Evaluation and Stability Analysis of Climbing Bean (*Phaseolus vulgaris* L.) Genotypes in High Potential Areas of Ethiopia

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Abstract

Climbing bean (Phaseolus vulgaris L.) is an important pulse crop to ensure food and nutritional security in Ethiopia. However, its productivity is below its potential due to use of low yielding local varieties, biotic and abiotic stresses in different growing environments. Limited research was done on climbing bean and a few varieties were developed so far. This study is therefore undertaken to evaluate and identify high yield potential and stable performance. The trial was conducted at Jimma, Metu, Haru, Bako and Pawe during 2019-2020 main crop seasons using randomized complete block design with three replications. The combined analysis of variance showed highly significant difference ($P \le 0.01$) among genotypes (G), locations (L), year (Y) and their interaction (G x LxY) for most of the traits. Based on mean grain yield performance of the genotypes over environments, Genotype NUV-54 (G1) scored maximum grain yield (2.67 tha⁻¹) followed by GenotypeNUV-76 (G15) (2.57 tha⁻¹), which exhibited a yield advantage of (23.61% and 18.14) and (18.98% and 13.72%) from the checks Dandesu (2.16tha⁻¹) and Tibe (2.26 tha⁻¹), respectively. Stability view of GGE biplot showed that G1 and G15 exhibited the first and the second-highest mean grain yield and relatively ideal genotypes and moderate stability to stable across environments, respectively. These genotypesG1 and G15 are characterized by small seed size with red and white seed color, respectively. Fast cooking time is the other major attributes of outstanding varieties G1 (83 minute) and G15 (88 minute). The performance of these two genotypes also showed resistance to common bacterial blight; angular leaf spot and floury leaf spot. These two promising genotypes were promoted to verification plot for official release. Based on the gain yield performance, disease resistance and quality, the National Variety Release Committee (NVRC) approved the release of the first candidate varieties NUV-54 (G1) for commercial production since June 2022. The variety is recommended for Southwest, West and other similar agro ecologies with high rainfall areas of the country.

Keywords: Climbing bean, Yield, GGE, NUV 54

Introduction

Common bean is an important pulse in terms of production and area coverage

in Ethiopia. The national area coverage and production is estimated as 311,583.58hectares and 552, 564.074tons, respectively(CSA,

2021). The production and utilization of common bean has increased due to the rising of global demand and the hunger particularly expansion in vulnerable subset of small holder farmers in the country. Nutritionally, common bean is rich in dietary source of vitamins protein, and essential minerals such as iron and zinc (which are key elements for mental development) and B-vitamins. It plays a critical role in cropping systems and soil fertility improvement via nitrogen fixation (Beebe et al., 2000)..

Common bean is classified into four major groups by CIAT, depending on their growth habit. Class I has a determinate growth habit (bush type bean) while class II-IV has an indeterminate growth habit. Classes IIIb and IV are referred to as climbing beans or pole beans. Climbing beans originated from medium to highaltitude regions of the Andes and Central America (Voysest, 2000). The most outstanding characteristic of climbing beans is their high yield potential: up to 4 to 5 tonha⁻¹ versus 3 tonha⁻¹ for bush beans under optimal conditions (CIAT, 2004). The nature of their growth habit and yield potential allows significant harvests in areas where population pressure is high and arable land is scarce and Muyaneza, (Sperling 1995). Climbing beans are grown in East and Central African countries, including: Rwanda, Central Kenya highlands, Western Kenya, Burundi, and Eastern Democratic Republic of Congo and Southern, southwestern and Western

mid-highlands of Ethiopia (Ramaekers *et al.*, 2013; Raphaël, 2013; CGIAR, 2018; Berhanu *et al.*, 2019). The majority of these regions are characterized by high rainfall, high population density and land scarcity. Climbing beans are more common on altitudes of 1750-2300 meters above sea level (Woolley *et al.*, 1991).

Climbing bean in Ethiopia is mainly produced around homestead gardens, along the fences and sometimes intercropped with maize/pigeon peas. It can also be planted in the production fields, but it requires providing supporting sticks (Berhanu et al., 2019). Therefore, climbing beans which have high grain yield can provide the best option for intensification and production where arable landholdings are diminished due to population pressure. Despite the potential of climbing beans to maximize income per unit area for small holder farmers, limited number of climbing bean varieties were released as compared to bush type beans. Hence, this study was conducted to evaluate the stability of high yielding climbing bean genotypes along with disease resistance and acceptable quality across different testing locations and thereby to identify and advance elite genotypes to variety verification trial and release..

Materials and Methods

The experiment was conducted in Jimma, Metu, Haru, Bako and Pawe during 2019-2020 cropping season.

The description of experimental locations is presented in Table1. A total of 17 climbing bean genotypes including two checks (Dandesu and Tibe) were evaluated as a national variety trial across five locations during 2019-2020 except at Pawe where the experiment was conducted in 2020 only(Table 2). The tested introduced materials were from International Centre for Tropical Agriculture (CIAT). The genotypes were arranged in randomized complete block design with three replications.

Planting was done in a plot of four rows with 4m length with regular spacing of 10 cm between plants and 50cm between rows. Fertilizer NPS at the rate of 121kgha⁻¹ was applied at planting. The plants were supported

Table1. Description of experimental locations

with sticks starting from one month after planting and hands weeding along with manual digging were done to control weeds. Harvesting and threshing were done manually after physiological maturity.

Two candidate climbing bean varieties; namely, NUV-54 and NUV-76 along with two checks Dendesu and Tibe were tested under verification plot. The verification plot was planted at Jimma, Metu Bako and Pawe research stations and on two farmers field surrounding each research center. The trial was planted in a 10m X 10m single plot. All cultural practices for climbing were carried out as stated above. The verification plots were evaluated by variety release technical committee.

Table 1. Description of experimental locations										
Location	Altitude	Latitude	Longitude	Temperature		Annual				
				Min(°C)	Max(°c)	rainfall				
Jimma	1754	7°46'N	36°00'0"E	11.6°c	26.3°c	1572mm				
Metu	1558	8°19' 0" N	35°35' 0"E	12.7°c	28.9	1829 mm				
Haru	1252	8°59' 0" N	35°47' 0"E	16°c	27°c	1227mm				
Bako	1650	9°6' 0" N	37°9' 0" E	13.3°c	28°c	1238mm				
Pawe	1120	11°19' 0"E	36°24' 0"E	16.3 °c	32.6°c	1587mm				

Table 2	Climbing bean	genotypes	tested at nine	environments	(at five	locations [·]	for two	vears)
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Genotype code	Genotype name	Location	Year	Environment code
1	NUV 54	Jimma	2019	JM19
2	NUV 27		2020	JM20
3	NUV20	Metu	2019	MT19
4	NUV 31		2020	MT20
5	NUV 40	Haru	2019	HR19
6	HUV219-9		2020	HR20
7	NUV 100	Bako	2019	BK19
8	NUV 115		2020	BK20
9	NUV 102	Pawe	2020	PW20
10	NUV 30			
11	NUV 90			
12	NUV42			
13	NUV 173			
14	NUV 56			
15	NUV 76			
16	Check 1(Dandesu)			
17	Check 2(Tibe)			

Agronomic characters such as days to flowering, days to maturity, plant height (cm), number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight (gm), yield per plant(gmplant⁻¹), and vield per hectare (Kgha⁻¹) were recorded. Disease such as common bacterial blight, angular leaf spot, and floury leaf spot were also recorded. The scoring system was 1-9 scale (1=immune, 9=Susceptible, then 1-3=resistant,4-6=moderately resistant and 7-9 = susceptible (Shrestha and Mishra, 1994). All the data including grain yield were collected from the middle two harvestable rows. All the data were subjected to combined analysis of variance (ANOVA) using SAS software. The data analyses for interpreting genotype by environment interaction were done by GGE stability analysis in R software.

The following ANOVA models have been used to test the performance of genotypes at each and combined locations, respectively (Singh and Ceccarelli 1996) as indicated below.

$$\begin{split} Y_{ij} &= \mu + G_i + B_j + e_{ij} and \ Y_{ijk} = \mu + G_i \\ &+ E_j + GE_{ij} + Bk \ (j) + e_{ijk}. \end{split}$$

Where, Y_{ij} = observed value of genotype i in block j, Y_{ijk} = observed value of genotype i in block k of environment j, μ = grand mean of the experiment, Gi =the effect of genotype i, B_j= the effect of block j, Bk_(j) = the effect of block k in environment j, e_{ij}= error effect of genotype i in block j,E_j= environment effect, GE_{ij}= the interaction effect of genotype i with environment j, e_{ijk} = error (residual) effect of genotype i in block k of environment j. The stability of the tested genotypes was performed using GGE Biplot of GUI package in Rsoftware.

Results and Discussion

The result from the combined analysis of variance across the five locations is presented in Table 3. The pooled analysis of variance revealed that mean squares due genotype was significant (P \leq 0.01) for most of the traits except pod per plant and common bacterial blight, indicating genotypes were responded differently for each trait. Mean squares due to location was significant ($P \le 0.01$) for all the traits considered, indicating the distinct nature of the five test locations. Mean square due to years differed significantly ($P \le 0.01$ with respect to all the traits indicating that climate changes were observed during the study.

Mean squares due to location x genotype were significant for most of traits except pod per plant, seed per pod and seed per plant, meaning that genotypes exhibited different relative performance in each location. Nonsignificant genotype x year was observed for most of the traits except days to flowering, days to maturity, floury leaf spot, hundred seed weight and yield hectare⁻¹, indicating that genotypes showed consistent performance for most of traits in each year. Location x year interaction

revealed significant effect for all traits, meaning the location of genotypes performance varied in the two years, suggesting climbing that bean genotypes performed differently in every location in each year. Means squares due to genotype x location x year interaction found significant effect for days to flowering, floury leaf and hundred seed weight. spot Generally, the result for yield and related traits indicated that phenotypic variability for these traits is dependent genetic factors, environmental on variables and the interaction between genotypes and environment.

Based on the combined mean performance of the genotypes over environment, G1 scored maximum grain yield (2.67 t/ha) followed by G15 (2.57 t/ha), which exhibited a yield advantage of (23.61% and 18.14) and (18.98% and 13.72%) from the check Dandesu (2.16 tha⁻¹) and Tibe

(2.26 t/ha), respectively (Table4). The performance of the tested genotypes also showed resistance to common bacterial blight, angular leaf spot and floury leaf spot. Highest plant height was recorded from genotype, G5 (291.37 cm) followed by G14 (269.88 cm), while the lowest was recorded from genotype G4 (213.57 cm). Separate analysis for each of the test environments showed consistently large variation among test genotypes for grain yield. Generally, based on the combined mean vield and other agronomic traits over 9 environments, G1 relatively was top-ranking genotype followed by G15. Moreover, G1 had also showed the highest yield across most of the environments than the two check varieties. Thus, G1 and G15 are the first and the second candidate varieties promoted for variety verification trial.

Source	DF	DTF	DTM	PH(cm)	NPP	NSD	SPP	CBB	ALS	FLS	HSW (gm)	YLD _{pl} (gm/plant	YLD _{ha} (t/ha)
yr	1	24350.7**	9676.9**	17817.4**	1664.3**	58.4**	65156.4**	9.7**	19.9**	23.5**	161.5**	3452.0**	196.1**
loc	4	8934.0**	21564.3**	1139**	5696.1**	90.7**	111505.7**	145.3**	49.0**	32.0**	8585.6**	5054.6**	104.6**
Geno	16	55.3**	118.8**	8493.9**	139.7ns	15.7**	3404.2**	1.3ns	1.6*	1.4**	903.1**	127.2**	1.3**
Loc*rep	10	22.5**	28.4*	1302.2ns	297.5*	8.1ns	14249.6**	4.7**	0.6ns	0.3ns	31.4ns	30.3ns	1.7**
Geno*yr	16	21.2**	26.5*	18.1ns	159.1ns	6.1ns	1596.2ns	1.0ns	1.1ns	1.8**	111.9**	23.9ns	0.6*
yr*loc	3	22986.5**	10192.8**	59697.0**	502.1*	21.0*	22690.5**	5.2**	9.5**	23.5**	2107.4**	5516.7**	96.5**
Geno*loc	64	15.1**	25.0**	2018.7**	136.2ns	7.7ns	1134.3ns	1.7**	2.5**	1.7**	79.9**	65.5**	0.8**
yr*geno	16	24.3**	20.7ns	1874.5ns	203.3ns	6.5ns	1603.1ns	1.0ns	1.0ns	1.5**	103.0**	16.2ns	0.6*
geno*yr*loc	48	12.9*	15.3ns	1602.4ns	151.8ns	7.8ns	1415.6ns	0.6ns	0.8n5	1.1**	60.3**	20.6ns	0.5ns

Table 3. Mean squares values of combined analysis of variance for yield and related characters of 17climbingbean genotypes evaluated at nine environments during 2019-2020.

Where, * = significant at ($P \le 0.05$) and **= significant at ($P \le .01$), yr=year,loc=location, Geno=genotype, DF=degree of freedom, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP =pod per plant, NSD=seed per pod, NSP= seed per plant, CBB=common bacterial blight, ALS= angular leaf spot,FLS=floryleaf spot, HSW=hundred seed weight, YLD_{pl}=yield per plant, YLD_{ha}= yield ha^{-1.}

		2019 2020									Overall mean
No.	Genotype	Jimma	Metu	Haru	Bako	Jimma	Metu	Haru	Bako	Pawe	(tha-1)
1	NUV 54	2.07	1.83	2.92	1.77	5.74	2.07	5.00	1.21	1.48	2.67
2	NUV 27	0.77	1.53	3.37	1.90	4.27	1.55	4.38	1.21	1.28	2.25
3	NUV20	1.30	1.23	2.73	2.06	4.82	1.99	3.96	1.62	0.94	2.30
4	NUV 31	0.37	1.50	2.47	1.37	3.06	1.82	3.75	1.13	1.35	1.87
5	NUV 40	1.17	1.28	2.01	1.05	4.96	1.97	3.13	1.44	1.71	2.08
6	HUV219-9	0.97	1.50	2.49	2.17	5.05	1.59	3.96	1.26	1.05	2.23
7	NUV 100	0.73	1.54	3.08	1.91	3.86	1.69	3.54	0.88	1.70	2.10
8	NUV 115	0.40	0.84	2.35	1.35	5.19	1.68	4.17	0.98	1.40	2.04
9	NUV 102	0.87	0.97	2.73	1.88	5.12	1.81	5.42	0.78	1.67	2.36
10	NUV 30	0.77	1.45	1.72	1.36	4.14	1.63	4.58	1.44	1.36	2.05
11	NUV 90	0.77	1.49	3.41	1.57	5.46	1.77	4.58	1.08	1.09	2.36
12	NUV42	0.47	0.92	2.17	1.48	3.41	1.58	3.96	0.90	1.54	1.82
13	NUV 173	0.43	1.51	3.19	1.46	5.64	1.89	5.75	1.13	1.65	2.52
14	NUV 56	0.43	1.31	2.07	1.06	3.81	2.23	3.75	1.08	1.70	1.94
15	NUV 76	0.60	1.91	3.28	1.80	5.90	2.03	5.71	0.70	1.21	2.57
16	Dandesu	0.57	1.14	2.83	1.70	5.52	1.48	4.42	0.83	0.97	2.16
17	Tibe	1.37	1.23	2.25	1.96	5.57	1.53	3.58	1.25	1.63	2.26
	mean	0.83	1.36	2.65	1.64	4.80	1.78	4.33	1.11	1.4	2.21
	CV	42.70	22.04	15.33	19.45	13.54	32.56	27.17	33.37	14.2	26.92
	LSD	0.59	0.50	0.68	0.53	1.08	ns	Ns	ns	0.33	0.32

Table 4 . Mean grain yield performance (t ha-1) of 17 climbing bean genotypes evaluated in five locations in 2019 and 2020 cropping season

geno		DF	DM	PH	NPP	spd	SPP	CBB	ALS	FLS	HSW	Yld(gm/pl	Yld(t/h
	Name											ant)	a)
1	NUV 54	56.63	105.85	256.77	15.17	4.97	68.43	3.07	2.41	1.44	29.34	17.80	2.68
2	NUV 27	52.15	101.26	240.36	12.89	5.55	68.55	2.85	2.67	1.37	29.36	16.07	2.25
3	NUV20	52.19	101.81	235.42	13.93	5.23	69.22	2.89	2.70	1.52	28.62	14.83	2.30
4	NUV 31	52.19	99.00	213.57	14.39	4.64	58.54	2.67	2.26	1.74	41.29	13.32	1.87
5	NUV 40	54.70	105.48	291.37	11.21	4.81	53.60	2.48	2.07	1.81	34.91	15.50	2.08
6	HUV219-9	54.37	99.59	253.37	13.43	7.10	83.52	2.74	2.48	1.15	25.31	15.95	2.23
7	NUV 100	52.41	100.26	221.85	13.59	6.79	69.98	3.04	2.70	1.15	28.56	13.71	2.10
8	NUV 115	53.37	101.59	246.78	10.57	5.21	52.65	2.70	2.56	1.22	29.35	13.61	2.04
9	NUV 102	54.44	100.22	246.43	15.17	5.55	74.99	2.44	2.44	1.00	26.32	17.75	2.36
10	NUV 30	52.22	102.48	245.23	10.45	5.00	46.00	2.70	1.96	1.52	42.43	15.34	2.05
11	NUV 90	52.70	100.81	256.23	14.00	6.08	79.34	2.89	2.48	1.22	24.47	15.30	2.36
12	NUV42	52.48	101.52	249.52	13.14	5.07	68.65	2.67	2.15	1.52	33.95	14.26	1.82
13	NUV 173	52.89	98.07	244.77	11.43	5.90	64.09	2.81	2.15	1.44	25.84	17.70	2.52
14	NUV 56	55.81	103.22	269.88	10.85	5.23	53.92	2.56	2.15	1.74	40.08	15.43	1.94
15	NUV 76	53.59	99.48	238.24	13.00	7.21	82.64	2.67	2.07	1.00	25.55	16.30	2.57
16	Dandesu	54.67	99.67	263.27	14.29	6.23	78.23	3.11	2.56	1.15	27.39	20.50	2.16
17	Tibe	53.85	100.07	256.88	21.55	5.64	78.75	2.81	2.67	1.00	29.76	21.29	2.26
	mean	53.57	101.20	248.82	13.47	5.66	67.71	2.77	2.38	1.35	30.74	16.16	2.21
	CV	5.64	3.76	14.50	89.88	48.23	57.75	31.59	37.4	51.72	15.71	31.21	26.92
	LSD	1.62	2.04	19.31	NS	1.46	20.94	NS	0.48	0.37	2.58	2.70	0.32

Table 5. Mean grain yield performance (ton ha-1) and other growth parameters of 17 climbing bean genotypes evaluated in five locations for the period 2019-2020

GGEBiplot and stability analysis of the test genotypes across environments

The GGE biplot method consists of a set of biplot interpretation methods to evaluate genotype and testenvironment (Yan, 2007). The analysis showed that genotype G1 performed best at Jimma and Metu followed by G15. The check Tibe (G17) better performed at Jimma and Pawe. Pawe. Genotype G4, G7, G14, and G12 did not perform best in any of the environments (Figure 1). Mean vs. Stability" view of GGE biplot is an efficient tool to compare genotype based on mean performance and stability across environments within a mega environment (Yan et al., 2007). Mean vs. stability view of GGE biplot is presented in Figure 2. G1 showed higher mean grain yield but had less stability across environment. Genotype-15 scored the secondhighest mean grain yield performance relatively and stable across environments. Besides according to Yan and Hunt (2001), the GGEBiplot explains a small portion of the total variation that can contribute to this discrepancy.

The "which-won-where" view of the GGE biplot is an effective feature for mega-environment analysis (Yan *et al.*, 2007). Therefore, in this study based on the mean yield performance of climbing bean genotypes, all environments and genotypes fall into a four sector (figure 3). The Biplot contains a polygon drawn on genotypes that are furthest from the

biplot origin so that all other genotypes are contained within the polygon and these genotypes located the vertices of the polygon on performed either the best or the poorest in one or more environments (Yan, 2006). Environments within the same sector share the same winning environments genotypes and in different different sectors have winning while, genotypes the genotypes within the polygon and nearer to origin were less responsive than vertex genotypes (Yan and 2006).Besides Tinker, the high fluctuation in the performances of the genotypes, the significant interaction effect was observed over year by location. Yan and Tinker (2006) indicated the genotypes in the corner of the polygon are the best performing one in each set of environments within the angle of the polygon formed by the broken lines. In this assumption, the G1, G5, G4, and G13 performed best in their respective environments. Genotypes 1 performed well in JM19 and JM20 and moderately adapted to MT19, MT20, and BK20. Three vertex genotypes, G5, G4, and G13 had the highest vield in their vertex environments (MT20. PA20and BK20), (PW20), and (BK19,HR19 and HR20 and, respectively. The other thirteen genotypes were fallen in with their respective sectors environment markers.

The ideal genotype is located in the first concentric circle in the bi-plot. An ideal genotype has the highest mean yield and stable across environments (Farshadfar*et al.*, 2012). Genotype

near to the concentric circle is G15 which can be desirable and benchmarks for evaluation of climbing bean genotypes followed by G11, G9, and G17 (figure 4).



Figure 1. Mean grain yield performance and stability of genotypes based on the G × E data



Figure 2. Mean grain yield performance and stability of genotypes based on the G × E data



Figure 3. GGE bi-plot on genotypes using symmetrical scaling for mean lint yield and stability of 15climbingbean genotypes

Tested across seven environments



Figure 4. The average- environment view to rank genotypes to ideal genotypes

[63]

Important seed Characteristics and cooking time of candidate varieties

The candidate varieties NUV-54and NUV-76 are characterized by small seed size with red and white seed color, respectively. Fast cooking time is the other major attribute of outstanding candidate varieties NUV-54 (83 minutes) and NUV-76 (88 minutes). Whereas, check varieties; Dandesu and Tibe were characterized by red seed color, medium and small seed size with their acceptable cooking

time (87 and 85 minutes), respectively (Table 6). Therefore, these two genotypes were promoted to variety verification trial and submitted to variety releasing committee as candidate varieties and evaluated by the technical committee in the 2021 cropping season. Finally, based on the gain yield performance, disease resistance/tolerance and acceptable quality, the national variety release standing committee approved the release of the first candidate varieties NUV-54 (G1) for commercial production purposes since June 2022.

Table 6. Seed Characteristics and cooking time of climbing bean Candidate and check varieties

N <u>o.</u>	Variety	Seed color	Seed size	Cooking time (minute)	Decision of the committee (NVRC)	Year of release
1	NUV-54 (candidate1)	white	small	83	released	2022
2	NUV 76(candidate2)	red	small	88	rejected	-
4	Dandesu(check1)	red	medium	87	check	2012
5	Tibe (check2)	red	small	85	check	2004

Conclusion and Recommendation

The combined analysis of variance showed highly significant ($P \le 0.01$) due to genotypes, location, year and their interaction for most traits. The mean yield performance of the genotypes showed that G1 (NUV 54) scored maximum grain yield (2.67 tha ¹) followed by G15 (NUV76) (2.57 tha⁻¹). which exhibited а vield advantage of (23.61% and 18.14) and (18.98%) and 13.72%) from the standard check Dandesu (2.16 t/ha) and Tibe (2.26 t/ha), respectively. The performance of the genotypes also showed resistance to foliar disease. These genotypes G1 and G15 are characterized by small seed size with red and white seed color, respectively. Fast cooking time is the other major attribute of outstanding varieties G1 (83 minutes) and G15 (88) minutes).Generally, G1showed higher mean grain yield value than the other test genotypes and had moderate stability for some environments. GenotypeG15 scored the secondhighest mean grain yield and relatively a good stable candidate across

environments. Therefore, based on the gain vield performance, disease resistance and acceptable quality, the variety release national standing committee approved the release of the first candidate varieties NUV-54 (G1) for commercial production since June 2022. The variety is recommended for Southwest, West and other similar agro-ecologies with high rainfall areas of the country.

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Reference

- Beebe S, Skroch PW, Tohme J, Duque MC, Pedraza F and J NienhuisStructure of genetic diversity among common bean landraces of Middle American origin based on correspondence analysis of RAPD. Crop Sci.2000; 40: 264–273.
- Berhanu Amsalu, Kassaye Negash, Tigist Shiferaw, Kidane Tumssa, Dagmawit Tsegaye, Rubyogo Jean Claude, and

Clare Mugisha Mukankusi, 2019. Progress of Common Bean Breeding and Genetics Research in Ethiopia. *Ethiop. J. Crop Sci. Special Issue Vol. 6 No.3 (2018).*

- Central Statistical Authority (CSA), 2021. Agricultural sample survey, Area and production of temporary crops, private holdings for the 2021.
- CGIAR (2018). Common Bean Grain Legumes - A CGIAR Research Program. Intuition theme by CPOThemes. http://grainlegumes.cgiar.org/crops/c ommon-bean/
- CIAT, International Centre for Tropical Agriculture, 2004, . Impact of Improved bean varieties in Western Kenya, Highlights. No.18 December. 2004.
- Farshadfar E., Mohammadi R., Aghaee M, Vaisi Z. 2012. GGE biplot analysis of genotype x environment interaction in wheat-barley disomic addition lines. Australian Journal of Crop Science 6, 1074–1079.
- Ramakers L, Micheni A, Mbogo P, Vanderleyden J & Maertens M. 2012. Adoption of Climb.ing beans in the central highlands of Kenya: An empirical analysis of farmers' adoption decisions. African Journal of Agricultural Research, Vol 8, No 1, pp 1-19.
- Raphaël P (2013). Potential and challenges of climbing bean production in western Kenya. Some back ground (theory and case studies) in technology adoption and adaptation by smallholder farmers. Minor thesis –N2Africa pp. 1-37.
- Shrestha, S. M., and N. K. Mishra, 1994. Evaluation of common cultivars of rice against leaf and neck blast in Nepal. Institute of Agriculture and Animal Science Journal, 15: 101–103.

Singh and Ceccarelli 1996

- Sperling L, Muyaneza S (1995). Intensifying production among smallholder farmers: the impact of improved climbing beans in Rwanda. Afr. Crop Sci. J. 3(1):117-125.
- Voysest, 2000. Mejoramientogenetico del frijol (Phaseolus vulgaris L.): legado de variedadas de America Latina 1930-1999.
- Woolley J, Davis JHC (1991). The agronomy of intercropping with beans. In: Common beans: Research for crop improvement (van Schoonhoven, A. and Voysest, O., eds). C.A.B. Intl. Wallingford UK and CIAT Cali Colombia. pp. 707-735.Voysest. 2000.

Mejoramientogenetico del frijol (Phaseolus vulgaris L.): legado de variedadas de America Latina 1930-1999.

- Yan W, Hunt LA. 2001. Interpretation of genotype by environment interaction for winter wheat yield in Ontario. Crop Sci 41:19–25.
- Yan W, Kang MS, Ma B, Woods S and Cornelius PL. 2007. GGE biplot vs. AMMI analysis of genotype-byenvironment data. Crop Science, 47: 643-653.
- Yan, W., and Tinker NA., 2006. Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci. 86: 623–645.