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Variation in Traits Related to Water use Efficiency and Pod Yield in Groundnut (*Arachis hypogaea* L.) Mapping Population

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Abstract Two fifty water use efficient recombinant inbred lines of cross GKVK 4 × NRCG 12473 of groundnut were evaluated for genetic parameters viz., variability, heritability and genetic advance as percent of mean. The estimates of GCV and PCV were high for pod yield per plant, kernel yield per plant, number of pod per plant and specific leaf area surrogate trait of water use efficiency. High heritability coupled with high genetic advance as percent of mean was noticed for number of pod per plant, kernel yield per plant, plant height, specific leaf area, sound mature kernel percent and pod yield per plant. This indicates that these traits are mainly governed by additive gene action and responsive to selection. Therefore, it would be rewarding to lay due emphasis on the selection of these characters for rapid improvement genotypes with high water use efficiency and pod yield. Based on the mean performance of the RILs viz., 1647-4-8, 1642-1-9, 1625-8-3, 1348-6-6, 1586-6-1, 1570-5-1, 1026-6-10, 1008-9-15, 1663-4-8, 1326-2-2, 1035-3-4, 1036-1-3, 1085-10-9, 1040-14-2, 1089-11-3 and 1037-12-11 could be considered as elite genotypes for improving groundnut genotypes with high pod yield and high WUE under moisture stress/rainfed condition or can be used as parents in hybridization for the improvement of pod yield in Groundnut.

Keywords Water use efficiency, SLA, SCMR, RILs, Groundnut.

Introduction

Groundnut (*Arachis hypogaea* L.) is a leguminous plant of high nutritional value and is a protein and energy source in developing regions; it produces high quality oil, is rich in essential fatty acids, as well as in the vitamin E, B_1 and B_2 and has an easy digestibility. Gorundnut is grown under rain-dependent production conditions in India. Due to erratic rainfall and frequent drought, and also lack of high yielding adapted cultivars, groundnut yields are gradually low

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and unstable under rain-dependent conditions. Though, groundnut is known for its relative ability to withst and periods of water limited conditions still produce biomass and kernels requires thorough investigations to increase water use efficiency (WUE), to assure sustained food security for the benefit of resource poor farmers in the semi-arid regions. Therefore, sustaining crop productivity under water limited conditions is most important aspects that needs to be addressed immediately.

Water Use Efficiency is one such important trait which is correlated with Specific Leaf Area (SLA), Soil Plant Analysis Development (SPAD) Chlorophyll Meter Reading (SCMR), Carbon Isotopic Discrimination ($\Delta\ ^{13}C$) and transpiration efficiency ($\delta\ ^{18}O$) and these traits have been suggested as surrogate traits in selecting for WUE in groundnut. $\Delta^{13}C$ and SLA are inversely related to WUE and yield. SCMR and $\delta\ ^{18}O$ are positively related to yield and WUE [1].

For effective selection for high yielding Water Use Efficient genotypes, knowledge on genetic parameters such as genetic variability, heritability, genetic advance is essential. Genetic variability for trait of interest in any breeding material is a pre-requisite as it provides basis for selection. The present study has been undertaken to determine the estimates of variability, heritability and genetic advance for physiological traits related to Water Use Efficiency, pod yield associated parameters in F_8 recombinant inbred line populations of cross GKVK 4 × NRCG 12473 in groundnut.

Materials and Methods

The material for the present investigation comprised of 250 water use efficient F_8 recombinant inbred line (RIL) population of groundnut grown in 30 × 10 augmented design during *rabi*/summer 2015 at the Ghandhi Krishi Vigyan Kendra, University of agriculture sciences, Bangalore representing the Southern region of Karnataka. Observations were recorded on five randomly selected plants in each RIL on plant height (PH), number of branches per plant (NB/P), days to 50% flowering (DFF), number of pods per plant (NP/P), pod yield per plant (PY/P), shelling percentage (SH %), kernel yield per plant (KY/P), sound mature kernel percentage (SMK %), traits related to water use efficiency (WUE) viz., SPAD chlorophyll meter reading (SCMR) and Specific leaf area (SLA). Genotypic and phenotypic co-efficient of variation were computed according to the formula suggested by Burton and Devane [2]. Heritability in broad sense was computed by the formula as suggested by Lush [3]. Genetic advance was calculated as per the formula given by Johnson et al. [4]. The elite water use efficient genotypes were identified based on their mean performance along with the checks for the characters governed by additive genes.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the existence of sizable variability for all the characters and considerable improvement can be achieved in these characters by simple selection. However, analysis of variance by itself is inconclusive in explaining all the inherent genetic variability among the RILs. Hence, actual variance has to be estimated for the characters to know the extent of existing variability. The mean, range, standardised range, coefficients of genotypic and phenotypic variation, heritability and genetic advance of various characters are given in the Table 1. The range of variation was quite high in F_8 RILs suggesting that this trait may be improved by individual plant selection. The estimates of standardised range was high in F_8 RILs acress traits provide clues about the occurrence of genotypes with extreme expression. Magnitude of variation was found to be high for specific leaf area, days to 50 flowering, plant height, number of branches per plant, number of pod per plant, pod yield per plant, kernel yield per plant, shelling percentage, sound mature kernel percentage and SPAD chlorophyll content. Presence of high variability for these characters were in agreement with the results obtained by Nandini et al. [5], Savita et al. [6] and Anusha and Savithramma [7].

The phenotypic co-efficient of variability (PCV) and genotypic co-efficient of variability (GCV) estimates were relatively high for specific leaf area, num-

Table 1. Genetic variability parameters for growth, traits related to WUE, yield and its component traits in F_8 recombinant inbreed line population of the cross GKVK 4 × NRCG12473 in groundnut.

Characters	Mean	Range		Standardized range	GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)
		Min	Max					
SCMR	42.27	29.50	53.60	0.57	9.24	9.75	89.83	18.03
SLA (cm^2/g)	137.38	44.16	252.12	1.62	18.59	18.97	96.62	43.73
DFF	39.10	32.00	47.00	0.38	6.25	8.67	52.58	9.27
PH (cm)	37.00	18.00	43.00	0.68	13.03	15.16	72.56	23.34
NB/P	6.40	2.00	10.00	1.56	29.03	38.51	56.81	45.07
NP/P	17.50	4.30	39.60	2.02	29.95	33.72	78.79	54.76
SH (%)	55.50	26.00	76.00	0.90	12.02	16.65	53.70	18.41
SMK (%)	59.76	28.26	90.74	1.05	22.33	23.29	79.33	32.03
KY/P (g)	6.37	0.68	22.40	1.84	37.09	40.11	85.49	70.65
PY/P (g)	19.83	3.00	38.95	1.72	28.73	31.21	85.07	54.53

ber of branches per plant, kernel yield per plant, pod yield per plant and number of pods per plant. These findings are in accordance with the reports of Suvarna et al. [8], Gopinath Jatti et al. [9], John et al. [10] and Anusha and Savithramma [7]. The PCV and GCV estimates were moderate for plant height, shelling percentage and sound mature kernel percentage. Moderate PCV and GCV estimates for shelling percentage and sound mature kernel percentage has also been reported by Nandini et al. [5] and Savita and Savithramma [11]. Low GCV and PCV values obtained in the present study for SPAD chlorophyll meter reading and days to 50% flowering are accordance with the result of Nandini et al. [5] and Savita and Savithramma [11]. The high magnitude of genotypic coefficient of variation further revealed greater extent of variability present in these characters, thereby suggesting good scope for improvement through selection. Low values of genotypic coefficient of variation indicated the need to create variability either by hybridization or mutation followed by selection.

High heritability estimates have been obtained for pod yield per plant followed by kernel yield per plant, sound mature kernel percentage, number of pods per plant, specific leaf area, plant height, oil content and pod yield per plant indicating that they are least influenced by the environment. These results are in accordance with reports of Golakia et al. [12] and Nandini et al. [5] Alan Cruickshan et al. [13]. Veeramani et al. [14] reported high broad sense heritability for pod and kernel yield and John et al. [10] reported high heritability for sound mature kernel percentage along with kernel yield and pod yield in groundnut. On the contrary, moderate to low heritability estimates is being reported Suvarna et al. [8] for these characters. Days to 50% flowering, number of branches per plant and shelling percentage showed moderate heritability estimates, indicating substantial influence of environment on these characters. These results are in accordance with the reports of Nandini et al. [5] and Savita and Savithramma [11].

Heritability is a measure of the genetic relationship between parents and progeny and widely used in determining the degree to which a character may be transmitted from parents to off-springs. Heritability value along cannot provide information on the amount of genetic progress that would result from selection of best individuals [9]. Jonson et al. [4] reported that heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selecting the best individuals. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in the selection program for better efficiency in the selection.

High heritability coupled with high genetic advance as percent of mean has been noticed for the characters specific leaf area, number of pods per plant, pod yield per plant, plant height, sound mature kernel percentage and kernel yield per plant indicated the presence of lesser environmental influence and preva-

Table 2. Superior RILs with high WUE, pod yield and related attributes selected in F_8 recombinant inbred lines of the cross GKVK 4 × NRCG 12473 in groundnut.

RILs	SCMR	SLA (cm^2/g)	NP/P	SH (%)	SMK (%)	KY/P (g)	PY/P (g)
1647-4-8	42.70	132.77	25.60	64.58	78.75	17.23	26.68
1642-1-9	40.50	152.10	26.60	65.86	74.36	18.23	27.68
1625-8-3	46.90	145.64	35.60	74.24	81.00	27.23	36.68
1348-6-6	48.80	160.85	31.20	70.72	75.00	22.83	32.28
1586-6-1	49.10	139.72	28.80	68.37	79.62	20.43	29.88
1570-5-1	49.90	145.48	22.80	60.43	72.16	14.43	23.88
1026-6-10	47.00	144.05	23.50	61.55	69.99	15.13	24.58
1008-9-15	42.90	147.08	22.80	60.43	67.72	14.43	23.88
1663-4-8	43.10	140.88	24.00	62.32	70.00	15.63	25.08
1326-2-2	43.10	156.55	28.00	67.50	78.70	19.63	29.08
1035-3-4	44.50	157.55	27.20	66.58	75.47	18.83	28.28
1036-1-3	40.30	144.89	27.00	66.35	80.10	18.63	28.08
1085-10-9	42.90	153.72	28.60	68.16	72.97	20.23	29.68
1040-14-2	41.60	159.80	29.20	68.79	80.30	20.83	30.28
1089-11-3	43.00	159.14	31.40	70.91	75.00	23.03	32.48
1037-12-11	41.60	145.52	31.60	71.08	79.67	23.23	32.68
Mean ± SE	41.06±0.28	159.01±1.86	16.82±0.45	54.37±0.58	64.61±0.83	12.45±0.16	22.9±0.22
GKVK-4 (PI)	41.39	139.73	18.12	60.35	67.33	14.75	21.20
NRCG 12573 P2)	42.37	155.40	17.06	52.23	60.92	9.69	14.14
TMV-2**	40.65	118.33	18.40	51.49	57.05	10.03	19.48
KCG-2*	43.73	114.72	17.28	68.11	66.93	12.91	20.36

lence of additive gene actions in their expression. These results were in accordance with Nandini et al. [5] and Savita and Savithramma [11]. High heritability coupled with moderate genetic advance as percent reported for SPAD chlorophyll meter reading. This moderate value may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters and selection differential is always constant. Moderate heritability and genetic advance as percent of mean observed for shelling percent. Moderate heritability coupled with low GAM observed for days to 50% flowering in the present study, which indicated considerable influence of environment apart from non-additive gene action.

Higher heritability coupled with high genetic advance revealed the presence of lesser environmental influence and prevalence of additive gene action in their expression. But lower values of genetic advance indicated the prevalence of narrow range of variability, high G × E interaction or non-additive gene action. For moderate values of genetic advance, both additive and non-additive gene action might be responsible for the expression. High estimates of heritability along with high genetic advance provides good scope for further selection and stabilising the superior RIL genotypes.

The data on the mean performance of the water use efficient RILs for the characters governed by additive genes are given Table 2. The 1647-4-8, 1642-1-9, 1625-8-3, 1348-6-6, 1586-6-1, 1570-5-1, 1026-6-10, 1008-9-15, 1663-4-8, 1326-2-2, 1035-3-4, 1036-1-3, 1085-10-9, 1040-14-2, 1089-11-3 and 1037-12-11 exhibited superiority for traits related to WUE, pod yield and its related characters compared to the parents (GKVK 4 and NRCG 12473) checks (KCG 2 and TMV 2). Hence, these genotypes could be considered as elite genotypes for improving groundnut pod yield and high WUE under moisture stress / rainfed condition or can be used as parents in hybridization for the improvement of pod yield in Groundnut.

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