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Assessment of Yield, Variability, Heritability and Genetic Advance in Ten Genotypes of Groundnut (*Arachis hypogaea)* in South-East Nigeria

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Abstract
Ten genotypes of Groundnut (*A. hypogaea*) were assessed for yield and yield components in a randomized complete block design with three replicates at the Research Farm of the Michael Okpara University of Agriculture, Umudike in 2018 and 2019. In each year, the experiment consisted of 30 plots, each measuring 1m by 1m with a distance of 1m separating the plots and blocks. Seeds were planted at intra and inter-row spacing of 0.5m to give a population of 40,000 plants^{-1}. Data were collected on the number of leaves plant^{-1}, number of branches plant^{-1}, length of branches plant^{-1}, days to flowering plant^{-1}, number of pods plant^{-1}, the weight of pods plant^{-1}, number of seeds plant^{-1}, the weight of seeds plant^{-1}, 100 seed weight, pod yield^{-1} and seed yield^{-1}. Analysis of variance showed that the genotypes were significantly different (P<0.01) in all the characters studied. In both years the number of leaves plant^{-1}, number of seeds plant^{-1}, 100 seed weight, the weight of seeds plant^{-1} and pod yield^{-1} were positive and highly significant (p<0.01) with seed yield^{-1}. Enormous variability existed among the genotypes of *A. hypogaea* as shown by the genetic component analysis. Genotypes with a high genotypic coefficient of variation, a high broad sense heritability estimates and a high genetic advance for the number of leaves plant^{-1}, the number of seeds plant^{-1}, 100 seed weight, the weight of seedplant^{-1}, pod yield^{-1} and seed yield^{-1} could be selected for improvement in seed yield of *A. hypogaea.* High genetic gain (faster progress) could be expected from selection based on the number of leaves plant^{-1}, the number of branches plant^{-1} and the weight of seeds plant^{-1} because they are predominantly under the control of addictive genes.
Keywords: Yield, Variability, Heritability, Genetic advance, Groundnut

Introduction

Groundnut (*Arachis hypogaea* L.) is an annual herb in the Fabaceae family (Batioli *et al*. 2011). It is one of the most important oilseed crops grown in semi-arid and subtropical areas of the world (Ibrahim *et al*. 2022). According to Hamakareem *et al*., (2016), groundnut was taken across the Pacific to the Philippines by the Spaniards before spreading to Asia. The Portuguese imported it into West Africa (Waele and Swanevelders, 2011. The genetic diversity of the genes is classified into four gene pools: primary gene pool consisting of *A. hypogaea* and *A. monticola* secondary consisting of diploid species from section *Arachis* that are cross-compatible with *A. hypogaea*, tertiary consisting of species of section procumbent that are weakly-cross compactable with *A hyprogaea* and the fourth gene pool consisting of the remaining wild species classified into seven other sections (Pasupuleti *et al*. 2013). The wild species are used as forage (Waele and Swanevelder, 2011). A. *hypogaea* is a self-pollinating crop with cleistogamous flowers, natural hybridization can occur to a small extent where bees' activity is high. Flowering begins 17-35 days after seedling emergence depending on the cultivar and environmental conditions. Flowers, simple or compound are borne in the axils of leaves and never at the same node as vegetable branches. One or more flowers may be present at a node (Seabra *et al*. 2019). The stigma becomes receptive to pollen about 24 hours before anthesis and remains so for about 12 hours more, and the dehiscence of anthers takes place 2-3 hours before the opening of the flowers in the morning. Fertilization occurs about 6 hours after pollination (Yusuf *et al*. 2017).

Depending on the prevailing temperatures, the peg or gynophore carrying the ovary and fertilized ovule on its tips appears in 6-10 days and grows to enter the soil (Positive geotropic) where it develops into pods. The tip orients itself horizontally away from tap roots; (Yadlapalli; 2014), Yol *et al*., (2018) reported that groundnut is derived from the Greek word arachis (legume) and hypogaea meaning "below ground" referring to the formation of pods in the soil. Shalini *et al*., (2016) reported that groundnut is valued as a rich source of energy contributed by oil (48-50%) and protein (25-28%) in the kernels. They provide 564Kcal of energy from 100g of kernels. Groundnut oil is an excellent cooking medium because of its high smoking point (Ibrahim, 2021, Ibrahim, *et al,* 2022). Bodena (2018) reported that groundnut merge fix as much as 190kg of nitrogen per hectare. Groundnut is not produced in commercial quantity in the southeast even with its enormous potential that could favour its production. Identification of genotypes with high seed yield capacities, determination of the relationship between seed yield and yield components and the yield components that influenced seed yield^{-1} most, calculation of broad sense heritability, genetic advance and genetic gain to be able to predict breeding program for seed yield^{1} improvement are the objectives of this research work.

Materials and Methods

Ten groundnut genotypes which included, RRB, SUMNUT 10, SUMNUT 20, RMP 91S (Small seed), RMP91 (big seed), JL 12, JL24, ICGV 89754 and ICGV 15-87281 were evaluated for growth, pod and seed yieldha^{-1} in 2018 and 2019 cropping seasons. The experiment was a randomized complete block design with the genotypes as treatment, replicated 3 times and was carried out at the Research Farm of Michael Okpara University of Agriculture, Umudike (Longitude 07^{0} 33^{1}E, latitude 05^{0} 29^{1}N and altitude 122m) with a temperature of 26^{0}C. The seeds were planted at a spacing of 50cm by 50cm with a distance of 1m separating the plots and blocks. Nine stands per plot and ten plots per block, on a land area of 19m by 5m. Weeding was done manually using the hoe and hand-pulling methods as soon as they appeared. Data were collected on the number of leaves plant^{-1}, number of branches plant^{-1}, days to 50% flowering, number of pods plant^{-1}, the weights of pods plant^{-1}, the number of seeds plant^{-1}, the weight of seeds plant^{-1}, 100 seed weight, seed yield hectare^{-1} and pod yield hectare^{-1}. Data were analyzed by one-way analysis of variance and significant means separated with the least significant differences (Snedeco and Cochran 1989, Obi, 2001). The gross variability was partitioned into genetic and non-genetic components and phenotypic, genotypic and error variances were estimated using the method of Wrikke and Weber (1986)

$$\sigma^2P = \frac{\text{MSG}}{r}, \sigma^2G = \frac{\text{MSG}}{r} - \frac{\text{MSE}}{r} \qquad \sigma^2E = \frac{\text{MSE}}{r},$$

MSG, MSE and r are the mean square *genotypes*, means square error and number of replications while σ^2P, σ^2G and σ^2E are phenotypic, genotypic and error variances respectively. The phenotypic, genotypic and environmental components of variation were estimated according to Singh (2001).

$$\text{PCV} = \frac{\sigma\text{P}\times 100}{\text{Mean}}, \text{GCV} = \frac{\sigma\text{G}\times 100}{\text{Mean}}, \text{ECV} = \frac{\sigma\text{E}\times 100}{\text{Mean}}.$$

PCV, GCV and ECV are phenotypic, genotypic and environmental coefficients of variation respectively. Broad sense heritability was estimated according to Allard (1991). Genetic advance (GA) was calculated according to Johnson *et al* (1995),

$$\text{G.A} = \frac{\sigma^2\text{G}}{\sqrt{\sigma\text{P}}} \times \text{K}$$

Where K=2.063(selection differential at 5%), σ^2G= genetic variance.

$\sqrt{\text{QP}}$ = square root of phenotypic variances, Genetic gain (GG) was determined from genetic advance expressed as a percentage of the population mean.

Results and Discussion

The physical and chemical characteristics of the soil experimental site were taken and analyzed before planting. The results are given in Table 1. Soil textural class was sandy loam. Slight. The soil was relatively suitable for the cultivation of *A. hypogaea*, (Baughman *et al*. 2015). The soil was analyzed at the National Root Crop Research Institute Umudike, Soil Science Laboratory. The soil was slightly acidic with pH in H_2O of 5.8 in 2018 and 6.1 in 2019. The rise in organic carbon, total nitrogen and available phosphorus in 2019 was due to the residual effects of the application of organic manure, which released nutrients slowly. Table 2 shows the agro-metrological data of the experimental site in 2018 and 2019. The mean maximum temperatures were 31.75 and 32.22, while the mean rainfall (amount) was 193.56 and 171.76 for 2018 and 2019 respectively. The minimum temperatures in both years are also given. The weather conditions were good enough for the production of *A. hypogaea* in Umudike. The results of the analysis of variance are presented in Tables 3 and 4 which showed that the ten genotypes of *A. hypogaea* differed greatly in their vegetative, the reproductive characteristics as well as pod and seed yield hectare^{-1}. JL 24, ICGV 89754, JL 12, Rmp-91-B and ICGV-15-87281 vegetative characters (number of leaves and number of branches plant^{-1}) performed best in both 2018 and 2019. For reproductive characters (number of seed/pod, weight of seeds/pod and weight of pods) these genotypes recorded superior performance which translated into the height of pod and seed yield ha^{-1} in both years. The genotypes, JL 24, ICGV-89754, JL 12, Rmp-91-B and ICGV-15-87281 could further be reviewed for possible release in Umudike. High variance ratios in Table 5 suggest high variation in the 11 characters of the 10 genotypes of *A. hypogaea*. The correlation matrix showed that the number of leaves plant^{-1}, number of branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, weight of seeds plant^{-1} and pod yield hectare^{-1} associated positively and highly significantly ($P<0.01$) with seed yield hectare^{-1} in 2018 and 2019, (Table 5). This suggests that improvement in the performance of these characters will lead to an increase in seed yield hectare^{-1}. From Table 6, the weight of seed plant^{-1} (0.641 in 2018, 0.599 in 2019) was the single reproductive factor that directly contributed most to seed yield ha^{-1}. The weight of pods plant^{-1} (0.406 in 2018, 0.375 in 2019) was the second individual reproductive factor that directly influenced seed yield ha^{-1}. Pod yield ha^{-1} was the third most important single factor that directly influenced seed yield. This implies that Agronomic practices and other factors that could improve the performance of the weight of seeds plant ha^{-1}, weight of pod plant^{-1} and pod yield ha^{-1} will lead to an increase in seed yield ha^{-1} of these genotypes. The effectiveness of selection in any crop depends on the extent and nature of phenotypic and genotypic variability present in different agronomic traits of the population (Yeshiwas, *et al*. 2017). Generally, genetic parameters including genotypic coefficient of variation, heritability and genetic advance are prerequisites for genetic improvement of crops. A high genotypic coefficient of variation indicates the availability of high variation. The very low value of variation indicates that selection will not be effective for such traits because of narrow genetic variability (Dikshit, *et al*. 2015). From Table 7, very high variance ratios were observed among most of the characters studied.

Table 8 shows the means, estimates of phenotypic and genotypic variances, genetic advance and genetic gain in 2018 and 2019. Estimates of Phenotypic and Genotypic coefficients of variation were high in length of branches plant^{-1}, number of leaves plant^{-1}, number of branches plants^{-1}, number of pods plants^{-1}, weight of pods plants^{-1}, weight of seeds plants^{-1}, pod yield^{-1}and seed yield^{-1} High genotypic coefficient of variation indicates greater variability from these characters, thereby suggesting abundant scope from improvement through selection among these variations. Since phenotypic coefficients of variation were slightly higher than the genotypic coefficient of variation for all the characters studied, this indicates the presence of slight environmental influence to some degree in the phenotypic expression of the characters. Pandy *et al*. (2010) and Mulugeta, *et al*. (2012) also observed similar findings. The same trends were reported by Chinatu and Ukpaka (2016) in *Piper guineense*, Eze *et al*. (2016) In Taro, Chinatu, *et al*., (2016) in cucumber wide range of variation was observed from most of the characters under study. Shoba, *et al*. (2012) and Meta and Monpara (2010) reported high phenotypic and genotypic coefficient of variation for pod yield. Pradham and Patra (2011) reported low heritability estimates for days to 50% flowering and pod yield – *A. hypogaea*. Johnson et al. (1995) reported that heritability estimates together with genetic advances are more important than heritability alone to predict the effect of selecting the best individual genotypes. Genetic advances and genetic gains indicated moderate to high variability for length of branches, number of leaves, number of seeds/plants, weight of pods/plant, pod yield/ha and seed yield/ha in both years.

Conclusion

This study revealed that the genotypes JL 24, ICGV-89754, JL12, Rmp-91-B and ICGV-15-87281 performed well in Umudike. Further studies could be carried out for it to be released to farmers to encourage groundnut production in the Southeast. The high phenotypic and genotypic coefficients of variation with very low environmental coefficients of variation observed among most of the seed yield/ha and yield components studied revealed enormous and exploitable variability which is mostly heritable. Moderate progress in the improvement of seed yield of *A. hypogaea* could be achieved by selecting genotypes with the higher number of leaves plant^{-1}, longer and more branches plant^{-1}, higher seed weight plant^{-1}, higher pod weights plant^{-1}, higher pod and seed yield hectare^{-1} since they have high broad sense heritability genotypic coefficient of variation and genetic advance. High genetic gain (faster progress) could be expected from selection based on the number of leaves plant^{-1}, number of branches plant^{-1} and weight of seeds plant^{-1} because they are predominantly under the control of addictive genes.

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Table 1: Physicochemical properties of the experimental site in 2018 and 2019

Physical Characteristics	2018	2019	Method of Analysis
Sand (%)	75.6	74.2	Hydrometer (Jackson, 1962)
Silt (%)	10.3	11.8	Hydrometer (Jackson, 1962)
Clay (%)	14.0	13.9	Hydrometer (Jackson, 1962)
Textural class	Sandy-loam	Sandy-loam	
Chemical properties			
PH (H_20)	5.8	6.1	pH meter
Organic Carbon (%)	1.12	1.3	Flame Photometric (Kjedahl, 1983
Total Nitrogen (%)	0.097	0.15	Kjedahl method (Kjedahl, 1983)
Available P (mgKg^{-1})	33.4	22.7	Flame photometric (Kjeldahl, 1983)
Exchangeable K(CmolKg^{-1})	0.221	0.3	Oxidation (Kjeldahl, 1983)
Exchangeable Ca(CmolKg^{-1})	3.20	4.0	A. A. S. (Kjeldahl, 1983)
Exchangeable Mg(CmolKg^{-1})	0.96	1.1	A. A. S. (Kjeldahl, 1983)
Cation exchange capacity (CmolKg^{-1})	5.72	7.0	
Base Saturation	83.21	84.9	

Source: National Root Crops Researches Institute Umudike, Abia State, Nigeria

Table 2: Mgro-Meteorological Data for Umudike Ecological Zone Showing Means for 2018 and 2019

	2018							2019						
	Rainfall		Temperature (^oC)		Relative Humidity (%)		Sunshine	Rain Fall AMT		Temperature		Relative Humidity (%)		Sunshine
Month	AMT	Days	Max	Min	0900 HRS	1500 HRS	(HRS)	(MM)	DAY	MAX	MIN	0900 HRS	1500 HRS	(HRS)
January	0	0	34	23	50	31	7	51	2	33	23	68	49	5.7
February	0	0	36	24	62	36	4.7	0	0	35	24	70	38	6.4
March	257	10	33	25	80	66	4.4	80.5	5	35	25	76	54	7.9
April	129.3	8	33	25	79	70	5.1	140.7	8	33	24	79	62	6.3
May	278..4	16	32	25	82	72	5.4	144.8	11	32	24	82	71	7.0
June	354.7	16	29	23	85	72	4.7	274.4	15	31	24	85	79	5.8
July	268.7	15	29	24	89	81	3.9	457.6	19	30	23	88	78	3.7
August	396.2	22	29	24	89	81	3.4	133.1	11	31	23	84	78	4.6
September	312.6	15	29	23	86	77	6.7	263.7	14	30	23	85	73	4.9
October	273.4	7	30	24	80	69	5.8	288.9	10	31	24	82	70	5.6
November	45	2	31	24	83	64	7.4	83	7	33	24	78	65	7.3
December	73	1	33	24	71	51	7.4	40	2	33	24	73	50	7.4
Total	2322.7	112	381	288	986	770	65.4	1957.8	104	387	285	717	582	50.4
Mean	193.56	9.33	31.75	24	78	64.17	5.45	163.14	163.14	32.25	23.7	79.67	64.67	5.6

Table 3: Mean of seed Yield and Yield Component of Ten Genotypes of Groundnut (*A. hyprogaea*) in 2018 Umudike

Varieties	Length of branches (cm)	No. of branches plant $^{-1}$	No. of leaves plant $^{-1}$	Days to 50% flowering	No. of pods plant^{-1}	Weights pods plant $^{-1}$	No. of Seeds plant^{-1}	Weight of seeds plant^{-1}	100 seeds plant $^{-1}$	Pod yield ha $^{-1}$ Kg	Seed yield ha^{-1} Kg
RRB	58.56	9.20	209.33	33.000	20.48	30.55	25.77	17.89	61.11	3457.6	1995.0
JL24	60.33	11.22	276.70	32.333	23.25	38.14	33.63	23.26	66.67	4279.4	2791.7
ICGV-15-87281	60.11	9.89	202.96	31.000	21.81	35.14	37.55	24.63	68.06	3934.9	2755.1
SAM NUT 20	40.56	7.44	126.81	32.000	23.22	25.66	28.85	16.81	60.00	2877.3	1701.6
ICGV-89754	57.11	10.22	229.59	32.000	24.22	37.77	37.63	27.22	66.67	43338.2	3045.1
JL12	50.44	9.78	243.15	31.667	23.25	36.63	34.44	20.70	63.33	4037.8	2618.9
ICGV-8124	58.44	9.22	204.81	32.000	25.00	28.44	32.07	17.00	64.17	3177.7	1929.6
RMP-91-5	44.00	9.67	229.63	31.667	24.00	35.55	38.22	20.55	63.06	3980.2	2310.7
RMP-91-B	51.89	8.22	189.85	31.667	24.00	32.33	34.45	21.55	66.94	3646.9	2402.4
SAM NUT 10	48.69	8.67	158.40	31.333	22.11	31.37	29.59	19.44	65.56	3515.2	2179.0
LSD 0.05	2.117	0.499	4.708	0.09955	1.238	0.748	0.662	1.198	1.425	71.66	68.85

Table 4: Mean of seed Yield and Yield Component of Ten Genotypes of Groundnut (*A. hypogaea*) in 2019 Umudike

Varieties	Length of branches (cm)	No. of branches plant $^{-1}$	No. of leaves plant $^{-1}$	Days to 50% flowering	No. of pods plant^{-1}	Weights pods plant $^{-1}$	No. of Seeds plant^{-1}	Weight of seeds plant^{-1}	100 seeds plant $^{-1}$ (g)	Pod yield ha $^{-1}$ (Kg)	Seed yield ha^{-1} Kg
RRB	61.78	9.22	195.07	33.000	21.44	33.40	26.59	16.51	62.5	3433.6	1842.7
JL24	60.89	10.89	221.18	32.333	24.85	33.03	30.66	18.48	64.17	3700.4	2072.0
ICGV-15-87281	60.67	8.67	207.33	31.000	24.77	26.66	29.96	18.74	64.72	3293.9	2090.8
SAM NUT 20	39.33	8.11	153.92	32.667	22.33	24.99	28.03	15.63	60.56	2861.3	1755.1
ICGV-89754	52.67	10.78	237.92	31.667	28.11	32.66	31.14	20.92	67.22	3689.7	2331.2
JL12	57.89	11.00	225.92	31.667	22.70	32.29	29.77	18.22	65.83	3618.9	2043.2
ICGV-8124	59.89	10.56	240.11	32.000	23.33	29.18	30.11	17.74	63.06	3260.9	1989.7
RMP-91-5	40.33	8.67	150.18	31.556	26.89	27.81	33.77	15.77	56.94	3120.2	1771.6
RMP-91-B	45.22	8.56	205.89	32.333	25.92	32.22	30.81	19.18	65.56	3681.9	2137.8
SAM NUT 10	51.78	8.22	162.96	31.000	24.17	27.25	30.66	16.92	65.28	3069.2	1906.1
LSD 0.05	2.001	1.037	3.981	0.099	0.67	0.856	0.484	1.251	1.483	91.02	53.71

Table 5: Correlation Matrix of means values of yield and yield components of Ten Genotypes *A. hypogaea* at Umudike in 2018 and 2019

					2018						
Character:	LB	NBP	NLP	DF	NPP	WPP	NSP	WSP	100SW	PYH	SYH
LB	1.000										
NBP	0.145	1.000									
NLP	0.482**	0.751**	1.000								
DF	-0465**	-0.209	-0.289	1.000							
NPP	0.575**	-0.156	0.434*	0.060	1.000						
WPP	0.355	-0.277	0.035	0.094	0.379*	1.000					
NSP	0.287	-0.356	0.337	0.134	0.551**	0.734**	1.000				
WSP	0.355	-0.573**	0.304	0.278	0.602**	0.809**	0.402*	1.000			
100SW	0.755**	-0.086	0.488*	0.278	0.729**	0.555**	0.855**	0.654**	1.000		
PYH	0.388*	0.286	0.419*	-0.104	0.433*	0.984**	0.752**	0.821**	0.603**	1.000	
SYH	0.302	0.494**	0.664**	-0.200	0.558**	0.891**	0.891**	0.951**	0.605**	0.834**	1.000
					2019						
LB	1.000										
NBP	0.235	1.000									
NLP	0.519**	0.415*	1.000								

*implies that correlation is significant at 0.05, ** correlation is significant at 0.01, LB= Length of branch, NBP= Number of branches plant^{-1}, NLP= Number of leaves plant^{-1}, DF= Days to flowering, NPP= Number of pods plant^{-1}, WPP= Weight of pods plant^{-1}, NSP= Number of seeds plant^{-1}, WSP= Weight of seeds plant^{-1}, SW=Seed weight, PYH= Pod yield hectare^{-1}, SYH= Seed yield hectare

Table 6: Estimates of direct and indirect effects between seed yield and yield components for 2018 and 2019

Indirect effects				2018					
TRAITS	PYH	WSP	100SW	NSP	WPP	NPP	NBP	SYH	**Direct effects on SYH**
PYH	1.000								
WSP	0.942	1.000							
100SW	0.803	0.859	1.000						
NSP	0.665	0.881	0.865	1.000					
WPP	0.949	0.935	0.792	0.861	1.000				
NPP	0.836	0.915	0.865	0.942	0.823	1.000			
NBP	0.484	0.436	0.433	0.323	0.489	0.254	1.000		
SYH	0.956	0.995	0.863	0.885	0.950	0.915	0.474	1.000	
					2019				
PYH	1.000								
WSP	0.586	**1.000**							
100SW	0.576	0.859	**1.000**						
NSP	0.484	0.626	0.332	**1.000**					
WPP	0.976	0.612	0.591	0.661	**1.000**				
NPP	0.812	0.652	0.426	0.745	0.302	**1.000**			
NBP	0.544	0.402	0.562	0.594	0.495	0.369	**1.000**		
SYH	0.639	0.924	0.866	0.611	0.637	0.540	0.574	**1.000**	

Residual effect = 0.34, NB= Number of branches plant^{-1}, NPP= Number of pods plant^{-1}, WPP = Weight of pods plant^{-1},
NSP= Number of seeds plant^{-1}, 100SW= 100 seed weight, WSP= Weight of seeds plant^{-1}, PHY= Pod yield ha^{-1}, SYH= Seed yield ha^{-1}

Table 7: Variance Ratios of Agronomic Character of 10 varieties of *A. Hypogaea* in 2018 and 2019

Characteristics.	*Mean Square Genotype*	*Mean Square Error*	*Variance Ratio*
Length of branches	682.721	4.498	151.77**
Number of leaves	258798.40	24.89	1034.97***
Number of branches	17.931	0.28	64.02**
Days to 50% flowering	4.026	0.011	362.33**
Number of seeds/pod	155.409	0.491	316.37***
Number of pods/plant	39.702	0.484	81.99**
Weight of pods/plant	165.607	0.628	263.600**
Weight of seeds/plant	103.105	1.613	63.940*
100 seed weight	81.397	2.471	32.94*
Pod yield KgHa^{-1}	2030153.000	5767.000	352.020***
Seed yield KgHa^{-1}	1453260.000	5324.000	272.97***

Table 8: The mean, range, phenotypic, Genotypic and environmental variances, Phenotypic, genotypic and Environmental coefficient of variation, Heritability, Genetic advance and Genetic Gain

Characters	Mean	Range	VP	VG	VE	PCV	GCV	ECV	H_2B	GA	GG
Length of branches	54.04	23.45	227.57	226.08	1.49	429.054	426.244	2.809	99	30.917	61.78
Number of leaves	200.05	89.93	3413.09	3413.15	5.93	1709.118	170.148	2.964	99.8	120.42	60.19
Number of branches	9.47	2.89	4.28	3.88	0.4	50.531	40.971	4.224	91	3.869	40.86
Days to flowering	31.922	2	1.342	1.338	0.004	4.204	4.191	0.013	99.7	2.384	7.47
Number of pods	23.19	4.52	5.72	5.58	0.57	24.665	22.208	2.456	90	4.442	19.15
Number of seeds	30.42	7.55	15.49	15.41	0.09	50.867	50.867	0.296	99	8.077	26.55
Weight of pods	29.95	8.41	29.07	28.8	0.27	97.055	97.055	0.901	99	11.019	36.79
Weight of seeds	17.81	5.29	8.14	7.55	0.59	45.705	45.705	3.313	93	5.459	30.65
100 seed weight	63.58	6.66	27.3	26.31	0.82	42.671	42.671	1.289	97	10.421	16.39
Pod yield ha^{-1}	3353	839	316741.33	313642.66	3098.66	9354.091	9354.091	92.415	99	1149.693	34.29
Seed yield ha^{-1}	1994	575.6	96479	95399	1080	4784.305	4784.305	54.162	99	633.617	31.78