Phenotypic And Genotypic Variance And Heritability Estimates For Oil Content And Other Agronomic Traits In Groundnut (Arachis Hypogaea L.)

M. S. Jibrin
Plant Science Department, Institute for Agricultural Research Ahmadu Bello University Zaria
Email: mohasjibrin@gmail.com

C. A Echekwu
U. S. Abdullahi
I. S. Usman
Plant Science Department, Institute for Agricultural Research Ahmadu Bello University Zaria

S. H. Habu
National Horticultural Institute (NIHORT) Bagauda Station, Kano

Abstract: The success of any crop improvement programme depends largely on the amount of genetic variability present in the plant materials. This study was conducted to estimate Phenotypic and Genotypic Variance and Heritability Estimates for oil content and other agronomic traits in groundnut, a total of 25 genotypes were used in the study that were laid out in a 5 x 5 lattice design with three replications. The analysis of variance showed significant difference among the genotypes. The genetic variability as shown by the genotypic coefficient of variation (GCV) and phenotypic coefficient of variations (PCV), showed that the PCV was higher than GCV for all the studied traits. Portraying the importance of environment in the variation exhibited. Estimate of broad sense heritability were moderate to high for most traits except for seed size that recorded low values. This indicates that selection for traits with high heritability will lead to fast genetic improvement of a trait that is by increasing the frequency of favourable alleles by repeated mass selection or hybridization between selected genotypes.

Keywords: Arachis hypogaea Phenotypic and Genotypic Variance, Heritability and oil content.

I. INTRODUCTION

Groundnut (Arachis hypogaea L.) is the 13th most important food crop and 5th most important oilseed crop in the world Mondal et al., (2009). The kernel is rich in oil (48-50 %) and protein (25-28 %) Pasupuleti et al., (2013). Groundnut seed are nutritional source of vitamin E, niacin, falcin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium Stigter et al., (2006). Groundnut kernels are consumed directly as raw, roasted or boiled kernels or oil extracted from the kernel is used as culinary oil. It is also used as animal feed (green material and straw) and industrial raw material (oil, cake and fertilizer). Groundnut has potential as a source of bio-fuel, but because it must compete for food use, increase in oil production on per acre basis are essential if the crop is to be used as a source of oil for bio-fuel conversion.

The selection of potential genotypes from the existing germplasm, utilizing them in the hybridization programme and isolation of the superior segregants in the segregating population is the usual breeding strategy in highly self-pollinated crops like groundnut. The success of selection programme depends upon the magnitude of genetic variability and the actual heritable variation in the progeny. The magnitude of variability, heritability and genetic advance differ depending upon the material and environment in which the material is raised (Kavera, 2008). The phenotypic
expression of the plant character is mainly controlled by the genetic makeup of the plant and also the environment. So it is necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameter such as phenotypic and genotypic coefficient of variation, heritability and genetic advance (Hiremath, 2009). Estimate of heritability assists breeder to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources (Smalley et al., 2003). Broad sense heritability is estimated using the total genetic variance. As a rule, traits with greater heritability can be modified more easily by selection and breeding, than traits with lower heritability. 

Vegetable oils are in high demand due to diseases associated with fat from animal source. About two-thirds of the total groundnut production is crushed for oil and the remaining one-third is used in confectionery products. With increasing consumer demand for edible oil of good quality, there is a need to investigate and understand various factors that influence groundnut oil content and quality Dwivedi et al., (1993). This study was undertaken to estimate the extent of genetic variability and heritability for oil content and other agronomic parameters in groundnut, to aid in the formulation of an effective breeding program.

II. MATERIALS AND METHODS

The experimental material comprises of 25 genotypes obtained from institute for Agricultural research (IAR) ABU Zaria, Nigeria, consisting of releases varieties, breeding lines and their crosses with two checks (SAMNUT 25 AND SAMNUT 26) included. The F1 progenies were generated during 2013/2014 raining season at the Screen house using 3 X 5 North Carolina mating design II. The genotypes were laid in a 5 X 5 lattice design with three replications and inter and intra row spacing of 50cm X 25cm at Samaru IAR research farm faculty of agriculture Ahmadu Bello University Zaria, (11 °11’ N, 7° 38’E), 600m above sea level in the Northern guinea Savanna, all agronomic practices were carried out according to IAR recommended. The observations were recorded on five randomly selected plants from each entry and replication for studied different characters. The following biometric data were collected: plant height, days to maturity, haulm weight, pod number per plant, pod weight per plant, pod length, pod diameter, pod size seed length, seed diameter, seed size, seed yield per plant, shelling percentage, hundred seed weight, oil content, protein and carbohydrate content. The data collected was subjected to analysis of variance (ANOVA) using the generalised linear model (GLM) procedure of Statistical Analysis system (SAS) and significant means were compared using Least Significant difference (LSD). Phenotypic and genotypic coefficient of variation as well as the broad sense heritability were computed using the formulae given by Singh and Chaudhary (1985). The formulae for the above parameters were as given below:

The phenotypic and genotypic coefficient of variation as well as broad sense heritability were computed using the formulae given by Singh and Chaudhary (1985).

### Analysis of variance

The data related to each trait was subjected to analysis of variance (ANOVA) using the Generalised Linear Model (GLM) procedure of Statistical Analysis System (SAS) and significant means were compared using Least Significant Difference (LSD). Phenotypic and genotypic coefficient of variation as well as the broad sense heritability were computed using the following formulae given by Singh and Chaudhary (1985).

- **Phenotypic coefficient of variation (P.C.V %)**
  \[
  \text{Phenotypic coefficient of variation} = \frac{\sqrt{\sigma_{ph}^2}}{X} \times 100
  \]

- **Genotypic coefficient of variation (P.C.V %)**
  \[
  \text{Genotypic coefficient of variation} = \frac{\sqrt{\sigma_{g}^2}}{X} \times 100
  \]

- **Genotypic Coefficient of variation**: \(\sigma_g^2\)
- **Phenotypic Coefficient of variation**: \(\sigma_{ph}^2\)

- **Broad sense heritability**
  \[
  h_b^2 = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100
  \]

### Results

#### Table 1

<table>
<thead>
<tr>
<th>Characters</th>
<th>MEAN</th>
<th>CV (%)</th>
<th>Mean Square Between df=39</th>
<th>Error df=66</th>
</tr>
</thead>
<tbody>
<tr>
<td>plant height</td>
<td>24.06</td>
<td>14.57</td>
<td>54.43**</td>
<td>12.29</td>
</tr>
</tbody>
</table>

#### Table 2

<table>
<thead>
<tr>
<th>Characters</th>
<th>MEAN</th>
<th>CV (%)</th>
<th>Mean Square Between df=39</th>
<th>Error df=66</th>
</tr>
</thead>
<tbody>
<tr>
<td>plant height</td>
<td>24.06</td>
<td>14.57</td>
<td>54.43**</td>
<td>12.29</td>
</tr>
</tbody>
</table>

---

www.ijres.com
days to maturity 109.23 3.78 47.84** 17.09
hull weight 720.23 28.09 116455.74** 40935.32
pod number per plant 52.96 24.30 304.42* 165.56
pod weight per plant 54.35 21.23 320.30** 133.23
pod length 28.58 1.97 28.06** 0.32
pod diameter 13.41 2.44 2.99** 0.11
pod size 2.15 4.09 0.11** 0.01
seed length 14.12 8.69 4.84* 1.51
seed diameter 10.25 9.50 4.14** 0.95
seed size 1.39 10.50 0.03* 0.02
seed yield per plant 26.68 22.52 109.49** 36.08
shelling percentage 50.01 24.59 249.10* 151.27
hundred seed weight 56.91 14.03 104.07* 63.79
oil content 49.11 2.92 14.89** 2.06
protein content 26.83 19.57 117.67** 27.56
carbohydrate content 10.74 35.92 86.50** 14.87

Table 2: Mean value, coefficient of variation and mean square of measured character

IV. DISCUSSION

The genetic variability as shown by the genotypic coefficient of variation (GCV) and phenotypic coefficient of variations (PCV), showed that the PCV was higher than GCV for all the studied traits. Portraying the importance of environment in the variation exhibited, similar result was reported by Nath and Alam, 2002. The breeder make rapid progress where heritability is high using selection methods that are dependent solely on phenotype (example mass selection). However, where heritability is low, the method of selection based on families and progeny testing are more effective and efficient (Acquaah, 2007). Estimate of broad sense heritability were moderate to high for most traits except for seed size that recorded low values. This indicates that selection for traits with high heritability will lead to fast genetic improvement of a trait that is by increasing the frequency of favourable alleles by repeated mass selection or hybridization between selected genotypes, showing varying degree of variation for such traits. This agreed with the finding of Patil et al., 2015. The moderate to high value of broad sense heritability signifies the preponderance of additive gene action in the inheritance of those traits. Hence selection for such traits would be effective. This study corroborates with the work of Patil et al., 2015 and is not in agreement with the work of John and Raghava, 2015 and Noubissié et al., 2012.

<table>
<thead>
<tr>
<th>Traits</th>
<th>( \sigma_k^2 )</th>
<th>( \sigma_e^2 )</th>
<th>( \sigma_{ph}^2 )</th>
<th>( h_b^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plant height</td>
<td>11.07</td>
<td>4.16</td>
<td>17.23</td>
<td>75.86</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>11.38</td>
<td>5.49</td>
<td>16.87</td>
<td>67.47</td>
</tr>
<tr>
<td>Hull weight</td>
<td>2537.33</td>
<td>8531.86</td>
<td>29051.19</td>
<td>71.47</td>
</tr>
<tr>
<td>Seed length</td>
<td>51.27</td>
<td>47.72</td>
<td>98.99</td>
<td>51.79</td>
</tr>
<tr>
<td>Seed weight</td>
<td>85.48</td>
<td>50.18</td>
<td>135.66</td>
<td>61.01</td>
</tr>
</tbody>
</table>

\( \sigma_k^2 \) = Genotypic variance,

\( \sigma_e^2 \) = Environmental variance,

\( \sigma_{ph}^2 \) = phenotypic variance,

\( h_b^2 \) = Broad sense heritability.

Table 2: Variance Components for measured traits of groundnut genotypes during 2014/2015 dry season

REFERENCES


