

Performance and Adaptability of Common Bean-Released Cultivars at Three Agro-Ecological Zones in Tanzania

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ABSTRACT

This study focused on examining the genetic performance and stability of common bean genotypes across multiple environments in Tanzania using an alpha-lattice experimental design. The aim was to minimize environmental variability and maximize genetic expression. Three experimental sites were selected to represent the ecologies of the main bean growing areas of Tanzania, which are Tropical Savannah represented by TARI-Selian, Tropical highlands represented by TARI-Uyole and semi-arid regions represented by Babati region. The sites were planted with diverse common bean genotypes, all of which were released for use in Tanzania. Agronomic practices, such as hand-hoe weeding and fertilizer application, were consistently applied. Key data collected included days to 50 percent flowering, growth habit, plant height, pod and seed count, yield per plot, and 100 seed weight. Advanced statistical analyses, including ANOVA, AMMI, and stability tests, were conducted using R software to evaluate yield and yield components. This paper findings discuss about the yield performance, stability, and the discriminating versus representative power across locations. In terms of yield, Babati was the leading site with mean yield of 1413.07 kilogram per hectare (kg/h) with Uyole 96 being the lead genotype (2845.567kg/h). Genotypes that were found to be stable and high-yielding in multiple locations include, Rojo, SUA Kalima, SAKILA, Fibe, and Nyeupe Uyole with the mean yields of 1045.83kg/h, 1023.73kg/h, 1003.33kg/h, 670.4kg/h and 544.77kg/h respectively. In discriminativeness and representativeness, Babati was the most discriminating site among the three locations while Seliani was the most representative among the three. These findings revealed significant variations and allowed the assessment of genotype performance and environmental interactions.

Key Words: Common bean genotypes, Genotype by environment interaction, lattice design, Environmental stability, Discriminativeness, Representativeness.

1. INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is an important source of vegetable protein, minerals, and vitamins and is the most popular legume for human consumption globally. It is cultivated for domestic use and as a source of revenue at the household level and at the national level. Regardless of the fact that common bean cultivars vary considerably in terms of seed shape, size, and colour, most are remarkably similar when it comes to their nutritional composition [1]. Due to its high nutritional content, the crop is a good and cheap source of protein, carbohydrates, vitamins, minerals, and unsaturated fatty acids for the poor throughout the world, particularly in Latin America and Africa [2]. 662 and 700 million people in Latin America and eastern/southern Africa, respectively, depend on its inexpensive, nutrient-rich grains for protein and micronutrients like iron and zinc; yearly intake can approach 66 kg per capita [3] , [4]. Millions of resource-poor farmers, particularly in developing nations, rely on common beans (*Phaseolus vulgaris* L.) for dietary proteins, vitamins, and minerals [3]. Common beans are the most important grain legume crop in Tanzania, where they are frequently intercropped with maize, sorghum, bananas, or other crops [5]. According to PABRA 2022, common bean cultivation can be found in most locations in Tanzania with around 5,803,747 households in rural Tanzania depending solely on beans for their daily food [6]. The range of growth habits (from determinate bush types to vigorous climbers) and the range of growth cycles (from 2 to 10 months in length) make beans a crop that fits many production niches. Nevertheless, common beans are becoming increasingly commercial with the trends of urbanization and market globalization [4].

There is a widening gap between the demand and supply of common bean (*Phaseolus vulgaris* L. 2n = 22) in Tanzania [7]. The reason may be due to an increase in insect pests and diseases affecting common beans, changing dietary preferences where people prefer more beans, an increase in the number of people to be fed, the loss of genetic diversity of the germplasm used in breeding programs to develop high-yielding varieties, and the effects of climate change, particularly a rise in temperature accompanied by a reduced amount of rainfall [8]. Considering bean originated in the mid-latitude neo-tropics and, by nature, is not well adapted to a warm and dry climate, the crop is mainly cultivated in the northern zone, the Great Lakes region in the west, and the Southern Highlands of Tanzania.

2. LITERATURE SURVEY

Common beans continue to face biotic and abiotic stresses that negatively affect yields and the quality of the crop. As a result, the average yield is low (1.1 tons/ha), and the production is not sufficient to meet the country's demand for the growing population of the country. Tanzania's population is predicted to grow steadily by ten million people (+15.79 percent) between 2023 and 2028. The population is predicted to reach 73.36 million after the tenth year of population growth, marking a new peak in 2028. [9] This is also supported by the prediction made by FAO, 2019, of an increase in the global population to approximately 10 billion people by 2050, requiring at least up to 60% increase in production to meet the food demand [10]. The genus *Phaseolus* contains five domesticated species in decreasing order of importance: common bean (*Phaseolus vulgaris* L.), lima beans (*P. lunatus* L.), runner bean (*P. coccineus* L.), tea bean (*P. acutifolius* A. Grey), and year bean (*P. polyanthus* Greenman), all with distinct adaptation and reproductive systems. About 111,000 years ago, common beans diverged into three gene pools. These are Mesoamerican and Andean, known as the major gene pools that included both wild and domesticated forms, and the third gene pool consisting of a relatively narrow distribution of wild types that grow in a restricted region between Northern Peru and Ecuador [11], [12]. During domestication, morphological, physiological, biochemical, and genetic changes occurred that resulted in diverse seed colours, shapes, and sizes [13]. Selection for desirable traits within the gene pools continued based on natural genetic variability in the populations. Among the recorded criteria were reduced seed dispersal and dormancy, compact growth habits, reduced sensitivity to day length, and an increase in the size of the harvested parts [14]. In this regard, the superior genotypes were selected by farmers while neglecting other undesirable genotypes. In general, this may lead to a reduction in inferior alleles over generations, affecting the gene and genotypic frequencies of the population [15].

The genotype-environment (GxE) interaction has a significant impact on crop yield components [16]. A complicated variable, yield is influenced by both direct and indirect influences. Grain weight and the number of pods per plant are two examples of direct factors. These are low heredity features whose expression is heavily influenced by environmental influences [17]. Genotypes that yield well in one area may not perform well in other areas due to GxE interaction. This restricts the cultivars that can be recommended for various situations and encourages the selection of genotypes appropriate for each environment [18].

3. OBJECTIVE OF RESEARCH

This study investigated the performance and adaptability of Tanzanian common bean released cultivars across three diverse locations in Tanzania. By conducting assessments in these diverse locations, we sought to gain insights into how these cultivars perform under varying agro-ecological conditions, such as soil types, climatic patterns, and other geographical factors and also recommend on the most representative site for conducting breeding activities.

4. RESEARCH METHODOLOGY

4.1 Experimental sites and considered genotypes

The study was conducted in the 2022–2023 cropping season at three diverse sites: the Tanzania Agriculture Research Institute, TARI-Seliani (representing the northern highlands), TARI Uyole (representing the southern highlands), and Babati region (representing the central regions), comprising different climatic conditions, representing tropical savanna regions (with distinct wet and dry seasons), tropical highlands (with relatively mild and moderate rainfalls), and semi-arid areas (with low rainfalls and hot temperatures), respectively. The selected sites are part of a wide range of agro-ecological zones present in Tanzania, as shown in Figure 1. Additional details about the experimental sites, including their weather conditions are presented in Table 1. A total of 45 released bean varieties in Tanzania which were obtained from research stations at TARI Uyole, TARI Seliani, SUA and ASA were used for the study. The genotypes include; Uyole 94 Uyole 96 Uyole 98 Wanja Uyole 03 Uyole 04 Urafiki Njano Uyole Calima Uyole Fibe Pasi Rosenda Uyole 16 Nyeupe Uyole Uyole 17 Uyole 18 Selian 14 Selian 15 TARIBEAN 1 TARIBEAN 2 TARIBEAN 3 TARIBEAN 4 TARIBEAN 5 TARIBEAN 6 Selian 13 Selian 12 Selian 09 Selian 10 Selian 11 Jesca Selian 05 Lyamungo 90 Lyamungo 85 Cheupe Selian 94 Selian 06 Selian 97 Rojo Pesa Mshindi SAKILA20 SUA Kalima SUA-KIKATITI Kablanketi progeny Gloria Sweet Violet VTTT 923/23-10 NUA 48 NUA 64 and Kipapi.

Table 1: Characteristics of the experimental sites, their weather conditions and respective climatic zones

Study area	Annual average rainfall (mm)	Average temp (°C)	Average relative humidity (%)	Climatic zone
TARI-UYOLE	600-2600	15-30	70-90	Tropical Savanna
TARI-SELIANI	900	15-25	60-80	Tropical highlands
BABATI REGION	600	25-30	40-60	Semi-Arid

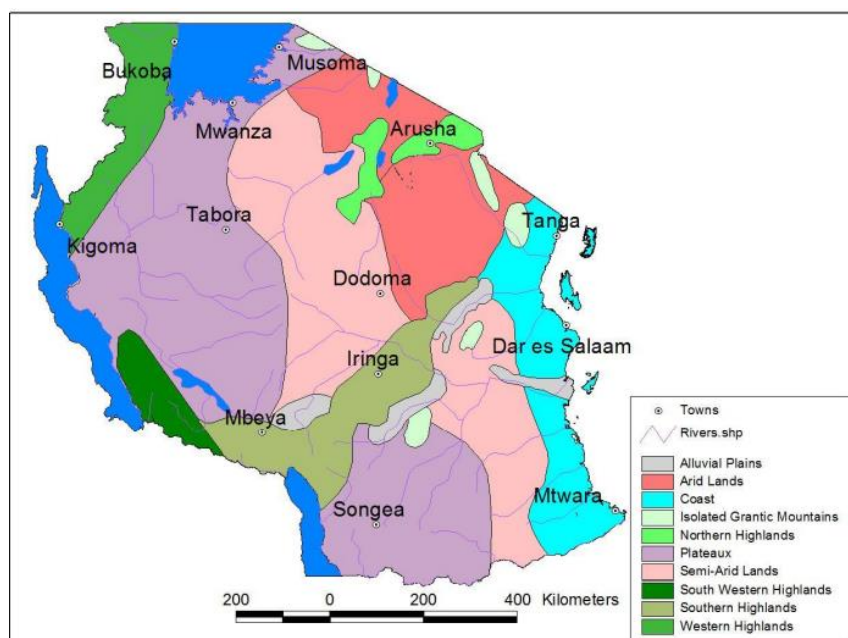


Figure 1: A map of Tanzania showing the different agro-ecologies

4.2 Experimental design and field layout

The experiment was carried out using the Alpha lattice design. The choice of this design was informed by the need to reduce the effect of environmental variables, hence maximising the genetic variables by ensuring that each treatment is exposed to similar conditions. This minimizes the effects of factors such as soil type, topography, shades, among other factors that might have cause variability. All three experimental sites were laid out using Alpha-lattice design

Table 2: Table showing a summary of the mean of all traits across different locations

ENV; Environment, GEN; Genotype, df50; day to 50% flowering, pdpl; Number of pods per plant, sdpd; Number of seeds per pod, pht-cm; Plant height(cm), ydpl; Yield

ENV	GEN	DF50	PDPL	SDPD	PHT-CM	SWT100	YLDPL-KG/H
Babati	Calima Uyole	47	9.5	6.33	38.19	40.33	1632.23
Babati	Fibea	50.33	13.07	5.33	67.88	42	1040
Babati	Gloria	51	15.1	12.67	67.17	45.33	1057.77
Babati	Jesca	47.67	22.33	9.33	34.13	41.33	2683.33
Babati	Kablanketi progeny	48.33	13	10.33	46.6	37.67	980
Seliani	Rojo	37	11.67	8.67	46.52	43	1000
Seliani	Rosenda	36	11.27	7.67	56.43	48	1235.57
Seliani	SAKILA20	39.67	9	8.33	52.5	53.33	892.23
Seliani	Seian 15	38.33	18.73	10.33	204.8	37	657.77
Seliani	Selian 05	38	4.63	7	33.6	27.67	273.33
Seliani	Selian 12	34	14.17	9.33	30.9	44	636.67
Uyole	Uyole 17	47	17.55	4.65	42	41	1033.33
Uyole	Uyole 18	49	12.05	4.25	85.8	34	1005
Uyole	Uyole 94	50	15.46	4.15	65.27	40	915
Uyole	Uyole 96	50	17.62	4.6	98.73	43	800
Uyole	TTTT 923/23-10	51	14.66	7.8	62.05	40	1410
Uyole	Wanja	47	10.02	5	33.56	37.5	756.67

Involving three replications, each replication containing 5 blocks of 10 plots. Each experimental plot was planted with one common bean genotype in 4 rows of 2m length spaced at 50cm between the rows. Within rows, plants were spaced at 10cm from one plant to another and one seed was placed per hole. Table 3 illustrates how the design was laid out in field conditions. Hand- hoe weeding was done twice when beans had one trifoliate leaf and before flowering. Fertilizer application was done once during planting and the fertilizer used was NPK: 20:10:10 at recommended rate. All recommended agronomic practices for common bean productions were followed on all locations.

4.3 Data collection

Data was collected for the following key traits; Number of Days to 50% flowering (DF50), Growth habit (GH), Plant height (PH), Number of pods per plant (PDPL), Number of seeds per pod (SDPD), Yield per plot, and 100 seed weight (100SWT). The Number of Days to 50% flowering was obtained by counting the days from emergence to at least when half of the plants in the plot had flowers. The growth habit was assessed by assigning growth types (Bush, semi-climber, climber and aggressive climber respectively) depending on the climbing tendency of the variety. Plant height was estimated by selecting five random plants in the middle row and measuring with a ruler and the average recorded. The number of pods per plant was obtained by first sampling a total of five plants per variety from the middle row and counting the number of pods for each plant. The average was then obtained by taking the total number of pods obtained per variety for each location, then divided by three. Number of seeds per pod was estimated by

counting seeds from five pods for each variety and the average was obtained. Yield per plot; Two middle rows of the plot were harvested and the grain yield was estimated at 14% moisture content. 100 seed weight; Seed weight was estimated by counting 100 seed per variety and measured using a weighing balance to obtain the weight in grams.

4.4 Statistical analysis

The data was first analysed using conventional analysis of variance (ANOVA) for days to 50% flowering, plant height (cm), pods per plant, plants per pod, 100 seed weight and yield in (g/plot) across all environments using the metan package in R. For variables with significant GxE interactions, an Additive main effects and multiplicative interaction (AMMI) ANOVA and performance across the three sites. For variables with non-normal distribution, a mixed linear model, mini-mum norm quadratic unbiased estimation (MINQUE) was used to get variance components expressed as proportions to the phenotypic variance and predict genotypic effects. The minque package in R was used for the above with a randomized x-group (3,10,45) jackknife method. Pearson's correlation between yield and other variables were tested at 0.05 and 0.01.1.

5. RESULT AND DISCUSSION

5.1 Results

5.1.1 Genotypes seed yield and yield components variation

Table 2 shows the means of the traits recorded across location. The highest common bean seed yield was recorded at Babati, followed by TARI-Uyole and lastly TARI-Seliani. Seed yield mean at Babati, ranged from 286.67 kg/h to 3726.67 kg/h with a mean of 1413.07 /kg/h, while at TARI-Uyole, seed yield ranged from 276.67kg/h to 2026.67kg/h with a mean yield of 1010.5kg/h, and at TARI-Seliani it has a range of 70 kg/h to 2323.33kg/h with mean yields of 968.9kg/h.

The highest seed yielding genotypes at Babati was Uyole 96 with the mean of 2845.567kg/h, closely followed by SUAKIKATITI with the mean value of 2771.1kg/h and Jesca 2683.33kg/h. Among the common bean genotypes harvested at TARI Uyole, SUA-KIKATITI recorded the highest seed yield of 1816.67kg/h followed by TARI-Bean 3 (1635kg/h) and TARI-Bean 1 (1595kg/h). At TARI-Seliani, the highest seed yielding genotypes was SUA-KIKATITI (1924.43kg/h), followed by TARI Bean 1 (1494.43kg/h) and TARI-Bean 6 (1471.1kg/h). At Babati, the highest number of pods per plant was recorded from Seliani 05 (25.33), followed by Seliani 14 (24.13) and lastly Seliani 15 (23.93). In TARI-Uyole the leading genotype was Seliani 14 (23.66), followed by Seliani 15 (23.55) and lastly, Rojo (21.41). Also, in TARI-Seliani, the leading Genotype was Seliani 14 (20.53), followed by Seliani 15 (18.73) and lastly Fibea (18). For number of seeds per pod, in Babati the leading genotype was Gloria (12.67g), followed by Kablanketi progeny (10.33) and lastly Seliani 97 and SUA 90 both with the mean of 9.67g. At TARI-Seliani the leading genotype was Uyole 94 with a mean of 13.33g, followed by NUA 64 with a mean of 13g and lastly Uyole 96 and Gloria both with a mean of 12.33g. For TARI-Uyole, the leading genotype was SUAKARANGA with a mean of 9.5g, followed by TARIBEAN 1 with a mean of 8.05g and lastly Kablanketi progeny and SAKILA 20 with a mean of 8g. At Babati the genotypes with the highest seed weight were recorded for Uyole 03 (48.33g) followed by Uyole 96 with a mean of 46.67g and lastly Gloria, Nyeupe Uyole and SUA-KARANGA all with a mean of 45.33g. At TARI-Uyole, Seliani 13 was leading with a mean of 45g, followed by NUA 48 with a mean of 44.5g and lastly Gloria, Seliani 15 and Uyole 96 all with a mean of 43g. And lastly, at TARI-Seliani, Uyole 03 was leading with a mean of 57 g, followed by SUA-Kalima and Sweet Violeth both with a mean of 56.33g and lastly Kipapi with a mean of 55g.

5.1.2 AMMI analysis and yield stability index

Across location, the effect of genotypes, environment and genotype by environment interaction was highly significance ($P < 0.001$) on the number of days to 50% flowering, number of pods per plant, 100 seed weight and the seed yield. The genotype and environment significantly impacted the number of seeds per pod but no significance was observed on genotype by environment interactions. Mean seed yield across sites ranged from 276.67kg/h to 3726.67kg/h. AMMI analysis showed that the main effects of genotypes and environment accounted for 27.47% and 10.32% of seed yield treatment sum of squares total, respectively, whereas genotype by environment interaction effect represented 19.49% of seed yield treatment sum of squares total. Considering the interaction principal component axe (IPCA), IPCA 1 showed high significance ($P < 0.001$) for seed yield and accounted for 93.73% of the genotype by

interaction for seed yield sum of squares while IPCA 2 showed no significance ($P > 0.001$) contributing to 18.98% respectively. (Table 3).

As shown in Table 3, the results of AMMI analysis indicated that the main effects of environment and genotypes accounted for 87.86% and 5.25% of the total sum of squares for the days to 50% percent flowering, respectively, while the interaction effect between genotype and environment accounted for 1.54% of the total sum of squares for the days to 50% percent flowering. Regarding the IPCA, IPCA 1 and IPCA 2 contributed 77.6% and 22.4% of the genotype by interaction for seed yield sum of squares respectively and showed no significance ($P > 0.001$) on number of days to 50% percent flowering.

For 100 seed weight the interaction effect between genotype and environment accounted for 2.6% of the total sum of squares, while the main effects of environment and genotypes accounted for 21.5% and 38.2% of the total sum of squares, respectively. IPCA 1 and IPCA 2 contributed 60.9% and 39.1% of the genotype by interaction for seed yield sum of squares, respectively, and there was significant difference ($P < 0.001$) in 100 seed weight of common beans genotypes in the side interaction principal component axe (IPCA).

The number of pods per plant treatment sum of squares total was determined by AMMI analysis to be influenced by genotypes and environment, accounting for 25.24% and 2.99% of the total, respectively. The genotype by environment interaction effect accounted for 17.79% of the total. Regarding the IPCA, IPCA 1 contributed 67.4% and had a high significance ($P < 0.001$) for number of pods per plant, accounting for 32.6% of the genotype through interaction for the sum of squares for number of pods per plant, while IPCA 2 had no significance ($P > 0.001$) for number of pods per plant. (Table 4).

For number of seeds per pod, the environment and genotypes accounted for 28.92% and 11.10% of the total sum of squares respectively, while the interaction effect between genotype and environment accounted for 13.95% of the amount. While IPCA 2 showed no significance ($P > 0.001$) contributing to 45.5% of the genotype by interaction for number of seeds per pod sum of squares, IPCA 1 demonstrated high significance ($P < 0.001$) for number of seeds per pod and accounted for 54.5% of the genotype by interaction on the side interaction principal component axe (IPCA).

Table 3: AMMI analysis of variance for Yield, 50% days to flowering, Number of seeds per pod, Pods per plant, and 100 seed weight of common bean genotypes across sites

SV	D F	YIELD		DF50		SDPD		PDPL		100SWT	
		MS	F	MS	F	MS	F	MS	F	MS	F
Total	43 0	3126 4.04		31.4 5		8.1 4		28.2 5		62.4 8	
Treatment	5	1670 0.25	1.2 5	4.9	2.2 9** *	12. 02	2.5 3	120. 46	6.89 ***	26.5 6	1.27
Genotypes	44	8394 4.41	6.3 ***	16.1 3	7.5 6	8.8 3	1.8 6** *	69.7 2	3.99 ***	233. 54	11.1 8***
Environments	2	6938 72.1	52. 0** *	5941 .31	278 2.5 3	506 .04	106 .40 ***	181. 6992	10.3 9***	2890 .03	138. 32** *
Block	32	1116 0.61	0.8 4	2.8	1.3 1	4.5 1	0.9 5	15.6 2	0.89	21.7 2	1.03 9
Interactions	83	3156 7.76	2.3 7** *	2.50	1.1 2	5.8 8	1.2 4	26.0 5	1.49 ***	34.7 1	1.66 ***

IPC A 1	45	5457 4.1	4.0 9** *	4.04	1.8 9	6.8 8	1.4 5** *	35.6 0	2.04 ***	46.3 3	2.22 ***
IPC A 2	43	1156 2.28	0.8 7	1.22	0.5 7	6.0 2	1.2 7	18.0 6	1.03	31.1 3	1.49 ***
Error	17 6	1334 3.54		2.14		4.7 6		17.4 8		20.8 9	

*** significance at a P-value of 0.001 SV=Source of variation; DF=Degree of freedom; MS=Means square; F=F-value; DF50=Days to 50% flowering; PDPL=Number of pods per plant; SDPD=Number of eds per pod; 100SWT=100 seed weight

Figure 2, representing the AMMI Biplot, shows the genotypic and environmental additive main effects against their corresponding first interaction principal component axis (PC1). Genotypes placed on the right-hand side of the plot have higher yield compared to those placed on the left-hand side of the plot. From the plot, the genotypes G42 (SUA-Kalima) and G50 (Kipapi) were high yielding and low PC1 values close to zero making them the high yielding and most stable genotypes among the 45 genotypes. The genotypes G39 (Pesa) and G37 (Seliani 97) had high yielding and had positive genotype by environmental interactions while the genotype G49 (SUA Karanga) had the high yield and showed negative genotype by environmental interaction. Among the three environments, Seliani showed to have low contribution to the genotype by environment interaction while Uyole and Babati had high contribution to the genotype by environment interaction as they a both have high PC1 score placing them far away from the middle line.

Figure 3, shows the ranking of 45 genotypes by mean yield and stability. The average environment axis (AEA) is the line that crosses the biplot origin from upper left to lower right. It is determined by averaging the first and second scores for each environment’s principal component. Greater mean yield is indicated by proximity to the circle. The stability of genotypes is represented by the double arrowed line that goes through the origin and is perpendicular to the AEA.

On this axis, any direction away from the biplot origin indicates a larger G×E interaction and less stability. The best genotypes for broad selection are those with high mean yield and high stability. They have the shortest vector from the average environment axis in the biplot and are situated close to the origin. These genotypes include G38 (Rojo), G42 (SUA Kalima), G41 (SAKILA 20), G10 (Fibea), and G14 (Nyeupe Uyole) with the yield means of 1045.83kg/h, 1023.73kg/h, 1003.33kg/h, 670.4kg/h and 544.77kg/h respectively. These genotypes indicate that they are both high yielding and stable across the three locations. The genotypes that had high yield but low stability and respond best to particular environments include; G39 (Pesa), and G37 (Seliani 97) with the mean yields of 482.25 kg/h and 260.44 kg/h are ideal genotypes for Seliani and Uyole, while G35 (Seliani 94) and G17 (Seliani 14) are ideal genotypes for Babati with the mean yields of 397.56 kg/h and 269 kg/h respectively.

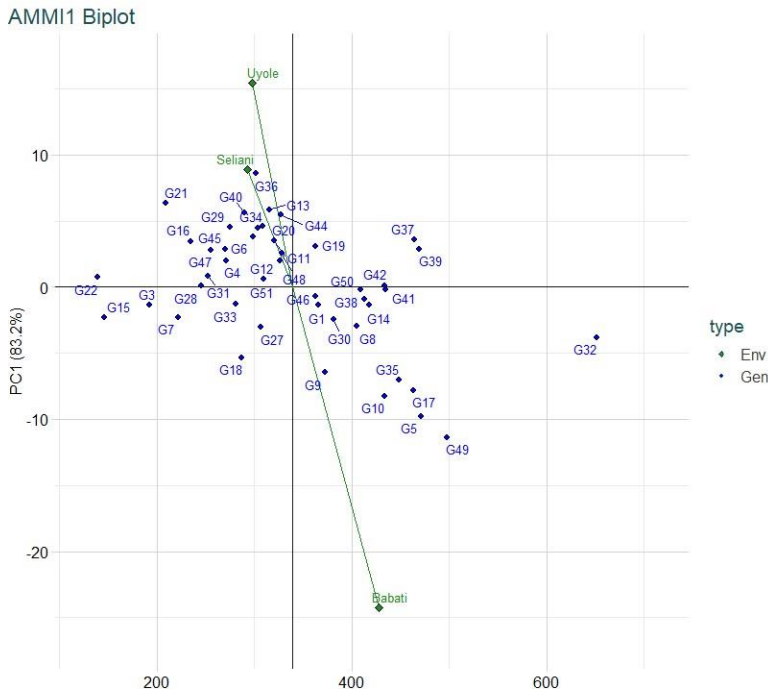


Figure 2: AMMI-1 Biplot for yield (kg/h) presenting the means of 45 genotypes (G) and three environments (E) against their corresponding first interaction principal component axis score (PCI).

Mean vs. Stability

Scaling = 0, Centering = 2, SVP = 1

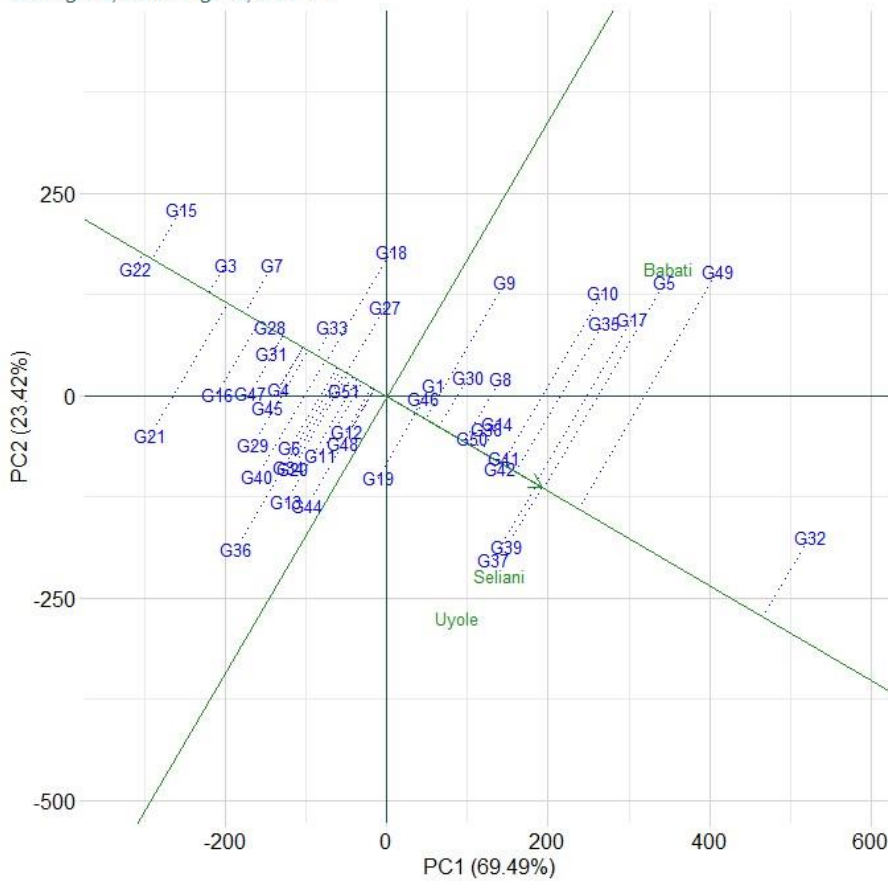


Figure 3: GGE biplot displaying mean performance vs stability of common bean genotypes (G) across locations (E).

Discriminateness vs. representativeness

Scaling = 0, Centering = 2, SVP = 2

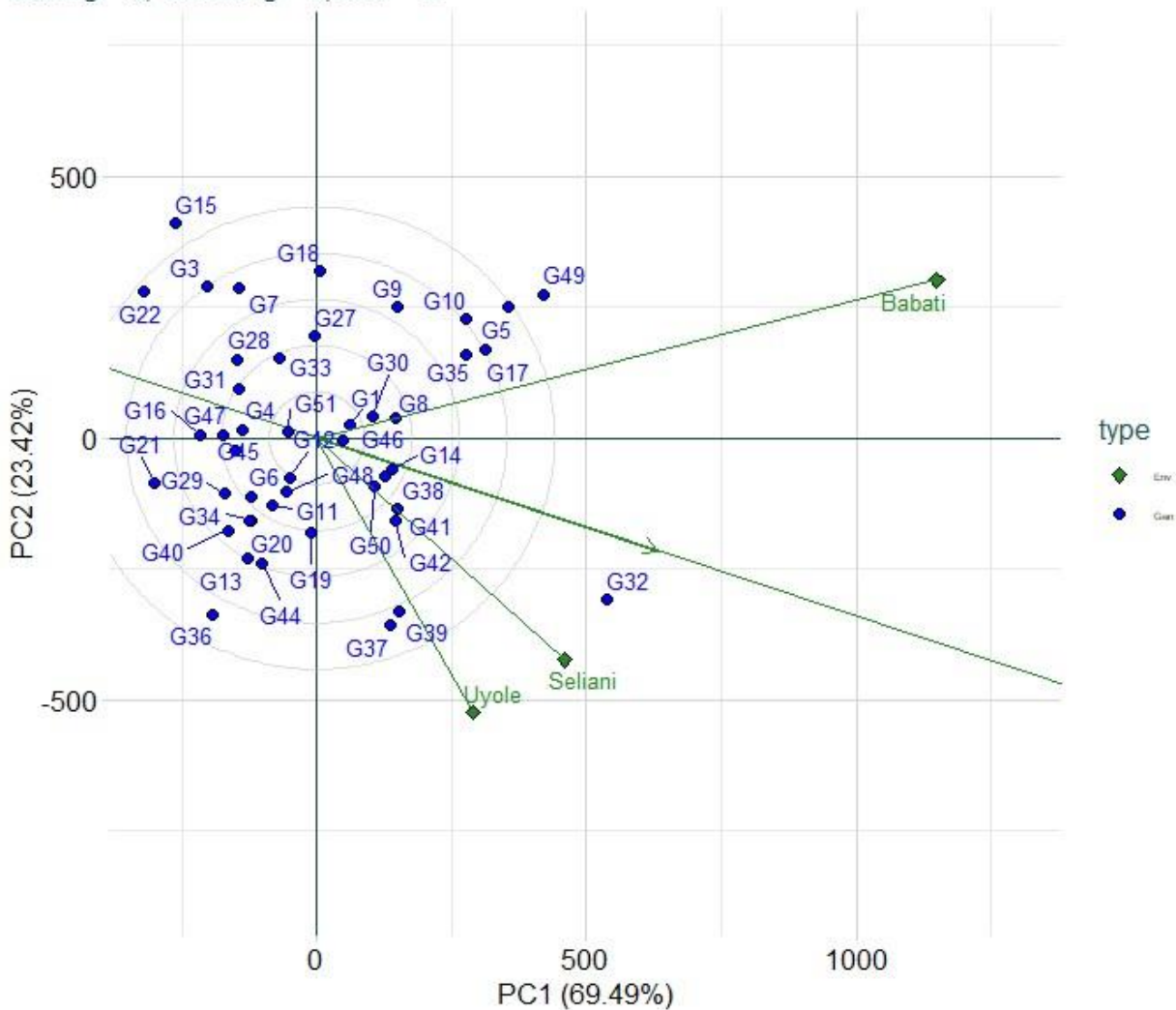


Figure 4: GGE biplot showing experimental sites (E) discriminating power and representativeness on common bean genotypes (G) seed yield.

The GGE biplot (Figure 4) shows the discriminating power and the representativeness of the experimental sites on the yield of common bean genotypes. An experimental site showing a longer vector from the point of origin of the biplot shows that it had a larger discriminating ability in terms of superior seed yield genotypes while those with shorter vector from the point of origin of the biplot shows that it had a low discriminating ability terms of superior seed yield genotypes. Also, the experimental site vector having a small angle from the average environmental axis (AEA), is described as a more representativeness of the common bean seed yield evaluation experiment. From the graph (Figure 4), Babati had the longest vector from the point of origin among the three environments showing that it had higher discriminating ability while Seliani had the shortest vector indicating that it had a low discriminating ability. The experimental site Seliani has a small angle with AEA hence more representative compared to other sites where as Uyole had a larger angle with the AEA hence the least representative site among the experimental sites.

DISCUSSION

Three agro-ecological zones had genotype seed yields and yield component variations that varied significantly from one zone to the next. Genetic materials of common bean genotypes, site conditions, and their interactions all had a significant impact on yield and yield components of common bean genotypes. Common bean genotype yields vary depending on the type of genotype grown, ideal environmental conditions (PH of 5.5 to 6.8), and meteorological factors (temperature range of 160C to 240C, average annual rainfall of 500mm to 2000mm). It has been well-described by Barili [19], how common bean genotype, environment, and genotype by environment interaction interact. Genotypes of common beans, especially landraces that produced large yields at particular locations, can be utilised to improve varieties that are specific to those areas where they have outperformed. The greatest seed yield was noted at Babati, which was followed by TARI-Uyole and TARISelian. This could have been brought about by interactions between the environment and the well-distributed rainfall and soil characteristics. Thus, compared to other agro-ecological zones, Babati has favourable conditions that promote the growth of common beans, resulting in a higher yield. Genotype selection for the corresponding bean traits is based on the high variations of common bean genotypes observed within location [20].

On the other hand, AMMI analysis revealed that the genotype main effect (27.47%) had a greater influence on common bean seed yield than the environmental main effect (10.32%). This suggested that the experimental sites and genotypes employed were varied and suitable for both specialised and broad studies on genotype adaptability. Similar to how Horn et al., 2018 study found that cowpea genotypes contributed significantly to seed yield (38.0%) as opposed to environmental effects (5.0%)[21], Tadesse et al., 2019 research found that genotype main effects on rice seed yield were 41.3% as opposed to environmental main effects (31.9%). [22]. In contrast, this study Philipo et al., 2021 found that the environmental effect contributed more (78.2%) than the genotype main effect (6.5%) [23]. The variation in the number of common bean genotypes and locations used the current study used 99 diverse bean genotypes, whereas Philipo et al., 2021 used 14 all white bean genotypes could account for the variation in the genotype main effect reported by this study [23]. This trait selection needs to be done in multiple environments to have a genotype that can be grown across several agro-ecological zones and perform more or less the same, because of the nearly equal influence of environment and genotype main effect on seed yield.

When it came to seed yield, the study's findings regarding days to 75% flowering, number of pods/plants, number of seeds/pods, and 100 seed weight showed that common bean genotypes had a greater influence on these traits than did the environment within agro-ecological zones and the interaction between genotype and environment. The experiment requires to be repeated and conducted in more locations and during more seasons of the year in order to make this study more realistic. Plant breeders typically employ a number of adaptabilities and stability analysis techniques to select plant genotypes that perform roughly similarly in a variety of environments; this has been adequately explained by Rono et al., 2016 and Adjebeng-Danquah et al., 2017 24-25].

The AMMI model is a hybrid analysis that applies principal component analysis to the sum's squares assigned by the ANOVA to the genotype and environment interaction, incorporating both the additive and multiplicative components of the two-way data structure. Analysis of variance is used first. For analysing genotype versus environment, additive main effects and multiplicative interaction (AMMI) stability value (ASV) has become a potent tool. This indicates that is a contemporary technique for identifying and choosing plant genotypes that are adaptable to a range of environmental conditions. Consequently, it is said that plant genotypes with low ASV values, which are closer to zero, are more stable, whereas those with high values are impacted by environmental factors [26]. Due to the fact that genotype stability is independent of yield, some common bean genotypes that were ranked as stable by ASV had very low yields [27].

Because it combines stability and high yielding traits into a single index, the yield stability index (YSI) is used to identify stable and high seed yielding bean genotypes [28]. Because they have high mean yield and stability traits, genotypes with lower YSI are more valuable [24]. According to YSI's analysis of the study's data, the genotypes Lyamungo 85 and Tari bean 4 demonstrated strong yielding and stability. The ideal experimental site, which has a high ability to distinguish superior genotypes and is representative of all experimental sites, can be seen with the aid of the concentric circles [29].

Therefore, TARI-Selian has both the high discriminating ability of superior common bean genotypes and representativeness of other experimental sites, thus it is an ideal site for a selection of the widely adapted common bean genotypes, as this site provided more information on seed yield performance of the tested genotypes. The

experiment can be further conducted into other sites to provide more information on this, the sites with high environment variations so as to assess the diverse of the genotypes among various environments. Yan, 2002 used GGE biplot to determine the discriminating power and representativeness of the experimental sites on sorghum genotypes yield and suggested the sites with strong discriminating power as the one located far from the point of origin and negative correlations from the other experimental sites [30].

6. CONCLUSION

This study investigated the performance and adaptability of Tanzanian common bean released cultivars across three diverse locations in Tanzania. It offers insightful information about the differences in seed yield and yield components of common bean genotypes in Tanzania's various agro-ecological zones. It also emphasizes the significance of genotype selection suited to particular growing conditions and desired results in each location. Moreover, the results point to the possibility of genetic improvement in seed weight through selective breeding of specific genotypes, highlighting the necessity of location-specific agronomic practices and targeted breeding programs to improve crop productivity and increase seed weight. Lastly, further research may be required to pinpoint specific genetic factors that contribute to variations in seed weight and to devise targeted breeding strategies for increasing seed weight in different genotypes and locations. Overall, the study underscores the significance of considering genotype and location-specific factors for optimizing seed weight in crop production.

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REFERENCES LIST

- [1] I. and N. G. and V. V. and K. A. and N. T. and S. C. and A. E. and R. A. and S. L. and T. F. and others} Karavidas, "Agronomic practices to increase the yield and quality of common bean (*Phaseolus vulgaris* L.," *AGRONOMY*, vol. 12, p. 271, 2022.
- [2] T. Celmeli, S. Id, H. Canci, D. Sari, A. A. Id, and C. Toker, "The Nutritional Content of Common Bean (*Phaseolus vulgaris* L.) Landraces in Comparison to Modern Varieties", doi: 10.3390/agronomy8090166.
- [3] W. J. Broughton, G. Hernández, M. Blair, S. Beebe, P. Gepts, and J. Vanderleyden, "Beans (*Phaseolus* spp.) - Model food legumes," *Plant Soil*, vol. 252, no. 1, pp. 55–128, May 2003, doi: 10.1023/A:1024146710611/METRICS.
- [4] S. E. Beebe, I. M. Rao, M. W. Blair, and J. A. Acosta-Gallegos, "Phenotyping common beans for adaptation to drought," *Front Physiol*, vol. 4 MAR, p. 28034, Mar. 2013, doi: 10.3389/FPHYS.2013.00035/BIBTEX.
- [5] R. J. Hillocks, C. S. Madata, R. Chirwa, E. M. Minja, and S. Msolla, "Phaseolus bean improvement in Tanzania, 1959-2005," *Euphytica*, vol. 150, no. 1–2, pp. 215–231, Jul. 2006, doi: 10.1007/S10681-006-9112-9/METRICS.
- [6] P. Onyango, "Making the Bean Corridor work: Lessons from Tanzania | PABRA." Accessed: Feb. 07, 2024. [Online]. Available: <https://www.pabra-africa.org/making-the-bean-corridor-work-lessons-from-tanzania/>
- [7] S. E. Beebe, I. M. Rao, M. J. Devi, and J. Polania, "Common beans, biodiversity, and multiple stresses: challenges of drought resistance in tropical soils," *Crop Pasture Sci*, vol. 65, no. 7, pp. 667–675, May 2014, doi: 10.1071/CP13303.
- [8] E. Katungi, A. Farrow, J. Chianu, and S. Beebe, "Common bean in Eastern and Southern Africa: a situation and outlook analysis," 2009, Accessed: Dec. 11, 2023. [Online]. Available: <https://nru.uncst.go.ug/handle/123456789/9206>
- [9] "Tanzania - total population 2018-2028 | Statista." Accessed: Mar. 24, 2024. [Online]. Available: <https://www.statista.com/statistics/447624/total-population-of-tanzania/>

- [10] M. Van Dijk, T. Morley, M. L. Rau, and Y. Saghai, "A meta-analysis of projected global food demand and population at risk of hunger for the period 2010-2050," *Nat Food*, doi: 10.1038/s43016-021-00322-9.
- [11] V. and D. J. P. and B. J.-P. and D. D. G. chmit, "Use of chloroplast DNA polymorphisms for the phylogenetic study of seven Phaseolus taxa including P. vulgaris and P. coccineus," *Theoretical and applied genetics*, vol. 87, pp. 506–516, 1993.
- [12] S. Mamidi *et al.*, "Demographic factors shaped diversity in the two gene pools of wild common bean Phaseolus vulgaris L.," *Heredity* 2013 110:3, vol. 110, no. 3, pp. 267–276, Nov. 2012, doi: 10.1038/hdy.2012.82.
- [13] Y. Rezene, "GGE-Biplot Analysis of Multi-Environment Yield Trials of Common Bean (Phaseolus vulgaris L.) in the southern Ethiopia," *J Plant Stud*, vol. 8, no. 1, p. 35, Feb. 2019, doi: 10.5539/JPS.V8N1P35.
- [14] D. Sicard, L. Nanni, O. Porfiri, D. Bulfon, and R. Papa, "Genetic diversity of Phaseolus vulgaris L. and P. coccineus L. landraces in central Italy," *Plant Breeding*, vol. 124, no. 5, pp. 464–472, Oct. 2005, doi: 10.1111/J.1439-0523.2005.01137.X.
- [15] D. K. Ray, J. S. Gerber, G. K. Macdonald, and P. C. West, "Climate variation explains a third of global crop yield variability," *Nature Communications* 2015 6:1, vol. 6, no. 1, pp. 1–9, Jan. 2015, doi: 10.1038/ncomms6989.
- [16] S. Mohammed, M. Elias, M. Mekiso, and E. Lere, "Muluneh Mekiso. Genotype x Environment Interaction and Stability Analysis of Some Selected Field Pea (Pisum sativum L.) Varieties in Northern Part of South Regional State," *Article in International Journal of Biochemistry Biophysics & Molecular Biology*, vol. 7, no. 1, pp. 5–11, 2022, doi: 10.11648/j.ijbbmb.20220701.12.
- [17] G. Ligarreto–Moreno and C. Pimentel–Ladino, "Grain yield and genotype x environment interaction in bean cultivars with different growth habits," *Plant Prod Sci*, vol. 25, no. 2, pp. 232–241, Apr. 2022, doi: 10.1080/1343943X.2021.1981141.
- [18] E. Pérez-Vega, A. Pañeda, C. Rodríguez-Suárez, A. Campa, R. Giraldez, and J. J. Ferreira, "Mapping of QTLs for morpho-agronomic and seed quality traits in a RIL population of common bean (Phaseolus vulgaris L.)," *Theoretical and Applied Genetics*, vol. 120, no. 7, pp. 1367–1380, May 2010, doi: 10.1007/S00122-010-1261-5/TABLES/4.
- [19] L. D. and V. N. M. do and P. A. L. do and C. J. E. de S. and S. F. F. and N. M. Barili, "Genotype-environment interaction in common bean cultivars with carioca grain, recommended for cultivation in Brazil in the last 40 years," *Crop Breeding and Applied Biotechnology*, vol. 15, pp. 244–250, 2015.
- [20] George. Acquah, "Principles of plant genetics and breeding," p. 569, 2007, Accessed: Mar. 15, 2024. [Online]. Available: https://books.google.com/books/about/Principles_of_Plant_Genetics_and_Breedin.html?id=6dGwVvFvF9wC
- [21] L. and S. H. Horn, "Importance of cowpea production, breeding and production constrains under dry areas of Africa," *RUFORUM Working Document series*, vol. 17, pp. 499–514, 2018.
- [22] T. and T. Z. and A. H. and A. D. Tadesse, "Determination of Nitrogen and Phosphorous Fertilizer Rates on Lowland Rice Production," *Results of Crop Improvement and Management Research 2018*, 2019.
- [23] M. and N. P. A. and M. E. R. Philipo, "Environmentally stable common bean genotypes for production in different agro-ecological zones of Tanzania," *Heliyon*, vol. 7, 2021.
- [24] J. K. and C. E. K. and O. J. O. and N. V. W. and M. J. K. and O. J. and O. M. and K. A. M. and others Rono, "Adaptability and stability study of selected sweet sorghum genotypes for ethanol production under different environments using AMMI analysis and GGE biplots," *The Scientific World Journal*, vol. 2016, 2016.

- [25] J. and M.-A. J. and G. V. E. and A. I. K. and O. S. K. and others Adjebeng-Danquah, “AMMI stability analysis and estimation of genetic parameters for growth and yield components in cassava in the forest and Guinea savannah ecologies of Ghana,” *International Journal of Agronomy*, vol. 2017, 2017.
- [26] G. and W. L. G. and M. A. S. and de B. O. I. and Z. A. D. and Z. R. and C. A. S. G. and F. T. and B. G. Matei, “Genomic selection in soybean: accuracy and time gain in relation to phenotypic selection,” *Molecular Breeding*, vol. 38, pp. 1–13, 2018.
- [27] C. and G. N. and B. A. B. and B. C. and C. R. and H. A. and H. L. and M. P. and V. C. and A. A. and others Sirami, “Increasing crop heterogeneity enhances multitrophic diversity across agricultural regions,” *Proceedings of the National Academy of Sciences*, vol. 116, 2019.
- [28] J. L. and T. C. and R. D. A. and M. V. and M. J. and Q. R. Rolando, “Key ecosystem services and ecological intensification of agriculture in the tropical high-Andean Puna as affected by land-use and climate changes,” *Agric Ecosyst Environ*, vol. 236, pp. 221–233, 2017.
- [29] M. Shiri, “GRAIN YIELD STABILITY ANALYSIS OF MAIZE (ZEA MAYS L.) HYBRIDS UNDER DIFFERENT DROUGHT STRESS CONDITIONS USING GGE BILOT ANALYSIS,” *Crop Breed J*, 2013.
- [30] W. and R. I. Yan, “Biplot analysis of test sites and trait relations of soybean in Ontario,” *Crop Sci*, vol. 42, 2002.