

Adaptability Performances of Cowpea [*Vigna Unguiculata* (L.) Walp] Genotypes in Ethiopia

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Abstract

Sixteen cowpea genotypes were tested at seven environments in experiment laid out in 4 x 4 triple lattice designs during 2016/17 cropping season. The combined analysis of variance over environments showed significant differences among genotypes, environments, and significant effect of GEI on grain yield, days to flowering, days to maturity, plant height and pods per plants. Analysis of variance for grain yield from AMMI model, indicated the contribution of genotype, environment and GEI accounted for about 63.3%, 5.3%, and 29.7% of the total sum of squares, respectively. The result indicated environment was contributed much to the observed variations suggested the need to test cowpea genotypes at diverse environments. Two genotypes, IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to both environments but more to favorable environments suggested the need to further test to develop as varieties. Other two genotypes, 95K-1095-4A and 93K-619-1, identified as highly responsive to environments suggested to consider the genotypes as candidate varieties where they performed best.

Keywords: Additive Main Effects and Multiplicative Interaction, Triple lattice and GIE.

1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp] is an annual herbaceous legume that belongs to Fabaceae family. It is one of the widely cultivated and consumed grain legumes globally, especially in the arid and semi-arid tropics (Noubissietchiagam *et al.*, 2010; Baidoo and Mochiah, 2014). Generally, cowpea production and utilization in Ethiopia is very low as compared to other African countries though the country is claimed to be center of diversity and/or origin. The country has high potential for the production of the crop that more than 66.5% of the arable land is very suitable for cowpea production (CCRP, 2015). It plays a critical role in the lives of millions of people in the developing world, providing them a major source of dietary protein that nutritionally complements low protein staple cereal and tuber crops. Its grain is the most important part of the plant for human consumption (Agbogidi and Egho, 2012).

Drought is the most important abiotic stress limiting production of all crops worldwide, even the most drought tolerant cowpea (Hall, 2004). More importantly, Ethiopia is known as a victim with recurrent drought that causes for partial or total crop failure and, subsequently, famine in the country. In such a situation, cowpea can be a potential crop to reduce the consequences of drought because of its drought tolerant nature more than other staple crops. The relative magnitude of environment, genetic and their interaction effects are a challenge that makes production difficult (Hall *et al.*, 2003). Therefore, in the process of developing cowpea varieties for desirable traits, it is necessary to evaluate genotypes in contrasting environments in the country. However, information on the effect of genotype, environment, and their interaction on cowpea grain yield under diversified agro-climatic conditions of Ethiopia is limited. Therefore, this research was initiated to estimate the magnitude of genotype, environment and genotype by environment interaction for grain yield of cowpea across different environments.

2. Material and Methods

Table 1: Description of test environments

Environments	Soil type	Altitude (masl)	Average rainfall	Temperature(°C)		Geographical location	
				Min	Max	Latitude (N)	Longitude (E)
Arbaminch	vertisols	1216	1000mm	16	37	06° 06' 841"	37° 35"
Babile	*	1650	671mm	15.5	28.1	9° 13' 09"	42° 19"
Sekota	*	*	1043mm	12.9	32.9	38° 56'	12° 14'
Kobo	vertisol	1450	673.4mm	13	34	12° 8' 21"	39° 18'
Melkassa	Andosol	1500	763.0mm	14.0	24.8	8° 30'	39° 21'
Jinka	vertisol	1383	1274.7mm	16.6	27.6	5° 52'	36° 38'
Meisso	Vertisol	1332	787.0mm	14.9	28.2	9° 28'	38° 08'

Source: Arbaminch University and Melkassa Agricultural Research Center and *= Data not available

Table 2: List of experimental materials

Code	Genotype	Status
G1	KENKETI	Standard check
G2	86D-378	Advanced line
G3	IT-89KD	Advanced line
G4	MEL-NURL-96-3	Advanced line
G5	IT-96D-610	Advanced line
G6	IT-93K-556-4	Advanced line
G7	IT-97K-568-18	Advanced line
G8	IT-99K-1060a	Advanced line
G9	95K-1095-4A	Advanced line
G10	IT-87D-1137	Advanced line
G11	IT-96D-604	Advanced line
G12	93K-619-1	Advanced line
G13	IT-93K-293-2-2	Advanced line
G14	IT-99K-1060	Advanced line
G15	IT-960-604	Advanced line
G16	TVU	Standard check

Source: Melkassa Agricultural Research Center

The experiment was conducted at seven environments during 2016/17 cropping season in Ethiopia (Table 1). Sixteen cowpea genotypes (14 advanced lines and two standard checks) were used for this study (Table 2). The experiment was laid out in 4 x 4 triple lattice experimental design. The seeds of the experimental genotypes were planted on 4 m x 3.6 m plots (14.4 m²) having six rows, with inter-row spacing of 60 cm and 20 cm within rows. Fertilizer (DAP 100 kg/ha) was applied for the experiment and other agronomic managements were applied based on the recommendation. Data were collected on the basis of five sample plants randomly taken from the four central rows, viz. plant height at maturity, number of pods per plant, and number of seeds per pod, and on the basis of entire plot, such as days to 50% emergence, days to 50% flowering, days to 75% maturity, grain yield per net plot and 100 seeds weight. All data were subjected to analysis of variance (ANOVA) separately for individual environment and over environments. ANOVA is important in revealing the presence of GEI but it does not indicate genotypes contribution to the interaction. Mean that differ significantly were separated by Duncan Multiple Range Test.

3. Result and Discussions

The combined analysis of variance over environments showed significant ($P < 0.01$) mean squares of environment, genotype and the interaction of genotype x environment (GEI) for grain yield, (Table 3). The results indicated the presence of significant variations among genotypes and environments and the genotypes had inconsistent performance across the test environments for the mentioned traits. Akande (2009) in cowpea, Kaya *et al.* (2002) in wheat, Solomon *et al.* (2008), Wende (2013), Workie *et al.* (2013) in maize and Yayis *et al.* (2014) in field pea also reported the significant effect of genotype, environment and GEI on yield and some other yield related traits and they suggested the importance of further stability analysis.

Table 3. combined analysis of variance for yield

Source of variation	Degree of freedom	DF	DM	PH(cm)	PPP	GY(kg)
Replication	14	0.8	2.5	33.0	16.1	206.8
Genotype(G)	15	52.4**	122.8**	479.0**	107.4**	210611.0**
Environment(E)	6	2387.4**	1611.6**	14274.5**	1894.7**	6251125.2**
GxE	90	35.8**	65.8**	774.0**	69.2**	195706.1**
Error	210	8.5	6.1	81.8	23.7	4788.8
CV%		4.8	2.7	15.3	23.4	5.6
SEM		1.7	1.4	5.2	2.8	39.9
Mean		61.0	90.3	59.0	20.5	1237.4

**, significant at $P \leq 0.01$, DF= days to flowering, DM=days to maturity, PH (cm) = plant height in centi meter, PPP= pods per plant, GY (kg) = grain yield in kilo gram, CV (%) =coefficient of variation in percent and SEM=mean standard error

Mean Performance of Genotypes for grain yield

The first three genotypes with highest mean grain yield were IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) without significant difference between the two followed by 95K-1095-4A (1321.8 kg/ha). The three genotypes with lowest mean grain yield were IT-96D-610 (1112.5 kg/ha) and Kenketi (1128.5 kg/ha) without

significant difference among the two and IT-97K-568-18 (1007.0 kg/ha) (Table 4).

The AMMI analysis of variance for grain yield showed the significant ($P < 0.01$) effect of environment, genotype, and genotype by environment interaction. Environment, genotype, and genotype by environment interaction accounted for about 63.3, 5.3, and 29.7% of the total sum of squares, respectively. Most of the total sum of squares of the model was attributed to the environment and the interaction effect. This result was in agreement with the results reported by Akande (2009), Sarvamangala *et al.* (2010) and Nunes *et al.* (2014) in cowpea and Taye *et al.* (2000) in fieldpea that the contribution of environment to the observed variation of yield was large. The larger sum of squares of GEI compared to the genotype indicated larger differences in genotypic response across environments. Santos *et al.* (2015) in cowpea and Zali *et al.* (2012) in chickpea also reported the larger contribution of GEI than genotype effect for the observed yield variation. The greater contribution of the treatment (98.3%) than the error (1.53) indicated the reliability of the multi-environment experiment. The AMMI model further partitioned the genotype by environment interaction sum of square in to interaction principal component axes (IPCA) and residual term. The mean squares of the first three IPCAs were significant and all together contributed 79.33% of the total sum of squares of GEI. The IPCA 1, IPCA 2 and IPCA 3 accounted for 37.93%, 24.67, and 16.73%, respectively, for the observed variation due to GEI. For the validation of the variation explained by GEI, the first three multiplicative component axes are adequate (Gauch, 2006). This is because of notable reduction of dimensionality and graphical visualization for the stability patterns of genotypes (Annicchiarico, 2002) (Table 5).

Table 8. Mean grain yield (kg/ha)

Genotype	Environment								R
	Arbaminch	Babile	Sekota	Kobo	Melkassa	Jinka	Meisso	Gm	
Kenketi	1206.7ef	856.0c	1766.3c	1415.0gh	645.3g	1013.7e	996.7ef	1128.5hi	14
86D-378	1947.7a	524.0fg	2078.7a	1736.7e	851.0de	1478.3b	1023.7ef	1377.1a	2
IT-89KD	1520.7d	450.3g	1795.7c	2351.7a	783.0def	977.7ef	1033.7de	1273.2cde	7
MEL-NURL-96-3	1222.3ef	848.3cd	1951.7b	2069.7b	799.7def	766.7gh	1254.7b	1273.3cde	6
IT-96D-610	1563.0cd	1026.0b	1523.3e	1332.3h	614.7g	674.0h	1054.3cde	1112.5i	15
IT-93K-556-4	1011.7g	780.3cd	2139.7a	1541.3f	693.3fg	1620.7a	1056.0cde	1263.3cde	8
IT-97K-568-18	900.7h	879.7c	1395.7f	1134.0i	840.3de	706.0h	1192.7bc	1007.0j	16
IT-99K-1060a	1629.0c	802.7cb	1754.3c	1985.7bc	1514.0a	1020.3e	1085.3cde	1398.8a	1
95K-1095-4A	1727.7b	610.0ef	1593.7de	1734.3e	1115.3c	1009.7e	1461.7a	1321.8b	3
IT-87D-1137	1208.0ef	1149.3a	1819.3c	1512.7fg	709.3efg	749.7gh	1013.3ef	1166.0gh	13
IT-96D-604	1544.0cd	752.0d	1648.0d	1723.0e	816.0def	1336.3c	883.3f	1243.2def	9
93K-619-1	2014.3a	626.3e	1845.3c	1925.0cd	819.0def	876.0fg	990.0ef	1299.4bc	4
IT-93K-293-2-2	1490.0d	780.7cd	1430.7f	1183.7i	1273.3b	1043.0e	1479.3a	1240.1ef	10
IT-99K-1060	1142.7f	1066.0ab	1566.7de	1411.7gh	790.3def	1286.7cd	1176.3bcd	1205.8fg	11
IT-960-604	1255.3e	985.7b	1540.7e	1501.0fg	863.3d	1010.0e	1241.3b	1199.6fg	12
TVU	1543.3cd	994.3b	1426.7f	1850.3d	831.7def	1171.0d	1199.3bc	1288.1bcd	5
Over all mean	1432.9	820.7	1704.8	1650.5	872.5	1046.2	1133.9	1237.4	
CV(%)	4.1	7.4	3.4	4.2	7.5	7.9	6.7		
SEM	32.17	31.27	30.78	37.55	42.5	42.9	45.5		

Means in the same column followed by the same letters are not significantly different at 5% level of significance, Gm=grand mean of genotypes, R=mean grain yield rank of genotype in descending order and CV (%) =coefficient of variation in percent

Table 5. AMMI analysis of variance for grain yield

Source of variation	DF	SS	MS	Sum of square explained		
				%Total	% GxE	% GxE cumulative
Total	335	59287984	176979			
Treatments	111	58279428	525040**	98.3		
Genotypes	15	3159168	210611**	5.3		
Environments	6	37506751	6251125**	63.3		
Block	14	100417	7173ns	0.2		
Interactions (GxE)	90	17613509	195706**	29.7		
IPCA 1	20	6680777	334039**	11.3	37.93	
IPCA 2	18	4349683	241649**	7.3	24.67	62.6
IPCA 3	16	2946860	184179**	4.97	16.73	79.33
Residuals	36	3636189	101005**	6.1		
Error	210	908139	4324			

ns and **, nonsignificant and significant at $P < 0.01$, respectively. DF = Degree of freedom, SS = Sum of square, MS = Mean square, G = Genotype, E = Environment, G x E = Genotype by environment interaction, IPCA 1, IPCA 2 and IPCA 3 = Interaction principal component axis one, two and three, respectively.

4. Conclusion

IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to favorable environments suggested the need to further test to develop as varieties. Other two genotypes, 95K-1095-4A and 93K-619-1, identified as highly responsive to environments suggested to consider the genotypes as candidate varieties where they performed best.

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