YIELD AND YIELD STABILITY OF 21 GROUNDNUT (*ARACHIS HYPOGAEA* L.) GENOTYPES IN THE GUINEA SAVANNA OF GHANA

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Background

Groundnut (Arachis hypogaea L.) production is an integral component of the livelihoods of the people in the Guinea savanna of Ghana. The Guinea savanna of Ghana lies within the semi-arid tropical region. The area is characterised by erratic rainfall pattern, high temperatures, coarse textured soils low in organic matter content and cation-exchange capacity with a moderately acidic pH. Yet this area accounts for over 70% of total groundnut produced in Ghana. It is estimated that up to 90% of a typical farming household in this area is involved in groundnut production on marginal lands. The yield of groundnut is constrained by the use of low potential genetic materials, poor soil fertility, inadequate soil moisture and foliar diseases caused by *Cercospora arachidicola* S. Hori and *Cercosporidium personatum* (Berk. & Curt.). Current recommendations to overcome these problems come at a high cost. An effective approach to overcoming these challenges is through the development and use of superior groundnut genotypes. This study therefore aimed at identifying groundnut genotypes with high and stable pod and haulm yield across the guinea savanna of Ghana.

Materials and Methods

Five experiments over a two-year period were conducted with 21 groundnut genotypes comprising of 17 advanced breeding lines at Nyankpala, Damongo and Yendi in the Guinea savanna of Ghana. Soils at these locations are sandy loam, slightly acidic and low in nutrients. Genotypes were arranged in randomized complete blocks with four replications. Data was collected on haulm and pod yield. Data was analysed to determine the yield stability and G x E effect on shoot biomass and pod yield. Mega-environments for groundnut in the Guinea savanna of Ghana was also determined.

Table 1: BLUP means and stability of 21 groundnut genotypes tested across 5 environments

	Pod yield (t ha^{-1})			Biomass (t ha^{-1})		
Genotype	**Mean**	b_i	P_i	**Mean**	b_i	P_i
CHINESE	0.82	0.07	1.124	4.65	0.57	11.1
ICG (FDRS) 4	1.37	1.23	0.562	5.17	0.69	9.1
ICG 6222	1.39	1.76	0.757	6.86	1.74	2.9
ICGV 00068	0.96	1.58	0.935	6.27	3.33	3.1
ICGV 00362	0.58	0.37	1.169	5.36	1.18	7.2
ICGV 03166	0.86	1.50	1.252	4.31	0.92	11.9
ICGV 03179	0.80	0.68	1.144	4.31	0.37	13.6
ICGV 03196	0.85	1.09	1.124	4.45	0.31	12.8
ICGV 03206	0.65	0.67	1.36	3.90	0.69	14.3
ICGV 03315	1.05	1.36	0.898	5.65	1.28	6.4
ICGV 91317	0.91	1.56	1.224	4.57	0.56	11.7
ICGV 91324	0.75	1.26	1.28	4.72	0.56	12.1
ICGV 91328	0.82	0.89	1.136	5.06	0.57	10.9
ICGV 97188	0.85	1.03	1.14	4.23	0.34	14.0
ICGV 99029	0.79	1.13	0.971	5.66	0.98	6.8
ICGV 99247	0.76	0.98	1.571	4.34	1.19	10.7
ICGV-IS 08837	2.03	0.61	0.115	5.50	1.49	6.2
ICIAR 19BT	0.91	0.32	0.984	4.43	0.48	13.4
KPANIELLI	0.92	0.97	1.093	5.05	1.51	7.6
NKATIESARI	1.27	0.76	0.578	5.15	0.85	8.6
SUMNUT 22	0.86	1.06	1.221	4.35	0.50	12.8

P_i – cultivar superiority estimate, b_i – linear regression coefficient

Results

Mean pod yield ranged from 0.58 to 2.1 t ha-1. Genotype ICGV-IS 08837 emerged as the overall best by producing almost 2.5 fold more pods than CHINESE which is the most commercially important variety in the region. There was a high significant G x E effect on pod yield and haulm yield. The AMMI2 model successfully handled the G x E interaction as the first two principal components explained more than 80% of total G x E interaction. The low correlation among environments was mostly responsible for the significant G x E interaction implying that selection for much wider varietal adaptation to the region may not be effective. The study revealed that Nyankpala and Damongo were the most discriminating environments and constituted a mega environment each where adapted genotypes could be recommended for cultivation.

Table 2: ANOVA analysis from the application of the AMMI2 model

		Pod yield (t ha^{-1})		Haulm Yield (t ha^{-1})	
Source of variation	d.f.	s.s.	% Var	s.s.	% Var
Genotypes	20	12090547		65.7	
Environments	5	33736298		179.7	
Interactions	100	13660348		183.8	
IPCA 1	24	7351410***	53.81	105.5***	57.13
IPCA 2	22	4912536***	35.96	40.3**	21.93
Residuals	54	1396403		38.1	

Table 3: Spearman's rank correlation between genotype ranks based on means and stability estimates

	Pod yield		Haulm Yield	
	Mean	b_i	Mean	b_i
b_i	-0.33*		-0.66***	
P_i	0.77***	-0.05	0.92***	-0.86***

Figure 1: Management of experimental plots

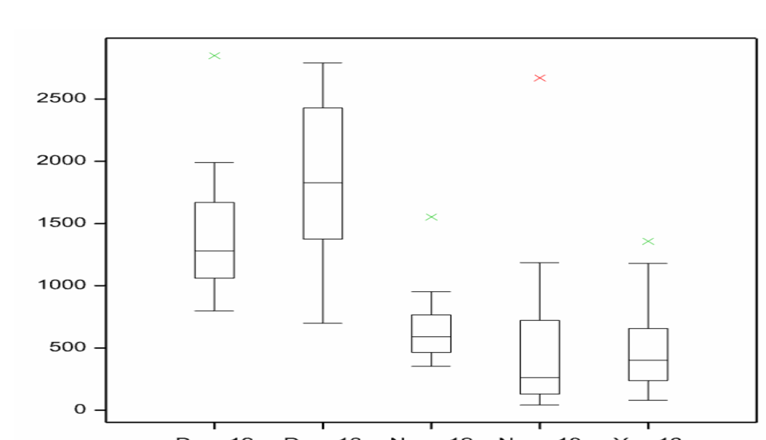

Figure 2: Box plot pod yield (kg ha^{-1}) displaying the total range, interquartile range and median

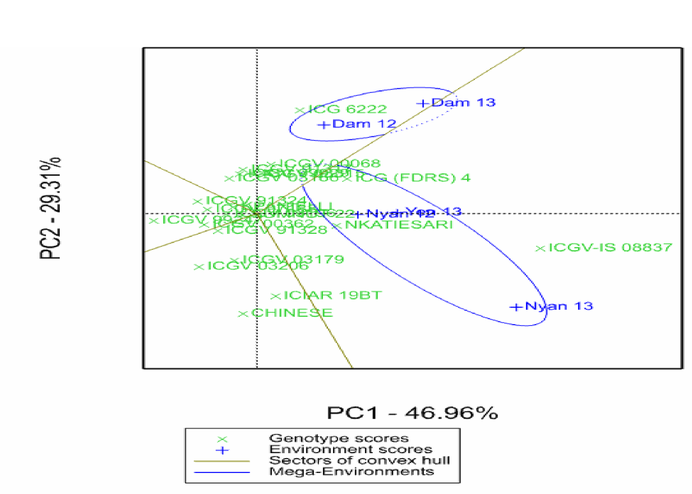

Figure 3: Mega-ggebiplot displaying mega environments for groundnut pod yield

Conclusion

In conclusion, the study identified high yielding genotypes (ICGV-IS 08837, ICG 6222, ICGV 03315) with consistent high yields across the environments tested. These genotypes are currently being evaluated by independent on-farm agronomists for onward submission for registration and release

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