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Genotype x Environment Interaction Evaluation for Mungbean (*Vigna radiata*) in Tanzania

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Mungbean is one of the major pulses in Tanzania alongside soybeans, chickpeas, cowpeas, pigeon peas, and beans. Factors causes' low productivity includes lack of improved varieties, disease severity, and drought. This study was objected on evaluating and identifying mungbean genotypes (G) with the most desirable traits. The study consists of five breeding lines and two checks laid in Randomized Complete Block Design (RCBD) with three replications in three environments (E) for two growing seasons. The reaction of *Mungbean Yellow Mosaic Virus (MYMV)* across three environments was not significant, while *Cercospora* Leaf Spot and anthracnose (ANTH) was significant ($p=0.05$) for Selian across 2019/20 season. Genotypes AVMU 1601 and AVMU 1693) showed <40 days to flowering and they had an average of 79 and 76 to maturity. Significant differences ($p=0.05$) were observed for 100 seed weight across the environment in both source of variations. Significance ($p=0.05$) grain yield was observed for only genotypes in all years and the GxE interaction for 2018/19 season. The AVMU 1601 and AVMU 1693 showed high yielding capacity with a range of 779 - 1711 kg/ha compared to checks. This gives more attention to end users to adapt these genotypes in their mungbean farming operation for enhanced productivity.

Key words: Adaptability, climate change, variation, effect, traits.

INTRODUCTION

Mungbean (*Vigna radiata* L, Wilczek) is a leguminous crop commonly known as green gram and most widely distributed *Vigna* species. It is a commercial pulse crop in Asia and Africa as a major source of food (Pandey et al., 2020). It plays an important role in food system transformation because it provides a plant-based source

of dietary proteins and other essential micronutrients. Furthermore, it fixes nitrogen from the atmosphere which is important to agricultural sustainability (Ali and Gupta, 2012). The world's total mungbean cultivated area is estimated to be 6 million ha (Hou et al., 2019). Global annual production of mungbean is estimated to be

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between 2.5 and 3 million metric tonnes (Hou et al., 2019). However, India alone contributes about 65% of global acreage and 54% of global production but still; this production is not enough to meet the country's mungbean demand (Sherasia et al., 2018). In Tanzania, mungbean is mainly grown in Dodoma, Morogoro, Simiyu, Mtwara, Tabora and Kilimanjaro regions and it is estimated to be cultivated in an area of 217,000 ha (Mmbando et al., 2021). However, the productivity is still low with the average of 0.336 t/ha as compared to the potential yields of 1.5t/ha (Nair and Schreinemachers, 2020). Foliar diseases cause low productivity, for instance *Mungbean Yellow mosaic virus* cause yield loss of between (10 to 100%) (Bashir et al., 2006), cercospora leaf spot up to 50% (Chankaew et al., 2011) and anthracnose between 40 to 46% (Kulkarni, 2009). Currently, there are only two improved varieties named Nuru and Imara that were released in 1978 and 1982 respectively, by the Tanzania Agricultural Research Institute (TARI-Ilonga). These varieties currently have been reported to be succumbed to foliar diseases and other biotic factors (Mbeyagala et al., 2016; Sequeros et al., 2021) across different agro ecologies in Tanzania. Genotype by environment interaction effects mungbean productivity because of dynamism for diseases occurrence, genetic deterioration, drought variation, infestation of insect pests with different genotypes from one season to another (Baraki et al., 2020). The objective of this study was to evaluate mungbean genotypes for their adaptability and improved productivity for various agronomic and yield traits as per genotype x environment (GxE) interaction, specifically, to evaluate and identify high yielding and adapted genotypes to the main growing areas with desirable attributes of tolerance to biotic and abiotic stresses.

MATERIALS AND METHODS

Descriptions of the experimental sites

The three experimental agro-ecological experimental sites were TARI – Ilonga found at 498m above sea-level (a.s.l), characterized by sandy clay to clay loam with an average annual rainfall of 731 mm and temperature range of 19.0°C to 30.8°C, TARI Ukiriguru (17.0°C to 28.2°C) and TARI Selian (14.3°C to 25.8°C) with 1265 and 1373 m a.s.l respectively through sandy towards sandy clay loam with annual rainfall ranging between 500 to 650 mm from both sites.

Planting materials and experimental procedures

The study consisted of five mungbean breeding lines sourced from World Vegetable Centre and two old released mungbean varieties. These seven genotypes were tested for adaptability, stability, and uniformity across different agro ecologies in Tanzania during mungbean growing seasons between 2018/19 and 2019/2020. The established trials received basal application of phosphorus fertilizer Di-ammonium phosphate (DAP) at a rate of 123.50 kg per hectare and weeded twice at 3rd and 7th week after planting depending on weeds infestation. The trials were laid out in Randomized Complete

Block Design (RCBD) with three replications. The plot size was four rows each 5 m long spaced 50 cm apart and 20cm between plants within a row for mungbean. The net plot size was 4.2 m² across the testing sites. Mechanical weeding was done four times using hand hoe.

Data collection

Data were collected on the following phenological (days) parameters and were used in determining yield (kg/ha), yield components and acclimatization of the genotypes across the agro ecological zones. This data collection was made on days to 50% flowering, diseases scores, days to maturity, grain yield and other yield parameters. Disease score for MYMV was done using scale of 1 to 6 and for Cercospora leaf spot (CLS) the score was done using scale of 0 to 5 while for anthracnose (ANTH) the scoring was done using the scale of 1 to 9 (WVC, 2018).

Data analysis

The collected and organized data were analysed using GenStat 16th Edition with the following linear model $Y_{ijk} = \mu + G_i + v_j + G_i*v_j + \delta_k + G_i*v_j*\delta_k + e_{ijk}$, where; Y_{ijk} = Response variable (Yield) with genotype i , environment j and season k ; μ = Overall mean for all the observed response; G_i = Fixed effect of genotype; v_j = random environmental effect of the observed response; G_i*v_j = Interaction effects between variety and environment; δ_k = Random effect of replication within a season; $G_i*v_j*\delta_k$ = Interaction effect of variety, environment and season; e_{ijk} = Random term error which is assumed to be normally distributed with 0 mean and variance δ^2 which were summarized in a given results. The collected and organized data were analysed by using Analysis of Variances (ANOVA) by observing three sources of variations namely, genotype, location, and the interaction of genotype by location. The significance test was ($p=5\%$) under least significant differences (LSD) and separation means were tested under Fisher protected.

RESULTS

Characteristics of the genotypes used

The identified five genotypes previously selected from 10 genotype (data not shown) tested in previous mungbean growing season namely (AVMU 1601, AVMU 1624, AVMU 1625, AVMU 1692 and AVMU 1693 including two local check varieties Nuru and local (Table 1) were evaluated in three agro-ecologies. From these genotypes, six had dark green colour and one was brown. Also, five were dull and two were shiny for their seed luster Table 1.

Reaction to diseases

The reaction of *MYMV* across three environments was not significant, while *Cercospora Leaf Spot* was significant ($p=0.05$) for Selian environment only and ANTH at Ilonga (Tables 2 and 3). Through mean value magnitude, the infection of diseases showed to be higher at Selian in 2018/19 than the rest locations but higher at Ukiriguru in 2019/20 probably because of seasonal

Table 1. Seed characterization of mungbean genotypes used in this study.

Elite selected Genotypes and checks		Seed color	Seed luster
1.	AVMU 1601	Dark green	Dull
2.	AVMU 1624	Dark green	Shine
3.	AVMU 1625	Dark green	Dull
4.	AVMU 1692	Dark green	Dull
5.	AVMU 1693	Brown	Dull
6.	Nuru	Dark green	Shine
7.	Local Var	Dark green	Dull

Source: Author

Table 2. Mungbean genotype trials for disease reactions with their respective mean values per location in 2018/19 season.

Genotype	Mungbean Yellow Mosaic Virus			Cercospora Leaf Spot			Anthracnose				
	IL	UK	SL	IL	UK	SL	IL	UK	SL		
AVMU 1601	2.00	2.00	3.00	2.00	1.00	2.00	1.00	2.00	2.00		
AVMU 1624	3.00	2.00	4.00	3.00	1.00	2.00	4.00	3.00	2.00		
AVMU 1625	4.00	2.00	4.00	3.00	2.00	1.00	3.00	3.00	2.00		
AVMU 1692	3.00	3.00	4.00	2.00	1.00	2.00	3.00	3.00	2.00		
AVMU 1693	2.00	2.00	3.00	2.00	2.00	2.00	3.00	3.00	2.00		
Local		4.00	3.00	4.00		3.00	3.00	3.00	5.00	4.00	3.00
Nuru	4.00	4.00	4.00		3.00	2.00	5.00		4.00	3.00	3.00
Mean	3.00	3.00	4.00	3.00	2.00	2.00	3.00	3.00	2.00		
CV%	28.90	36.60	23.30	34.10	54.30	38.00	23.00	21.90	26.20		
LSD	1.64	1.83	1.58	1.62	1.79	1.51	1.36	1.87	1.11		
P=0.05	ns	ns	ns	ns	ns	*	*	ns	ns		

Scale for MYMV 1 to 6 (1=highly resistant; 6=highly susceptible). CLS scale 0 to 5 (0=highly resistant; 5=highly susceptible). Scale for ANTH is 1 to 9 (1=free from disease; 9=highly susceptible), ns=not significant, *=significant, **=highly significant, LSD=Least

Significant Differences, CV=Coefficient variation, IL=Ilonga, UK=Ukiriguru, SL=Selian.

Source: Author

variations of rainfall and relative humidity which creates conducive environment for disease development and severity. For instance, the higher infection of anthracnose was expressed at Ilonga at the scale of 4.00 for local cultivars while at the rest locations with other genotypes were lower (Tables 2 and 3). The new advance lines, AVMU 1601 and AVMU 1693 expressed the trait of resistance to these diseases. However, both Local and Nuru cultivars were highly susceptible to MYMV followed with ANTH and the least being CLS (Tables 2 and 3).

These two genotypes with promising resistance are suggested to be considered for release so that can replace the old varieties which showed to be susceptible to all assessed potential diseases across the testing sites.

Phonological characteristics

More days to flowering were observed at Selian and

Ukiriguru (mid altitude) compared to Ilonga (low altitude) across the growing seasons in their respective agro ecologies. Check cultivars like Nuru showed higher number of days to flowering of >40 days to most of the environment and seasons while the candidates (AVMU 1601 and AVMU 1693) showed <40 days (Tables 4). Moreover, the genotypes including AVMU 1601 and AVMU 1693 took an average of 79 and 76 days respectively to maturity. One of the genotypes named AVMU 1601 matures early (62 to 64 days) at low altitudes (Eastern zone) and late (88-96 days) at mid altitude (Lake zone) while in Northern zone took 80 to 83 days to mature. Genotype named AVMU 1693 matures early (64 days) at low altitudes (Eastern zone) and late at high altitude (96 days at Lake Zone) while in Northern zone takes 68 days to mature (Table 4). Generally, these lines AVMU 1601 and AVMU 1693 are early maturing compared to local cultivars and Nuru variety which takes an average of 79 and 83 days respectively to mature at Lake and Northern zones. Higher variation was observed

Table 3. Mungbean genotype trials for disease reactions with their respective mean values per location in 2019/20 season.

Genotype	Mungbean Yellow Mosaic Virus			Cercospora Leaf Spot			Anthracnose			
	IL	UK	SL	IL	UK	SL	IL	UK	SL	
AVMU 1601	N/A	1.00	1.00	1.00	2.00	2.00	1.00	2.00	1.00	
AVMU 1624	N/A	2.00	3.00	3.00	2.00	3.00	3.00	3.00	3.00	
AVMU 1625	N/A	3.00	2.00	2.00	2.00	2.00	3.00	3.00	1.00	
AVMU 1692	N/A	2.00	2.00	2.00	3.00	3.00	3.00	3.00	2.00	
AVMU 1693	N/A	1.00	2.00	2.00	2.00	2.00	1.00	3.00	1.00	
Local		N/A	4.00	4.00	3.00	3.00	4.00	4.00	4.00	3.00
Nuru		N/A	4.00	4.00	4.00	3.00	3.00	4.00	4.00	3.00
Mean	-	3.00	2.00	3.00	2.00	3.00	3.00	3.00	2.00	
CV%	-	20.90	18.70	35.50	33.20	13.80	16.40	24.40	19.10	
LSD	-	0.94	0.82	1.62	1.44	0.65	0.79	1.36	0.73	
P=0.05	-	**	**	ns	ns	**	**	ns	**	

Scale for MYMV 1 to 6 (1=highly resistant; 6=highly susceptible). CLS scale 0 to 5 (0=highly resistant; 5=highly susceptible). Scale for ANTH is 1 to 9 (1=free from disease; 9=highly susceptible), ns=not significant, *=significant, **=highly significant, LSD=Least Significant Differences, CV=Coefficient variation, IL=Ilonga, UK=Ukiriguru, SL=Selian, N/A= Data Not available.

Source: Author

Table 4. Comparative Mungbean genotype trials 2018/19 across three testing sites for phenological traits 2018/19 and 2019/20 Season.

Genotype	Days of flowering			Days to maturity			Days to flowering			Days to maturity			
	IL	UK	SL	IL	UK	SL	IL	UK	SL	IL	UK	SL	
AVMU 1601	31.00	41.00	45.00	62.00	96.00	80.00	31.00	43.00	37.00	62.00	87.00	81.00	
AVMU 1624	35.00	41.00	39.00	62.00	95.00	69.00	35.00	42.00	39.00	62.00	88.00	82.00	
AVMU 1625	43.00	40.00	39.00	61.00	95.00	68.00	43.00	45.00	39.00	61.00	88.00	78.00	
AVMU 1692	38.00	43.00	39.00	64.00	97.00	73.00	38.00	44.00	34.00	64.00	90.00	77.00	
AVMU 1693	40.00	44.00	43.00	64.00	96.00	68.00	40.00	43.00	35.00	64.00	86.00	78.00	
Local	32.00	41.00	43.00		68.00	93.00	88.00	44.00	50.00	46.00	68.00	91.00	84.00
Nuru	45.00	46.00	43.00	64.00	93.00	80.00	32.00	42.00	45.00	64.00	88.00	87.00	
Mean	38.00	42.00	41.00	64.00	95.00	75.00	38.00	44.00	39.00	77.00	88.00	81.00	
CV%	3.10	3.10	5.6	3.30	2.10	5.80	3.10	2.60	7.10	3.30	1.90	3.70	
LSD	2.09	2.29	4.12	3.76	3.60	7.79	2.06	2.03	4.94	3.78	2.92	5.33	
P=0.05	**	*	**	*	ns	**	**	**	**	*	*	*	

IL=Ilonga, UK= Ukiriguru, SL=Selian, ns=not significant, **= highly significant, *significance.

Source: Author

across the environment with higher significance ($p=0.05$) (Table 4).

Grain yield and yield parameter

Significant differences ($p<0.05$) were observed for 100 seed weight across the testing sites in both source of variations of genotype, environment, and its respective interactions (Table 5). The AVMU 1693 showed higher mean values magnitude which has a range of 4.00 to

6.33g for 100 seed weight than others (Table 5). However, for the grain yield, the significance difference was observed for only genotypes in all years and the GxE interaction for 2018/19 mungbean growing season. Quantitatively, AVMU 1601 and AVMU 1693 found to be a high yielding genotypes despite the weather variations transversely three locations they were able to yield greater than others with a range of 779 to 1711 kg/ha (Table 5). Compared to current productivity of 0.4t/ha (Mmbando et al., 2021), these varieties if recommended for commercialization it will increase the productivity to

Table 5. Interaction for genotype by environment for 100 seed weight and grain yield in two growing seasons.

Genotypes	Environment	100SW (g)		Grain yield (Kg/ha)	
		2018/19	2019/20	2018/19	2019/20
AVMU 1601	Ilonga	4.33	4.33	1264.00	1088.00
	Ukiriguru	3.97	3.93	1544.00	885.00
	Selian	4.43	4.56	1487.00	842.00
AVMU 1624	Ilonga	4.33	4.33	856.00	387.00
	Ukiriguru	4.53	4.77	1143.00	522.00
	Selian	2.77	5.27	799.00	682.00
AVMU 1625	Ilonga	4.60	4.60	923.00	341.00
	Ukiriguru	5.30	5.10	1094.00	624.00
	Selian	3.67	5.60	799.00	471.00
AVMU 1692	Ilonga	6.00	6.00	1132.00	466.00
	Ukiriguru	4.90	5.00	955.00	518.00
	Selian	3.77	5.50	728.00	438.00
AVMU 1693	Ilonga	6.33	6.33	1711.00	933.00
	Ukiriguru	5.37	5.40	1409.00	946.00
	Selian	4.00	5.90	1349.00	779.00
Local	Ilonga	5.40	5.40	863.00	399.00
	Ukiriguru	3.80	4.37	857.00	465.00
	Selian	4.73	4.87	924.00	352.00
Nuru	Ilonga	5.60	5.60	809.00	444.00
	Ukiriguru	4.63	4.63	924.00	435.00
	Selian	5.00	5.23	1093.00	427.00

SW = Seed weight.

Source: Author

>49% that is, from 0.4 t/ha to a range of 0.8 to 1.7 t/ha.

The results presented in three sources of variations which are genotype, environment and GxE interaction across the seven traits which are grouped into diseases, phenological and yield (Table 6). Significance differences for days to flowering, days to maturity and 100 seed weight were observed across two seasons with their respective source of variations. However, disease variations were observed 2018/19 season significantly compared to 2019/20 season as well as to grain yield particularly for genotype and GxE interactions (Table 6). These variations show how agro-ecologies play significant roles towards evaluation of various genotypes which later support the identification of the genotypes with desirable traits as per breeding objectives.

DISCUSSION

Reaction of fungal diseases to Mungbean genotypes

The main mungbean diseases are yellow mosaic virus, anthracnose, powdery mildew, Cercospora leaf spot, halo blight, bacterial leaf spot, and red spot while the major

main abiotic stresses affecting mungbean production are drought, waterlogging, salinity, and heat stress (Nair et al., 2019). The mungbean breeding has been important in developing biologically resistant varieties and organisms, but there are many obstacles that are still being addressed, which include the accurate and precise identification of (sources) resistant to some traits and traits brought by many genes (Bhaskar, 2017). In this study which was conducted in Tanzania three diseases were observed namely yellow mosaic virus, anthracnose and Cercospora leaf spot. The MYMV found affecting some of the genotypes across the locations. However, two of the genotypes expressed the trait of resistance. This disease is caused by yellow mosaic viruses which is a key importance especially in South and Southeast Asia. Also, the virus affects various leguminous crops including blackgram (*Vigna mungo*), mothbean (*Vigna aconitifolia*), Lima bean (*Phaseolus lunatus*), pigeonpea (*Cajanus cajan*), French bean (*Phaseolus vulgaris*), cowpea (*Vigna unguiculata*), Dolichos (*Lablab purpureus*), horsegram (*Macrotyloma uniflorum*), and soybean (*Glycine max*) with variation in percentile losses (Dikshit et al., 2004; Rashid et al, 2020). This study is aligned with that of Habib et al., (2007) which screened the mungbean

Table 6. Summary for source of variations across the seasons.

Season	Source of variation	MYMV	CLS	ANTH	DF	DM	100SW	Grain yield
2018/19	Genotypes (G)	0.003	<.001	<.001	<.001	<.001	<0.002	<0.001
	Environment (E)	0.003	0.038	<.001	<.001	<.001	<.001	0.182ns
	GXE interaction	0.676ns	0.097ns	0.317ns	<.001	<.001	0.003	0.004
2019/20	Genotypes (G)	-	0.013	<.001	<.001	<.001	<.001	<.001
	Environment (E)	-	0.766	<.001	<.001	<.001	<.001	0.629
	GXE interaction	-	0.962	0.060	<.001	0.013	0.001	0.678

MYMV=Mungbean Yellow Mosaic Virus, CLS=Cercospora Leaf Spot, ANTH=Anthracnose, DF=Days to flowering, DM=Days to Maturity, SW=Seed weight.

Source: Author

germplasm for resistance to *MYMV* and identified resistance genotypes as well as that of Nair et al. (2017) for identification of mungbean lines with tolerance to or resistance to yellow mosaic in the field of India.

Cercospora leaf spot is another economical fungal disease of mung bean leading to significant damage to the crop production. The occurrence needs to be observed during early dry season or in rainy season as that provide ideal environment for the spread of this disease (Mansoor, 2022). The disease occurs on other legumes, including cowpea and soybean. Among the environment favouring this development of disease include warm temperature, frequent rain, and high humidity and over-crowded plants with poor air flow and low sunlight penetration among plants. In this study, the disease affected more the checks rather than the improved one. Possibly these checks found to be susceptible because it has been used for the last 40 years and are recycled from season to season across the mungbean growing season. The study found to be similar with that of Raje and Rao (2002) where by thirty-five genotypes were found to be resistant to *Cercospora* leaf spot out of two hundred and six genotypes across four sowing dates spread over two seasons under field conditions in India. Furthermore, other studies found that the environmental factor play an important role in increasing the severity of this disease make disease control more difficult. An attempt has been made to unravel the genotype x environment interaction towards identification and validation of resistant cultivars against *Cercospora* leaf spot in multi-environment trials whereby initial screening with 246 genotypes under artificial epiphytotic conditions was conducted to provide a subset of 22 mungbean cultivars for further evaluation in field trials in six consecutive environments over two years. They found that the environmental influence towards the genotypic response and confirmed the existence of a non-linear interaction with a non-specific genotypic response, thus advocating the urgency of multi-site testing for further exploration (Das et al., 2020). Also Mahapatra et al. (2022) determined that the components

for CLS resistance is associated with leaf spot intensity in the field, which is estimated from the area under the disease progress curve (AUDPC). However, our study was experimented following the recommended agronomic practices within the country and had recommended spacing in the field. Other studies conducted and did not find any resistance genotypes neither under the laboratory nor field screening (Habib et al., 2007; Abbas et al., 2020). This indicates the complexity of this disease when it comes to develop, evaluate, and identify resistance genotype or variety under any condition.

Screening of mungbean germplasm in the field under natural disease pressure is always recommended, as it provides a longer period of host, pathogen and environment interactions and leads to more accurate and reproducible results (Kaur et al., 2011). Same scenario was observed in this study whereby some genotypes found to be susceptible to anthracnose across the testing environment and three genotypes had trait of anthracnose resistance. Same study by Pandey et al., (2021) found 22 accessions consistently anthracnose resistant under the categories of highly resistant and resistant with scores ranging from ≥ 1.0 to ≤ 3.0 during the period of study.

Phonological characteristics

The mungbean phenology characteristics play significant roles in crop growing cycle depending on the type of the environment (Chauhan and Williams, 2018). Days to flowering and maturity showed variation among genotypes and environments being tested. The phenological traits considers timing of the biological events in plants such as flowering, leafing, hibernation, reproduction, and migration (Liang, 2019) in relation to changes in season and climatic environments. This study found to be related to that of Malaviarachchi et al. (2016) on response of mungbean to increased temperature in various locations and different season. Same variation observed in terms of days to flowering and maturity. Time

to flowering of mung bean crops varies appreciably depending on the genotype, environment and the daylengths and temperatures prevailing during the period after sowing (Imrie and Lawn, 1990). In our study, some environment received prolonged rainfall, and this caused the maturity to be more than 80 days and others less rainfall with moderate temperature made the maturity to be short less than 70 days as like that of Malaviarachchi et al. (2016). Various mathematical models describe the dynamic control of time to flowering by daily values of maximal and minimal temperature, precipitation, day length and solar radiation. The models are always validated by cross-validation and used to demonstrate that the phenology of adaptive traits, like flowering time, is strongly predicted not only by local environmental factors but also by plant geographic origin and genotype (Yimram et al., 2009; Kozlov et al., 2020).

Grain yield and yield parameters

Globally, the yield potential of mungbean ranges from 2.5 to 3.0 t/ha; however, the global average productivity of mungbean is ~0.5 t/ha (Pratap et al., 2020; Pandey et al., 2021). For Tanzania productivity is less than 0.4 t/ha which shows that it is below the global average (Mmbando et al., 2021). However, from this study two genotypes showed higher productivity of between 0.8t/ha towards 1.7 t/ha basing on genotype and environment. However, other studies have shown that choosing the right combination of parental genotypes which has desirable traits like 100 seed weight, plant height, disease resistance and good number of pods per plant has influence on grain yield (Yimram et al., 2009).

This was observed in this study whereby AVMU 1693 for instance, had high weight of 100 seed weight which resulted to higher grain yield. Looking on the influence of high temperature stress on growth, phenology, and yield performance of mungbean it has showed that high temperatures (<40/28 °C) were found to be detrimental for potential productivity of mungbean in various growth environment (Sharma et al., 2016).

Conclusion

Numerous factors restraining mungbean productivity in Tanzania found to be lack of improved varieties, inadequate skills on good agricultural practices and choice of the environment that suit mungbean production. In this study, some genotypes had high yield in one location and less in another location which was attributed by environmental factors like rainfall, temperature, heat, and relative humidity. This gives more attention to researchers to consider and review some important features like planting dates, type of variety, plant density, fertilizer use and maturity variation. If these features are well explored and taken to farmers for adoption, the

productivity of mungbean in Tanzania will be improved significantly. This is because, the significant higher grain yields with higher net benefit from farmers in connection to mungbean reliable market are the promising indicators for adopting new crop varieties in any agricultural community.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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