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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN F_8 ADVANCED BREEDING LINES OF GROUNDNUT (*Arachis hypogeaea* L.)

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Abstract

Genetic variability is a basic requirement for crop improvement as this provides wider scope for selection. The effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable. The pesent experiment was conducted to study the variability in F_8 advanced breeding lines of groundnut across four environments in the savannah ecological zone of Nigeria. Twenty three advanced breeding lines were evaluated using a randomized complete block design during 2012/13 rain season in each zone. Analysis of variance was carried out for all the traits under study using SAS computer software. The results showed highly significant (P <0.10) variation among genotypes, location and genotype x location interaction (GLI) for all traits. Significant GLI suggested that the linear function of additive environmental effects was reflected by the change in ranking order of genotypes under varying environmental conditions. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits studied, which suggested the presence of environmental influence to some degree in the phenotypic expression of the traits. Pod weight per plant had the highest PCV (24.88%) and GCV (22.85 %). The estimates of broad sense heritability (H^2) were observed to be high (63.26-84.33) for all the traits. High heritability estimate coupled with higher genetic advance (37.25) for pod weight per plant indicating that the character is controlled by additive genes and therefore further improvement is possible through selection.

Keywords: *PCV, GCV, Heritability and Genetic Advance as percent of mean, Groundnut*

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a major annual oilseed legume crop in Africa valued as a rich source of protein, minerals and vitamins. Nigeria ranks the highest in groundnut production in Africa with an area of 2.63 million hectares and a production of 3.0 million tons during 2013 (FAOSTAT, 2014). The average groundnut yield in the country is low (less than 1 t/ha) compared to world average of above 2 tons ha^{-1}. The low productivity of the crop is ascribed mainly due to foliar diseases namely late leaf spot (causal organism: *Phaeoisariopsis personata* [(Berk. and Curt.) Deighton]), rust (causal organism: *Puccinia arachidicola* Speg.) and groundnut rosette disease (Padmaja, *et al.*, 2015). Late leaf spot and rust diseases often occur together and causeup to 50-70% of yield losses in the crop (Subrahmanyam *et al.*, 1985). Sporadic yield loss of 30% annually has been reported for groundnut rosette disease in Nigeria whose epidemics could result to total yield loss. Development of cultivars resistant/tolerant to these diseases could be effective in decreasing the production costs, improving production quality and quantity and reducing the detrimental effects of chemicals on our ecosystem.

For any crop improvement program, germplasm collection and assessment of genetic variability is an important step. The knowledge of nature and magnitude of variability available in the genotypes for different characters is an important prerequisite for making simultaneous selection over more number of characters to bring remarkable improvement in groundnut. Being a complex character, pod in yield in groundnut is influenced by a

number of yield and yield-attributing characters, environment and polygenes. Thus, the variability in the collections for these characters is the sum total of heredity effects of concerned genes and the influence of the environment. Hence, it is very essential to partition the observed variability into heritable and non-heritable components measured as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (H^2), genetic advance (GA), and genetic advance expressed as percent mean (GAM%).

Surveys of genetic variability using suitable parameters such as GCV, heritability estimates, and GAM are absolutely necessary to start an efficient breeding program (Atta *et al.,* 2008). Heritability value alone may not provide clear predictability of the breeding value. Heritability in conjunction with genetic advance over mean (GAM) is more effective and reliable in predicting the resultant effect of selection (Patil *et al.*, 1996; Ramanjinappa *et al.,* 2011). GAM is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.,* 2003).

Achieving a superior groundnut cultivar with satisfactory pod yield is an important objective for selection and further improvement. Thus, the present study was conducted to evaluate genetic variation for agronomic traits in 23 genotypes of groundnut.

MATERIALS AND METHODS

Study Site

The field experiment was carried out at the Institute for Agricultural Research (IAR) Samaru, Ahmadu Bello University Zaria, Nigeria ($11^0$06.69"N, $7^0$69'.96"E) and three other locations: Minna ($9^0$61.44"N, $6^0$56.62"N), Lafia ($8^0$48' 33"N, $8^0$51'67"E) and Markurdi ($7^0$72.97 "N, $8^0$53.64"E). The experimental material for the present study comprised of twenty three advanced breeding lines (F_8) of groundnut which were planted at four locations in a randomized complete block design with three replications. The description of these lines is presented in Table 1. In Samaru, planting was done on 23/6/, 2012, while Minna, Lafia and Markurdi plantings were carried out on 16/6/2012, 12/6/2012 and 02/05/2012, respectively. Plot size in each location is 0.25m x 0.75m x 2 rows as plot of 4 m in length. Foliar diseases were controlled by spraying calixin at the rate of 1 ml/litre. Other cultural operations including plant protection measures were followed as recommended practices for groundnut ensuring uniform and healthy crop. Observations on the traits of the breeding lines were recorded on 5 individual plants, randomly selected from each plot. Parameters considered for the present study were plant height (cm), days to maturity, number of mature pods per plant, pod weight (g) per plant, seed weight per plant, hundred seed weight, shelling percent, and haulm weight per plant.

Data Analysis

Data analysis was carried out for all the traits using SAS computer software. Heritability in the broad sense (H^2) was estimated according to Falconer (1989). In the present investigation two types of coefficient of variations were estimated viz., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) to compare the variations among the traits. They were computed as employed by Singh and Chaudhury (1985). Genetic advance (GA) and Genetic advance expressed as percentage of means (GAM %) were calculated using the procedure recommended by Singh and Chaudhury (1985) and Allard (1960). Correlations were estimated using the standard procedure suggested by Miller *et al.* (1958) and Kashiani and Saleh (2010) from the corresponding variance and covariance components.

RESULTS AND DISCUSSION

One of the components of the breeding programme of IAR is a replicated field experiment conducted over a range of environmental conditions. Each experiment is analyzed separately. In an experiment with crop plant, the assumption that the experimental error variance (σ_e^2) are the same in all environmental conditions is seldom attainable. In general this assumption will only hold if all experiments have been conducted in the same way, with the same amount of control over all environmental conditions and the experimental materials possess similar variability. Because of natural variability that often occurs within any piece of land the a *priori* expectation is that σ_e^2 would change from place to place (Cochran and Cox, 1957). It is assumed that heterogeneity of σ_e^2 would be due to variable environments in which the performance trials were conducted.

In this study, Cochran test of homogeneity of σ_e^2 was used on combined analysis of variance and the results indicated homogeneity for all the traits. For the four locations, and based on the results of Cochran test of homogeneity of σ_e^2, there was highly significant ($P < 0.01$) difference for genotype x location interactions for all the traits considered in this study (Table 2 and 3). Significant G x E interaction suggested the linear function of additive environmental effects (Mather and Jinks, 1982) and was reflected by the change in ranking order of the genotypes under varying environmental conditions. However, overall performance of the genotypes depends on the magnitude of genotype x environmental interaction.

The lack of consistent pattern in terms of significance of σ_{gl}^2 affirms the unpredictable nature of genotype x environmental interaction. Since σ_{gl}^2 was significant for all traits measured in this study, the genotype x location arose from distinct and exclusive conditions existing in a particular experiment. Furthermore, the presence of significant σ_{gl}^2 is indicative that stability and adaptability must be resorted to. The aim of the breeders must now be to breed for varieties stable and adaptable over predictive and un-predictive environmental variations.

The quantitative measurement of individual character provides the basis for an interpretation of different variability of parameters. The phenotypic variability which is observable includes both genotypic and environmental variation. It changes under different environmental conditions. Estimation of variance components for the nine characters studied is presented in Table 3. The highest variability (σ_p^2 and σ_g^2) was recorded for number of pod per plant (145.32 and 196.21) followed by pod weight per plant (73.71 and 87.41), respectively. The low values were observed for Seed weight (t/ha^{-1}) (0.05 and 0.07). This result clearly indicates that variation for the characters was not only due to genotypes but also due to influence of wide range of phenotypic (σ_p^2) and genotypic variance (σ_p^2) observed in the experimental material for all the traits studied implying that location played a significant role.

Mean pod yield of genotypes over environmental index ranged from 0.85 ton ha^{-1} in genotype (ICGX-SM99010/6/P_1/P_2) to 1.79 ton ha^{-1}in genotype (RS006F4B1-6) (Table 4). Genotype ICGX-SM99010/6/P_1/P_2 produced the highest pod yield over two location viz: 1.95 ton ha^{-1} at Samaru and 2.08 ton ha $^{-1}$ at location Lafia, and genotype also produced the highest pod yield over two location as follows: 2.00 ton ha^{-1} and 1.76 ton ha $^{-1}$ at Minna and Makurdi, respectively (Table 4). RS006F4B1-10 (B) has the second highest pod yield over environmental index with pod yield of mean pod yield of 1.69 ton ha^{-1}. The highest site mean yield (1.42 ton ha^{-1}) was recorded at Minna followed by Makurdi (1.34 ton ha^{-1}) and the lowest was at Lafia (1.14 ton ha-1). G

× L interaction makes it very difficult to choose variety (ies), and in most cases, it is not practical to recommend specific ones for each location. Therefore, further analysis is needed to simplify this interaction.

The analysis of variance in this study indicated the presence of significant difference among all the traits in the accessions. The heritable (genotypic) variation is usually masked by non-heritable variation creating difficulty in exercising selection. Hence it becomes necessary to partition overall variability into heritable and non-heritable components to enable the breeders to plan for proper breeding programme. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (PCV) were calculated for all the characters under study (Table 5). The PCV ranged from 8.23 % for shelling percentage to 26.42% for number of pod per plant. The highest PCV (26.42 %) recorded for number of pod per plant was followed by that of pod weight per plant (24.88%) and seed weight per plant 23.48%. GCV had a similar trend as PCV. The range varied from 6.54% for shelling percentage to 22.85% for pods weight per plant. The maximum GCV was observed for number of pods per plant (22.85 %) followed closely by pod weight per plant (22.74%), Seed weight per plant (t/ha^{-1}) (21.26%) and pod weight (t/ha^{-1}) (18.12%). Higher GCV estimates which were recorded for number of pod per plant, pod weight per plant (g) and total pod weight in ton ha^{-1} indicated the presence of significant genetic variability in these characters. Selection pressure can be applied on these traits to isolate promising genotypes. The estimates of GCV and PCV indicated that the values of the latter were always higher than that of the former suggesting the influence of environmental factors. Less difference observed between PCV and GCV in certain cases indicated greater role of genetic components and less influence by environment. Similar results were obtained by John *et al*. (2006), Ladole, *et al*. (2009) and Shinde *et al.* (2010). High GCV values indicate greater variability for a trait and that it can be improved through selection.

In a population, the observed variability is a combined measure of genetic and location, whereas the genetic variability is the only estimate heritable from generation to generation. However, a measure of heritability alone does not give an idea about the expected gain in the next generation but it has to be considered in conjunction with genetic advance. The traits which expressed high heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process. According to Panes and Sukhatme (1995) such traits were found to be governed by additive genes and had minimum location influence. The heritability estimates recorded in this study ranged from 63.26% for shelling percentage to 84.33% for pod weight per plant. According to Deshmukh *et al*. (1986) PCV and GCV values greater than 20% are regarded as high, whereas less than 10% are considered to be low and values between 10 – 20% to be medium. Based on this argument, all the traits recorded high heritability estimates with pod weight per plant depicting the highest (84.33%) estimates. High heritability with high genetic advance is an indication that selections may be effective for these populations. This indicates additive gene effects playing an important role in the expression of this trait. The finding of Vijayasekhar (2002) was in contrast with the findings of the present study. These results however, are in conformity with the findings of John *et al.* (2008) who reported high PCV and GCV for most agronomic traits in F_2 segregating populations of Spanish x Virginia crosses of groundnut. Mohitlal *et al.* (2004) reported high estimates of heritability and genetic advance as per cent of mean. The results indicate that, the traits are most likely governed by additive genes and had

contributed some positive alleles for increase expression of the traits. Hence, selections may be effective.

For efficient selection, we cannot completely depend on heritability alone. The combinations of high heritability with high genetic advance will provide a clear base on the reliability of that particular trait in selection of variable entries. The genetic advance expressed as percent of mean for traits studied ranged from 9.24 for shelling percentage to 37.25% for pod weight per plant. The highest genetic advance as percent of mean was recorded by pod weight per plant (37.25%) followed by number of pod per plant (34.74 %), seed weight per plant (g) (34.16 %) and pod weight (t/ha^{-1}) (28.76 %). The lowest value of 9.24 % was observed in shelling percentage.

High heritability coupled with high genetic advance as per cent of mean in all the populations, indicating that additive effects are substantial and environmental effects are small and hence, selection is effective. The results are in accordance with the findings of Khedikar (2008) who reported genetic advance as per cent of mean (18.58, 19.82) with high heritability (71.88, 74.41) were noticed in both the crosses (JL 24 × ICG 11337 and JL 24 × ICG 13919) for pod yield per plant. Similar results were reported by Sarvamangala (2009) and Dolma *et al.* (2010) for moderate estimates of PCV and GCV values for this trait. The results revealed that the traits are controlled by both additive and non-additive gene action. The correlations between pod yields with other traits are indicated in Table 6. Pod yield is the results of combine contribution of many traits which are independent. Breeders always look for variation among traits to select desirable genotypes. Some of the traits in this study had high association among themselves and with pod yield. The analysis of the relationships among these traits and their association with pod yield is essential to establish selection criteria (Singh, 1990).

Pod weight per plant had positive and significant correlation with number of pod per plant (0.623, $P < 0.01$), pod weight in ton ha-1 (0.804, $P < 0.01$), seed weight per plant (0.542, $P < 0.01$) and total seed weight in ton ha^{-1} (0.750, $P < 0.01$). This indicates that genotypes with high magnitude for these traits are high yielding. Similarly, days to maturity had positive and significant correlation with 100 – seed weight (0.610, $P > 0.01$) which implies that selection for late maturing genotypes may improve 100 – seed weight. Generally, positive and significant association of pairs of traits justify the possibility of correlated response to selection

CONCLUSIONS

From the results of the present study, it can be concluded that direct selection can be done for most of the yield attributing traits since they exhibited high genetic variability and high range of variation. High genetic variability in the form of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for all the traits studied. High heritability of these traits accompanied with high genetic gain expressed as a percentage of mean indicates that whatever variation occurred is mainly genetic and less influenced by the location (Rudra Naik *et al.*, 2009). Therefore, priority should be given to these traits studied during selection.

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Table 1 Description of the experimental materials

Identity	Pedigree	Source
ICGX-SM99010/6/P1/P2	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P1/P3	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P3/P6	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P3/P7	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P5/P9	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P9/P12	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P12/P13	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P12/P14	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99010/6/P12/P16	ICG129917 x ICGV-SM 90704	ICRISAT
ICGX-SM99013/6/P3/P1	ICG129917 x ICGV-SM 94584	ICRISAT
ICGX-SM99013/6/P3/P2	ICG129917 x ICGV-SM 94584	ICRISAT
ICGX-SM99013/6/P3/P3	ICG129917 x ICGV-SM 94584	ICRISAT
ICGX-SM99013/6/P4/P4	ICG129917 x ICGV-SM 94584	ICRISAT
ICGX-SM99013/6/P5/P6	ICG129917 x ICGV-SM 94584	ICRISAT
ICGX-SM99013/6/P6/P8	ICG129917 x ICGV-SM 94584	ICRISAT
RS006F4B1-1	ICGV-IS 96814x ICGV 93470	ICRISAT
RS006F4B1-2	ICGV-IS 96894 x ICGV 93470	ICRISAT
RS006F4B1-3	19 BT x UGA 8	ICRISAT
RS006F4B1-4 (R)	12 AR x UGA 8	ICRISAT
RS006F4B1-6	18 AT x UGA 4	ICRISAT
RS006F4B1-7	18 AT x UGA 5	ICRISAT
RS006F4B1-8	10 B x UGA 5	ICRISAT
RS006F4B1-10 (B)	ICGV-IS 96806 x ICGV 93470	ICRISAT

Source: ICRISAT Breeding Nursery, Samanko, Mali 2008

Table 2: Combined analysis of variance for agronomic character of groundnut grown across four locations (Samaru, Minna, Lafia and Markurdi) in 2012

Sources of variation	DF	PHT	DTM	NOP	PWT	PTT	SWT	STT	HST	SHP
Replication	2	16.52	67.55	21.61	320.99	0.01	14.06	0.01	1.20	13.98
Rep(loc)	6	1.99	6.04	7.42	333.55	0.03	2.00	0.01	3.30	13.76
Location (L)	3	152.31**	293.4**	1077.15**	1143.03	2.62**	100.33**	1.00**	91.68**	21.24
Genotype (G)	22	208.30**	840.71**	1946.98**	920.44**	1.38**	374.98**	0.71**	161.38**	305.57**
G x L	66	53.33**	229.41**	616.22**	432.56	0.32**	79.87**	0.19**	57.93**	165.55**
Error	176	2.99	9.05	6.68	324.69	0.01	3.46	0.01	1.99	19.77

PHT=Plant Height (cm), DTM=Days to Maturity (days). NOP=Number of pod per plant, PWT=Pod weight per plant (g), PTT= Pod weight (t/ha^{-1}), SWT = Seed weight per plant (g), STT =Seed weight (t/ha^{-1}), HST 100 – seed weight and SHP= Shelling percentage (%)

Table 3: Estimates of variance components for agronomic character of groundnut grown across four locations (Samaru, Minna, Lafia and Markurdi) in 2012

	Variance component estimates				
Character	σ_g^2	σ_l^2	σ_{gl}^2	σ_p^2	σ_e^2
Plant Height (cm)	15.96	1.96	16.78	20.20	2.99
Days to Maturity (days)	63.94	3.19	73.45	82.43	9.05
Number of pod per plant	145.32	12.67	203.18	196.21	6.68
Pod weight per plant (g)	73.71	16.04	35.96	87.41	324.69
Pod weight (t/ha^{-1})	0.11	0.04	0.11	0.14	0.01
Seed weight per plant (g)	29.13	1.08	25.47	35.55	3.46
Seed weight (t/ha^{-1})	0.05	0.01	0.06	0.07	0.01
100 – seed weight	11.89	1.06	18.65	16.58	1.99
Shelling percentage (%)	21.41	-0.4	48.59	33.84	19.77

$\sigma_e^2 =$ M_e = mean square of error

$\sigma_{gl}^2 = \frac{M_{gl} - M_e}{r}$ M_{gl} = mean square of genotype x location

$\sigma_g^2 = \frac{M_g - M_{gl}}{rl}$, M_g = mean square of genotype

$\sigma_l^2 = \frac{M_l - M_{gl}}{rg}$, M_l = mean square of location

$\sigma_p^2 = \sigma_g^2 + \sigma_{gl}^2 / l + \sigma_{rl}^2 / rl$

Table 4: Overall mean pod yield (ton ha^{-1}) of groundnut germplasm grown across four locations in 2012

	Locations				
Genotypes	Samaru	Minna	Lafia	Makurdi	Mean
ICGX-SM99010/6/P1/P2	0.94	0.92	0.69	0.83	0.85
ICGX-SM99010/6/P1/P3	1.16	1.62	0.92	1.69	1.35
ICGX-SM99010/6/P3/P6	1.79	0.95	1.37	1.49	1.40
ICGX-SM99010/6/P3/P7	1.01	1.61	0.82	1.66	1.28
ICGX-SM99010/6/P5/P9	1.69	1.70	1.18	1.59	1.54
ICGX-SM99010/6/P9/P12	1.76	1.58	1.67	1.43	1.61
ICGX-SM99010/6/P12/P13	0.98	1.36	0.89	1.52	1.19
ICGX-SM99010/6/P12/P14	1.00	1.41	0.88	1.27	1.14
ICGX-SM99010/6/P12/P16	1.02	2.00	0.93	1.71	1.41
ICGX-SM99013/6/P3/P1	1.14	1.53	1.04	1.43	1.29
ICGX-SM99013/6/P3/P2	1.08	1.92	0.96	1.66	1.41
ICGX-SM99013/6/P3/P3	1.15	1.37	1.10	1.15	1.19
ICGX-SM99013/6/P4/P4	1.52	1.15	1.51	1.00	1.29
ICGX-SM99013/6/P5/P6	1.32	1.49	1.24	1.37	1.36
ICGX-SM99013/6/P6/P8	1.52	1.90	1.46	1.45	1.58
RS006F4B1-1	0.98	0.97	0.93	0.93	0.95
RS006F4B1-2	0.86	1.19	0.51	1.15	0.93
RS006F4B1-3	1.95	1.70	2.08	1.41	1.79
RS006F4B1-4 (R)	1.18	1.13	1.20	1.00	1.13
RS006F4B1-6	1.44	1.80	1.64	1.65	1.63
RS006F4B1-7	1.53	1.06	1.42	1.01	1.26
RS006F4B1-8	1.14	1.24	1.12	1.16	1.17
RS006F4B1-10 (B)	0.72	1.19	0.72	1.22	0.97
Mean	1.26	1.42	1.14	1.34	1.29
SE±	0.54	0.57	0.37	0.65	

Table 5: Mean and genetic parameters in F_8 Advanced breeding lines of groundnut germplasm grown across four locations in 2012

	Mean	PCV (%)	GCV (%)	H^2	GA	GAM
Plant Height (cm)	38.84	11.57	10.29	79.02	6.77	16.23
Days to Maturity (days)	95.67	9.49	8.36	77.57	10.77	13.07
Number of pod per plant	53.01	26.42	22.74	74.06	14.83	34.74
Pod weight per plant (g)	37.57	24.88	22.85	84.33	11.36	37.25
Pod weight (t/ha^{-1})	1.83	20.27	18.12	79.92	3.11	28.76
Seed weight per plant (g)	25.39	23.48	21.26	81.95	8.17	34.16
Seed weight (t/ha^{-1})	1.29	19.79	17.33	76.75	3.00	26.95
100 – seed weight	26.49	15.37	13.02	71.71	6.22	19.57
Shelling percentage (%)	70.73	8.23	6.54	63.26	7.40	9.24

Phenotypic coefficient of variation (PCV) = $\frac{\sigma_p^2}{\bar{x}}$,

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{\bar{x}}$

Heritability (broad sense) = $\frac{\sigma_g^2}{\sigma_g^2 + \sigma_{gl}^2 / l + \sigma_{rl}^2}$

Genetic gain = $i \times h \times p$

Genetic gain expressed as percentage of mean = $i \times h \times GCV$

Table 6: Pearson correlation coefficient among yield and yield components of advanced breeding lines groundnut grown at Samaru in 2012

Characters		2	3	4	5	6	7	8	9
Plant Height (cm)	1	0.343	0.472**	0.178	0.169	0.095	0.136	0.291	-0.011
Days to Maturity (days)	2	1	0.243	-0.062	0.054	0.155	0.123	0.610**	0.245
Number of pod per plant	3		1	0.623**	0.603**	0.485**	0.611**	0.154	0.069
Pod weight per plant (g)	4			1	0.804**	0.542**	0.750**	0.092	-0.072
Pod weight (t/ha^{-1})	5				1	0.656**	0.927**	0.119	-0.108
Seed weight per plant (g)	6					1	0.812**	0.324	0.472**
Seed weight (t/ha^{-1})	7						1	0.269	0.262
100 – seed weight	8							1	0.459**
Shelling percentage (%)	9								1