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Genetic variability and association analysis for yield, physiological and quality traits in drought tolerant groundnut genotypes

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ABSTRACT

Thirty drought tolerant groundnut genotypes developed at Agricultural Research Station, Kadiri of Anantapur District, Andhra Pradesh were evaluated for their variability with regards to yield, physiological and quality traits. Estimates of heritability, genetic advance and genetic advance as per cent mean were also obtained for the above traits. The results revealed high to moderate GCV and PCV in addition to high heritability and high genetic advance as per cent mean for haulm yield per plant and free proline content. Further, pods per plant, pod yield per plant, and 100 kernel weights were observed with high positive direct effects and strong positive associations with kernel yield per plant. Consequently, these attributes are identified as effective selection criteria for kernel yield improvement in groundnut.

Key words: Correlation, Genetic advance, Groundnut, Heritability, Path analysis, Variability, Yield

India ranks first in groundnut cultivated area but occupies second place in production. The productivity of groundnut in India is also low, primarily due to cultivation of the crop mostly under rainfed conditions with frequent dry spells. Therefore, there is an urgent need for development of high yielding drought tolerant varieties in groundnut. Kernel yield in groundnut however is influenced by different yield components, physiological and quality traits, which makes direct selection for kernel yield ineffective, owing to its complex nature of inheritance. In this context, information on variability of the experimental material, heritability of the traits conditioning kernel yield and their genetic advance, the nature and extent of association between the yield component traits and their association with kernel yields are pre-requisites for planning of effective crop improvement programmes. Information on the direct and indirect effects of these component traits on kernel yield also aids in targeted selections and superior crop improvement. The present investigation was undertaken in this context to study the variability, heritability, genetic advance, character associations and path effects of yield components, physiological and quality traits on kernel yield with a view to identify suitable selection criteria for higher kernel yield in drought tolerant groundnut.

MATERIALS AND METHODS

Experimental material for the present investigation comprised of 30 drought tolerant groundnut genotypes developed at Agricultural Research Station, Kadiri of Acharya N.G. Ranga Agricultural University. These genotypes were sown during *kharif* 2015 at Agricultural Research Station, Kadiri of Ananthapuram District in Andhra Pradesh state. Each genotype was sown in continuous two row plots of 5m row length at spacing of 30cm between rows and 10cm between plants within the row in a Randomized Block Design with two replications. The crop was raised under rainfed conditions and all recommended practices were followed to raise a healthy crop. Observations were recorded on yield and physiological and quality traits, such as days to 50 per cent flowering, pods per plant, pod yield per plant mature kernel per cent, kernel yield per plant, 100 kernel weight, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA), oil, protein and free proline content in seed. The observations were recorded from five randomly selected plants for each genotype in each replication, while observations on days to 50 per cent flowering, oil, protein and free proline content in seeds were recorded on plot basis. The data collected was subjected to standard statistical procedures. Genotypic, phenotypic and environment co-efficient of variation, in addition to broad sense heritability and genetic advance as per cent mean were calculated and categorized as per standard procedures. Genotypic and phenotypic correlation coefficients in addition to the direct and indirect effects of different yield attributes were also estimated and categorized.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant mean squares due to genotypes for all traits, indicating the existence of sufficient variation among the genotypes for yield, physiological and quality characters studied in the present investigation. Leading in a scope for their effective selection. Information on mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability, genetic advance and genetic advance as per cent mean for yield, physiological and quality traits studied indicate the genetic variability (Table 1) in frequent genotype.

In the present study, higher PCV, compared to GCV were noticed for all the traits studied, indicating the influence of environment. The extent of environmental influence (Environmental Coefficient of Variation – ECV) as explained by the amount of the difference between GCV and PCV ranged from ranged from 0.02 (Oil content) to 5.02 (pod yield per plant) in the present study. Further, it was noticed to be low for protein content, free proline content, SLA, 100 kernel weight, days to 50 per cent flowering in addition to SCMR, indicating the minimal influence of environment on these traits. Further, low (<10%) PCV and GCV were recorded for days to 50 per cent flowering, sound mature kernel per cent, SCMR, SLA, oil and protein content. In contrast, moderate values (10-20%) were recorded for pods per plant, pod yield per plant, kernel yield per plant, 100 kernel weight and free proline content while, higher (>20%) PCV and moderate GCV were recorded for haulm yield per plant. The results are in broad conformity with the findings of Patil *et al*. (2014).

High (>60%) estimates of heritability were recorded for days to 50 per cent flowering, 100-kernel weight, SLA, haulm yield per plant, in addition to oil content, protein and free proline content in seed the present investigation. The findings are in broad agreement with the reports of Patil *et al*. (2014) for majority of the above traits. Moderate (30-60%) heritability values were recorded for pods per plant, pod yield per plant, mature kernel per cent, kernel yield per plant and SCMR. The findings are in agreement with the reports of Vishnuvardhan *et al*. (2012) for most of the traits.

Genetic advance as per cent mean also revealed high values (>20%) for haulm yield per plant and free proline content in seed. The results are in agreement with the reports of Patil *et al*. (2014). Further, moderate (10-20%) estimates of genetic advance as per cent mean were noticed for pods per plant, pod yield per plant, kernel yield per plant, 100 kernel weight and SLA. The results are in broad agreement with the reports of Vishnuvardhan *et al*. (2012). However, low estimates of genetic advance as per cent mean were recorded for days to 50 per cent flowering, mature kernel per cent, SCMR, oil and protein content in seed and the findings are in conformity with earlier reports for SCMR (Thankur *et al*. 2011), days to 50% flowering (Vishnuvardhan *et al*. 2012), mature kernel per cent, oil and protein content (Patil *et al*. 2014).

High heritability coupled with high genetic advance as percent mean was recorded for haulm yield per plant and free proline content in seed the present study which indicated high heritability due to additive gene effects; and therefore, selection would be effective for the characters. However, days to 50 per cent flowering, 100 kernel weight, specific leaf area, oil and protein content in seed had high heritability coupled with moderate to low genetic advance as per cent mean indicating the role of both additive and non-additive gene effects for control of these characters. The findings are in broad agreement with the reports of Zaman *et al*. (2011) for 100 kernel weight Satish (2014) for days to 50 per cent flowering and Patil *et al*. (2014) for oil and protein content in seed. Further, pods per plant, pod yield per plant, sound mature kernel per cent, kernel yield per plant and SCMR had moderate to low heritability and genetic advance as per cent mean indicating the role of non-additive gene effects for control of these characters. The results are in agreement with the findings of Vishnuvardhan *et al*. (2012) for number of pods and pod yield per plant and Patil *et al*. (2014) for mature kernel per cent.

Kernel yield in groundnut is a complex trait as it is based on various yield component traits and hence, direct selection for yield is largely ineffective. Therefore, selection for various component traits responsible for conditioning of kernel yield in groundnut is advocated. In this context, the nature and magnitude of association among kernel yield and its component traits was also studied in the present investigation study revised (Table 2). Genotypic correlations recorded a higher magnitude compared to phenotypic correlations indicating the masking effect of

Table 1. Estimates of variability and genetic parameters for yield, physiological and quality traits in groundnut.

Character	Mean	Range		Coefficient of variation (%)			Heritability in broad sense (%)	Genetic advance as per cent of mean
		Minimum	Maximum	Genotypic (GCV)	Phenotypic (PCV)	Environment (ECV)		
Days to 50% flowering	29.06	27.50	30.33	2.69	3.34	0.65	65.1	4.50
Pods per plant	17.76	14.30	21.90	10.12	14.16	4.04	51.0	14.90
Pod yield per plant	12.87	9.73	15.48	10.25	15.27	5.02	44.9	14.15
Mature kernel (%)	81.54	76.33	84.67	2.58	3.71	1.13	48.5	3.71
Kernel yield per plant	8.16	5.05	9.52	10.39	14.85	4.46	49.0	14.95
100 kernel weight (g)	32.02	27.42	39.91	10.19	11.41	1.22	79.9	18.77
SPAD chlorophyll meter reading	43.73	38.88	47.38	5.01	6.70	1.69	56.0	7.73
Specific leaf area	163.61	132.66	184.53	8.67	8.90	0.23	94.8	17.38
Haulm yield per plant (g)	11.33	7.93	16.33	17.25	20.73	3.48	69.3	29.58
Oil content (%)	46.29	43.22	48.40	2.93	2.95	0.02	98.8	6.00
Protein content (%)	24.34	22.33	26.25	4.01	4.08	0.07	96.9	8.14
Free proline content (mg)	2419.80	1661.00	3080.17	15.41	15.58	0.17	97.8	31.41

Table 2. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among yield, physiological and quality traits.

Character	r	Pods per plant	Pod yield per plant	Sound mature kernel per cent	100 kernel weight	SPAD chlorophyll meter reading	Specific leaf area	Haulm yield per plant	Oil content	Protein content	Free proline content	Kernel yield per plant
Days to 50%	r_p	0.2822	0.1157	-0.2263	-0.0588	0.0515	0.2302	0.0794	-0.1348	0.0792	-0.3117	0.2560
flowering	r_g	0.3114	0.3219	-0.2983	-0.0653	0.1371	0.2995	0.0540	-0.1728	0.0918	-0.3302	0.2776
Pods per plant	r_p		0.4065*	-0.1238	-0.3498*	0.3622*	-0.2508	0.3936*	0.3511*	0.3916*	-0.1737	0.3515*
	r_g		0.4628**	-0.1317	-0.3682*	0.4096*	-0.3392	0.4316*	0.4399*	0.4376*	-0.2446	0.3724*
Pod yield per	r_p			0.4064*	0.3663*	0.3680*	0.1317	0.4896**	0.3560*	0.4376*	-0.1570	0.6617**
plant (g)	r_g			0.5176**	0.4327*	0.3852*	0.3241	0.5218**	0.3970*	0.4737**	-0.2929	0.8336**
Mature kernel (%)	r_p				0.4218*	0.3240	-0.0994	-0.0642	0.1860	-0.0326	0.0772	0.3627*
	r_g				0.4887**	0.3896*	-0.1476	-0.1080	0.2802	-0.0397	0.1319	0.3859*
100 kernel weight	r_p					0.1758	0.1981	0.2793	-0.2125	0.3729*	-0.0700	0.3925*
(g)	r_g					0.2519	0.2351	0.2989	-0.2400	0.4177*	-0.0897	0.4080*
SPAD chlorophyll	r_p						0.4759**	0.2736	0.2503	0.2204	0.0019	0.3621*
Meter Reading	r_g						0.6633**	0.3249	0.2929	0.2663	-0.0029	0.6066**
Specific leaf area	r_p							0.2170	0.2734	0.6343**	0.0126	0.2790
	r_g							0.2360	0.2909	0.6684**	0.0082	0.3216
Haulm yield per	r_p								0.2896	0.3002	-0.0329	0.2596
plant (g)	r_g								0.3103	0.3232	-0.0404	0.2843
Oil content (%)	r_p									0.4516**	-0.0003	0.3717*
	r_g									0.4606**	0.0011	0.5998**
Protein content	r_p										-0.0314	0.3575*
(%)	r_g										-0.0284	0.3772*
Free proline	r_p											-0.0757
content(%)	r_g											-0.1097

r_p= Phenotypic correlation; r_g = genotypic correlation; *, ** Significant at 5% and 1% levels, respectively

environment. Further, positive and significant association of kernel yield (was noticed in the present study) with pods per plant, pod yield per plant, mature kernel per cent, 100 kernel weight, SCMR, oil content and protein content indicating an increase in kernel yield with an increase in these characters. The findings are in broad agreement with the reports of Pavan Kumar *et al.* (2014).

Study on inter-character associations revealed significant and positive association of pods per plant with pod yield per plant, SCMR, haulm yield per plant, oil content and protein content; pod yield per plant with sound mature kernel per cent, 100 kernel weight, SCMR, haulm yield per plant, oil content and protein content; sound mature kernel per cent with 100 kernel weight; 100 kernel weight with protein content; SCMR with SLA; SLA with protein content; and oil content with protein content in the present investigation, indicating a scope for simultaneous improvement of these traits through selection. The findings are in broad agreement with the reports of earlier workers (Pavan Kumar *et al.* 2014 and Venkatesh *et al.* 2015). In contrast, significant and negative association of pods per plant with 100 kernel weight was noticed in the present investigation. The negative association may be attributed to competition for a common factor such as nutrient supply indicating the need for balanced selection while making simultaneous improvement for these traits Rao *et al.* (2014).

Path co-efficient analysis provides an effective means of finding out the direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation and also measures the relative importance of each causal factor. In the present investigation, to genotypic path co-efficient were observed to be of higher magnitude compared to phenotypic as per results of masking effect of environment. The results also revealed high residual effect for both phenotypic (0.5967) and genotypic (0.5300) path coefficients, respectively explaining about 41 (phenotypic) and 47 (genotypic) per cent of the variability in kernel yield per plant and therefore, other attributes besides the characters studied are contributing for kernel yield. The results also revealed high (>0.30) positive direct effects of pod yield per plant, pods per plant, and 100 kernel weight on kernel yield per plant. Similar results were also reported for pods per plant and 100 kernel weight (Kwaga 2013) and pod yield per plant (Venkatesh *et al.* 2015). These traits had also exhibited highly significant and strong positive association with kernel yield per plant. High direct effects of these traits are the main factor for their strong association with kernel yield per plant. Hence, these traits should be considered as important selection criteria in all groundnut improvement programmes and direct selection for these traits is recommended for kernel yield improvement. Although, SLA and free proline content had high positive direct effects on kernel yield per plant. Yet there non-significant association with it indicated the need for adoption of restricted simultaneous selection model to nullify the undesirable indirect effects while ending use of the high direct effects.

Although non- significant, at high negative direct effects were noticed for days to 50 per cent flowering and haulm yield per plant on kernel yield per plant which

Table 3. Phenotypic (P_p) and genotypic (P_g) path analysis for kernel yield in groundnut over seasons

Character	p	Days to 50% flowering	Pods per plant	Pod yield per plant (g)	Mature kernel (%)	100 kernel weight (g)	SPAD chlorophy ll meter reading	Specific leaf area	Haulm yield per plant (g)	Oil content (%)	Protein content (%)	Free proline content (%)	Correlation with Kernel yield per plant
Days to 50% flowering	p_p	**-0.3027**	0.1305	0.2243	0.0084	0.1042	-0.0019	-0.0085	-0.0029	0.0959	-0.0029	0.0115	0.2560
	p_g	**-0.3477**	0.1925	0.4409	0.0739	0.1262	-0.0340	-0.0742	-0.0234	0.0428	-0.0227	-0.0966	0.2776
Pods per plant	p_p	0.0625	**0.4313**	0.2102	-0.0274	0.1084	-0.1145	-0.0210	-0.1650	-0.0511	-0.0757	-0.0063	0.3515*
	p_g	0.1854	**0.4505**	0.2019	-0.0593	0.2250	-0.1802	-0.0447	-0.1885	-0.1215	-0.0918	-0.0046	0.3724*
Pod yield per plant (g)	p_p	-0.0992	0.1457	**0.7017**	-0.0544	0.1563	-0.1167	0.0624	-0.0970	-0.1770	0.0694	0.0704	0.6617**
	p_g	0.1516	0.2734	**0.7184**	-0.0693	0.2395	-0.1863	-0.1032	-0.1661	-0.2219	0.0978	0.0996	0.8336**
Mature kernel	p_p	0.0095	0.1252	0.1945	**-0.0322**	0.1190	-0.0111	-0.0083	0.0057	-0.0378	-0.0046	0.0028	0.3627*
	p_g	0.0238	0.1505	0.1973	**-0.0796**	0.0971	-0.0953	-0.0174	0.1574	-0.1002	0.0498	0.0025	0.3859*
100 kernel weight(g)	p_p	-0.0064	0.1154	0.2388	0.0024	**0.3281**	-0.1758	0.0166	-0.1142	0.0432	-0.0531	-0.0025	0.3925*
	p_g	-0.0218	0.1568	0.2445	0.0296	**0.3339**	-0.1566	0.0192	0.0599	-0.1658	-0.0900	-0.0017	0.4080*
SPAD chlorophyll Meter Reading	p_p	-0.0546	0.1459	0.1694	0.0052	0.0180	**0.0399**	-0.0427	0.0335	-0.0404	0.0877	0.0002	0.3621*
	p_g	0.0798	0.2025	0.3129	0.0130	0.2611	**0.0582**	-0.0286	-0.4394	-0.1509	0.2996	-0.0017	0.6066**
Specific leaf area	p_p	0.0187	0.0550	0.0672	0.0032	0.0184	-0.0399	**0.3099**	-0.0534	-0.0481	-0.0532	0.0011	0.2790
	p_g	0.0353	0.1718	0.2082	0.0118	0.0785	-0.0783	**0.3180**	-0.1751	-0.0697	-0.1789	0.0001	0.3216
Haulm yield per plant(g)	p_p	-0.0005	0.1919	0.2212	0.0004	0.1534	-0.0012	-0.0033	**-0.3095**	0.0996	-0.0912	-0.0012	0.2596
	p_g	0.0223	0.2275	0.2952	0.0446	0.2363	-0.2152	-0.2023	**-0.4125**	0.2148	0.0745	-0.0008	0.2843
Oil content (%)	p_p	-0.0274	0.1156	0.2104	-0.0078	-0.0261	-0.0916	0.1167	0.0032	**-0.0134**	0.0919	0.0001	0.3717*
	p_g	0.1618	0.2531	0.2892	0.0629	0.1701	0.2156	-0.9113	0.2517	**-0.0575**	0.1647	-0.0004	0.5998**
Protein content (%)	p_p	-0.0113	0.1877	0.2103	0.0014	0.0803	-0.0598	-0.0943	-0.0032	0.0643	**-0.0104**	-0.0075	0.3575*
	p_g	-0.0110	0.3458	0.2326	0.0032	0.1725	-0.0677	-0.0800	-0.2570	0.0551	**-0.0196**	0.0034	0.3772*
Free proline content(%)	p_p	-0.0526	0.0384	0.1157	-0.0733	0.0076	-0.0701	-0.0895	-0.0962	-0.0751	-0.0911	**0.3104**	-0.0757
	p_g	-0.0073	-0.1102	0.1355	-0.0209	0.0299	-0.0001	-0.2813	0.0167	0.0000	-0.1905	**0.3186**	-0.1097

*, ** Significant at 5% and 1% levels, respectively, p_p= Phenotypic path coefficient, p_g= Genotypic path coefficient, Phenotypic residual effect= 0.5300, Genotypic residual effect= 0.5967

indicating a major role of indirect effects. Kernel yield per plant is mostly influence by pod yield per plant, pods per plant and 100 kernel weights. These findings are in agreement with those of Venkatesh *et al.* (2015) for mature kernel per cent and SCMR and Pavan Kumar *et al.* (2014) for oil and protein content. Thus, pod yield per plant, pods per plant and 100 kernel weightscould be used as the effective selection criteria for enhancing of kernel yield per plant in groundnut.

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