to maturity (99.87%, 62.50%). High heritability coupled with moderate genetic advance as percent of mean were noticed for grain filling periods, and spike lets per spike. Moderate heritability associated with high genetic advance was observed for the number of kernels per spike, biomass yield, and harvest index, whereas moderate heritability coupled with moderate genetic advance as percent of mean was observed for seeds per spike, and harvest index.

The estimates of genetic advances help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh 2009). Accordingly, Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al*., 1955). high heritability associated with high genetic advance was observed for days to heading, grain filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand-grain weight, grain yield per plot, biomass yield per plot, and harvest index respectively. These are simply inherited traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Kalimullah *et al*. (2012) reported similar findings for plant height, biomass yield per plot, and 1000 grain weight, which supports the present studies.

Table 2: Estimates of Ranges, Mean, Phenotypic (PV) and Genotypic (GV) Coefficient of Variation, Broad Sense Heritability and Genetic Advance as Percent of Mean of traits

Traits	Range	Mean+ SE	PCV (%)	GCV (%)	H^2B (%)	GA	GAM (%)
Days to heading (days)	17-65	38.79 ± 1.16	82.89	16.21	19.56	3.67	9.46
Grain filling period(days)	42-83	57.66 ± 1.02	15.87	15.74	98.30	18.56	32.20
Days to maturity (days)	23-107	63.22 ± 2.17	30.29	30.25	99.87	39.51	62.50
Plant height (cm)	41.6-74	56.17± 0.66	92.85	85.76	85.31	1.63	2.90
fertile tillers/plant (no)	1.2-5.8	2.31 ± 0.08	30.77	12.57	17.65	0.11	4.84
spikelets/spike (no.)	2-6	3.29 ±0.16	31.62	25.60	64.91	1.39	42.35
Spike length(cm)	0.2-12.8	10.16 ±0.10	16.81	8.25	24.11	0.85	8.36
kernels/ spike (no)	10.2-41.4	17.35±0.50	24.61	14.78	46.07	3.75	18.31
Seeds per spike(no)	12-46.2	24.90±0.66	26.71	11.46	18.36	2.52	10.12
1000-kernel weight (g)	11.8-32.5	19.95 ±0.66	19.77	13.41	46.07	3.75	18.79
Grain yield (kg/ha)	183.3-1333.3	691.38±0.08	45.44	45.04	97.67	636.62	92.08
Biomass yield (kg/plot)	0.4-4.8	1.75 ±0.37	49.21	28.44	33.41	0.59	33.92

Note: PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; H2b = Broad sense heritability; GA = Genetic advance and GAM = Genetic advance as percent of mean

3.5. Clustering of genotypes

The D2 values based on the pooled mean of genotypes resulted in classifying the 36 bread wheat genotypes into six clusters (eight groups and one solitary). It was indicated that the tested bread wheat genotypes were moderately divergent. The genotypes were clustered in such a way that 40% genotypes in cluster I (38.88%), 10% in cluster II (27%), 6% genotypes in III (16.67%), 3% genotypes in cluster IV (8.33%) whereas another 2% genotypes in cluster V (5.56%) and 1% genotypes in cluster VI (2.78), respectively (Table 3). This indicates that the crossing between superior genotypes of the above diverse cluster pairs might provide desirable recombinants for developing high-yielding bread wheat varieties.

3.6. Average intra and inter-cluster distance (D2)

The average inter-cluster distance (D2) values are presented in (Table no.10). Maximum inter-cluster distance was observed between clusters V and VI (D2 = 777.98770), followed by that between clusters III and IV (D2 = 525.49337). The lowest inter-cluster distance D2 was recorded in clusters III and VI (D2=62.04524) (Table 3). According to Rahim *et al*. (2010) Hybrid of genotypes with maximum distance resulted in high yield; the crosses between those genotypes can be used in a breeding program to achieve maximum heterosis. Therefore, more emphasis should be on clusters V and VI for selecting genotypes as parent for crossing with the genotype of the cluster, which may produce new recombinants with desired traits. This indicates that the crossing between superior germ plasm of above diverse cluster pair's might provide desirable recombinants for

developing high-yielding bread wheat varieties. Similarly, Degewione and Alamerew (2013) grouped 26 bread wheat genotypes into six clusters; Shashikala (2006) grouped 169 wheat genotypes into 11 clusters.

Table 3: Average intra (bold) and inter-cluster (off-diagonal) distance values (D2) among six clusters in 36 bread wheat genotypes

	I	II	III	IV	V	VI
I	**31.14**	109.67856**	310.81179**	19.80514ns	36.66184*	506.65355**
II		**22.00**	70.91886**	63.07811**	251.71101**	205.14023**
III			**7.41**	243.29602**	525.49337 **	62.04524*
IV				**24.04**	78.46869**	436.79455**
V					**0.01**	777.98770**
VI						**13.23**

x2 = 82.529 at 5% probability level and x2 =92.010 at 1% probability level, *= Significant at 0.05 probability level ,**= Highly significant at 0.01 probability level., where = X^2 is Chi-square.

3.7. Genetic divergence

Genetic divergence analysis quantifies the genetic distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence. Divergence analysis is a technique used to categorize genotypes that are as similar as possible into one group and others into a different. D-square statistics (D2) developed by Mahalanobis (1936). It has been used to classify the divergent genotypes into different groups. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization.

The lowest intra cluster distance D2 was recorded in cluster IV (19.80514), which shows the presence of less genetic variability or diversity within this cluster. The diversity among clusters or inter cluster distance D2 ranged from 85.15 to 174.32. Cluster V and VI showed maximum inter cluster distance of (D2 = 777.98770), followed by that between clusters III and IV (D2 = 525.49337) and I and VI (D2 = 506.65355). The lowest inter cluster distance was noticed between clusters I and IV (19.80514), followed by that between clusters I and V (36.66184). Evaluation of genetic diversity can be useful for the selection of the most efficient genotypes. The results of this study showed the presence of a high genetic divergence among wheat genotypes, which is similar to the findings of Ali et al. (2008) who reported that cluster analysis can be useful for finding high yielding wheat genotypes. According to Rahim et al. (2010) hybrids genotypes with maximum distance resulted in high yield. Thus the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Therefore, more emphasis should be given on cluster V and VI for selecting genotypes as parents for crossing with the genotypes of cluster, which may produce new recombinants with desired traits.

The chi-square test for the clusters indicated that there was a statistically significant difference in all characters (Table 7). The $\chi 2$- test for the six clusters indicated that there was a statistically significant difference in all characters.

Table 4: Bread wheat genotypes in six clusters tested based on D2 analysis

Clusters	Number and (%) of Genotypes	Genotypes (G*)
I	14 (38.88%)	G13,G16,G22,G14,G15,G10,G11,G25,G7,G8,G26,G28,D5,G33
II	10 (27%)	G30, G32, G3 ,G19, G34, G36, G17, G18, G2, G9
III	6 (16.67%)	G27, G31, G21, G29, G1,G24
IV	3(8.33%)	G12 , G23, G4 (Atila-7)
V	2 (5.56%)	G6 (ETBW5957), G35(kakaba)
VI	1 (2.38%)	G20 (ANGI-2/HUBARA-3)

G*=genotype number

3.8. Principal component (PC) analysis

The eigenvalues are often used to determine how many factors to retain. The first four components together accounted for about 75.6% of the total variation among the genotypes with respect to all the 13 traits evaluated and showed the presence of considerable genetic diversity among the genotypes for most of the traits under consideration. Individually, PC1, PC2, PC3, PC4, PC5, and PC6 in that order accounted for about 22%, 13%, 12%, 11%, 9% and 7% of the gross variation among the 36 bread wheat genotypes evaluated for 13 traits. The traits, which contributed more to PC1, were days to heading, plant height, grain filling period, and Spike length. Whereas for second PC grain yield, days to maturity, fertile tiller/plant, 1000-kernel weight, and harvest index. For the third PC, biomass yield, No. of kernels/ spike, and harvest index while for the fourth PC, Fertile tiller/plant and The first two principal components PC1 and PC2 with values of 22% and 13% respectively, contributed more than half to the total variation. Therefore, the present study confirmed that the bread wheat genotypes showed significant variations for the characters studied and it suggested the many opportunities for genetic improvement through selection. Similar results were reported by Sajjad et al (2011), El-Mohsen et al. (2012) and Degewione and Alamerew (2013).

Table 5: Eigenvalues and Eigenvectors of the first six principal components (PCs) for 13 traits of 36 bread wheat genotypes tested at Benatsemay weyito kebele during the 2020 growing season

Characters	PC1	PC2	PC3	PC4	PC5	PC6
Days to heading(days)	0.744	0.189	-0.135	-0.185	0.384	0.120
Grain filling period (days)	0.594	0.163	0.177	-0.020	-0.167	-0.408
Days to maturity (days)	0.028	0.498	0.056	0.766	-0.171	0.025
Plant height(cm)	0.783	0.171	0.237	0.246	0.004	0.160
Fertile tiller (no)	0.198	0.509	-0.149	-0.247	-0.110	0.606
No. of spikelet/spike (no.)	0.088	0.259	-0.631	0.204	-0.110	0.297
Spike length (cm)	0.594	0.204	-0.268	-0.009	0.202	-0.465
No. of kernels/ spike (no.)	-0.320	0.753	0.559	0.452	-0.365	0.208
Thousand-kernel weight (g)	-0.320	0.753	0.187	-0.129	0.221	-0.160
Grain yield (t/ha)	-0.135	0.536	-0.131	-0.208	-0.630	-0.208
Biomass yield (t/ha)	0.077	-0.111	0.569	-0.435	0.184	0.168
Eigen value	3.083	1.926	1.698	1.548	1.311	1.028
Variance explained (%)	22	13.7	12.1	11	9.3	7.3
Cumulative variance explained (%)	22	35.7	47.9	58.9	68.3	75.6
Difference	1.156	0.227	0.150	0.237	0.282	0.112

4. Conclusion

The present study comprises thirty-six bread wheat germplasm that were evaluated at weyito Nasa agricultural farm with the objective of assessing the genetic variability of yield and yield-related traits. Analysis of variance revealed that highly significant differences were obtained among the treatments for all thirteen traits. Selected quantitative characters indicated adequate variability among the germplasm considered in this study. The estimates of ranges of mean values revealed that bread wheat germplasm possesses a good amount of genetic variability. Productive tillers per plant, spike length, kernel per spike, thousand-grain weights, biomass yield per plot, and grain yield per plot showed a high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values. Heading date, maturity date, grain filling period, and plant height showed a medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The high to a medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values of characters suggest the possibility of improving the desired traits through selection. The values of heritability for all the quantitative characters were high. The expected genetic advance as a percentage of the mean ranged from 0.11% No of fertile tiller per plant to 636.62% 5% for grain yield(GY) Characters with high genetic advance as a percent of mean allow the improvement of the characters through selection. The cluster analysis based on D2 analysis on the pooled mean of

genotypes classified the thirty-six genotypes into six clusters, which makes them moderately divergent. There was a statistically approved difference between all the clusters. It was obvious from the analysis that three PCs out of thirteen were selected having >1 Eigenvalues and contributed 75.6 % variation among thirty-six bread wheat genotypes for all parameters. It was noted that the principal component first contributed 22%, the principal component second 13%, and the principal component third 12%, of the total genetic variability for all the genotypes Productive tillers per plant, spikelet per spike, spike length, kernel per spike thousand-grain weight and harvest index showed high heritability with the high genetic advance of percent mean, these traits may be included as components of indirect selection.

Acknowledgements

The authors would like to thank the South Agricultural Research Institute (SARI) in South Nations and Nationalities People State for its financial support. And also, our special thanks go to Werer Agricultural Research center for providing planting materials for the research purpose.

Conflict of interest

The authors declare no conflict of interest

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ISSN: 2616-3721 (Online); 2616-3713 (Print)