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Analysis of Phenotypic Stability in 25 Cowpea Genotypes Across Six Environments

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ABSTRACT

Twenty-five cowpea (*Vigna unguiculata* L.) genotypes were evaluated across six contrasting environments for phenotypic yield stability. Combined analysis of variance revealed significant differences among the genotypes and the main effects. A1B×D, BC×M, L1B×M, A1B×M, and BA×I were the best performing and stable genotypes. The non-parametric analysis showed that genotype IT93K-503-1 had the highest yield and BC×D had the lowest yield. Shukla stability analysis revealed Beledi A and Dan lla as the most stable across test environments and genotypes A1B×D, BC×M and BA×I were good performers. The coefficient of variability graphical approach showed that genotypes BC×I, A1B×M, A1B×D, Dan lla, TA×M, Mouride, L1B×I, BC×M and L1B×D were high yielding. This implies they would do well across the testing sites. However, genotype IT93K-503-1 should be promoted for cultivation in drought-prone environments.

Key words: Adaptability, Cowpea, Environment, Genotype, Stability, Yield.

INTRODUCTION

Agricultural drought stress is highly variable and unpredictable over seasons and years making it difficult to identify a representative environment that could be considered a drought stress condition. One of the main factors for variability in yield of cowpea genotypes across environments is the genotype and genotype by environment interaction (GEI) effects. Stability is an important aspect of breeding for drought tolerance. Since drought tolerance is polygenic, it is hard to select tolerant genotypes in drought-prone environments. This makes it important to conduct factor stability analyses in the selection of cowpea genotypes for release.

Plant breeders commonly use different stability analyses to investigate GEI effects. Firstly, Finlay and Wilkinson (1963) and Francis and Kannenberg (1978) approaches to measure the stability of genotypes over small environmental variability. Secondly, Plaisted (1960) and Shukla (1972) approaches suggest that a genotype is considered to be stable if its mean response in a trial is parallel to environmental response. Lastly, several authors (Eberhart and Russell, 1966; Lin and Binns, 1988, Kang and Gorman, 1989; Crossa, 1990) suggest that a genotype is considered stable if the error means square from the regression model on the environmental index is small. Kang (1988) reported that the most commonly used stability analysis is the rank sum which incorporates yield and stability. Another frequently used approach is the coefficient of variability (Francis and Kannenberg, 1978) which assesses both performance and stability of genotypes concurrently. This approach measures the overall performance and coefficient of variability (CV) for each genotype across environments. The mean yield is then plotted against the CV. This approach was found to characterize genotypes into clusters rather than an estimate of stability per se. Use of approaches that give better stability estimates are crucial for selecting promising genotypes that combine high yield and stability which are most desired by farmers in the recent increase of frequent occurrence of drought in farmers' fields.

Ombakho and Tyagi (1987) reported that correlation coefficient analysis at times fails to reveal the true nature of the association between yield and its components. Thus, the use of path-coefficient analysis is a much better option. This method relays on the cause and effect situation among variables. It is a standardized partial regression coefficient and has a direct influence of one variable (independent) upon another (dependent).

Moisture deficit and flooding are major production constraints encountered in sub-Saharan Africa (SSA) over the seasons and years, between and within environments. Despite an increase in incidences of drought stress during the cropping season, cowpea has the ability to withstand drought stress better than other field crops. This study was designed to assess the effects of GEI and identified a sound and logical approach for identifying high yielding and stable genotypes.

MATERIALS AND METHODS

Field layout and genetic materials: Yield trial was carried out across six contrasting environments (drought stress and optimal conditions) in three locations Legon (Coastal Savanna) 5º 38' N, 0º 10' E, Fumesua (Forest-Savanna)

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6°41' N, 1º 28' W and Nyankpala (Guinea Savanna), 9°24' N, 0°59' W) in 2018. The unfavourable conditions were due to drought-stress, whereas the optimum conditions occurred in well-watered experiments. The trial was planted in two adjacent blocks spaced 50 m apart denoting two water regimes. The first block (Block 1) was designated as well-watered (WW) and the second (Block 2) as severe stress (SS). Plants planted in Block 2 were subjected to severe water stress-imposed by withdrawing irrigation water for three weeks at the flowering stage. Then watering was resumed for two weeks, twice a week, in order to score recovery and regrowth parameters of the genotypes. Twenty-five genotypes used in this study are A1B×D; BC×D, BC×I, BC×M, Beledi A, Beledi C, Dan lla, IT93K-503-1, L1B×D, L1B×I, L1B×M, A1B×I, Laduni 1B, Mouride, TA×D, TA×I, TA×M, Titinwa A, A1B×M, AGRAC-216, Apagu 1B, Asontem, BA×D, BA×I and BA×M. The genotypes were evaluated using 5 × 5 lattice square design with three replications. Each entry was planted in a two-row plot of 2 m spaced 0.6 m between rows and 0.20 m between hills within a row. All the recommended cultural practices were carried out to raise a good crop. Data were collected on an individual plant basis and means were computed.

Data analysis: Each water treatment and location were considered as an environment. Analyses of data combined across six environments were performed using GenStat 18th Edition considering all effects as random except genotypes according to Vargas *et al*. (2013). Phenotypic stability was computed using GEA-R and coefficient of variability percent and seed yield graphical analysis. The path-coefficient analysis was carried out using SPSS 22nd edition Statistical Software.

The combined analysis across environments was computed following the procedure of Vargas *et al*. (2013):

$$Y_{ijk} = \mu + Rep_i + Block_j(Rep_i) + Gen_k + Cov + \varepsilon_{ijk} \quad \text{.....(1)}$$

where Y_{ijk} is the trait of interest, μ is the mean effect, Rep_i is the effect of the *i*th replicate, $Block_j(Rep_i)$ is the effect of the *j*th incomplete block within the *i*th replicate, Gen_k is the effect of the *k*th genotype, Cov is the effect of the covariate and ε_{ijk} is the error associated with the *i*th replication, *j*th incomplete block, and *k*th genotype, which is assumed to be normally and independently distributed, with mean zero and homoscedastic variance σ^2. The $Si^{(1)}$ and $Si^{(2)}$ statistics are two rank stability approaches; $Si^{(1)}$ statistic measures absolute rank difference of genotype over

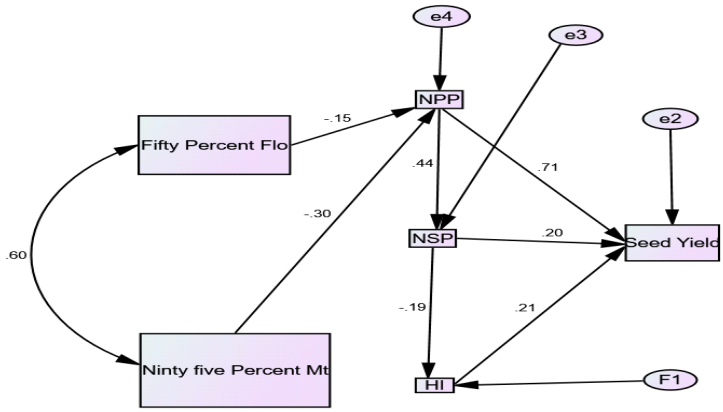

Fig 1: Path diagram of cause (traits studied) and effect (seed yield) relationship among 25 cowpea genotypes.

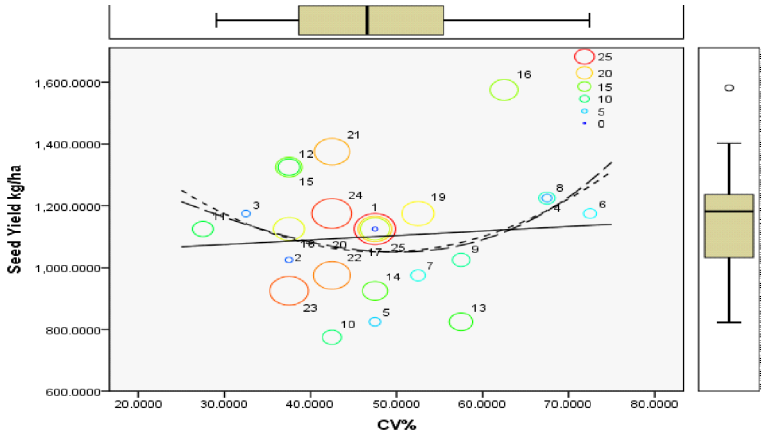

Fig 2: Cowpea seed yield vs CV percent of 25 genotypes across six environments.

GENOTYPES: Dan lla (15), Asontem (6), AGRAC-216 (4), IT93K-503-1 (16), Mouride (21), BC×M (12), Beledi C (14), BC×D (10), BA×I (8), BA×D (7), Laduni 1B (12), Titinwa A (25), TAM (24), L1B×I (18), L1BM (19), L1BD (17), BAM (9), 1BCI (10), Beledi A (13), TA×D (22), Apagu 1B (5), TA×I (23), A1B×M (3), A1B×D (1) and A1B×I (2).

environment, if $Si^{(1)}=0$ for a genotype, then it shows maximum stability, whereas $Si^{(2)}$ gives the variance between the ranks over environments, with zero variance being an indication of maximum stability. The exact variance and expectation of $Si^{(1)}$ and $Si^{(2)}$ were given by Huehn (1979).

RESULTS AND DISCUSSION

Combined analysis of variance: The combined analysis of variance across the six test environments revealed that genotypes and environments were significantly different. The main effect of genotype contributed 10.8% to the total variability and environment accounted for 63.8%. The interaction between genotype and environment accounted for 25.4% of the total variation of the mean square (Table 1). This indicates both favourable and unfavourable conditions existed during the trial. The differential yield response to environments could be utilized to identify genotypes targeted to specific environments. Mean performance for seed yield and some yield components is presented in Table 2. Genotype IT93K-503-1 had the highest seed yield (1,526.1 kg ha^{-1}) and BC×D had the lowest yield (766.6 kg ha^{-1}).

Table 1: Combined analysis of variance of seed yield (kgha^{-1}).

Source of variation	DF	MS
Geno	24	607686***
Env	5	16418495***
Geno × Env	120	270609***
Pooled Error	294	129843
Total	449	

*, **, *** Significantly different at 0.05, 0.01 and 0.001 levels of probability, respectively.

Path analysis: The number of days to 50% flowering and 95% maturity are exogenous variables, and tend to negatively relate to the number of pods per plant as shown in the association between harvest index and the number of seeds per pod. It was observed that the harvest index was positively associated with seed yield as was the number of pods per plant with number of seeds per pod. The study also found that the number of seeds per pod and number of pods per plant had a positive influence on seed yield (Fig 1). Total positive association ($r = 0.91$, $P<0.001$) was observed for the number of pods per plant, number of seeds per pod, harvest index and seed yield. This suggests that an increment of a variable by a unit will significantly increase the seed yield. Thus, high seed yield could be obtained through selection for increased harvest index, number of pods per plant, number of seeds per pod. This result agrees with the study of dos Santos *et al*. (2014).

Yield stability analyses: Results of yield stability analyses using the sum rank method are presented in Table 3. The genotypes with highest seed yield were IT93K-503-1, Mouride, A1B×D, BC×M and BA×I. Among these good performers, three are population developed for drought tolerance (A1B×D, BC×M and BA×I). Genotype superiority according to Lin and Binn (1988) revealed that IT93K-

Table 2: Mean yield of individual environments.

	Seed yield kg/ha			100-seed weight			NSP			NPP		
Geno	WW	DS	Mean	WW	DS	Mean	WW	DS	Mean	WW	DS	Mean
Apagu 1B	1007	685.6	1349.8	8.94	8.5	13.2	13.55	11.14	19.1	17.03	8.54	21.3
Laduni 1B	1444	868.8	1878.4	11.13	11.85	17.1	14.66	11.69	20.5	19.37	7.6	23.2
Mouride	1604	1078	2143.0	17.09	16.28	25.2	10.97	10.22	16.1	15.49	7.03	19.0
Beledi A	1044	548	1318.0	10.09	10.07	15.1	12.09	10.87	17.5	17.9	5.26	20.5
Beledi C	999	795.4	1396.7	8.21	8.89	12.7	11.45	10.72	16.8	20.69	8.72	25.1
Dan lla	1435	1112.2	1991.1	17.33	16.64	25.7	11.3	10.86	16.7	16.41	6.97	19.9
IT93K-503-1	2232	876.5	2670.3	13.89	14.69	21.2	13.75	11.2	19.4	26.66	6.02	29.7
Titinwa A	1487	774.7	1874.4	11.44	11.03	17.0	12.16	9.98	17.2	21.49	6.99	25.0
A1B×D	1472	807.9	1876.0	9	7.61	12.8	11.94	10.86	17.4	17.01	8.39	21.2
A1B×I	1068	826.9	1481.5	9.33	8.96	13.8	12.62	11.11	18.2	16.52	7.86	20.5
A1B×M	1374	986.8	1867.4	12.11	11.44	17.8	12.13	10.79	17.5	16.81	6.97	20.3
BA×D	1303	656	1631.0	9.52	8.76	13.9	12.19	10.89	17.6	19.06	6.54	22.3
BA×I	1622	748.4	1996.2	11.41	11.11	17.0	11.81	11	17.3	20.44	5.79	23.3
BA×M	1306	774.1	1693.1	10.97	10.16	16.1	11.76	10.42	17.0	20.37	5.17	23.0
BC×D	940	556	1218.0	8.68	8.43	12.9	11.66	10.07	16.7	17.12	5.9	20.1
BC×I	1202	1017.8	1710.9	10.6	9.94	15.6	10.98	10.68	16.3	20.03	8.05	24.1
BC×M	1553	1062.7	2084.4	10.85	9.99	15.8	11.1	10.31	16.3	21.01	8.21	25.1
L1B×D	1474	830.6	1889.3	11.09	10.5	16.3	13.51	11.46	19.2	17.73	6.9	21.2
L1B×I	1365	955.1	1842.6	11.35	9.09	15.9	13.31	12.48	19.6	15.76	7.29	19.4
L1B×M	1438	897.2	1886.6	11.67	11.04	17.2	13.24	11.55	19.0	16.74	6.58	20.0
TA×D	1168	702.3	1519.2	11.82	10.66	17.2	11.43	9.55	16.2	15.52	6.76	18.9
TA×I	976	800.5	1376.3	10.17	10.53	15.4	10.4	9.86	15.3	17.64	6.18	20.7
TA×M	1304	895	1751.5	12.28	13.08	18.8	11.55	10.35	16.7	16.99	6.41	20.2
AGRAC-216	1521	963.4	2002.7	18.72	17.64	27.5	10.98	9.63	15.8	13.61	5.77	16.5
Asontem	1554	874	1991.0	14.24	13.65	21.1	14.1	11.57	19.9	14.8	6.22	17.9

Table 3: Sorted stability coefficients of 25 cowpea genotypes evaluated across six contrasting environments in 2018.

Geno	Superiority	Means	Geno	Stability	Means	Geno	Ecovalence	Means	Geno	Mean ranks	Means
IT93K-503-1	26163.0	1384.3	BC×M	2409.00	1257.90	Laduni 1B	722.00	1007.20	IT93-503-1	2.67	1384.30
Mouride	53212.0	1219.3	Mouride	21028.00	1219.30	BA×D	4734.00	868.80	Mouride	4.33	1219.30
BC×M	60476.0	1257.9	BC×I	22409.00	964.80	Titinwa A	5210.00	1025.40	BC×M	5.67	1257.90
Dan lla	71092.0	1162.6	A1B×I	23759.00	885.80	A1B×M	14789.00	1098.10	Dan lla	6.67	1162.60
A1B×M	100405.0	1098.1	TA×I	24720.00	817.80	Beledi C	15045.00	828.10	A1B×M	7.33	1098.10
Titinwa A	136018.0	1025.4	BC×D	29803.00	697.60	L1B×I	18165.00	1015.70	A1B×D	10.33	1083.10
BA×I	139045.0	1070.3	TA×D	30156.00	871.20	L1B×D	18228.00	995.30	TA×M	10.33	1038.10
TA×M	140353.0	1038.1	A1B×M	41500.00	1098.10	Dan lla	20460.00	1162.60	L1B×I	11.00	1015.70
Laduni 1B	142596.0	1007.2	Beledi A	54029.00	725.10	Apagu 1B	24376.00	759.00	L1B×M	11.00	1055.90
L1B×I	144761.0	1015.7	Dan lla	63496.00	1162.60	TA×D	28204.00	871.20	Laduni 1B	11.00	1007.20
L1B×M	154032.0	1055.9	BA×D	69241.00	868.80	BA×M	34229.00	898.70	Titinwa A	11.00	1025.40
L1B×D	156005.0	995.3	Beledi C	69790.00	828.10	Mouride	36595.00	1219.30	BC×I	12.33	964.80
AGRAC-216	157078.0	1090.0	Laduni 1B	80478.00	1007.20	BC×I	37623.00	964.80	AGRAC-216	12.67	1090.00
A1B×D	166629.0	1083.1	Titinwa A	84450.00	1025.40	BC×D	40138.00	697.60	L1B×D	13.00	995.30
BC×I	170046.0	964.8	L1B×I	89256.00	1015.70	A1B-I	42062.00	885.80	Asontem	13.33	1045.10
Asontem	183357.0	1045.1	L1B×D	99738.00	995.30	TA×M	44545.00	1038.10	BA×I	13.33	1070.30
BA×M	212574.0	898.7	Apagu 1B	105827.00	759.00	IT93K-503-1	52530.00	1384.30	A1B×I	15.33	885.80
A1B×I	219681.0	885.8	TA×M	121096.00	1038.10	TA×I	58334.00	817.80	TA×I	16.67	817.80
TA×D	227426.0	871.2	BA×M	148925.00	898.70	Beledi A	108751.00	725.10	BA×D	17.00	868.80
BA×D	227672.0	868.8	A1B×D	168314.00	1083.10	L1B×M	144380.00	1055.90	BA×M	17.33	898.70
Beledi C	258510.0	828.1	IT93K-503-1	184654.00	1384.30	BA×I	174747.00	1070.30	TA-D	17.67	871.20
TA×I	263077.0	817.8	L1B×M	254930.00	1055.90	BC×M	179825.00	1257.90	Beledi C	19.33	828.10
Apagu 1B	313858.0	759.0	BA×I	271716.00	1070.30	AGRAC-216	291809.00	1090.00	Beledi A	20.00	725.10
Beledi A	339472.0	725.1	Asontem	387394.00	1045.10	A1B×D	309827.00	1083.10	Apagu 1B	22.67	759.00
BC×D	355094.0	697.6	AGRAC-216	412226.00	1090.00	Asontem	408808.00	1045.10	BC×D	23.00	697.60

503-1, BC×M, Dan lla, L1B×I, Laduni 1B, Mouride, Titinwa A and A1BM were stable with high yields. The non-parametric analysis according to Nassar and Huehn (1987) revealed that IT93K-503-1 had the highest mean yield among the genotypes evaluated (Table 2). Vaezi *et al*. (2017) reported a similar trend when they used parametric and non-parametric measures for selecting stable and adapted barley genotypes.

The yield stability differences among the 25 cowpea genotypes were further assessed by using the graphical method (Francis and Kannenberg, 1978). The percent CV on the x-axis was plotted against seed yield on the y-axis (Fig 2). The mean percent CV computed was 47.73%. The cowpea genotypes with CV and seed yields above the grand mean were considered high yielding with low stability, whereas those with low CV percent and seed yields below the grand mean were considered highly stable and low yielding. Genotype IT93K-503-1 was found to be the highest yielding and BC×D was the lowest yielder. However, genotypes in the first quadrant as presented in (Fig 1), 11 (BC×I), 3 (A1B×M), 1 (A1B×D), 13 (Dan lla), 24 (TA×M), 21 (Mouride), 18 (L1B×I), 12 (BC×M) and 17 (L1B×D) yielded above the grand mean. This implies that they could thrive well across the testing sites under stress and optimal growing conditions.

CONCLUSION

Breeding cowpea for high yield, farmer preferred characteristics and broad adaptability should be the research focus for the cowpea improvement programme. Testing genotypes across environments and time will enable identification of stable and high yielding genotypes. In addition, this study found stability analysis to be a useful statistical tool for adaptability and selection of stable and high yielding genotypes. Our study revealed that when breeding for drought tolerance, breeders should consider other abiotic stresses including heat stress which, in most cases, occur simultaneously in farmers' fields.

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