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RESEARCH ARTICLE

ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTIONS ANALYSIS OF YIELD PERFORMANCES IN COWPEA GENOTYPES UNDER UGANDAN ENVIRONMENTS.

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Abstract

Yield in legumes is the result of many plant processes, which are usually expressed in yield and have been shown to be affected by management, genotype and environment. The objectives of this study were to assess the extent of genotype x environment interaction and to select the stable cowpea genotypes in Ugandan environments over seasons. Seventy-two cowpea genotypes were evaluated for yield in three locations and two seasons in Uganda. The yield data were subjected to analysis of variance and additive main effects and multiplicative interactions (AMMI) analysis. The results showed a highly significant (P<0.001) genotype by location and by year (season) interaction effects for grain yield, with 69.16% of the total variation attributable to environmental effects, 5.36% to genotypic effects and 12.74% to G x E interactions effects. Genotype MU9 had the highest yield (854.68 $kgha^{-1}$) but was only adapted to specific environments (Arua 2015B and 2016A). Hence, genotypes WC 30, NE 45, NE 31, NE 51 which were equally high yielding, stable and adapted to the tested environments, and should be recommended for genetic improvement of cowpea germplasm in Uganda.

Introduction:-

Cowpea (*Vigna unguiculata* L. Walp) is one of the most important legume crops grown in the semi-arid tropical regions of Africa (Afiukwa et al., 2013). The crop is majorly produced in West Africa, accounting for 61% in Africa with Nigeria being the leading producer and consumer, (FAOSTAT, 2013). Cowpea is an important staple food legume and cheap source of protein, used as an excellent substitute to animal proteins by many low-income Africans in the low-land humid and dry savannah tropics and for vegetarians (Boukar et al., 2016). Indeed, some cultivars with seed protein content of about 30%, close to that obtained for soybean (*Glycine max*) have been reported (Santos et al., 2012). Immature pods, immature seeds and young leaves of cowpea are also used as vegetables (Olawale, and Bukola, 2016), and its plant residues could be used as fodders and compost.

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Among the African biggest cowpea producers, Uganda is ranked 8th with production of about 84,000 metric tons (Ddamulira et al., 2015). This volume of production demonstrates the importance of cowpea cultivation as a component of Ugandan farming system and with cultivation expanding beyond northern and eastern regions traditionally known for the crop in recent time (Karungi et al., 2000a; Ronner et al., 2012). In Uganda, cowpea is ranked 4th legume after beans, groundnuts, and soybean (Ronner et al., 2012). Cowpea is mostly grown in the drier eastern and northern parts of Uganda (Dungu et al., 2015) because of its tolerance to drought and adaptation to warm weather, hence enabling it to produce significant yield where other legumes like beans fail to grow (Bisikwa et al., 2014).

Farmers-traditional cultivars are known to be well adapted to the low input conditions, but generally poor in yield and highly susceptible to the major diseases and pests. These production constraints are the main target of cowpea breeding program both at the national and regional levels in sub-Sahara Africa. Although past research efforts have brought some improvement into farmer's yield, available statistics still indicate significant instability in yield across locations and years (FAO, 2013) and yield at farm-gate is far below optimum.

Yield has been described as a complex phenotypic trait in plants because of being a final aggregate product of many interwoven physiological and development traits controlled by different arrays of genes. Understanding interrelationship between yield and environments (Nwofia, 2012) is vital to achieving high and stable yield. In addition, unregulated seed distribution system and research centers resource limitations have led to poor release and distribution of 'improved' varieties with doubt on yield stability. This problem could be addressed through a decentralized system where improved lines from research and seed centers are subjected to post-varietal-release evaluation to ascertain genetic stability, in this case yield.

The venture to develop high yielding genotypes on par with traditional cultivars is still in progress. The developed cultivars adapted to a wide range of environments, is the eventual goal of plant breeders. Hence, pattern of response of genotypes is studied by the plant breeders by testing genotypes in different environments to study genotype x environment (GxE) interaction. To estimate the level of interaction of genotypes to environments and to eliminate as much as possible the unexplainable and extraneous variability contained in the data, several statistically techniques have been developed to describe GxE and measure the stability of genotypes.

Since GxE interaction is naturally multivariate, the Additive Main effects and Multiplicative Interaction (AMMI) offers an appropriate first statistical analysis of yield trial that may have a GxE interaction (Zobel et al., 1988). The objectives of this study were to assess the extent of GxE interaction and to select the stable genotypes of cowpea genotypes in Ugandan environments over seasons.

Material and Methods:-

Study Sites and Plant Materials:-

Seventy-two cowpea genotypes were evaluated at Makerere University Agricultural Research Institute of Kabanyolo (MUARIK), National Semi-Arid Resources Research Institute of Serere (NaSARRI), and Abi-Zonal Agricultural Research and Development Institute of Arua (Abi-ZARDI) for two consecutive seasons, 2015B and 2016A. Information of coordinates, climatic and soil characteristics of the experimental sites are provided in Table 1.
The cowpea cultivars used in this study were obtained from cowpea collection at MUARIK (Table 2). Eight breeding lines from International Institute of Tropical Agriculture (IITA), 16 breeding lines from Uganda, and 48 Ugandan landraces were used.

Experimental Design:-

The genotypes were planted in an alpha lattice design (8 blocks x 9 genotypes per block) with two replications in three locations and two seasons. The first planting was done in September 2015 and the second in April 2016. Three seeds were planted per hole and the seedlings were thinned to two plants per stand 10 days after sprouting. Each plot consisted of 4 rows of 5m long and 0.75m apart with an intra-rows space of 0.25m. Regular weeding of the fields till maturity were done with hand hoe.

The cultivars were given protection against aphids during the vegetative stage by spraying with the insecticide chlorpyrifos (as Ascoris 48 EC) applied at the rate 2.5 g (a.i.) ha^{-1} once at 15 days after planting. They were also given protection against podding stage pests, by spraying with λ-cyhalothrin (as Karate 2.5 EC) applied at the rate 2.5 g (a.i.) ha^{-1} using a CP-15 knapsack sprayer at 50 % podding (Abudulai et al., 2006).

At maturity, the whole plot was harvested and the total dried grain weight (g) was taken using electronic weighing scale. Harvesting was done twice and the yield (kg.ha^{-1}) was estimated from the total dried grain weight per plot.

Statistical Analysis:-

A combined analysis of variance was done on the yield data across locations and seasons using linear mixed model (REML) procedure in GenStat 12.0 software (Payne et al., 2009). The model described by Smith et al. (2005) was used as follow:

$$y_{ijklm} = \mu + \rho_i + \iota_j + s_k + r_l + b_{m(l)} + \iota s_{kj} + \rho s_{ki} + \rho\iota_{ji} + \rho\iota s_{ijk} + \varepsilon_{ijklm}$$

Where, y_{ijklm} is the observed value for the i^{th} genotype from j^{th} location, k^{th} season, m^{th} block nested within the l^{th} replication; μ is the general mean effect; ρ_i is the i^{th} genotype effect (considered as fixed); ι_j is the j^{th} location effect (considered as fixed); s_k is the k^{th} season effect (considered as random); r_l is the l^{th} replication effect (considered as random); $b_{m(l)}$ is the effect of mth replicated nested within the l^{th} replication (considered as random); ιs_{kj} is the k^{th} season and j^{th} location interaction effect (considered as random); ρs_{ki} is the interaction effect of k^{th} season and i^{th} genotype (considered as random); $\rho\iota_{ji}$ is the interaction effect of j^{th} location and i^{th} genotype (considered as random); $\rho\iota s_{ijk}$ is the effect of the three-way interaction between k^{th} season, j^{th} location and i^{th} genotype (considered as random); and ε_{ijklm} is the experimental error considered as random.

Yield means were separated using Least Significant Difference (LSD) at 5% level.

To establish the adaptability and the stability of the genotypes to the different environments, an additive main effects and the multiplicative interaction (AMMI) analysis was performed. AMMI is a unified approach that fits the additive effects of genotypes and the environments by the usual analysis of variance and then describes the non-additive parts by principal component analysis fitted to the AMMI model according to the following equation:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n\tilde{\alpha}_{gn}\delta_{en} + \theta_{ge} + \varepsilon_{ger}$$

Where Y_{ger} = yield of genotype g in environment e for replication r, μ =grand mean; α_g=mean deviation of the genotype g (genotype mean minus grand mean); and β_e=mean deviation of environment mean; λ_n=the eigenvalue of the principal component (IPCA) axis n; $\tilde{\alpha}_{gn}$= the genotype g eigenvector value for IPCA axis n; δ_{en}= the environment e eigenvector value for IPCA axis n; θ_{ge}= the residual; and ε_{ger}= the random error (Zobel et al., 1988).

Results:-

Cowpea Grain Yield as Influenced by Genotypes, Locations and Years (Seasons):-

The results from the analyses of variance are presented in Table 3. Genotypes, locations, and seasons significantly (P<0.001) affected the grain yield in cowpea. In terms of interactions, genotypes significantly (P<0.001) interacted with locations and with seasons for cowpea grain yield. The three-way interaction (Y x L x G) effects were also highly significant (P<0.001). The factors explained revealed that cowpea grain yield was mostly affected by locations (72.06%), genotypes (5.73%) and the interaction year x location x genotype (2.75%).

The data from the Table 4 showed that the highest cowpea grain yield were recorded in Arua in year 2015 and 2016 (979.3 and 1029.7 kg ha^{-1}, respectively) while the lowest yields were recorded in Serere in 2015 and 2016 (31.9 and 188.70 kgha^{-1}, respectively). The highest grain yield in MUARIK in 2015 was observed on the genotype WC48 (1219.68 kgha^{-1}) and the lowest on NE4 (34.29 kgha^{-1}). In ARUA 2015, the variety NE5 recorded the highest grain yield (1514.92kgha^{-1}) while the lowest yield was observed on NE37 (518.10 kgha^{-1}). In Serere 2015, the highest grain yield was recorded on the cultivar NE20 and the lowest value on NE15 (83.02 and 1.41kgha^{-1}, respectively). In the second year 2016, the cultivars IT91, NE5, NE20 presented highest grain yield 753.65, 1760.84 and 239.81 kgha^{-1} in MUARIK, ARUA and Serere, respectively. The lowest grain yields were observed on WC67 (180.32 kgha^{-1}), NE37 (524.09 kgha^{-1}), and NE15 (158.20 kgha^{-1}) in MUARIK, Arua and Serere, respectively (Table 5). Across locations and years, however, only MU9 surpassed all other genotypes with a mean grain yield of 854.68 kgha^{-1}.

Additive Main Effects and Multiplicative Interactions Analysis of cowpea grain yield:-
The AMMI analysis of variance for cowpea grain yield (kgha^{-1}) of the 72 genotypes tested in six environments showed that 69.16% of the total sum of squares was attributable to environmental effects; only 5.36% to genotypic effects and 12.74% to G x E interactions effects (Table 6).

The first linear interaction term (IPCA1) of the AMMI analysis, accounted for 58.00% of the GxE sum of squares, and the second accounted for 34.41% using 75 and 73 degree of freedom (*df*) respectively (Table 6). The two first bilinear terms accounted for 92.41% of the GxE sum of squares and used 148 of the 355*df* available in the interaction. They were significant at P<0.001. The obtained data confirmed the adequacy to the AMMI model used. This made it possible to construct the biplots (Fig 1A and 1B). In Fig1A, the biplot indicated that genotypes: G18 (MU 9), G25 (NE 30), G28 (NE 36), G37 (NE 48), G44 (NE5), G52 (WC 26), G61 (WC48A), G66 (WC64), G67 (WC 66), G70 (WC 68), G71 (WC 68A) and G3 (EBERAT * NE51) were high yielding cultivars in the environments E2 and E5 (Arua 2015B and 20156A) since AMMI placed them at the right hand side of the midpoint of the axis on the biplot. In contrast, genotypes: G2 (EBELAT * NE 39), G4 (IT109), G5 (IT2841* BROWN), G17 (MU24C), G21 (NE18), G29 (NE 37), G30 (NE39 * SEC2), G32 (NE4), G50 (WC18), G54 (WC29), G69 (WC67A), G71 (WC68A) and G72 (WC8) were low yielding in the environments E1(MUARIK 2015B), E3 (Serere 2015B), E4 (MUARIK 2016A) and E6 (Serere2016A), given that they were placed at the left hand side of the midpoint of the axis on the biplot (Fig1A)

In Fig 1B, the IPCA 1 scores for both the genotypes and environments were plotted against the grain yield for the genotypes and the environments, respectively. The IPCA scores of a genotype in the AMMI analysis are an indication of the adaptability over environments. The graph space of Figure 1B was divided into 4 quadrants from lower yielding environments in quadrant 1 and 4 to high yielding in quadrant 2 and 3. The biplot showed not only the average yield of a variety but also how it is achieved. The cultivars 2419, IT 2841 * BROWN, MU 24C, NE 13, NE 18, NE 21, NE 4, NE 49, SEC 1 * SEC 3, SEC 5 * NE 39, SEC 5 * NE 51, WC 18, WC 29, WC 30, WC 44, WC 5, WC 67A, WC 68, WC 68A and WC 8 were posed in quadrat 3. The cultivars NE21, NE32, WC55, and WC17 had IPCA2 scores close to zero. The cultivars NE 48, NE5 and WC 26 had an IPCA 1 score greater than the other cultivars but were less stable. The biplot also showed that the cultivars NE30, NE67, NE48, WC48, WC26 and NE5 were best for high-yielding environments E2 and E5 (Arua 2015B and 2016A). With respect to the test environments, E1 (MUARIK 2015B) had the longest distance between its marker and the origin. In addition, the length of a genotype vectors reflects the amount of interaction for that genotype. Thus according to Fig1B, the genotype MU9 had a large IPCA 2 score.

Table 1:- Geographic coordinates, climatic characteristics and soils of the study locations

Locations	Geographical coordinates		Altitude (m.a.s.l)	Average annual temperature	Average annual rainfall	Soils
	Latitude	Longitude				
MUARIK (Wakiso)	0°28’N	32°37’E	1200	21.50 °C	1150 mm	Sandy clay loam
Abi-ZARDI (Arua)	3°4.58’N	30°56’E	1206	24 °C	1250 mm	Sandy clay loams
NaSARRI (Serere)	1°35’N	33°35’E	1140	26.05 °C	1419 mm	Black clays

m.a.s. l = meters above sea level
Source: Fungo et al. (2011); Sserumaga et al. (2015)

Table 2:- Characteristics of the cowpea cultivars used in the study.

Cultivars	Origin	Growth type	Seed coat characteristics	No of days to flowering	No of days to maturity
2419	Uganda	Semi-erect	cream	47	74
EBELAT X NE 39	Uganda	Semi-erect	cream	50	77
EBELAT X NE 51	Uganda	Erect	gray tainted black	48	73
IT 109	IITA	Semi-erect	creamish white	49	77
IT 2841	IITA	Semi-erect	light brown	52	78
IT 2841* Brown	IITA	Erect	cream	52	76

IT 71	IITA	Semi-erect	cream	50	77
IT 84	IITA	Erect	light brown	51	75
IT 889	IITA	Erect	gray tainted black	53	75
IT 91	IITA	Erect	light brown	50	75
IT 97	IITA	Semi-erect	cream	50	73
KVU27-1	Uganda	Erect	coffee brown	49	76
MU 15	Uganda	Erect	cream	49	75
MU 17	Uganda	Semi-erect	cream	52	75
MU 19	Uganda	Erect	cream	50	76
MU 20B	Uganda	Erect	black	52	77
MU 24C	Uganda	Semi-erect	cream	50	77
MU 9	Uganda	Erect	brown	49	74
NE 13	Uganda	Semi-erect	brown	50	78
NE 15	Uganda	Semi-erect	gray tainted black	52	75
NE 18	Uganda	Semi-erect	brown	50	76
NE 20	Uganda	Semi-erect	cream	49	73
NE 21	Uganda	Erect	cream	50	77
NE 23	Uganda	Semi-erect	brown	48	73
NE 30	Uganda	Semi-erect	light brown	51	76
NE 31	Uganda	Semi-erect	cream	51	77
NE 32	Uganda	Erect	coffee brown	52	77
NE 36	Uganda	Erect	cream	50	72
NE 37	Uganda	Semi-erect	cream	47	75
NE 39 X SEC 2	Uganda	Erect	cream	49	77
NE 39 X SEC 4	Uganda	Semi-erect	light brown	50	75
NE 4	Uganda	Semi-erect	cream	54	79
NE 40	Uganda	Semi-erect	cream	50	75
NE 41	Uganda	Erect	creamish white	49	75
NE 45	Uganda	Semi-erect	cream	50	76
NE 46	Uganda	Erect	light brown	51	77
NE 48	Uganda	Erect	brown	50	77
NE 49	Uganda	Semi-erect	cream	49	74
NE 5	Uganda	Semi-erect	cream	51	73
NE 50	Uganda	Erect	gray tainted black	52	77
NE 51	Uganda	Erect	light brown	49	75
NE 53	Uganda	Erect	gray tainted black	48	76
NE 6	Uganda	Erect	coffee brown	48	76
NE 67	Uganda	Erect	light brown	49	75
NE 70	Uganda	Semi-erect	cream	54	78
SEC 1 X SEC 3	Uganda	Erect	brown	51	75
SEC 5 X NE 51	Uganda	Semi-erect	cream	49	75
SEC5 X NE 39	Uganda	Semi-erect	cream	49	74
WC 17	Uganda	Erect	black	52	79
WC 18	Uganda	Semi-erect	cream	49	76
WC 2	Uganda	Erect	light brown	51	78
WC 26	Uganda	Semi-erect	cream	53	76
WC 27	Uganda	Erect	cream	48	74
WC 29	Uganda	Semi-erect	cream	52	77
WC 30	Uganda	Erect	brown	51	77
WC 32 * SEC 5	Uganda	semi-erect	cream	48	79
WC 35A	Uganda	Erect	cream	52	75
WC 36	Uganda	Semi-erect	cream	50	74
WC 41	Uganda	Semi-erect	cream	45	75

WC 44	Uganda	Semi-erect	black	50	76
WC 48A	Uganda	Erect	brown	51	76
WC 5	Uganda	Semi-erect	cream	52	76
WC 52	Uganda	Semi-erect	cream	48	72
WC 55	Uganda	Semi-erect	creamish white	50	76
WC 63	Uganda	Erect	gray tainted black	50	76
WC 64	Uganda	Erect	gray tainted black	49	74
WC 66	Uganda	Erect	gray tainted black	49	72
WC 67	Uganda	Semi-erect	black	50	74
WC 67 A	Uganda	Semi-erect	creamish white	50	76
WC 68	Uganda	Semi-erect	brown	52	77
WC 8	Uganda	Erect	brown	49	76
WC68A	Uganda	Semi-erect	cream	51	77

NE: Northern and Eastern Uganda lines, WC: Western and Central Uganda lines, MU: Makerere University lines, IT: IITA lines.

Table 3:- Analysis of variance for yield of cowpea genotypes across locations in 2015B-2016A, Uganda

Source of variation	DF	SS	MS	Explained (%)
Total	948	153881958.8		
Rep	1	644775	644775	
Years (Y)	1	665194	665194***	0.432
Locations (L)	2	110883636.8	55441818***	72.058
Locations/Seasons/Rep	6	907650	151275***	
Locations/Seasons/Rep/Blocks	84	4082232	48598***	
Genotypes (G)	71	8810106	124086***	5.725
Y x L	2	1111496	555748***	0.722
L x G	142	13154454	92637***	8.548
Y x G	71	2112605	29755***	1.373
Y x L x G	142	4225210	29755***	2.746
Residual	426	7284600	17100	

***significant at P<0.001.

Table 4:- Mean cowpea grain yield performance (kgha^{-1}) for different locations in 2015B-2016A, Uganda

Locations	Grain yield in 2015B	Grain yield in 2016A
SERERE	31.9a	188.70a
MUARIK	434.2b	443.9b
ARUA	979.3c	1029.7c
Grand mean	482	537.3
LSD	58.1	42.58

LSD: Least significant difference at P<0.05.

Table 5:- Grain yield (kgha^{-1}) of 72 cowpeas grown in six environments and IPCA scores for the GxE interactions effects as derived from AMMI analysis, Uganda

Genotypes	Genotypes codes	E1	E2	E3	E4	E5	E6	GxE means	Ranks	[IPCAg[1]
MU 9	G18	1186.03	1514.29	10.21	491.43	1759.11	167	854.68	1	-3.41
WC 66	G67	1116.19	1205.08	82.71	424.13	1207.08	239.5	712.45	2	-8.46
NE5	G44	306.03	1514.92	38.42	415.24	1760.84	195.21	705.11	3	11.48
WC 68	G70	869.84	1227.3	34.66	567.62	1250	191.45	690.14	4	-3.91
WC 48A	G61	1219.68	1057.78	56.44	496.51	1065.29	213.22	684.82	5	-12.36
NE 36	G28	1003.81	1238.73	24.21	310.48	1243.5	180.99	666.95	6	-6.2
NE 30	G25	401.9	1299.05	66.13	506.67	1468.74	222.92	660.9	7	6.21
NE 48	G37	390.48	1469.21	65.79	283.18	1473.59	222.57	650.8	8	7.58
EBERAT	G3	937.78	1100.95	24.11	465.4	1118.86	180.9	638	9	-6.97

* NE 51										
NE 53	G41	702.22	1029.84	18.82	713.65	1148.95	175.61	631.51	10	-3.23
NE67	G45	380.32	1262.86	8.7	497.14	1472.24	165.49	631.13	11	6.22
WC 63	G65	801.27	1101.59	37.93	393.65	1239.46	194.72	628.1	12	-4.84
NE 50	G39	688.25	1081.9	12.03	620.32	1182.72	168.82	625.67	13	-2.41
WC 64	G66	1156.19	857.78	19.37	511.75	998.97	176.16	620.04	14	-13.26
IT 889	G9	652.7	1109.21	48.85	565.71	1114.71	205.64	616.14	15	-2.07
WC 26	G52	145.4	1445.71	18.5	457.78	1453.23	175.29	615.99	16	11.32
NE 23	G24	949.84	1018.41	21.75	501.59	1023.42	178.54	615.59	17	-8.48
WC 67	G68	677.46	1078.73	41.31	611.43	1057.59	198.1	610.77	18	-3.04
NE 20	G22	725.71	1099.68	83.02	206.98	1281.75	239.81	606.16	19	-2.08
MU 15	G13	269.84	1179.68	61.48	487.62	1332.88	218.27	591.63	20	6.55
KVU 27-1	G12	382.86	1172.7	7.12	596.19	1207.93	163.9	588.45	21	3.24
IT 71	G7	303.49	1186.03	42.78	475.56	1294.73	199.57	583.69	22	5.69
NE 51	G40	278.1	1154.92	41.82	573.97	1159.64	198.61	567.84	23	4.89
IT 91	G10	307.94	969.52	65.57	753.65	1033.14	222.36	558.7	24	2.34
MU 20B	G16	419.68	1080.63	40.26	358.73	1226.03	197.05	553.73	25	2.45
NE 46	G36	311.75	1130.16	3.5	579.05	1135.02	160.28	553.29	26	3.88
NE 41	G34	323.17	1085.08	34.88	441.27	1135.05	191.67	535.19	27	2.98
WC 55	G64	389.21	1043.17	28.26	492.7	1066.52	185.05	534.15	28	1.48
IT 84	G8	551.75	1074.92	27.62	357.46	995.11	184.41	531.88	29	-1.05
WC 27	G53	498.41	960	45.31	324.44	1111.87	202.1	523.69	30	-0.58
2419	G1	1030.48	704.76	14.38	408.25	787.48	171.17	519.42	31	-13.85
NE 21	G23	406.35	1010.79	15.69	503.49	1004.06	172.47	518.81	32	0.47
NE 15	G20	1005.71	705.4	1.41	511.75	712.91	158.2	515.89	33	-14.01
NE 32	G27	413.97	954.29	10.67	461.59	1082.97	167.46	515.16	34	-0.36
NE 70	G43	1041.9	670.48	18.02	505.4	673.05	174.81	513.94	35	-15.13
SEC 5 * NE 39	G47	416.87	869.84	77.58	448.89	1012.37	234.37	509.99	36	-0.5
WC 17	G49	316.83	1048.25	5.79	387.94	1055.54	162.58	496.15	37	2.59
WC 41	G59	328.89	918.1	25.68	573.97	939.57	182.47	494.78	38	0.67
NE 45	G35	150.48	1024.76	38.74	382.22	1172.17	195.52	493.98	39	6.19
IT 2841x	G6	219.05	890.79	42.42	618.41	988.74	199.2	493.1	40	2.75
NE 6	G42	571.43	786.03	26.44	516.19	862.98	183.23	491.05	41	-4.93
SEC 5 * NE 51	G48	255.24	968.25	30.91	440.64	1063.48	187.7	491.04	42	2.41
WC 44	G60	150.48	1076.83	17.28	499.05	1021.2	174.06	489.82	43	5.88
WC 32 * SEC 5	G56	161.9	1009.52	27.83	426.67	1103.23	184.62	485.63	44	5.35
NE 31	G26	173.33	1165.08	60.12	343.49	952.86	216.9	485.3	45	6.84
WC 30	G55	88.89	1083.17	1.7	460.95	1113.21	158.49	484.4	46	7.12
NE 39 * SEC 4	G31	156.83	1019.68	19.58	495.24	980.46	176.37	474.69	47	4.94
WC 52	G63	564.44	788.57	32	405.08	791.88	188.79	461.79	48	-5.34
MU 19	G15	354.92	893.33	16.13	352.38	919.83	172.92	451.59	49	-0.15
WC 36	G58	861.59	563.81	40.83	457.14	581.67	197.62	450.44	50	-13.49
WC 5	G62	128.89	953.02	18.44	459.05	955.96	175.23	448.43	51	4.37
NE 49	G38	245.71	854.6	49.05	459.68	874.61	205.83	448.25	52	1.16
NE 13	G19	67.3	834.29	32.75	558.1	989.16	189.54	445.19	53	4.89
SEC 1 * SEC 3	G46	313.65	835.56	10.46	489.52	834.61	167.24	441.84	54	-0.5
WC 35A	G57	396.19	847.62	34.99	302.22	844.66	191.78	436.24	55	-1.71
NE 40	G33	174.6	949.84	15.39	316.19	972.38	172.18	433.43	56	3.68
IT 97	G11	280.63	720	44.07	525.71	801.9	200.86	428.86	57	-0.91

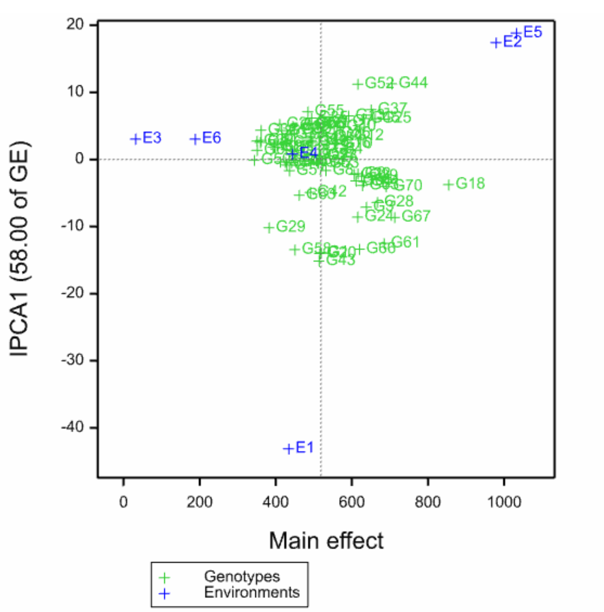
WC 68A	G71	204.44	909.84	21.49	337.78	915.27	178.28	427.85	58	2.47
WC 2	G51	237.46	866.03	30.04	358.73	886.42	186.83	427.58	59	1.42
IT 2841 * Brown	G5	273.02	731.43	19.33	509.84	841.18	176.12	425.15	60	-0.46
WC 8	G72	67.3	864.13	45.77	441.27	870.77	202.55	415.3	61	4.2
MU 17	G14	288.89	813.97	27.56	348.57	810.96	184.35	412.38	62	-0.4
EBELAT* NE 39	G2	67.94	944.13	4.89	336.51	946.17	161.67	410.22	63	5.21
NE 18	G21	217.14	886.98	13.21	216.51	886.04	170	398.31	64	1.84
MU 24C	G17	117.46	714.92	68.03	448.89	787.45	224.82	393.6	65	1.73
NE 37	G29	622.86	518.1	25.88	421.59	524.09	182.67	382.53	66	-10.26
WC 29	G54	60.32	758.73	20.6	385.4	767.54	177.38	361.66	67	2.73
NE 4	G32	34.29	836.83	29.27	238.1	842.82	186.06	361.23	68	4.28
IT 109	G4	67.94	606.35	45.65	354.92	879.87	202.44	359.53	69	1.09
WC 67A	G69	158.73	782.22	23.45	180.32	781.27	180.24	351.04	70	1.31
NE 39 * SEC 2	G30	52.7	701.59	34.33	336.51	787.79	191.12	350.67	71	2.64
WC 18	G50	171.43	678.1	49.51	258.41	697.78	206.3	343.59	72	-0.2

E1-MUARIK in 2015, E2-ARUA in 2015, E3-SERERE in 2015, E4-MUARIK in 2016, E5-ARUA in 2016, E6-SERERE in 2016.

Table 6:- AMMI analysis of variance for grain yield of 72 cowpea genotypes, Uganda

Source	DF	SS	MS	Explained %
Total	786	86896950		
Genotypes (G)	71	4659466	65626***	5.36
Environments (E)	5	60094702	12018940***	69.16
G x E Interactions	355	11071391	31187***	12.74
IPCA 1	75	6421263	85617***	58.00
IPCA 2	73	3809776	52189***	34.41
Residuals	207	840352	4060	7.59

***significant at $P<0.001$



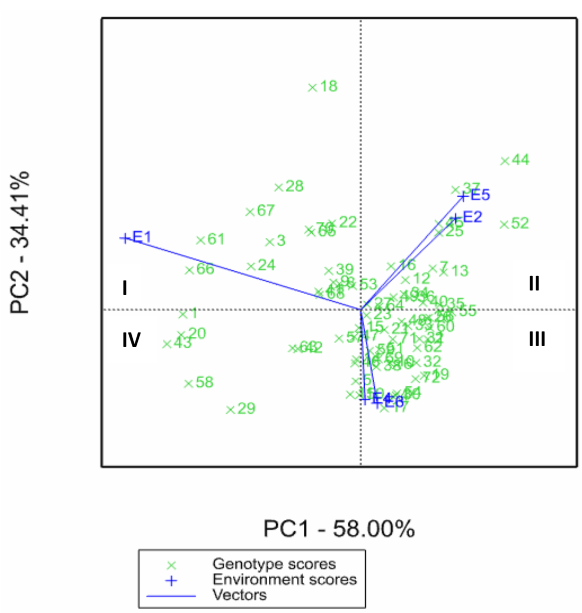


Fig.1:- AMMI biplots for grain yield (Kgha^{-1}) of the 72 cowpea cultivars in 6 environments using genotypic and environmental scores.

Environments codes: **E1**-MUARIK in season 2015B, **E2**-ARUA in season 2015B, **E3**-SERERE in season 2015B, **E4**-MUARIK in season 2016A, **E5**-ARUA in season 2016A, **E6**-SERERE in season 2016A.

Genotypes (G)*: **1**-2419, **2**-EBELAT * NE 39, **3**-EBERAT * NE 51, **4**-IT 109, **5**-IT 2841 * BROWN, **6**-IT 2841x, **7**-IT 71, **8**-IT 84, **9**-IT 889, **10**-IT 91, **11**-IT 97, **12**-KVU 27-1, **13**-MU 15, **14**-MU 17, **15**-MU 19, **16**-MU 20B, **17**-MU 24C, **18**-MU 9, **19**-NE 13, **20**-NE 15, **21**-NE 18, **22**-NE 20, **23**-NE 21, **24**-NE 23, **25**-NE 30, **26**-NE 31, **27**-NE 32, **28**-NE 36, **29**-NE 37, **30**-NE 39 * SEC 2, **31**-NE 39 * SEC 4, **32**-NE 4, **33**-NE 40, **34**-NE 41, **35**-NE 45, **36**-NE 46, **37**-NE 48, **38**-NE 49, **39**-NE 50, **40**-NE 51, **41**-NE 53, **42**-NE 6, **43**-NE 70, **44**-NE5, **45**-NE67, **46**-SEC 1 * SEC 3, **47**-SEC 5 * NE 39, **48**-SEC 5 * NE 51, **49**-WC 17, **50**-WC 18, **51**-WC 2, **52**-WC 26, **53**-WC 27, **54**-WC 29, **55**-WC 30, **56**-WC 32 * SEC 5, **57**-WC 35A, **58**-WC 36, **59**-WC 41, **60**-WC 44, **61**-WC 48A, **62**-WC 5, **63**-WC 52, **64**-WC 55, **65**-WC 63, **66**-WC 64, **67**-WC 66, **68**-WC 67, **69**-WC 67A, **70**-WC 68, **71**-WC 68A, **72**-WC 8.*

Discussion:-

Cowpea Grain Yield as Influenced by Genotypes, Locations and Years (Seasons):-

Evaluation of cultivars in contrasting environments and across years is an essential step in determining their desirability and cultivars with average response across the environments that have a wide scope of adaptation. Expression of wide genetic variability recorded in this study offers opportunity for quality improvement that would allow selection of individuals with better attributes for cowpea grain yield. Data on wide genetic variability in cowpea for grain yields are well documented (Idahosa et al., 2010; Manggoel et al., 2012; Nwosu et al., 2013). The analysis of variance across environments showed highly significant ($P<0.001$) genotypic effects for the grains yield. Furthermore, the mean sum of squares of environments and genotype x environment interaction were significant indicating broad range of diversity existed among the genotypes across the tested environments (Anandan et al., 2009). Such statistical interaction resulted from the changes in the relative ranking of the genotypes or changes in the magnitudes of differences between genotypes from on environment to another (Tarakanovas and Ruzgas, 2006). The significant L x G effects ($P<0.001$) demonstrated that genotypes responded differently to the variation in the environmental conditions of location and indicated the necessity of testing cowpea varieties at multiple locations. The significant Y x L x G effects ($P<0.001$) showed that cowpea yield largely depends on climatic conditions, in particular on the seasonal variation of temperature and the total precipitation in the experimental years. Similar results have been reported by Ddamulira et al. (2015) while evaluating the genotype by environments interaction effects on Brazilian cowpea yield in Uganda.

The best performing cultivars with regard to yield across locations and years was MU9 (854.68 $kgha^{-1}$). The high yield obtained at Arua 2016A was explained by the rainfall pattern that occurred in this area compared to two other environments where the experiments were conducted. Arua has a bimodal rainfall pattern with much longer first season rains. The rain was received during cowpea germination, vegetative and reproductive stage, yet sufficient soil moisture during the reproductive stage is known to enhance grain filling which result into increased grain yield as reported by Faisal and Abdel (2010) and Agoyi et al. 2017). On the other hand, Serere has been reported to be an ideal environment for cowpea production in Uganda with its sandy loamy soil suitable for proper and healthy cowpea growth because it does not restrict root development, has good aeration and drainage (Ecocrop, 2009; Directorate Agricultural Information Services, 2011). But in this study, the lowest cowpea grain yields were recorded in Serere 2015B and could be explained by the severe diseases infestation experienced in that year especially, scab and rust diseases. These disease infestations could be attributed to the fact that the trial of 2015B was set on the previous year site, so there may have been disease build up in the soil prior to planting. Different trends were reported earlier on 29 cowpea genotypes under diverse Ugandan environments by Ddamulira et al. (2015), who observed high cowpea yield in Namulonge and Serere. This shows the difficulties encountered by breeders in selecting new genotypes for release; these difficulties arise mainly from the masking effects of variable environments (Goncalves et al., 2003; Tarakanovas and Ruzgas, 2006). Thus, it is important to study adaptation patterns of genotypes response and their stability in multi-location trial.

Additive Main Effects and Multiplicative Interactions Analysis of Cowpea Grain Yield:-

In the current study, the contribution of the environment to the total variation was higher than the effect of the genotypes and genotype by environment (G × E) interaction. The environments were diverse and caused the greatest variation in grain yield. The AMMI analysis for the grain yield indicated that G x E interaction effects was highly significant ($P < 0.01$) with a sum of square 2.3 times larger than that for genotypes, which determined sustainable differences in genotypic responses across environments. Similar results were reported by Ddamulira et al. (2015) while evaluating the grain yield and protein content of Brazilian cowpea genotypes under diverse Ugandan environments. In this study, the G x E interaction effects were partitioned in the two first principal component axes (IPCA1 and IPCA2). The two first IPCA explained 92.41% of the interaction sums square (Table 6). This implied that the interaction of cowpea genotypes with the six environments was predicted by the two first component of genotypes and environment which is in agreement with the findings by (Gauch and Zobel, 1996) who recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. However, this contradicts the findings by Asio et al. (2005) while evaluating the local and improved cowpea genotypes in Uganda. These results indicate that the number of terms to be included in an AMMI model cannot be specified prior without first trying AMMI predictive assessment as reported by Kaya et al. (2002). In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa et al., 1990; Ddamulira et al., 2015).

The Interaction Principal Component Axes (IPCA) scores of a genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA 2 score are to zero, the more stable the genotypes are across their testing environments. Considering only the IPCA 2 scores it became clear that the genotypes WC30, NE 45, NE 31, NE 51 were the most stable genotypes, they were well adapted to high yielding environments that are more favorable. These genotypes have good potential for genetic improvement of Ugandan cowpea germplasm. The cultivars NE21, NE32, WC55, and WC17 posed close to zero of IPCA1 showed that they are more stable but with lower yield than WC 30, NE 45, NE 31 and NE 51. The cultivars NE48, NE5 and WC 26 had a yield significantly over grand mean grain yield and had an IPCA 1 score greater than the other cultivars but were less stable and may be characterized by specific adaptation in favorable environments. The biplot also showed the yield of a variety at individual sites. For instance, the cultivars NE30, NE67, NE48, WC48, WC26 and NE5 were best for high-yielding environments E2 and E5 (Arua 2015B and 2016A). The specific adaptability to certain environments possibly explained the highest variation in their grain yield. It is presumed that although in certain environments, NE30, NE67, NE48, WC48, WC26 and NE5 yielded highly, in other environments like Serere, the same genotypes might be less adapted due to limited ability to mobilize growth resources which reduces on their ability to produce high dry matter and grain yield as reported by Ddamulira et al. (2015). With respect to the test environments, E1 (MUARIK 2015B) was most discriminating as indicated by the longest distance between its marker and the origin. Thus, MUARIK could be recommended as best environment for cowpea genotypes evaluation. In addition, the length of a genotype vectors reflects the amount of interaction for that genotype. Thus according to Fig.1B, most of the GEI is due to the fact that the genotype MU9 has grain yield beyond average and large IPCA 2 score value in the trial. A similar result on the genotype MU9 was reported by Asio et al. (2005) in Uganda. As a result, this genotype is most suitable for poor environments.

Conclusion:-

This study was conducted to understand the yield performance of cowpea genotypes under diverse environments in Uganda. The grain yield varied based on the genotypes, environments and their interactions. Although genotype MU9 had the highest yield, it was only adapted to specific environments and could be used in those specific areas. Hence, genotypes WC 30, NE 45, NE 31, NE 51 were high yielding, stable and adapted to the environments tested, and should be recommended for genetic improvement of cowpea germplasm in Uganda. In terms of environments, the best grain yield was obtained from Arua, which implied that this environment was favorable for growing cowpea lines in Uganda. The genotype x environment interaction also affected grain yield which implied that, the grain yield of cowpea differed based on different environmental factors (soil types, temperature and rainfall).

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