

Research Article

Genotype \times Environment Interaction and Yield Stability in Early-Maturing Cowpea (*Vigna unguiculata* (L.) Walp.) Landraces in Ethiopia

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The study was conducted to estimate the effects of genotype, environment, and genotype \times environment interaction on grain yield and yield-related traits and to identify stability genotype. At six environments, twenty-four cowpea landraces and one check were evaluated in a 5×5 triple lattice during the 2019 cropping season. Data were collected on yield and yield-related traits. The analysis of variance for each environment and across environments showed significant differences among genotypes, environments, and GEI for most traits including yield. Environment, genotype, and GEI showed 27.45%, 20.9%, and 49.55% contribution to the total sum of squares, respectively, for grain yield. This indicated that the environments were diverse and most of the variation in grain yield was caused due to interaction and environmental means. G24 (2632 kg ha⁻¹) and G16 (2290 kg ha⁻¹) were the highest yielder and stable genotypes with mean grain yields above the grand mean (2049.28 kg ha⁻¹) and standard check (2273 kg ha⁻¹). G24 and G16 were the most stable genotypes according to cultivar superiority, Wricke's ecovalence, regression coefficient, and deviation from regression stability models.

1. Introduction

Cowpea is an annual herbaceous and self-pollinated grain legume crop that belongs to family Fabaceae and genus *Vigna*. It is a diploid species with $2n = 2x = 22$ chromosomes [1]. The precise primary center of origin and the exact center of diversity of cowpea is not known, but according to OECD [2], Ethiopia is the primary center of diversity of cowpea and more than 66.5% of the arable land is very suitable for cowpea production.

Cowpea is drought resistant and adapted to marginal soil due to the nitrogen-fixing ability that makes it a useful staple crop for farmers in harsh environments under moisture stress and hot temperatures [3, 4]. It is widely cultivated and consumed globally, especially in the arid and semiarid tropics and sub-Saharan Africa [5]. As documented by Abate et al. [6], about 38 million households (194 million people)

grow cowpea in sub-Saharan Africa that accounts for about 84% of the world production. Particularly, production in Nigeria and Niger accounts for more than 45% and nearly 15% of the world's total production, respectively, with more than 4 million hectares of cultivated land each. Nigeria is supposed to be the highest producer of cowpea in the world with the production of 850,000 tons followed by Niger and Brazil, whereas Niger is the largest cowpea exporter in the world with an estimate of 215,000 tons exported annually [1, 7]. The crop is cultivated primarily for its edible seeds, young leaves (as a vegetable), pods seeds, soil improvement, and forage value [8, 9]. Due to its fast growth habit, it covers the ground rapidly and, therefore, limits weed competition and soil erosion [10, 11].

In Ethiopia, cowpea is mostly produced in the Amhara region (North and South Wollo, Waghimra, and Oromia special zones), Tigray region, Oromia region (East Shewa

and East and West Harerghe zones), Gambella (Anywaa Zone), and SNNPR: South Omo, Gamo Gofa, and Wolayta zones [8, 9]. As documented by the aforementioned authors, Ethiopia has a great diversity of cowpea landraces (local farmers' varieties) in many traits and over 83% of cultivated cowpeas in Ethiopia are landraces. Cowpea production and utilization in Ethiopia is very low as compared to other African countries, though the country is claimed to be the center of diversity and/or origin and has a high potential for the production of the crop.

Despite the fact that cowpea is a multipurpose grain legume, its productivity is very low and unstable across environments and years due to biotic factors (weeds, insects, and diseases), abiotic factors (soil type, altitude, rainfall distribution, and intensity), and scarcity of widely adaptable and early-maturing varieties [12, 13]. The variability in environments such as location effect, seasonal fluctuation, and their interaction highly influences the production of cowpea in relation to yield potential [14, 15].

Genotype \times environment interaction (GEI) is a challenge for plant breeders since it complicates variety recommendation because of the inconsistency of best-yielding genotypes across cropping environments and season. The effect of GEI is most commonly minimized by repeating the experiment at several sites in a single year, or over several crop seasons in a single site, or both [16, 17].

Even though there are many opportunities for breeders to develop cowpea varieties possessing different agronomic characteristics and inherent tolerance to a wide range of biotic and abiotic factors, progress of cowpea breeding in Ethiopia is very limited either in exploiting the available genetic variability in the country or from introduction of improved varieties. Moreover, information on the effect of genotype, environment, and their interaction and the performance stability of cowpea landraces is scanty. Therefore, evaluating cowpea landraces in contrasting environments to generate such information is imperative. In view of this, this research was initiated with the following objectives:

- (i) To estimate the effects of genotype, environment, and genotype \times environment interaction on grain yield and yield-related traits
- (ii) To assess the stability of cowpea landraces for yield across environments

2. Materials and Methods

2.1. Description of the Study Area. The experiment was conducted at six cowpea-growing environments during the 2019 main cropping season in Ethiopia. The environments were as follows: Sekota, Kobo, Sirinka, Melkassa, Miesso, and Babile. The test environments were selected on the basis of representativeness for cowpea-producing environments. These six locations representing different agroecologies of cowpea-growing areas in Ethiopia and descriptions of the areas are presented in Table 1.

2.2. Experimental Materials and Design. Twenty-four Ethiopian cowpea landraces (Table 2) collected from the Amhara region, Tigray region, Oromia region, Gambella,

and SNNPR were evaluated along with one check (released variety: Kanketi). The experiment was conducted using a 5×5 triple lattice design at each location, and each genotype was assigned randomly. The seeds were planted on the first week of July at a plot size of $4 \text{ m} \times 2.4 \text{ m}$ (9.6 m^2) having four rows, with an interrow spacing of 60 cm and 20 cm between seeds within the row. The net harvest area was 4.8 m^2 per plot, the central two rows. The spacing between plots and blocks was 1 m and 1.5 m, respectively. All agronomic management practices were carried out equally and properly as per the recommendations.

2.3. Data Collection and Data Analysis. Data for plant height, number of pods per plant, and number of seeds per pod were collected on the basis of five sample plants which were randomly taken from the two central rows, and the average of five samples was used for analysis, while days to 50% flowering, days to 90% maturity, grain yield, and 100 seed weight were collected on the basis of the net plot (*i.e.*, two central rows).

Different statistical software packages were used to analyse the data. SAS [18] was used for analysis of variance of the individual environments and combined over locations [19]. SPAR 2.0 was used for regression coefficient (b_i) and deviation from regression (S^2_{di}), and GenStat (18th edition, 2015) was used for cultivar performance (p_i) and Wricke's ecovalence (W_i). The combined analysis of variance across the environment was carried out using a mixed model (genotype: fixed, location: random) in order to determine the differences between genotypes across environments, among environments and their interaction. The F-max method of Hartley [20] was used to assess the homogeneity of error variances prior to doing combined analysis over the environment. However, location four (Melkassa) was an outlier in terms of error variance; hence, it was removed from the combined analysis. Due to this, the combined analysis of variance for grain yield and yield-related traits of 25 cowpea genotypes tested was conducted for five environments. Various stability analyses were computed for grain yield. Mean comparison using Duncan's Multiple Range Test (DMRT) was performed to explain the significant differences among the means of genotypes and environments.

3. Results and Discussion

3.1. Analysis of Variance for Individual Environments. Analysis of variance for grain yield (kg ha^{-1}) of the 25 cowpea genotypes tested in six environments is presented in Table 2. Analysis of variance for each environment showed a highly significant ($P < 0.01$) variation in grain yield among cowpea genotypes in all tested environments. This indicated the presence of performance variation among the tested cowpea genotypes for grain yield. Likewise, El-Shaieny *et al.* [21]; Santos *et al.* [22]; Ishiyaku *et al.* [23]; and Tariku [24] in cowpea and Abele [25] and Tullu [26] in common bean reported large variation in grain yield

TABLE 1: Description of the test environments.

Environments	Soil type	Altitude (masl)	Average rainfall (mm)	Temperature (°C)		Geographical location	
				Min	Max	Latitude (N)	Longitude (E)
Sekota	Vertisol	1850	789	12.9	32.9	12° 14'	38° 30'
Kobo	Vertisol	1450	673.4	13	34	12° 8'	39° 18'
Sirinka	Vertisol	1880	876	13.6	27.3	11° 08'	39° 28'
Melkassa	Andosol	1500	763	14	24.8	8° 30'	39° 21'
Miesso	Vertisol	1332	787	14.9	28.2	9° 28'	38° 08'
Babile	Spodosols	1650	671	15.5	28.1	9° 30'	42° 21'

Source: the Melkassa Agricultural Research Center (MARC), Sirinka Agricultural Research Center (SARC), and Sekota Dry Land Agricultural Research Center (SDARC).

TABLE 2: Mean grain yield (kg ha⁻¹) of 25 cowpea landraces tested at six environments in the 2019 cropping season.

Code	Genotypes	Environments						GGM	Rank
		Sekota	Kobo	Sirinka	Melkassa	Miesso	Babile		
G1	NLLP_CPC_07-47	1761.1 ^{ef}	1776.5 ^{ghi}	2603.2 ^a	2642.1 ^{bcde}	1800.1 ^{efg}	2196.0 ^{cde}	2129.8 ^{b-h}	11
G2	NLL_CPC_07-74	1900.0 ^{abcde}	2538.3 ^{cd}	2401.6 ^{ab}	2581.5 ^{bcdef}	2729.5 ^{bcd}	1506.7 ^{ghij}	2276.3 ^{bc}	3
G3	NLLP_CPC_07-168	2261.1 ^a	1255.3 ^{lm}	2486.0 ^{ab}	1900.6 ^{ef}	2980.7 ^{abc}	1242.3 ^{ijkl}	2021.0 ^{g-j}	16
G4	NLLP_CPC_07-27	2094.4 ^{abcde}	2394.0 ^{cde}	1974.5 ^{cd}	2377.0 ^{bcdef}	3073.8 ^{abc}	1588.3 ^{ghij}	2250.3 ^{bcd}	6
G5	NLLP_CPC_07-05	1754.2 ^f	2170.4 ^{ef}	1765.3 ^d	2660.3 ^{bcde}	3065.4 ^{abc}	1055.0 ^l	2078.4 ^{c-i}	12
G6	NLLP_CPC_07-01	2014.6 ^{abcde}	1905.6 ^{efg}	743.2 ⁱ	2525.8 ^{bcdef}	2664.9 ^{bcd}	1446.6 ^{hijk}	1883.5 ^{i-l}	19
G7	NLL_CPC_07-49	1847.9 ^{cde}	1491.0 ^{ijkl}	1868.2 ^{cd}	2891.0 ^{abc}	2756.8 ^{abcd}	2724.8 ^a	2263.3 ^{bc}	5
G8	NLLP_CPC_07-77	1858.4 ^{bcde}	1406.8 ^{klm}	2458.4 ^{ab}	1905.2 ^{def}	2635.2 ^{bcd}	1408.0 ^{hijkl}	1945.3 ^{h-l}	18
G9	NLL_CPC_07-46A	2198.6 ^{abc}	1938.4 ^{efg}	1154.2 ^{efg}	1907.7 ^{def}	3074.6 ^{abc}	1969.9 ^{def}	2040.6 ^{g-i}	15
G10	ACC 211557	1775.0 ^{def}	1661.6 ^{hij}	1982.0 ^{cd}	2532.4 ^{bcdef}	2615.3 ^{bcd}	1710.7 ^{efg}	2046.2 ^{e-i}	14
G11	ACC222890	1712.5 ^{ef}	1299.7 ^{klm}	1625.8 ^{def}	2482.3 ^{bcdef}	1027.2 ^h	1062.6 ^{kl}	1535.0 ^o	25
G12	Dass 002	1393.1 ^f	2174.3 ^{cf}	1126.6 ^{efg}	1960.8 ^{def}	1465.3 ^{gh}	1661.3 ^{efghi}	1630.2 ^{no}	24
G13	Dass 007	1837.5 ^{cde}	2671.6 ^{bc}	1370.2 ^{ef}	2199.7 ^{cdef}	2994.6 ^{abc}	1246.8 ^{ijkl}	2053.4 ^{d-i}	13
G14	NLLP_CPC_07-69	1400.0 ^f	1729.0 ^{ghi}	1802.3 ^{cd}	1849.5 ^f	1705.1 ^{fg}	1396.1 ^{hijkl}	1647.0 ^{mno}	23
G15	NLLP_CPC_07_	1865.3 ^{abcde}	1206.2 ^m	1355.0 ^{ef}	2424.2 ^{bcdef}	2787.7 ^{abcd}	1311.0 ^{ijkl}	1824.9 ^{klm}	21
G16	ACC 233403	2038.9 ^{abcde}	2522.7 ^{cd}	992.9 ^{ghi}	3083.2 ^{ab}	2784.6 ^{abcd}	2320.1 ^{bcd}	2290.4 ^b	2
G17	NLLP_CPC_07-28	1406.9 ^f	1915.9 ^{efg}	809.3 ^{hi}	2360.2 ^{bcdef}	2256.8 ^{def}	1841.7 ^{efg}	1765.1 ^{mn}	22
G18	NLLP_CPC_07-46B	1868.8 ^{abcde}	1570.0 ^{ijk}	1415.3 ^{ef}	3433.4 ^a	1746.6 ^{fg}	1940.3 ^{ef}	1995.7 ^{g-k}	17
G19	ACC 244804	1768.1 ^{def}	2592.7 ^c	836.9 ^{hi}	2523.6 ^{bcdef}	1793.1 ^{efg}	1512.9 ^{ghij}	1837.9 ^{kl}	20
G20	NLLP_CPC_07-29	1997.2 ^{abcde}	2004.1 ^{fg}	1961.1 ^{cd}	2273.7 ^{cdef}	3090.4 ^{abc}	1952.2 ^{def}	2213.1 ^{b-f}	8
G21	ACC 223402	2118.8 ^{abcd}	2309.9 ^{de}	1667.3 ^{de}	2637.2 ^{bcde}	2708.0 ^{bcd}	1749.9 ^{efg}	2198.5 ^{b-f}	9
G22	NLLP_CPC_07_48B	1816.7 ^{cde}	1674.0 ^{hij}	2321.9 ^{ab}	2460.1 ^{bcdef}	2352.9 ^{de}	2340.5 ^{bc}	2161.0 ^{b-g}	10
G23	NLLP_CPC_07-03	2087.5 ^{abcde}	1525.3 ^{ijkl}	1199.6 ^{fg}	2691.6 ^{bcd}	3372.0 ^a	2578.8 ^{ab}	2242.5 ^{b-e}	7
G24	NLLP_CPC_07-55	2247.2 ^{ab}	3060.0 ^a	2150.4 ^{cd}	2928.5 ^{abc}	3205.1 ^{ab}	2203.3 ^{cde}	2632.4 ^a	1
G25	Kanketi	2181.3 ^{abc}	2871.6 ^{ab}	1831.7 ^{cd}	2945.1 ^{abc}	2534.1 ^{cd}	1275.9 ^{ijkl}	2273.3 ^{bc}	4
	EGM	1888.2 ^{**}	1986.6 ^{**}	1676.1 ^{**}	2487.1 ^{**}	2528.8 ^{**}	1729.7 ^{**}	2049.4	
	CV (%)	10.37	7.73	11.44	15.89	12.69	11.72		

** = significant at $P < 0.01$, GGM = genotypic grand mean, EGM = environmental grand mean, CV (%) = coefficient of variation in percent.

performance among different tested genotypes across environments.

Among the testing environments, the general performances of the genotypes for grain yield were the highest at Miesso as compared to the other six environments with a mean grain yield of 2528.8 kg ha⁻¹ followed by Melkassa (2487.1 kg ha⁻¹) and Kobo (1986.6 kg ha⁻¹). The superior performance of genotypes at Miesso and Melkassa can be attributed to the uniform distribution of rainfall during the season (Table 3). The lowest grain yield was obtained at Sirinka with a mean yield of 1676.1 kg ha⁻¹. This may be due to heavy rainfall and hail that occurred at the vegetative stage. Babile was the 2nd least-performing environment with

mean grain yield of 1729.7 kg ha⁻¹, which may be due to a small amount and erratic rainfall during the growing season.

As indicated in Table 2, the tested genotypes showed inconsistent yield advantage across environments. Genotype NLLP_CPC 70-55 scored the highest mean grain yield (3060.0 kg ha⁻¹) at Kobo followed by Kanketi (2871.6 kg ha⁻¹) and Dass 007 (2671.6 kg ha⁻¹), whereas NLLP_CPC_07-168 (2261.1 kg ha⁻¹), NLLP_CPC_07-55 (2247.2 kg ha⁻¹), and NLLP_CPC_46A (2198.6 kg ha⁻¹) were the three top-yielder genotypes at Sekota without a significant difference among them. At Sirinka, NLLP_CPC_07-47, NLLP_CPC_07-168, and NLLP_CPC_07-77 were the three best yielders with a mean grain yield of 2603.2 kg ha⁻¹, 2486.0 kg ha⁻¹, and

TABLE 3: Monthly meteorological data of the test locations during the growing period.

Location		Jun	July	August	September	October
Sekota	RF (mm)	57.4	125.6.0	110	76.4	0
	T min (°C)	17	16.2	16.1	17.6	18.5
	T max (°C)	28.5	26.8	27.1	28.1	28.4
	T mean	22.75	21.5	21.6	22.85	23.5
Kobo	RF (mm)	46.6	204.1	267.6	102.3	38.8
	T min (°C)	16.5	15.8	14.9	14.9	15
	T max (°C)	28.7	28.2	25.7	26.3	27.4
	T mean	22.6	22	20.3	20.6	21.2
Sirinka	RF (mm)	89.3	285.3	208.1	143.4	50.4
	T min (°C)	15.6	15.9	14.9	15.4	14.7
	T max (°C)	24.5	25.1	24.3	25.2	24.1
	T mean	20	20.5	19.6	20.3	14.7
Melkassa	RF (mm)	75.7	100.7	158.7	120.2	83.3
	T min (°C)	15	14.8	14.6	14.3	11.1
	T max (°C)	27	25.7	26.1	26.7	27.8
	T mean	21	20.3	20.4	20.5	19.5
Miesso	RF (mm)	42.5	70.7	123.1	92.6	53.9
	T min (°C)	15.6	14.6	14.2	14.6	14.3
	T max (°C)	25.9	22.5	23	24	25.8
	T mean	20.75	18.55	18.6	19.3	20.05
Babile	RF (mm)	82.2	5.2	112.8	55	86.4
	T min (°C)	18.6	18.6	17.5	16.3	14.7
	T max (°C)	29.2	28.2	30.5	31.7	31.3
	T mean	23.9	23.4	24	24	23

RF = rain fall; T = temperature; Min = minimum; Max = maximum; °C = degree centigrade; mm = millimeter.

2458.4 kg ha⁻¹, respectively. At the same time, NLLP_CPC-07-46B (3433.4 kg ha⁻¹), ACC 233403 (3083.2 kg ha⁻¹), Kanketi (2945.1 kg ha⁻¹), and NLLP_CPC 70-55 (2928.5 kg ha⁻¹) were the highest-yielder genotypes in Melkassa without a significant variation between them. At Miesso, NLLP_CPC_07-03 was the highest yielder (3372.0 kg ha⁻¹) followed by NLLP_CPC 07-55 (3205.1 kg ha⁻¹) and NLLP_CPC_07-29 (3090.4 kg ha⁻¹), respectively, without a significant variation between them. At Babile, NLLP_CPC_07-49, NLLP_CPC_07-03, and NLLP_CPC_07-48B were the three top yielders with grain yields of 2724.8 kg ha⁻¹, 2578.8 kg ha⁻¹, and 2340.5 kg ha⁻¹, respectively.

3.2. Combined Analysis of Variance over Five Environments. For combined analysis of variance, the homogeneity of error variances was tested using the F-max method of Hartley [20], which is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error as $F - \text{ratio} = \text{larger MSE} / \text{smaller MSE}$. If the larger error mean square is not three-fold larger than the smaller error mean square, the error variance was considered homogeneous [27] and allowed pooled analysis across environments. However, location four (Melkassa) was an outlier in terms of error variance; hence, it was removed from the combined analysis. Due to this, the combined analysis of variance for grain yield and yield-related traits of 25 cowpea genotypes tested was conducted for five environments (Tables 4 and 5).

The analysis showed that cowpea grain yield was significantly ($P < 0.01$) affected by the environment, genotype, and GEI. The significance of GEI indicated that the relative performances of the genotypes were not consistent across the test environments and the environments had different effects on the yield potential of the genotypes. This, in turn, suggested the need to conduct further analysis on the genotype by environment interaction to understand the nature of the interaction and to accomplish stability analysis for identifying genotypes with stable performances across environments and/or those that fit for specific adaptation. In agreement with this finding, El-Shaieny et al. [28]; Santos et al. [22]; and Ishiyaku et al. [23] in cowpea and Firew [29]; Abele [25]; and Tadele et al. [30] in common bean reported the significant effects of the genotype, environment, and genotype by environment interaction on yield and yield-related traits.

In this study, the largest variance was explained by the genotype by environment interaction (49.55%), followed by the environment effect (27.45%), genotype effect (20.9%), and 2.07% of replication effect (Table 4). Only 9.21% of total variation remained unexplained (as error). A large yield variation explained by the GEI and environment indicated that genotypes had various performances across environments and the environments were diverse, with large difference among environmental means causing most of the variation in grain yield. In line with this, many researchers reported the dominance of the environmental effect in the combined analysis of grain yield (Abele [25]; Tariku [24, 26]). Hence, the GEI maintained or exerted about more than double times larger effect than the genotype, which complicates the selection of superior and adaptable genotypes. Pham and Kang [31] indicated that, since GEI minimize the usefulness of genotype effects alone, it is, thus, imperative that yield levels, adaptation, and stability are taken into account in the multilocation trial. Therefore, simultaneous consideration of both high mean yield (genotype main effect) and GEI stability is very crucial in selecting superior genotypes from evaluated cowpea genotypes.

Combined analysis of variance revealed a highly significant ($P < 0.01$) variation among the tested genotypes for days to 50% flowering, days to 90% maturity, plant height, number of pods per plant, number of seeds per pod,

TABLE 4: Combined ANOVA for grain yield (kg ha⁻¹) of 25 cowpea genotypes tested at five environments.

Source of variation	Degrees of freedom	Sum of square	Mean square	Total variation explained (%)
Genotype	24	26479319.3	1103304.97**	20.9
Environment	4	34726016.9	8681504.24**	27.45
Rep (env.)	10	2615788.7	261578.87**	2.07
Interaction	96	62679547.1	652911.95**	49.55
Pooled error	240	11652665.5	48552.8	9.21
Total	374	126500672.0		

** = Significant at $P < 0.01$.

TABLE 5: Mean square from combined ANOVA for yield-related traits of 25 cowpea landraces tested at five environments.

Source	Df	DF	DM	PH	PPP	SPP	HSW
Genotype	24	41**	100**	1135**	26**	6**	1103305**
Environment	4	1668**	3060**	98526**	5579**	203**	8681504**
Rep (env.)	10	7ns	10 ns	243**	109**	4**	261579**
Interaction	96	28**	74**	733**	42**	7**	652912**
Pooled error	240	4	10	88	5	2	48553

** = Significant at $P < 0.01$; * = significant at $P < 0.05$, ns = nonsignificant; df = degrees of freedom; DF = days to flowering; DM = days to maturity; PH = plant height; PPP = pod per plant; SPP = seed per pod; HSW = hundred seed weight.

grain yield, and hundred seed weight (Table 6). In this study, the genotype \times environment interaction showed highly significant differences and the tested genotypes showed rank change and strong interaction. Therefore, the mean performance of genotypes cross the tested environments was interpreted using simple effects (i.e., mean of each genotype at each location) to provide relevant information.

3.3. Analysis of Variance for Grain Yield from Eberhart and Russell's Model. The significant mean squares for $G \times E$ interaction in the general ANOVA (Table 4) suggested the importance of partitioning the genotype by the environment interaction effect into the environment (linear), $G \times E$ (linear) interaction effects (the sum of squares due to regression or b_i), and unexplained deviation from linear regression (pooled deviation mean squares or S^2_{di}). The results of ANOVA for grain yield from Eberhart and Russell's model are presented in Table 7.

In the joint regression analysis of variance for grain yield, there was a highly significant difference for genotypes and a significant difference for genotype \times environment (linear) sources of variation. This indicated contrasts between the environments and the occurrence of the differential response of genotypes across environments. The linear and nonlinear parameters provide an adequate account of the dynamic response of genotypes to changing environments and are used with the mean performance of genotypes to assess the potentialities of different genotypes [32]. The significant $G \times E$ (linear) interaction indicated that the stability parameter " b_i " estimated by the linear response to change in environment was not the same for all genotypes, and the variability of genotypes for performance is partially unpredictable. These results are in agreement with those reported by Sarvamangala et al. [33] and Nunes et al. [34] in cowpea.

According to Eberhart and Russell's [21] model, a stable genotype should have high mean yield, the regression coefficient approximating to a unity ($b_i = 1$), and deviation from regression (S^2_{di}) nearly equal to zero. The regression coefficient (b_i) measures the response of genotypes to environments. When the regression coefficient of the genotype is nonsignificantly different from unity ($b_i = 1$), the genotype is said to have average response to environmental change and suitable to both poor and good environments, while if the b_i value of genotypes is significantly greater than unity ($b_i > 1$), the genotype is highly responsive to environmental change and it is suitable only for a good environment. When the genotype b_i value is significantly less than unity ($b_i < 1$), it indicates that the genotype is less responsive and it is suitable for poor environments [35]. Accordingly, many genotypes with mean grain yield lower and above the grand mean had b_i values which were nonsignificantly different from unity ($b_i = 1$), indicating their average response to both poor and good environments (Table 8). From those genotypes, G16, G20, G24, G2, and G7 had positive and nearly a unity ($b_i = 1$) regression coefficient values that indicated average responsiveness and that the genotypes were suitable for all environments. These genotypes had also higher mean yield than overall mean of genotypes, suggesting that they are desirable for cultivation in all environments. In contrast to this, genotypes G5, G6, G10, G15, and G23 had the b_i values significantly greater than unity, indicating that these genotypes are highly responsive to environmental change and are suitable only for good environments. Similarly, Rodriguez [36] and Adewale et al. [37] reported differences in cowpea genotypes for their responsiveness and stability for grain yield tested at different environments.

The mean sums of squares due to pooled deviation from regression were highly significant ($P \leq 0.01$) for grain yield of all genotypes except G21, indicating the importance of a nonlinear genotype by environment interaction, and the genotypes were unstable across environments (Table 8).

TABLE 6: Combined means of grain yield and yield-related traits of cow pea landrace grown at six environments in the 2019 main cropping season.

Code	Genotypes	DF	DM	PH	PDP	SDPP	GY	HSW
G1	NLLP_CPC_07-47	58.3 ^{cdef}	87.7 ^{bcde}	54.9 ⁱ	17.6 ^{ab}	11.8 ⁱ	2027.4 ^{cde}	11.3 ^{cdefg}
G2	NLL_CPC_07-74	58.7 ^{cdef}	85.4 ^{efg}	71.0 ^{defg}	15.1 ^{defgh}	10.9 ^{defg}	2215.2 ^{bc}	11.3 ^{bcdef}
G3	NLLP_CPC_07-168	56.5 ^{hijk}	84.5 ^{efgh}	60.4 ⁱ	15.1 ^{defgh}	11.6 ^{hi}	2045.1 ^{bcde}	8.3 ^{lmn}
G4	NLLP_CPC_07-27	56.1 ^{ijk}	82.6 ^{hi}	62.8 ^{gh}	14.8 ^{efgh}	11.8 ^{ab}	2225.0 ^b	8.9 ^{klm}
G5	NLLP_CPC_07-05	58.1 ^{cdefgh}	81.7 ⁱ	74.7 ^{bcdef}	15.1 ^{defgh}	9.8 ^e	1962.0 ^e	12.3 ^b
G6	NLLP_CPC_07-01	58.6 ^{cdef}	86.7 ^{cdef}	77.3 ^{bcd}	15.5 ^{cdefgh}	11.5 ^{abc}	1755.0 ^f	8.2 ^{lmn}
G7	NLL_CPC_07-49	61.4 ^a	89.0 ^{abc}	66.6 ^{fgh}	18.2 ^a	10.9 ^{bcde}	2137.7 ^{bcde}	10.8 ^{efgh}
G8	NLLP_CPC_07-77	58.5 ^{cdefg}	89.1 ^{abc}	83.1 ^{ab}	13.7 ^h	10.5 ^{cde}	1953.3 ^e	8.7 ^{klm}
G9	NLL_CPC_07-46A	55.5 ^{jk}	81.1 ⁱ	68.8 ^{defg}	13.9 ^h	9.9 ^e	2067.2 ^{bcde}	9.9 ^{hij}
G10	ACC 211557	57.4 ^{fghi}	87.9 ^{abcde}	85.6 ^a	16.8 ^{abcde}	10.5 ^{cde}	1948.9 ^e	11.1 ^{defg}
G11	ACC222890	57.9 ^{efgh}	88.7 ^{abc}	75.9 ^{bcde}	15.6 ^h	12.3 ^a	1345.6 ^h	7.9 ^{mn}
G12	Dass 002	58.4 ^{cdefg}	89.3 ^{abc}	75.9 ^{bcde}	14.7 ^{bcdefgh}	10.3 ^{de}	1564.1 ^g	7.3 ⁿ
G13	Dass 007	55.1 ^k	83.2 ^{ghi}	73.3 ^{cdef}	16.0 ^{fgh}	11.5 ^{abc}	2024.1 ^{de}	9.0 ^{kl}
G14	NLLP_CPC_07-69	58.1 ^{defgh}	87.9 ^{abcde}	77.4 ^{bcd}	14.1 ^{cbdefg}	10.4 ^{cde}	1606.5 ^{fg}	9.1 ^{jkl}
G15	NLLP_CPC_07_	58.0 ^{defgh}	88.6 ^{abcd}	70.6 ^{defg}	17.0 ^{gh}	10.8 ^{bcde}	1705.0 ^{fg}	10.0 ^{hij}
G16	ACC 233403	57.9 ^{defgh}	85.9 ^{def}	77.0 ^{bcd}	13.9 ^{abcd}	11.9 ^{ab}	2131.9 ^{bcde}	11.5 ^{bcde}
G17	NLLP_CPC_07-28	60.9 ^{ab}	89.7 ^{ab}	70.4 ^{defg}	14.4 ^h	10.8 ^{bcde}	1646.1 ^{fg}	10.6 ^{efgh}
G18	NLLP_CPC_07-46B	59.6 ^{bcd}	88.9 ^{abc}	77.2 ^{bcd}	14.4 ^{gh}	10.9 ^{bcde}	1708.2 ^{fg}	9.3 ^{ijk}
G19	ACC 244804	59.4 ^{cde}	87.2 ^{bcde}	67.4 ^{efgh}	16.7 ^{gh}	10.9 ^{bcde}	1700.7 ^{fg}	12.0 ^{bcd}
G20	NLLP_CPC_07-29	56.9 ^{fghi}	88.3 ^{abcd}	70.8 ^{defg}	14.9 ^{abcde}	10.9 ^{bcde}	2201.0 ^{bcd}	11.3 ^{bcdef}
G21	ACC 223402	56.3 ^{ijk}	87.0 ^{bcdef}	81.4 ^{abc}	16.0 ^{defgh}	11.2 ^{bcd}	2110.9 ^{bcde}	10.2 ^{ghi}
G22	NLLP_CPC_07_48B	61.4 ^a	90.5 ^a	69.6 ^{defg}	15.1 ^{bcdefg}	10.6 ^{cde}	2101.2 ^{bcde}	10.4 ^{fgh}
G23	NLLP_CPC_07-03	59.7 ^{bc}	88.7 ^{abc}	74.4 ^{cdef}	17.2 ^{defgh}	10.2 ^{be}	2152.6 ^{bcd}	13.6 ^a
G24	NLLP_CPC_07-55	59.3 ^{cde}	87.5 ^{bcde}	76.2 ^{bcd}	15.6 ^{abc}	11.5 ^{abc}	2573.2 ^a	12.2 ^{bc}
G25	Kanketi	58.3 ^{cdefg}	85.3 ^{efg}	75.2 ^{bcde}	13.6 ^{bcdefg}	11.1 ^{bcd}	2138.9 ^{bcde}	11.2 ^{cdefg}
	Mean	58.3 ^{**}	86.9 ^{**}	72.7 ^{**}	15.4 ^{**}	11.0 ^{**}	1961.9 ^{**}	10.3 ^{**}
	CV (%)	3.3	3.7	13.6	15.3	12	11.2	12.3

** = significant at $P < 0.01$; * = significant at $P < 0.05$; CV (%) = coefficient of variation in percent.

TABLE 7: Joint regression analysis of variance (ER's model) for grain yield of 25 cowpea genotypes grown at six environments during the 2019 cropping season in Ethiopia.

Source	Df	SS	MS
Total	149	508555146	3413121.8
Genotypes	24	9072930.8	378038.78 ^{**}
Env. + (gen \times env.)	125	41782215	334257.7232 ^{**}
Environment (linear)	1	17321917	
Gen \times env. (Linear)	24	4107016.6	171125.69 [*]
Pooled deviation	100	20353282	203532.82 ^{**}
G1	4	856817.19	214204.30 ^{**}
G2	4	606995.12	151748.78 ^{**}
G3	4	2052402.5	513100.62 ^{**}
G4	4	373236.43	93309.11 ^{**}
G5	4	429181.56	107295.39 ^{**}
G6	4	458759.21	114689.80 ^{**}
G7	4	1208845.2	302211.30 ^{**}
G8	4	1158939.3	289734.82 ^{**}
G9	4	1052930.2	263232.55 ^{**}
G10	4	221744.42	55436.105 ns
G11	4	1364846.2	341211.56 ^{**}
G12	4	654761.56	163690.39 ^{**}
G13	4	939623.1	234905.78 ^{**}
G14	4	155817.54	38954.385 ns
G15	4	422009.65	105502.41 ^{**}
G16	4	976218.16	244054.54 ^{**}
G17	4	556965.53	139241.38 ^{**}
G18	4	1762431.5	440607.88 ^{**}

TABLE 7: Continued.

Source	Df	SS	MS
G19	4	1406098.2	351524.55**
G20	4	342277.28	85569.32*
G21	4	67484.1	16871.025 ns
G22	4	487173.65	121793.41**
G23	4	1502497.6	375624.39**
G24	4	337378.94	84344.735*
G25 (ch)	4	957847.86	239461.97**
Pooled error	300	7300322.8	24334.41

** , *Significant at $P \leq 0.01$ and 0.05 , respectively, Df= degree of freedom; SS=sum of squares; MS = mean of squares, Env = environments, Gen = genotype.

TABLE 8: Stability parameters from Eberhart and Russell's models for grain yield across environments.

Genotypes	Grain yield (kg ha ⁻¹)	Rank	b_i	Rank	S ² di	Rank
G1	2129.83	11	0.07 ns	1	189869.89**	14
G2	2276.25	3	0.86 ns	8	127414.38**	12
G3	2021.01	16	0.71 ns	7	488766.21**	25
G4	2250.34	6	1.13 ns	15	68974.70**	6
G5	2078.41	12	1.76*	25	82960.98**	8
G6	1883.44	19	1.73*	24	90355.39**	9
G7	2263.27	5	1.09 ns	13	277876.89**	20
G8	1945.3	18	0.49 ns	6	265400.41**	19
G9	2040.57	15	1.11 ns	14	238898.14**	18
G10	2046.15	14	1.56*	21	31101.69**	3
G11	1535.02	25	0.40 ns	5	316877.15**	21
G12	1630.21	24	0.36 ns	4	139355.98**	13
G13	2053.39	13	1.48 ns	20	210571.37**	15
G14	1647	23	0.25 ns	2	14619.98**	2
G15	1824.91	21	1.58*	23	81168.00**	7
G16	2290.41	2	0.99 ns	11	219720.13**	17
G17	1765.12	22	1.27 ns	18	114906.97**	11
G18	1995.7	17	1.14 ns	17	416273.48**	24
G19	1837.86	20	1.04 ns	12	327190.14**	22
G20	2213.16	8	0.97 ns	10	61234.91**	5
G21	2198.51	9	1.13 ns	16	-7463.38 ns	1
G22	2161.01	10	0.28 ns	3	97459.00**	10
G23	2242.47	7	1.57*	22	351289.98**	23
G24	2632.42	1	0.91 ns	9	60010.33**	4
G25 (ch)	2273.28	4	1.27 ns	19	215127.56**	16

** = significant at $P \leq 0.01$, * = significant at $P \leq 0.05$, ns = nonsignificant, kg ha⁻¹ = kilogram per hectare of pooled mean over six environments, b_i and S²di, regression coefficient and deviation from the regression, respectively.

Likewise, Nigussie [38] have reported that twelve out of fifteen common bean genotypes evaluated at six environments had S²di values significantly different from zero.

From the tested genotypes, 11 genotypes had lower grain yield than the grand mean of genotypes, which showed that these genotypes were not desirable for cultivation though they were stable. The most stable genotypes with the lowest S²di values were G21, G14, G10, G24, G20, and G4, which ranked 1st, 2nd, 3rd, 4th, 5th, and 6th for deviation from regression, respectively, from the lowest to highest. However, genotype G21 showed a nonsignificant deviation from regression and negative S²di value with lower grain yield, indicating its suitability for unfavourable environments. The most unstable genotypes with the highest S²di values were G19, G23, G18, and G3, which ranked 22nd, 23rd, 24th, and 25th correspondingly among the tested genotypes. Therefore, these genotypes are best fit for specific adaptation in

favourable environments where there are high input levels. If the mean yield, regression coefficient value (b_i), and the deviation from the regression (S²di) are considered together, then the most stable genotype would be G24 with a mean grain yield of 2632 kg ha⁻¹ (ranked 1st in yield), 9th in regression coefficient ($b_i = 0.91$ close to 1), and 4th in deviation from the regression. Genotype G2 with a mean grain yield of 2276.23 kg ha⁻¹ and G20 (2213.16 kg ha⁻¹) would be the 2nd and 3rd most stable genotypes among the tested. Two genotypes (G5 and G23) among thirteen high yielder genotypes had a significant deviation of regression coefficient (b_i) values from unity, with a significant deviation of S²di value from zero (S²di > 0), indicating that they were unstable and desirable for cultivation in favourable environments. In agreement to this, Tariku [24] in cowpea and Firew [29], Abele [25], and Tullu [26] in common bean had identified the stable genotypes which are desirable for cultivation in all

TABLE 9: Stability analysis using Wricke's ecovalence (Wi) and cultivar superiority measure (Pi) of the Lin and Binns model.

Genotypes	Grain yield (kg ha ⁻¹)	Rank	Wi	Rank	Pi	Rank
G1	2130	11	1653466	22	439506	13
G2	2276	3	621011	8	255473	2
G3	2021	16	2110548	25	664236	19
G4	2250	6	384425	5	280255	3
G5	2078	12	827808	10	435876	12
G6	1883	19	827812	11	650874	18
G7	2263	5	1215161	18	320461	8
G8	1945	18	1337327	19	627385	17
G9	2041	15	1061949	15	528960	15
G10	2046	14	221842	2	415887	11
G11	1535	25	1617493	21	1126704	25
G12	1630	24	940800	13	887791	24
G13	2053	13	1097987	16	474959	14
G14	1647	23	545296	6	850599	23
G15	1825	21	656522	9	709147	22
G16	2290	2	1197791	17	296859	5
G17	1765	22	605750	7	702671	21
G18	1996	17	1776428	24	586899	16
G19	1838	20	1407161	20	697557	20
G20	2213	8	342873	3	301445	6
G21	2199	9	79422	1	290328	4
G22	2161	10	849857	12	360932	9
G23	2242	7	1729884	23	410594	10
G24	2632	1	343227	4	63329	1
G25	2273	4	1008432	14	306404	7

tested environments by using high mean grain yield, non-significant regression coefficient from unity, and nonsignificant deviation from regression values ($S^2_{di} = 0$).

3.4. Stability Analysis Using Wricke's Ecovalence (Wi) and Cultivar Superiority Measure (Pi) of the Lin and Binns Model. Wricke [39] defined the concept of ecovalence, to describe the stability of a genotype as the contribution of each genotype to the genotype \times environment interaction sum of squares. The ecovalence (Wi) or the stability of the i^{th} genotype is its interaction with environments, squared and summed across environments. According to this model, genotypes with low ecovalence have smaller fluctuations across environments and contributed the least to the genotype by environment interaction and, thus, are stable genotypes. The analysis in Table 9 showed that G21, G10, G20, G24, G4, and G14 were the most stable genotypes that ranked 9th, 14th, 8th, 1st, 6th, and 23rd, for grain yield, respectively. In harmony to this, Ishiyaku et al. [23] in cowpea and Tadele et al. [30] in common bean had reported the highest yielder genotypes having relatively low ecovalence values. The most unstable genotypes according to the ecovalence method were G3, G18, G23, and G1, showing relatively higher ecovalence % of GXE sum squares for grain yield, and ranked 16th, 17th, 7th, and 11st in mean grain yield, respectively. According to Asrat et al. [40], genotypes with high ecovalence mean and large estimated values are suitable for high-input environments.

As a stability statistic, the cultivar performance measure (Pi) of Lin and Binns [41] is estimated by the square of differences between a genotype's and the maximum genotype mean at a location, summed and divided by twice the number of locations. The most stable genotype is the one with the least deviation from the maximum yield of each environment, i.e., with the lowest (Pi) value. From the present investigation, the most stable genotype ranked first for Pi and for mean grain yield was G24 followed by G2, G4, G21, and G16, respectively (Table 9). These stable genotypes had the least contribution to the total variation due to the genotype by environment interaction. In contrast, G11, G12, G14, and G15 were the most unstable genotypes, and they contributed a large portion of the total variation due to GEI. These results are in agreement with the work of Alemayehu et al. (2016), and Tadele et al. [30], who reported the most stable cowpea genotypes having the lowest Pi value and high mean grain yield in their study.

4. Conclusions and Recommendation

Analysis of variance for each location and combined over five locations showed significant differences among genotypes, environments, and genotypes \times environments interaction (GEI) for grain yield and most of the yield-related traits. The significant genotypes \times environments interaction effects indicated the inconsistent performance of genotypes across the tested environments and the differential discriminating ability of the tested environments.

Among the tested environments, the highest mean grain yield (2529 kg ha⁻¹) was registered at Miesso followed by Melkassa (2487 kg ha⁻¹), while Sirinka (1676 kg ha⁻¹) and Babile (1730 kg ha⁻¹) were the least-yielding environments. The highest grain yield was obtained from NLLP_CPC_07-55 (2632.4 kg ha⁻¹), ACC233403 (2290.4 kg ha⁻¹), and NLLP_CPC_07-74 (2276.3 kg ha⁻¹). These three genotypes gave mean grain yield above the standard check Kanketi among the tested genotypes. The lowest mean grain yield was registered from ACC222890 (1535.0 kg ha⁻¹), Dass 002 (1630.2 kg ha⁻¹), and NLLP_CPC_07-69 (1647.0 kg ha⁻¹).

The significant effects of GEI on traits suggested the need to assess the stability of genotypes overall environments. The stability of 25 cowpea genotypes for grain yield over six environments was estimated by using cultivar superiority (Pi), Wricke's ecovalence (Wi), regression coefficient (b_i), and deviation from regression (S^2_{di}) models. Among the tested genotypes, NLLP_CPC_07-55 (2632 kg ha⁻¹), NLLP_CPC_07-74 (2276 kg ha⁻¹), NLLP_CPC_07-27 (2250 kg ha⁻¹), NLLP_CPC_07-29 (2213 kg ha⁻¹), and ACC 233403 (2290 kg ha⁻¹) were most stable genotypes without a statistically significant difference in mean grain yield; however, only the first three genotypes exceed the standard check variety Kanketi in grain yield. Therefore, these genotypes have been identified as a candidate to release for wider adaptation and commercial production.

Data Availability

The data that support the findings of this study are openly available in Yirga at https://www.researchgate.net/profile/Yirga_Wasihun.

Conflicts of Interest

The authors declare no conflicts of interest on submission of this manuscript.

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