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Multi-location Evaluation of Advanced Mungbean Lines under Different Climatic Conditions in Uganda

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Abstract
Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata],* or greengram is a popular crop especially in the drought prone areas of East Africa. It is rich in micronutrients and protein thus can help ameliorate malnutrition if incorporated in diets. Yield stability across target population of environments is a critical trait for mungbean breeding in the region. In this study, i) we examined the influence of climatic covariables on G X E for grain yield among mungbean genotypes ii) determined yield stability of mungbean genotypes across environments in Uganda. Field trials comprising of 40 mungbean genotypes were established in 9 environments in Uganda in an alpha lattice layout. Our findings showed that radiation and minimum relative humidity were the key factors responsible for G x E on mungbean yield. These contributed 40% of the G X E. Four mungbean genotypes; AVMU2021, AVMU2006, UMG2017-211 and UMG2017-263 exhibited both stability and adaptability across the test environments. Additional evaluation will be conducted for their potential release as varieties and also inclusion in the mungbean breeding program as parents.
Keywords: Factorial regression; Genetic variation; Stability; G X E; Greengram; Yield

Introduction

Mungbean (*Vigna radiata* (L.) also known as greengram is a key food and cash crop in several parts of the world especially in south Asia and east Africa. In Uganda, the crop is popular I the eastern and northern parts of the country especially among small-scale farmers (Mbeyagala et al., 2016, 2017). Mungbean has short growing cycle, requires less inputs compared to other crops, is tolerant to drought and also improves soil fertility through biological nitrogen fixation making it suitable for low input production systems (Nair and Schreinemachers, 2020). In terms of nutritional quality, mungbean grain is a rich source of essential nutrients e.g proteins (up to 31%), iron (>87 mg/kg) and zinc (up to 62mg/kg) (Nair et al. 2015; Anwar et al. 2007). The grain contains less flatulence causing factors compared to other legumes. This makes it an ideal food for children, the elderly and the convalescing (Adsule et al. 1986). Mungbean starch is also highly digestible with a high glycaemic index and thus more suitable for malnourished patients (Sandhu and Lim, 2008). Mungbean is consumed in a several ways as whole grain or as split grain, processed into flour or as bean/ vegetable sprouts (Nair and Schreinemachers, 2020).

Given its rich nutritional profile, mungbean has the potential to alleviate nutritional disorders especially in developing countries like Uganda where consumption of fortified foods and food supplements is still out of reach for the most vulnerable populations (Dahiya et al 2015). Iron deficiency is the most prevalent form

of nutritional disorder affecting mainly the poorest and vulnerable populations in resource constrained environments in developing countries (Stevens et al. 2022). For instance, in 2019, incidence of iron deficiency anaemia in east Africa was 53%, 31% and 39% among children (<5 years), non-pregnant women, and pregnant women, respectively (Stevens et al. 2022). A food based approach that promotes cultivation and consumption of popular nutrient rich crops/varieties is a more cost effective and sustainable approach (Dahiya et al 2015). Identification of best varieties/lines/cultivars for different locations or environments and which are also stable across environments requires the establishment of multi-environmental trials (METs). Cultivars tested in METs often vary in response from one environment to another due to genotype by environment interaction (G X E) phenomenon (Malosetti et al., 2013; Vargas et al. 1999). Several models such as ANOVA, regression on the mean model and AMMI have been used to describe G X E (Malosetti et al., 2013; Purchase et al. 2000; Purchase, 1997). However, these models do not make of use of explicit external environmental information but only rely on the phenotypic response variable of interest such as yield (Malosetti et al., 2013; Vargas et al. 1999). On the other hand, factorial regression model makes use of external environmental information directly to determine which variables influence G X E. In this study, i) we describe the influence of climatic variables on G X E for grain yield among mungbean genotypes using factorial regression model, ii) determine yield stability of mungbean genotypes across environments in Uganda.

Methods and Methods

Genetic Material

Forty mungbean genotypes comprising of 25 advanced lines from the World Vegetable Center (WorldVeg), formerly known as Asian Vegetable Research and Development Center (AVRDC), 13 accessions from the genebank at NaSARRI and two (2) released varieties (NAROGRAM1 and NAROGRAM 2) were evaluated (Table 1). The released varieties served as checks.

Test Environments

Multi-location field trials were established at five sites in Uganda; Serere at NaSARRI (2020B, 2021A and 2021B seasons), Arua at Abi Zonal Agricultural Research and Development Institute (AbiZARDI) during 2021A and 2021B seasons, Lira at Ngetta Zonal Agricultural Research and Development Institute (NgettaZARDI), Mayuge at Ikulwe satellite station (2021B season) and Kitgum at Kitgum District Farm Institute (DFI) during 2021B season. Each location and season combination constituted a different environment, hence there was a total of nine test environments. The coordinates of trial sites are as provided in Table 2.

Experimental Layout

Field trials were established in an alpha lattice design replicated twice in each environment. Designs were generated each season using Breeding Management System (BMS). The genotypes were planted in two (2) rows each with a length of two (2) metres long with a spacing of 0.5m x 0.1m. At each trial site, planting, weeding, thinning, pest management and harvesting were carried out manually. Pods harvested from each plot were sun-dried before manual threshing. Threshed grain was dried to a moisture content of 13% before determining plot grain weight.

Data Collection: Genotypes

Observations were recorded on several traits (Table 3) during the trials such as on number of days to 50% flowering, number of days to maturity, plant height, pod number, pod length, pod and seed weight, number of seeds per plant, plot pod weight, plot seed weight and seed size (100 seed weight). Plot seed weight was used to compute yield per ha. A description of the trait measured and corresponding stage of observation during field experiments is provided in Table 3 below.

Data Collection: Weather Variables

Records of weather observations during growing period were obtained from Automatic Weather Stations (ADCON Model) installed by Uganda National Meteorological Authority (UNMA) at or near the trial sites. The covariables recorded were average temperature, minimum temperature, maximum temperature, rainfall, radiation, average % relative humidity, minimum % relative humidity, maximum % relative humidity, average wind speed and maximum wind speed.

Data Analysis

Stability and Factorial regression analysis were carried using GEA-R (Genotype by Environment Analysis with R) Software version 4.1 (Pacheco et al., 2015). The climatic covariables listed above were in factorial regression analysis to guide in choosing which of the covariates provides greater proportion of the variability in G X E, explained by differential genotype sensitivity to explicit external environmental variables and have the advantage that hypotheses about the influence of those external variables on G X E of yield can be statistically tested. The factorial regression model for which G X E incorporates environmental covariates used as follows;

$$Y_{ij} = \mu + g_i + e_j + \sum_{g=1}^{H} Z_{ih}\,\zeta_{jh} + \varepsilon_{ij}$$

Where Y_{ij} is the yield of the i-th genotype (i=1,...,I) in the j-th environment (j=1,...,J); μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; z_{ih} are the environmental covariates; ζ_{jh} are the genotype factor; H (H < J) is the number of environmental covariates and ε_{ij} is the error term. Summary statistics were computed using doBy R package version 4.6.18 (Højsgaard and Halekoh, 2023).

Results

Performance of genotype for various traits

Number of days to 50% flowering ranged from 37 days (AVMU2015) to 49 days (UMG2017-235) with a mean of 40 days (Table 4). Average number of days to physiological maturity was 66 days with AVMU2001 as the earliest maturing genotype (60 days) and UMG2017-235 as the late maturing genotype (77 days). Average plant height was 27cm with the shortest genotype being AVMU2005 (21cm) and the tallest genotype (UMG2017-139) with a plant height of 40.2cm. On average, each of the genotypes had about 13 pods per plant with AVMU2002 having the lowest number of pods per plant (9pods) while UMG2017-222 had the highest number of pods per plant (20 pods). The genotype with the shortest pods was AVMU2001 (6.3cm) while UMG2017-139 had the longest pods (8.4cm). Genotype AVMU2022 had the lowest number of seeds per pod while UMG2017-139 had the highest number of seeds/pod. In terms of grain yield, the lowest yield genotype was AVMU2025 (681Kg/Ha) while the highest yielder was UMG2017-242 (1394kg/ha). The evaluated genotypes were generally large seeded (with 6.3g/100 seeds). UMG2017-97 had the smallest seed size (4.7g/100 seeds) while AVMU2020, AVMU2021 and UMG2017-211 had the largest seed size (7.4g/100seeds) [Table 4].

Across test environments, genotypes flowered earlier in Serere and later in Arua and Mayuge. Similarly, genotypes attained physiological maturity earlier in Serere compared to Arua (Table 5). on the other hand, yield/ha was highest in Mayuge, Lira and Serere but lowest in Kitgum and Arua. Results of factorial regression model fitted (Table 6) to the mungbean yield data showed that GEI was mainly explained by differential genotype sensitivities to radiation (F=2.36, $P\leq$0.00002) and minimum % relative humidity (F=1.61, P<0.015) during the growing period. Together, radiation and minimum % relative humidity, accounted for up to explained 40% of GEI with 76 degrees of freedom.

Yield stability analysis identified four genotypes that were both stable and adaptable (Fig. 1). These were; AVMU2021, AVMU2006, UMG2017-211, and UMG2017-263. Genotypes that only showed adaptability were; AVMU2018, AVMU2021, NAROGRAM2, AVMU2003, UMG2017-211, UMG2017-263, UMG2017-15, AVMU2006 and AVMU2007.

Discussion

In this study, variation in yield due to GEI was 40% and this was largely attributed to radiation and minimum relative humidity. This GEI variation is much higher than past findings reported by Imrie and Shanmugasundaram (1987). A recent study by Karimi et a. (2019) however, reported rainfall (distribution and amount) and temperature as key climatic parameters responsible for the variation. Other environmental variables such as soil characteristics (type, texture, fertility levels) contribute to differences in genotype performance (Karimi et al. 2019; Nair et al. 2015). However, these were not investigated in this study. This highlights the need to consider G X E in selection of suitable/potential genotypes. Variation was observed among genotypes across environments. Taller mungbean plants are often associated with yield advantage as such plants tend to have more branches and more pods that those with a short stature (Imrie and Shanmugasundaram, 1987). Additionally, mungbean genotypes with a high plant stature are preferred for both manual and mechanized harvesting, a key determinant for variety adoption (Karimi et al. 2019). On the basis of days to flowering and maturity, most of the genotypes tested were early maturing ($\leq$65 days). Similar results were reported by Yimram et al. (2009). Such genotypes are ideal for double cropping systems [2 seasons/year] (Mbeyagala et al. 2017; Yimram et al., 2009). Early maturity has also been reported as a key trait considered by farmers as a basis for mungbean variety selection in Kenya (Karimi et al 2019). Grain/seed size is another key trait for farmers in east Africa with large or bold seeded varieties preferred to small seeded types (<5g/100 seeds) (Mbeyagala et al., 2017). In this study, majority of the genotypes tested were large seeded, with average seed size of 6.3g/100 seeds.

This study identified four genotypes; AVMU2021, AVMU2006, UMG2017-211, and UMG2017-263 that were both adaptable and stable in yield across test environments. Information on stability and adaptability of performance of genotypes or breeding materials can aid farmers in making decisions about adoption and also for the variety release process by breeders (Ceccarelli, 2012).

Conclusion

In this study, radiation and minimum % relative humidity were the significant contributors to GEI for grain yield among mungbean genotypes. Among the genotypes tested, four (AVMU2001, AVMU2006, UMG2017-211, UMG2017-263) were both adaptable and stable in yield performance across environments. These genotypes were also large seeded, a key farmer preferred trait. Further evaluation of these potential genotypes geared towards release as varieties and inclusion in the breeding program as parents is recommended.

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Table 1: List of mungbean genotypes used in the study

No.	Line code	Seed Lustre	Seed Color	Source
1	AVMU2001	Shiny	Pale green	WorldVeg
2	AVMU2002	Shiny	Pale green	WorldVeg
3	AVMU2003	Dull	Green	WorldVeg
4	AVMU2004	Shiny	Pale green	WorldVeg
5	AVMU2005	Shiny	Pale green	WorldVeg

6	AVMU2006	Dull	Green	WorldVeg
7	AVMU2007	Dull	Green	WorldVeg
8	AVMU2008	Dull	Green	WorldVeg
9	AVMU2009	Shiny	Pale green	WorldVeg
10	AVMU2010	Shiny	Pale green	WorldVeg
11	AVMU2011	Shiny	Pale green	WorldVeg
12	AVMU2012	Dull	Green	WorldVeg
13	AVMU2013	Dull	Green	WorldVeg
14	AVMU2014	Shiny	Pale green	WorldVeg
15	AVMU2015	Dull	Green	WorldVeg
16	AVMU2016	Dull	Pale green	WorldVeg
17	AVMU2017	Dull	Green	WorldVeg
18	AVMU2018	Dull	Green	WorldVeg
19	AVMU2019	Dull	Green	WorldVeg
20	AVMU2020	Dull	Green	WorldVeg
21	AVMU2021	Dull	Green	WorldVeg
22	AVMU2022	Dull	Brown	WorldVeg
23	AVMU2023	Shiny	Pale green	WorldVeg
24	AVMU2024	Dull	Green	WorldVeg
25	AVMU2025	Shiny	Pale green	WorldVeg
26	UMG2017-222	Shiny	Pale green	NaSARRI
27	NAROGRAM1	Dull	Green	NaSARRI
28	NAROGRAM2	Shiny	Pale green	NaSARRI
29	UMG2017-97	Dull	Green	NaSARRI
*30	UMG2917-156	Dull	Green	NaSARRI
31	UMG2017-197	Dull	Green	NaSARRI
32	UMG2017-35	Dull	Green	NaSARRI
33	UMG2017-211	Dull	Green	NaSARRI
34	UMG2017-263	Dull	Green	NaSARRI
35	UMG2017-306	Shiny	Pale green	NaSARRI
36	UMG2017-23	Dull	Green	NaSARRI
37	UMG2017-15	Dull	Green	NaSARRI
38	UMG2017-235	Dull	Green	NaSARRI
39	UMG2017-242	Dull	Green	NaSARRI
40	UMG2017-139	Dull	Green	NaSARRI

*UMG2917-156 was not included in analysis because poor establishment across environments

Table 2: Location coordinates of trial sites

Location	Latitude	Longitude	Altitude (m)
Serere	1.536744N	33.447120E	1140
Lira	2.297487N	32.914027E	1084

Arua	3.078586N	30.947898E	1198
Mayuge	0.438806 N	33.476585E	1192
Kitgum	3.290085 N	32.887770E	941

Table 3: Description of traits measured in field evaluation of mungbean genotypes

Trait	Code	Description	Stage
Days to 50% flowering	DFF	Number of days from planting to when at least 50% of the plants in a plot have at least one unopened flower	Flowering
Plant Height (cm)	PH	Recorded on 5 randomly sampled plants per plot	Physiological maturity
Days to Maturity	DM	Days from sowing to when 90% of pods in a plot change color (to black or brown)	Physiological maturity
Pods per plant	NP	Mean number of pods from 5 random plants per plot	After harvest
Pod length (cm)	PL	Mean lengths measured from five randomly selected pods from each plant (up to 5 plants)	After harvest
Pod yield per plant (g)	PY	Mean weight for all pods measured from five randomly selected plants	After harvest
Number of Seeds per pod	NS	Mean number of seeds counted from five randomly selected pods from each plant (up to 5 plants)	After harvest
Seed yield per plant (g)	SY	Mean weight for all seeds measured from five randomly selected plants	After threshing
Plot seed weight (g)	PSW	Weight of all seeds from all plants in a plot	After threshing
Yield (kg)	SYHa	Weight of seeds per ha	After threshing
100 Seed weight (g)	SW_100	Weight of 100 randomly selected seeds	After threshing

Source: IBPGR. 1980.