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Assessment of Genetic Variability and Correlation for Drought Tolerance-Related Traits Among Groundnut (*arachis hypogaea* l.) Lines

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Abstract

Development of drought resilient groundnut varieties is pertinent to mitigating the effects of climate change. This study was conducted to determine the genetic diversity of groundnut genotypes for drought-related traits and to assess the association among agronomic and drought-related traits. One hundred and sixty-nine groundnut lines were evaluated under water stress and well-watered conditions at two locations for two years. The trial was laid out using 13 x 13 alpha lattice design with two replications. Data were collected on specific leaf areas, SCMR, pod yield, haulm yield, biomass, harvest index and drought tolerance index of pod yield. Data collected was analysed using R statistical software. The best linear unbiased predictions (BLUPs) and variance components were estimated using the linear mixed model. The association between agronomic and drought-related traits was assessed using Pearson's correlation. Significant genetic differences ($p < 0.05$) were observed for agronomic and drought-related traits among the groundnut genotypes with 20% of the genotypes identified as drought tolerant indicating that progress can be made from selections for improvement of drought tolerance. There was significant positive correlation of pod yield with SCMR (0.44**), harvest index (0.72**) and drought tolerance index of pod yield (0.17*) under water stress indicating that selecting for the improvement of these traits would improve pod yield. The findings from this research suggest the existence of genetic variability and presence of significant association between pod yield and drought-related traits to enhance identification of superior drought tolerant genotypes to mitigate the effects of drought.

Keywords: Correlation, drought-tolerance, genetic variability

Introduction

The cultivated groundnut (*Arachis hypogaea* L.) also known as peanut is an annual herb which belongs to the family, Fabaceae (also known as Leguminosae) and sub-family Papilionaceae. Annual world production of groundnut is about 53.9 million tons with an average yield of 1.6 t ha^{-1} (FAOSTAT, 2023). Groundnut seeds are highly nutritious possessing oil (35 – 60%), protein (22 – 30%) (Desmae *et al*., 2018), carbohydrate (10 – 20%) and minerals such as Vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium (Varshney *et al*., 2013).

Drought is the major abiotic stress of groundnut as 90% of its production is under semi-arid tropics characterized by low and erratic rainfall (Hamidou *et al*., 2012). Groundnut is widely grown under rain fed conditions characterized by erratic rainfall especially in Asia and Africa (Ghosh *et al*., 2022). Water deficiency is known to reduce groundnut yield by 70% (Manjonda *et al*. 2018; Ghosh *et al*., 2022). Flowering and pod setting stages have been reported as most critical for water stress in groundnut (Xiong *et al*. 2016). Additionally, drought affects the inherent symbiotic nitrogen fixation capacity of crops, limiting grain yield and quality affecting the feed quality of the haulm such as its nitrogen content, digestibility and metabolizable energy (Blummel *et al*., 2012). The Food and Agricultural Organization of the United Nations estimates that by 2025 approximately 480 million people in Africa will be living in areas with limited water supply, and as climatic conditions deteriorate, 60 million hectares currently classified as moderately constrained will become severely limited (FAO, 2007). Ravi *et al*. (2011) reported a slow pace of variety development, release and adoption of drought-tolerant groundnut which could be attributed to the polygenic nature of drought tolerance and the effect of genotype by environmental interaction which drags selection gains. Breeding approaches using drought-related traits with high heritability values and low G × E interactions have been reported to indirectly improve the selection efficiency of superior drought-tolerant genotypes (Chen *et al*., 2013).

Therefore, there is a need to explore genetic diversity in plant resources to enable plant breeders develop new and improved cultivars with desirable characteristics (Bhandari *et al*., 2017; Terfa and Gurmu, 2020). Assessment of genetic variability for agronomic and drought-related traits and their association is essential to enhance the selection of drought tolerant lines. This study was designed to determine the genetic diversity for agronomic and drought-related traits in groundnut genotypes and to assess the association among agronomic and drought-related traits in groundnut.

Materials and methods

Assessment of variability for agronomic and drought-related traits

One hundred and sixty-nine groundnut genotypes obtained from the groundnut breeding unit of the Institute for Agricultural Research, Samaru were evaluated for drought tolerance across two locations for two years. The locations include the Institute for Agricultural Research (IAR) farm Samaru (northern Guinea savanna) and Minjibir (Sudan savanna) in Kano State during the dry seasons of 2018 and 2019.

Field evaluation

The 169 groundnut genotypes were subjected to two treatment conditions; well-watered and water stress at Samaru and Minjibir during the 2018 and 2019 dry seasons. Groundnut genotypes in each treatment were laid out using 13 x 13 alpha lattice design with two replications. The seeds of the groundnut genotypes were sown in the field at a spacing of 0.75 m between rows and 0.25 m between plants in a row. Plot size was a single 4 m row. The well-watered treatment received irrigation twice a week from sowing till maturity. The water stressed treatment on the other hand received regular irrigation until drought imposition at pod filling stage (terminal drought) after which no irrigation was applied.

Data were collected on the following agronomic and drought-related traits. Leaf area (cm^2) of the second fully expanded leaves detached from five randomly selected plants per plot was measured using a leaf area meter. Leaf weight was obtained by weighing the detached leaves after oven drying at 80^0C for at least 48 h. Specific leaf area which is the leaf area per unit leaf dry weight ($cm^2\ g^{-1}$) was obtained by dividing the area of leaves detached from five randomly selected plants per plot by their weight. Pod weight ($g\ plot^{-1}$) was measured as the weight of pods obtained from five randomly selected plants per plot after air drying for 1 week and this was used to estimate the pod yield ($kg\ ha^{-1}$). Haulm weight ($g\ plot^{-1}$): the shoot and root weight of five randomly selected plants per plot at harvest. Their pods were removed before taking the haulm weight. This was used to estimate the haulm yield ($kg\ ha^{-1}$). Biomass ($kg\ ha^{-1}$): this is the total yield of a plant was estimated as the total yield of pods and haulms.

$$Total\ biomass = Haulm\ yield + pod\ yield$$

Harvest Index was computed as the proportion of pods produced to the total biomass as follows:

$$Harvest\ Index = \frac{Pod\ yield}{Total\ biomass}$$

SPAD chlorophyll meter reading (SCMR) was measured on the second fully expanded leaves from five randomly selected plants on the field. SCMR was recorded using a TSA SPAD chlorophyll meter.

Statistical analysis of phenotypic data

Analysis of variance: The descriptive statistics (mean, range, standard error) and analysis of variance (ANOVA) were done using R statistical software (R Core team, 2021). The best linear unbiased predictions (BLUPs) and variance components were estimated using the linear mixed model (LMM) fitted by the Restricted/Estimated Maximum Likelihood method (REML, Corbeil and Searle (1976)) in R package “lme4” (Bates *et al*., 2015). In the analysis of variance for each test environment, the genotypes and blocks were considered fixed and random effects, respectively. Mean separation was undertaken using LSD at 5% level of probability. Rank summation index (SI) was used to select the best performing groundnut lines under water stress condition.

Estimates of coefficients of variation and heritability: The phenotypic and genotypic coefficients of variation and broad sense heritability were computed using the formulae given by Singh and Chaudhary (1985).

(a) Genotypic coefficient of variation (GCV %)= $\frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$

(b) Phenotypic coefficient of variation (PCV %) = $\frac{\sqrt{\sigma_{ph}^2}}{\bar{X}} \times 100$

$$\sigma_{ph}^2 = \sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_e^2}{lr}$$

Where, σ_{ph}^2 is the phenotypic variance, σ_g^2 is the genotypic variance and σ_{gl}^2 is the genotype × environment variance, σ_e^2 is the error variance, *l* is the number of environments, and r is the number of replications

Phenotypic coefficient of variation and GCV values of more than 20% were regarded as high, whereas values less than 10% were considered as low and values between 10% and 20% as moderate (Shukla *et al*., 2006).

Broad sense heritability was estimated using variance components from combined ANOVA across environments (Goncalves-Vidigal *et al*., 2008; Mulugeta *et al*., 2023) as follows:

$$H_b = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_e^2}{lr}} X\ 100$$

The broad sense heritability estimates were classified as low (0 – 30%), moderate (30 – 60%), and high (60% and above) (Mehari *et al*., 2015).

Correlation analysis: The association between agronomic traits across environments was investigated using Pearson's correlation. The correlations between phenotypic traits were computed using cor function in R environment (R Core Team 2021).

Results

Phenotyping of agronomic and drought-related traits in groundnut genotypes

The analysis of variance revealed significant genotype mean squares ($p < 0.05$) for all traits measured across environments except root length under water stress (Table 1). Significant differences in haulm yield, biomass and drought tolerance index of pod yield (DTI (PY)) were observed in the performance of genotypes in the different environments under water stress. Under well-watered condition, the genotypes showed significant variations for traits evaluated except for SPAD chlorophyll meter reading (SCMR). Furthermore, there was significant G × E interaction for pod yield, biomass, harvest index and root dry weight.

Wide range of variations were observed for agronomic and drought-related traits under water stress and well-watered treatments. Across environments, mean performance of groundnut genotypes for agronomic and drought-related traits under water stress condition are presented in Table 2. Pod yield was highest for 1CGV 176249 (1000.80 kg/ha) and lowest for ICG 98294 (146.37 kg/ha) with a mean of 525.80 kg/ha. Mean SLA was 125.40 cm/g and ranged between 89.22 cm/g for SAMNUT 21 and 194.84 cm/g for 1CGV 176249. SCMR had a mean of 25.97 and ranged from 20.33 for SAMNUT 26 to 31.23 for SAMNUT 24.

Table 1. Mean squares of agronomic and drought-related traits of groundnut lines evaluated under water stress and well-watered conditions across Samaru and Minjibir in 2018 and 2019

Source	Df	Specific leaf area	SCMR	Pod yield	Haulm yield	Biomass	Harvest index	Root dry weight	Root length	DTI (PY)
WATER STRESS										
Environment, E		3	65240.00**	1520.07**	19596711.00**	338502962.00**	347817487.00**	0.24**	4.58**	1.66
Replication (E)	4	43925.00**	100.77**	72442.00**	3527107.00**	2850313.00**	0.01*	4.69**	19.46*	0.04
Block (Replication × E)	24	0.00	1.58	1215.00	8861.00	27410.00	0.00	0.02	0.10	0
Genotype (G)	168	1165.00*	20.63**	171848.00**	1584430.00**	1273914.00**	0.02**	0.83**	3.07	0.07**
G × E	504	875.00	14.71	128661.00	1318928.00**	1282738.00**	0.01	0.63	3.75	0.06**
Error		926.9.00	13.84	13610.00	726400.00	459500.00	0.01	0.60	3.56	0.02
WELL WATERED										
Environment, E	3	57459.00**	984.34**	48183624.00**	173510934.00**	363064176.00**	2.25**	63.84**	13.56	
Replication (E)	4	11887.00**	200.42**	572743.00**	16153119.00**	14382681.00**	0.05	3.18*	40.41*	
Block (Replication)	24	84.81	0.49	1779.00	11480.00	2619.00	0.00	0.05	0.13	
Genotype, G	168	3236.00**	11.20	252683.00**	3075845.00**	3639922.00**	0.06*	1.43**	12.35	
G × E	504	2692.00	9.97	190679.00**	2578682.00	2863015.00**	0.05*	0.92*	11.16	
Error		2382.00	10.47	59550.00	2186000.00	2213000.00	0.04	0.73	10.26	

SCMR- SPAD chlorophyll meter reading, DTI (PY)- drought tolerance index of pod yield

Table 2. Mean performance of 10 best and 10 worst groundnut genotypes evaluated for agronomic and drought-related traits under water stress at Samaru and Minjibir in 2018 and 2019

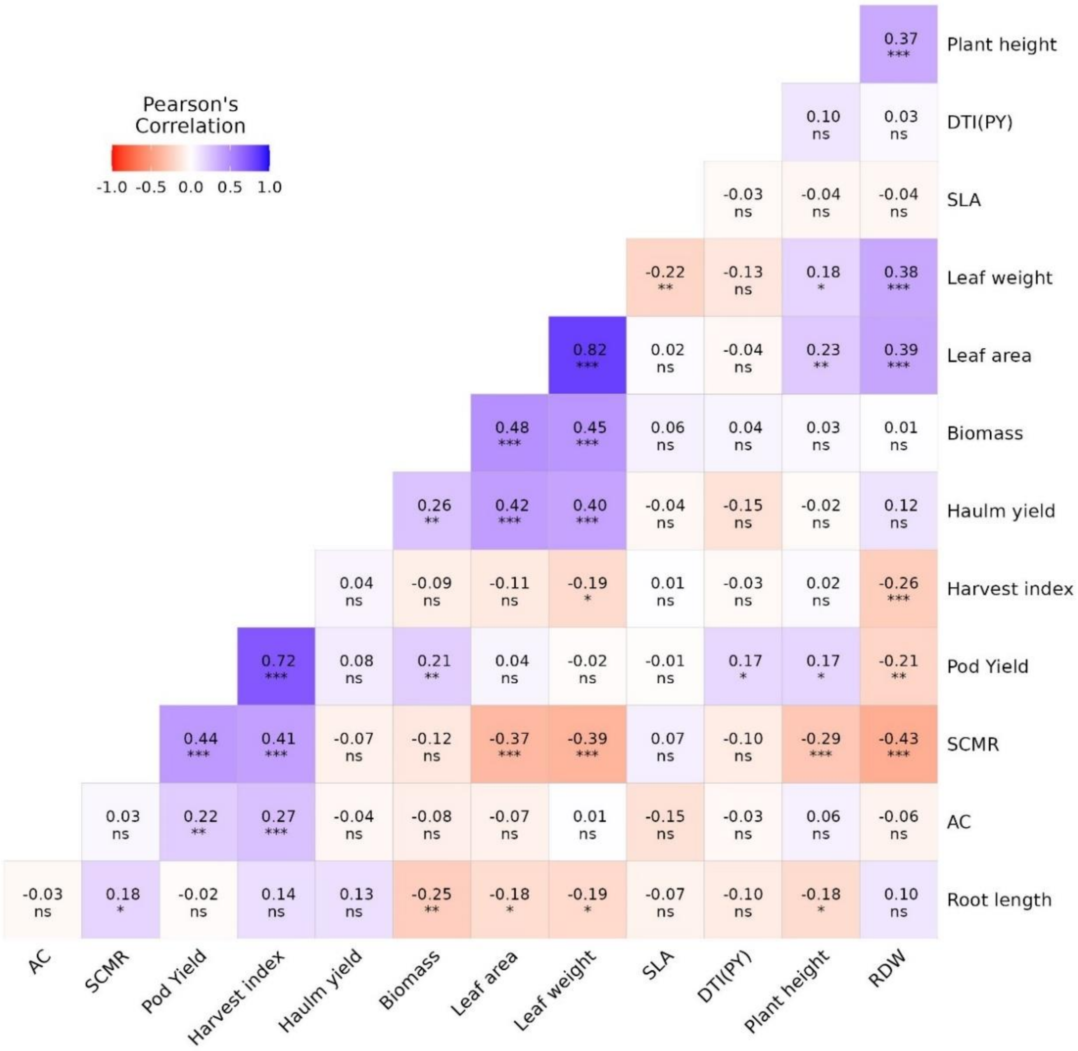
Designation	Pod yield (kg/ha)	SCMR	Specific leaf area (cm/g)	Haulm yield (kg/ha)	Biomass (kg/ha)	Harvest index	Plant height (cm)	Root length (cm)	Root dry weight (g)	Drought tolerance index	Rank
Best 10											
ICGV 176249	1000.80	26.90	194.85	3748.44	4984.43	0.23	11.12	10.71	2.23	0.51	1
ICGV 176151	963.70	31.11	152.64	2227.58	2816.29	0.28	13.44	9.42	2.02	0.42	2
IARGM 1457	658.75	28.75	151.26	2097.42	2854.06	0.35	14.54	11.04	2.71	0.43	3
ICG 14630	705.34	27.68	130.91	3020.93	2961.49	0.24	9.81	11.99	2.61	0.55	4
ICG 4764	602.35	26.63	127.38	3094.38	3395.20	0.17	13.92	9.47	1.75	0.42	5
ICG 02148	566.21	26.73	139.08	2643.84	3302.31	0.25	9.70	10.98	2.01	0.74	6
ICGV-IS 07891	865.75	27.60	132.97	2095.81	2935.59	0.32	11.92	10.42	2.65	0.47	7
ICG 97183	400.04	27.15	138.53	2967.60	3829.57	0.10	16.54	11.84	2.20	0.57	8
ICGV 176505	935.42	26.46	130.17	1882.25	3239.29	0.27	13.03	9.83	2.42	0.56	9
ICGV 176365	548.78	25.70	139.15	3212.26	3773.44	0.12	16.06	10.44	2.81	0.41	10
Worst10											
ICGV 176017	539.52	25.43	116.36	1784.83	2335.84	0.17	9.56	9.82	2.04	0.25	154
ICG 12672	326.49	24.65	111.85	1751.07	2174.97	0.17	12.24	11.14	1.82	0.32	155
ICG 851	359.72	26.08	119.54	2098.13	2676.73	0.11	8.75	10.75	2.49	0.30	156
RS006F4B1-85	192.76	25.21	125.74	1617.47	2365.71	0.08	15.13	10.77	1.86	0.24	157
ICGV 176239	241.22	26.10	120.10	2694.48	2563.29	0.09	8.08	12.53	3.07	0.23	158
ICGV-IS 07845	296.62	23.55	141.02	2104.77	2242.12	0.13	9.95	12.66	2.01	0.14	159
ICG 10474	283.76	23.67	137.61	2594.07	2440.76	0.06	8.95	10.51	1.82	0.20	160
ICG 93183	463.64	24.94	124.87	1524.69	2369.60	0.13	8.95	11.29	2.14	0.33	161
ICG 36	248.00	24.31	113.36	1962.75	2221.06	0.11	10.11	10.44	1.96	0.19	162
ICG 5755	195.99	21.39	121.62	1683.74	2160.50	0.10	8.85	10.29	1.73	0.15	163
Mean	525.80	25.97	125.36	2328.94	2885.00	0.17	11.43	10.93	2.18	0.39	
SE	222.66	2.67	5.86	876.64	1099.00	0.04	0.32	0.32	0.08	0.09	

Coefficients of variation and heritability of agronomic and drought-related traits

The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all measured traits as presented in Table 3. Low (<10%) to moderate (10 - 20%) genotypic coefficient of variation was observed for agronomic and drought-related traits under the water conditions. GCV was highest for harvest index under water stress (18.37%) and well watered (19.24%) conditions. The phenotypic coefficient of variation varied from 8.64% for SCMR to 37.10% for DTI (PY) under water stress. While phenotypic coefficient of variation ranged from 7.16% for SCMR to 50.42% for harvest index under well watered condition. Heritability estimates were moderate (30 - 60%) for SCMR and harvest index under water stress. Low (< 30%) heritability estimates were exhibited for SLA, SCMR, pod yield and haulm yield under both conditions. However, moderate (30 - 60%) heritability was observed for root dry weight under well watered condition.

Pearson's correlation analysis

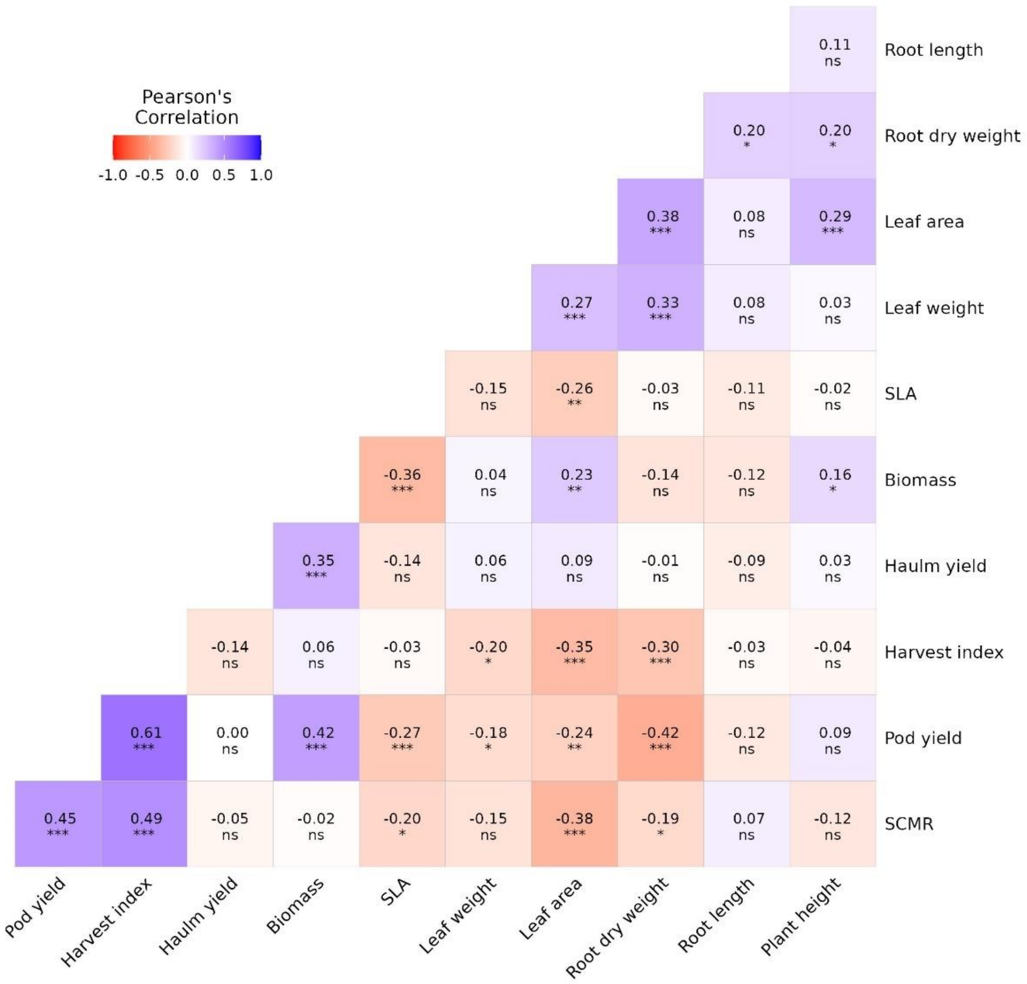
Significant correlations were observed for pod yield with SCMR, harvest index, and drought tolerance index under water stress. Specifically, harvest index showed a highly significant ($p < 0.01$) positive correlation (0.72**) with pod yield, followed by SCMR (0.44**) and biomass (0.21*) as shown on Figure 1. Similarly, pod yield was positively correlated with harvest index (0.61**), SCMR (0.45**) and biomass (0.42**) under well watered condition (Figure 2). However, significant negative correlations were observed between SLA and SCMR (r= -0.20**) as well as pod yield (r = -0.27**) under well watered condition. Among the drought surrogate traits (SLA and SCMR) for water use efficiency, SCMR had higher correlation with pod yield.



	AC	SCMR	Pod Yield	Harvest index	Haulm yield	Biomass	Leaf area	Leaf weight	SLA	DTI(PY)	Plant height	RDW
Plant height												0.37 ***
DTI(PY)											0.10 ns	0.03 ns
SLA										-0.03 ns	-0.04 ns	-0.04 ns
Leaf weight									-0.22 **	-0.13 ns	0.18 *	0.38 ***
Leaf area								0.82 ***	0.02 ns	-0.04 ns	0.23 **	0.39 ***
Biomass							0.48 ***	0.45 ***	0.06 ns	0.04 ns	0.03 ns	0.01 ns
Haulm yield						0.26 **	0.42 ***	0.40 ***	-0.04 ns	-0.15 ns	-0.02 ns	0.12 ns
Harvest index					0.04 ns	-0.09 ns	-0.11 ns	-0.19 *	0.01 ns	-0.03 ns	0.02 ns	-0.26 ***
Pod Yield				0.72 ***	0.08 ns	0.21 **	0.04 ns	-0.02 ns	-0.01 ns	0.17 *	0.17 *	-0.21 **
SCMR			0.44 ***	0.41 ***	-0.07 ns	-0.12 ns	-0.37 ***	-0.39 ***	0.07 ns	-0.10 ns	-0.29 ***	-0.43 ***
AC		0.03 ns	0.22 **	0.27 ***	-0.04 ns	-0.08 ns	-0.07 ns	0.01 ns	-0.15 ns	-0.03 ns	0.06 ns	-0.06 ns
Root length	-0.03 ns	0.18 *	-0.02 ns	0.14 ns	0.13 ns	-0.25 **	-0.18 *	-0.19 *	-0.07 ns	-0.10 ns	-0.18 *	0.10 ns

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Figure 1. Correlation coefficients of agronomic traits across four environments under water stress condition. Blue color indicates a positive relationship and red indicates a negative relationship between traits.



	Pod yield	Harvest index	Haulm yield	Biomass	SLA	Leaf weight	Leaf area	Root dry weight	Root length	Plant height
Root length										0.11 ns
Root dry weight									0.20 *	0.20 *
Leaf area								0.38 ***	0.08 ns	0.29 ***
Leaf weight							0.27 ***	0.33 ***	0.08 ns	0.03 ns
SLA						-0.15 ns	-0.26 **	-0.03 ns	-0.11 ns	-0.02 ns
Biomass					-0.36 ***	0.04 ns	0.23 **	-0.14 ns	-0.12 ns	0.16 *
Haulm yield				0.35 ***	-0.14 ns	0.06 ns	0.09 ns	-0.01 ns	-0.09 ns	0.03 ns
Harvest index			-0.14 ns	0.06 ns	-0.03 ns	-0.20 *	-0.35 ***	-0.30 ***	-0.03 ns	-0.04 ns
Pod yield		0.61 ***	0.00 ns	0.42 ***	-0.27 ***	-0.18 *	-0.24 **	-0.42 ***	-0.12 ns	0.09 ns
SCMR	0.45 ***	0.49 ***	-0.05 ns	-0.02 ns	-0.20 *	-0.15 ns	-0.38 ***	-0.19 *	0.07 ns	-0.12 ns

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Figure 2. Correlation coefficients of agronomic traits across four environments under well watered condition. Blue color indicates a positive relationship and red indicates a negative relationship between traits.

Table 3. Estimates of variance components and broad sense heritability of drought-related traits of groundnut genotypes evaluated under water stress and well watered conditions across Samaru and Minjibir in 2018 and 2019

	Trait	Genotype × environment variance (σ_{gl}^2)	Genotypic variance (σ_g^2)	Error variance (σ_e^2)	Phenotypic variance (σ_p^2)	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)
Water stress	Specific leaf area	0.44	42.10	113.63	156.17	5.18	9.97	26.96
	SCMR	0.11	1.56	1.74	5.25	4.95	9.06	30.00
	Pod yield	21632.50	5965	1812.50	29410	14.69	32.62	20.28
	Haulm yield	55014.75	42055.00	107548.50	204618.25	8.81	19.43	20.55
	Biomass	638.75	17008.00	115170.80	132817.55	4.52	12.63	12.81
	Harvest index	0.02	0.01	0.03	0.00	18.37	31.88	33.19
	DTI (PY)	0.01	0.01	0.00	0.02	15.38	37.10	17.20
	Root length	0.02	0.00	0.43	0.89	0.00	8.64	0.00
	Root dry weight	0.00	0.05	0.08	0.21	10.73	21.04	26.00
Well watered								
	Specific leaf area	14.40	56.14	310.75	381.29	5.53	14.40	14.72
	SCMR	0.00	0.20	1.30	2.81	1.93	7.16	7.26
	Pod yield	17985.75	7210.00	8000.00	33195.75	11.43	24.53	21.72
	Haulm yield	42395.25	97510.00	274480.00	414385.25	7.88	16.24	23.53
	Biomass	236151.00	129065.00	287359.25	475462.00	7.63	14.65	27.15
	Harvest index	0.01	0.00	0.06	0.07	19.24	50.42	14.56
	Root length	0.67	0.30	1.27	3.18	4.96	16.20	9.39
	Root dry weight	0.08	0.14	0.09	0.36	13.91	22.63	37.80

SCMR-SPAD Chlorophyll meter reading; DTI (PY) - drought tolerance index of pod yield; SCMR-

Discussion

Significant variation observed for measured traits indicated that adequate genetic variability existed among the genotypes. Similar findings in groundnut evaluated under water stress was reported by Salunke *et al*. (2018) and Abady *et al*. (2021). The significant G × E interaction observed for pod yield, haulm yield, biomass and harvest index showed that the genotypes performed differently with respect to these traits in the different environments. This implies that the traits are unstable across environments and the need to develop genotypes for specific environments. The non-significant G × E interaction for SCMR and SLA indicated their stability across environments under both water regimes and similar findings were also reported by Abady *et al*. (2021) to corroborate this submission. This indicates their reliability for utilization as surrogate traits for drought tolerance.

The GCV provides a measure for determining the extent of genetic variability in different traits and scope for genetic improvement. The difference between PCV and GCV values observed for measured traits indicate the influence of environment on the expression of these traits. Pod yield and harvest index with moderate GCV under water stress have higher potential response to selection which is essential for crop improvement than traits with low GCV. Similarly, Ali *et al.* (2020) reported moderate GCV for pod and seed yield under water stress. Results from this study also implied that selection would be less effective for traits like root length, biomass, SCMR and SLA which had low GCV estimates. There are conflicting reports in the literature concerning variability for drought-related traits under water stress condition. Pothula and Nadaf (2016) also reported low GCV estimates for drought-related traits under drought stress. In contrast, high GCV estimates were reported by Painawadee *et al*. (2009).

The information on the heritability and the relationship among the characters is important for plant breeders to formulate appropriate breeding strategies (Thakur *et al*., 2013). Moderate to high heritability estimates observed for SCMR under water stress in this study indicate that significant progress can be made for the improvement of this traits in early generations. On the other hand, the low heritability for pod yield and root dry weight indicated low genetic control and implies that direct selection in early generations for these traits may not be effective for crop improvement. Low heritability estimates for pod yield obtained under water stress are contrary to the findings of Ali *et al.* (2020). Recurrent selection was reported to be a powerful means of accumulating favorable alleles in a population and is the best method for improving traits with low heritability (Pereira de Castro *et al*., 2023).

Significant association of pod yield with SCMR, harvest index and biomass indicate the importance of these traits in determining pod yield under the two water regimes and the possibility of improving pod yield by selecting for these traits. Similarly, Abady *et al*. (2021) reported significant correlation of pod yield with harvest index and biomass. The positive relationship between pod yield and SCMR indicated that maintenance of photosynthesis rate under water stress due to the maintenance of high chlorophyll content would lead to increase in pod yield. Similar results were reported by Falke *et al.* (2019). The ability to maintain chlorophyll density under water stress conditions has been suggested as a drought tolerance mechanism in groundnut (Jongrungklang *et al*., 2008; Mamadou *et al*., 2017). Drought surrogate traits with low G × E interaction such as SLA and SCMR observed in this study are more reliable indices for selection under water stress conditions across multiple environments. These traits were recommended for the selection of drought tolerant genotypes (Nageswara Rao *et al*., 2001; Songsri *et al*., 2008).

Significant negative correlation observed between SLA with pod yield and SCMR under well watered condition shows that genotypes with higher pod yield and SCMR had lower SLA. Similar findings were reported by Salunke *et al*. (2018). Possession of small transpiration area evidenced by small leaves and plant body was suggested as an adaptive mechanism to reduce water loss to avoid drought effects (Blum, 2005; Yildrim and Kaya 2017). Nigam and Aruna (2008) suggested the selection of genotypes with high SCMR and low SLA for use as parents in drought resistance breeding programmes.

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Conclusions

Significant genetic differences ($p < 0.05$) were observed for agronomic and drought-related traits among the groundnut genotypes with 20% of the genotypes identified as drought tolerant indicating that progress can be made from selections for improvement of drought tolerance in groundnut. There was significant positive correlation of pod yield with SCMR (0.44**), harvest index (0.72**) and drought tolerance index of pod yield (0.17*) under water stress indicating that selecting for the improvement of these traits would improve pod yield.

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