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Yield performance stability of adapted and improved cowpea in the Equatoria region of South Sudan

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ABSTRACT

Cowpea is an important food crop with high nutritional and socio-economical values in South Sudan. However, the lack of improved varieties is one of the main production constraints. This study was undertaken to assess the yield stability performance of improved cowpea genotypes across six environments in South Sudan in 2014 and 2015. Nine genotypes were evaluated in a randomized complete block design with three replications. Genotype and genotype x environment biplot analysis method was used to determine yield stability. Highly significant ($p< 0.001$) genotype x environment interaction effect was detected for seed yield. IT90K-277-2 had the highest while ACC004 had the lowest grain yield. Palotaka was as highly discriminating and repeatable environment compare to the other testing sites. IT07K-211-1-8 and Mading Bor II were the most responsive genotypes, while IT90K-277-2 was the most stable high yielding genotype across the test environments and can be grown by farmers across the region.

Key words: Adaptability, Agro-ecological zones, Cowpea, Grain yield, Stability.

INTRODUCTION

South Sudan has diverse agro-ecologies with high potential of agricultural production for different crops (Galla and Ngalamu, 2013), including cowpea [*Vigna unguiculata* (L.) Walp]. The interest among farmers for cowpea production is increasing in the Equatoria region of South Sudan for food security and household income. However, the lack of quality seed and low grain yield of local varieties are the major production constraints among farmers. This has prompted the introduction of improved cowpea genotypes from different sources to select stable high yielding ones to boost production. Testing genotypes across locations are important for the identification of stable and high yielding genotypes and the target environment (Yan *et al*., 2000). However, genotype x environment interaction (GEI) plays a significant role in determining a stable high yielding genotype. A combined analysis of variance (ANOVA) can explain GEI and reveal the main effects, but it cannot explain the effects resulting from the interaction (Asnake *et al*., 2013). Hence, determination of varietal performance across test environments and ideal stable genotype(s) is crucial. Thus, the information drawn from such studies will facilitate the selection and release of the best performing genotypes to farmers.

Following the proposal of Gabriel (1971), the genotype and genotype by environment (GGE) biplot technique was used to display the GGE of multi-environment trials (MET) data which is referred to as GGE biplot (Yan, 2002). The GGE biplot analysis is the most powerful statistical tool to determine the pattern of genotypic responsiveness across environments (Kaya *et al.,* 2006). It displays both genotypic (G) and genotype × environment (GE) effects. However, the yield is the combined effects of G, E and GEI; only G and GEI are pertinent and concurrently significant in genotype evaluation (Yan *et al*., 2007). When selecting genotypes across contrasting environments for yield stability, plant breeders look for a non-crossover type of GEI or preferably the absence of GEI for general adaptation (Thomason and Phillips, 2006). Nevertheless, GEI is important for exploitation by GGE biplot to target suitable genotypes to a specific environment or group of environments.

GGE biplot uses visual analysis of MET data (Sozen *et al.,* 2018) and clearly identifies the best variety for specific environments and enables identification of MET. The MET can occur in more than one agro-ecological zone, defined by similar abiotic and biotic stresses (Cooper and DeLacy, 1994). Based on GGE biplot analysis of yield performance,

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genotypes can be assessed for both broad and specific adaption (Sozen *et al.,* 2018) which is crucial for assigning a particular genotype to a specific environment. The application of GGE biplot has helped breeders to select superior and high yielding genotypes since the package integrates both yield performance and stability (Kang, 1993, Kang and Magari, 1996; Fan *et al*., 2007). The objective of this study was to evaluate the yield stability performance of nine cowpea genotypes across six environments in South Sudan.

MATERIALS AND METHODS

The test locations were Palotaka (PAL) and Pajok (PAJ), in Magwi County, and Juba in Juba (JUB) County. PAL and PAJ are in the Greenbelt while JUB falls in Hills and Mountains agro-ecologies. The characteristics of the test locations are presented in Table 1. The genetic materials consisted of seven improved cowpea genotypes (IT90K-277-2, IT07K-274-2-9, IT07K-211-1-8, IT08K-193-15, IT07K-297-3, ACC004, and IT08K-1 80-11) introduced from the International Institute of Tropical Agriculture (IITA) and two farmers' preferred varieties (Mading Bor II and Titinwa). Based on yield performance, the best nine genotypes were selected from 147 cowpea genotypes evaluated in a preliminary yield trial. Mading Bor II (MBR II) is an adapted variety collected from Bor in the Flood Plains agro-ecology, while Titinwa, a landrace commonly grown by farmers, collected from Mundri in the Ironstone Plateau agro-ecology of South Sudan. Titinwa was used as a local check, because of its easy cooking ability.

The nine genotypes were evaluated in a randomized complete block design with three replications in each test location. The first evaluation was conducted during the first season in JUB and PAL (2014A), and PAJ in the second season (2014B), whereas in 2015, the genotypes were evaluated at the three sites in the second season (2015B). Each genotype was planted in a 4 m long, four-row plot with 0.50 m spacing between rows and 0.40 m between hills within a row. Two seeds were planted in a hill and thinned to one plant after 21 days to attain a population density of 33,333 plants ha^{-1} in each location.

Data were recorded in each plot using the cowpea descriptors developed by the International Board for Plant Genetic Resources (IBPGR) now Bioversity International. Grain yield adjusted to 12% moisture content was computed from the grain weight of harvested pods per plot. Although we measured many traits in this study, only data on grain yield and yield components are presented.

The ANOVA was performed using GenStat 18th Edition, considering all effects random except genotypes following the procedures of Vargas *et al*. (2013). Each season and location were considered as an environment. Analysis of variance was conducted for each environment separately and combined across the six environments to determine whether GEI was significant. Repeatability estimates were computed for grain yield and other six traits to determine

Table 1: Soil and climate characteristics of each environment where nine cowpea genotypes were evaluated.

Environment	Year	Local	Latitude	Longitude	Altitude (masl†)	Agro-ecology	Soil	Climate*	Average temperature (°C)**	Rainfall (Mm)**	Relative humidity (%) **	Code
A1a	2014	Palotaka	03.98°N	032.49°E	1017	Greenbelt	Ferrous soil	AW	25.5	1101	72	PAL
A1b	2014	Pajok	3.87°N	32.48°E	893	Greenbelt	Sandy Loam	AW	25.6	1166	74	PAJ
A2	2014	Juba	04.84°N	031.59°E	496	Hills and Mountains	Sandy Loam	AW	27.5	941	65	JUB
A3a	2015	Palotaka	03.98°N	032.49°E	1017	Greenbelt	Ferrous soil	AW	25.7	1169	75	PAL
A3b	2015	Pajok	3.87°N	32.48°E	893	Greenbelt	Sandy Loam	AW	25.6	1100	72	PAJ
A4	2015	Juba	04.84°N	031.59°E	496	Hills and Mountains	Sandy Loam	AW	27.5	963	66	JUB

†Meters above sea level; *According to Köppen-Geiger, AW: Wet-Dry Tropical Climate; **Data recorded during the experiment.

the precision of the trial (Allard, 1999). Phenotypic correlations were computed for these traits. To compute yield performance stability using GGE biplot (Yan, 2002), test environments were coded with the corresponding environmental characteristics and season as shown in Table 1. Mean grain yields of the nine cowpea genotypes from six environments were used to construct the GGE biplots. The analysis was based on singular value decomposition (SVD) of the first two principal components (PC1 and PC2) to identify genotypes adapted to specific or broad environments. The mean yield data used to generate the GGE biplot were environment centered without transformation which was then decomposed into principal components (PCs) via SVD Yan (2002).

RESULTS AND DISCUSSION

Analysis of variances

Combined ANOVA showed that environment had highly significant effects on grain yield, number of seeds per pod, number of branches per plant and number of days to 50% flowering, whereas year had significant interactions with genotypes for grain yield, number of pods per plant, number of branches per plant, and days to 50% flowering (Table 2). Estimates of repeatability varied with traits, with a number of seeds per pod scoring the highest (0.95) and grain yield (0.21) had the lowest score. Environment accounted for 60 to 75% of total variability in grain yield and yield components. Our results corroborate with the findings of other workers (Putto *et al*., 2008; Singh *et al.,* 2018) who reported that environment accounts for 50 - 80% of the total variation in MET data.

The mean grain yield of all genotypes was 735.8 kg ha^{-1}. The best genotype (IT90K-277-2) produced grain yields of 1,626.4 kg ha^{-1} and the worst one (IT07K-274-2-9) produced 343.7 kg ha^{-1}. The grain yield of the local check, Titinwa, was 628.3 kg ha^{-1}. Interestingly, the adapted variety MBR II was among the top three genotypes that - surpassed the local check Titinwa by 44 to 64.3%. Two of the best three genotypes (IT90K-277-2, IT07K-211-1-8) are improved lines introduced from IITA. MBR II had a competitive performance with the two best genotypes in PAJ during the second season in 2014. These genotypes had consistent performance during the second season with limited rains, suggesting that they can also adapt to marginal areas (Cooper *at al*., 1997; Meseka *et al*., 2016).

Phenotypic correlations

Phenotypic correlations between grain yield and six yield components showed that plant height, number of branches per plant, number of pods per plant, number of seeds per pod, days to 50% flowering and 100-seed weight were positively and significantly correlated with grain yield (Table 3). The strongest correlations were detected between grain yield and number of pods per plant and number of branches per pant ($r = 0.92$; $P<0.01$) and between grain yield and plant height ($r = 0.89$; $P<0.01$). This result indicated inherent contributions of these traits to grain yield showing a positive linear relationship between grain yield and the yield components, suggesting that improving one of these traits could positively influence grain yield. These traits can be used as an index for selecting high yielding cowpea genotypes. Our results corroborate the findings of Souza *et al*. (2007) and Menna *et al*. (2015) who reported significant

Table 2: Mean performance of nine cowpea genotypes tested for two years across six sites in Equatoria region of South Sudan.

Genotype	Yield (kg/ha)	100-seed weight (g)	Number of seed/pod	Number of pods/plant	Number of branches/plant	Number of days 50% flowering	Plant Height (cm)
IT90K-277-2	1626.4	19.87	11.84	46.09	9.786	45.29	64.17
IT07K-274-2-9	343.7	18.20	9.30	22.77	3.93	41.29	37.71
MBR II	947.1	10.56	15.59	30.00	6.04	48.14	62.10
IT07K-211-1-8	1479.4	19.04	11.19	44.00	9.26	40.14	60.76
IT08K-193-15	456.5	16.27	9.77	29.13	4.54	40.14	34.26
IT07K-297-3	355.4	15.97	10.89	26.39	4.34	38.86	49.74
Titinwa	628.3	16.53	10.74	23.96	4.70	33.43	68.97
ACC004	385.3	15.30	13.86	22.23	4.51	37.57	51.14
IT08K-180-11	399.7	16.29	11.56	23.37	4.07	37.86	40.43
Mean	735.8	18.28	11.00	37.92	5.49	42.11	66.4
LSD (0.05)	126.3	4.11	2.52	6.04	1.30	2.57	7.59
CV.%	9.15	20.67	17.93	16.78	18.89	5.61	9.49
Repeatability	0.21	0.16	0.95	0.86	0.51	0.48	0.41
Genotype	***	***	***	***	**	***	***
Environment	***	‡	***	‡	***	**	‡
Year	***	‡	‡	***	***	***	‡
Genotype × Environment	**	‡	‡	‡	‡	‡	‡
Genotype × Year	**	‡	‡	‡	‡	***	***

**, ***Significant at $P < 0.01$ and $P < 0.001$ probability levels, respectively; ‡ - non-significant at $P > 0.05$.

Table 3: Coefficients of phenotypic correlations between grain yield and some yield components of nine cowpea genotypes evaluated across three locations in 2014 and 2015.

Trait	Grain yield (kg/ha)
Plant height (cm)	0.89***
Days to 50% flowering (day)	0.49**
Number of seeds per pod (no.)	0.39*
Number of branches per plant (no.)	0.92***
Number of pods per plant (no.)	0.92***
100-seed weight (g)	0.29*

*, **, ***Significant at P < 0.05, P < 0.01 and P < 0.001 probability levels, respectively.

positive correlations of similar traits in cowpea. However, Aybegun *et al.* (2018) reported a negative and strong association between grain yield and number of days to 50% flowering in field pea.

GGE Biplot analysis

In this study, GGE biplot explained 88.4% of the total yield variation in the test environments. The vertex for "which-won-where-what" view identified IT07K-211-1-8 as the best genotype at PAJ, while IT90K-277-2 was the best genotype at PAL and JUB. MBR II had yield potential above average across the six environments. The check variety, Titinwa and most of the genotypes were not adapted to a specific location (Fig1 and Table 2). The poor performance of Titinwa and most of the genotypes across test environments can be attributed to GEI effects and their genetic backgrounds. However, different genotypes produced the highest grain yield in different test environments. The differential ranking of the genotypes across test environments demonstrates the existence of a mixture of crossover and non-crossover types of GEI as a common case with MET data (Kaya *et al.*, 2006).

Yield performance and stability of the nine cowpea genotypes determined by an average environment coordinate (AEC) method (Yan and Hunt, 2001; Yan, 2002) was defined by contributions of PC1 and PC2 in GGE biplot. A line passing through the AEC and biplot origin (average environment axis) serves as abscissa of the AEC, while the ordinate of AEC is the line that passes through the origin and perpendicular to the AEC abscissa (Fig 2). The AEC ordinate separates genotypes with above average grain yields from those with below average yields. Genotypic stability is crucial to sustainable performance across environments, the longer the projection to AEC ordinate, the greater tendency to more variability of genotypic performance across test environments. Consequently, IT90K-277-2 was identified as high yielding and most stable, while IT07K-211-1-8 was high yielding but unstable. MBRII was stable but had a lower yield compared to IT90K-277-2 and IT07K-211-1-8. Titinwa and five other genotypes had poor yield performance but were stable.

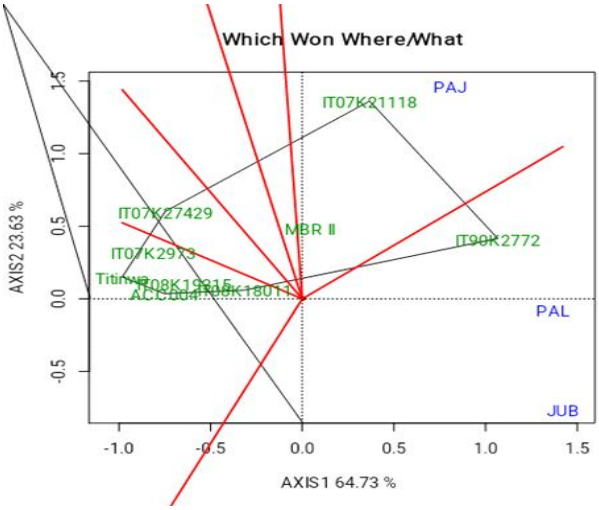

Fig 1: Polygon view of the GGE biplot showing the "which-won-where|what" using standardized yield data for nine cowpea genotypes.

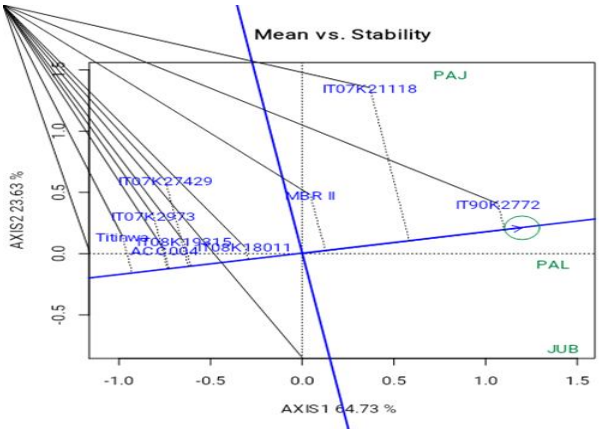

Fig 2: Mean performance and stability of nine cowpea genotypes using non-standardized yield data.

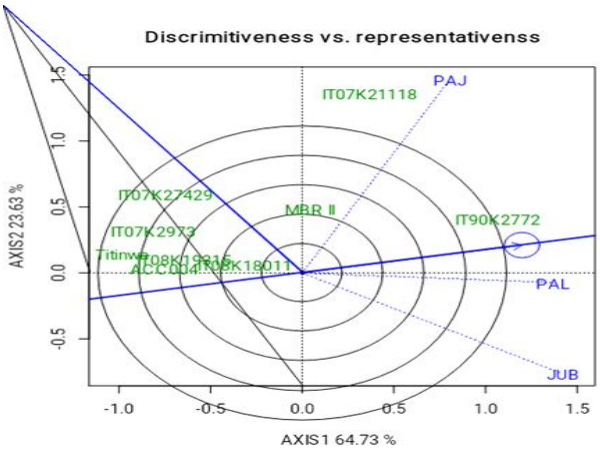

Fig 3: The relationship between three sites using standardized yield data of nine cowpea genotypes.

In the polygon view of the discriminating environments, JUB and PAL were strongly correlated and most discriminatory (Fig 3), suggesting that removing one of the two locations as a test environment would not lead to any loss of information and will cut down on resources that can be used in other locations (Yan *et al*. 2000; Yan and Rajcan, 2002; Yan and Tinker 2005; Kaya *et al*., 2006; Asnake *et al*., 2013). Yan and Tinker (2005) suggested that test environments that are non-discriminating provide no information on the genotypes and therefore should not be used as test environments. The first rainy season in PAJ characterized by high relative humidity and rainfall provided a perfect environment for insect pests and diseases, making it unsuitable for growing cowpea. Our results suggest that farmers in PAJ should grow improved cowpea varieties during the second season and concentrate on growing other crops like groundnuts (*Arachis hypogaea*), maize (*Zea mays* L.) and sorghum [*Sorghum bicolor* (L.) Moench] that require adequate rainfall which occurs during the first season. Although PAJ and PAL are grouped under the Greenbelt, PAL falls in mid-altitude (>1000 masl), while PAJ (893 masl) and JUB (496 masl) fall in the lowland that requires different germplasm classifications.

CONCLUSION

The present study revealed that environment interacted significantly with genotypes accounting for more than 60% of the total variability in grain yield and six yield components. Two improved genotypes introduced from IITA had high grain yields compared to farmers' preferred varieties. Interestingly, MBRII had competitive yield potential and other desirable traits compared to the two best-improved genotypes. IT90K-277-2 was the most stable and high yielding genotype that can also be grown in other lowland areas with similar environmental conditions. The study revealed that farmers in high rainfall lowland areas should avoid growing improved cowpea during the first season due to high insect and disease pressure. Farmers in lowland areas in Sub-Saharan Africa can tap into the stable performance of the best three genotypes for production and marketing to improve food security and household incomes.

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