Comparative genetic variability and traits’ heritability in vegetative and floral characters in accessions of two minor legumes

J.O. Agbolade¹, J.O. Popoola², J.I. Kioko², B.D. Adewale, A.A. Ajiboye², T.O. Ajewole², O.A. David⁵ and R.J. Komolafe²

Department of Crop Science and Horticulture, Federal University, Oye Ekiti, Nigeria.

Received: 13-06-2018 Accepted: 14-09-2018

ABSTRACT

This study evaluated genetic variability and heritability in vegetative and floral characters among two minor legumes (Sphenotylis stenocarpa Ex. A. Rich. Harms and [Cajanus cajan (L.) Millsp.] of five accessions each. Six (6) floral and ten (10) vegetative characters were pooled for analysis on one hundred (100) plants of the two minor legumes. Appropriate statistical analyses were employed for comparative evaluation. Significant differences (P = 0.05) were observed in all the traits except rachis length. Principal Component Analysis (PCA) revealed significant contributions of traits in lengths of calyx lobe, stipule, rachis and petiole; also in numbers of flowers per peduncle and of main branches to the expressed variability. The cluster analysis segregated the accessions into two major cluster groups. The broad sense heritability of traits was high (>95 %). The study is important in selection of valuable traits for conservation, management of genetic resources and hybridization programs of the two species.

Key words: Cajanus cajan, Floral, Sphenostylis stenocarpa, Variability, Vegetative.

INTRODUCTION

Genetic variability deals with the tendency of genetic characteristics to vary among taxa, it is closely related but not similar to genetic diversity which deals with the total number of genetic characteristics in the genetic make-up of a species (Ammar et al., 2015). Heritability, however deals with the extent to which observed differences between individuals are associated with the additive genetic variance, knowledge of this parameter helps geneticist to determine whether or not a particular trait can be improved by selection, management practices or both (Roman et al., 2000). The radiation of angiosperms has been closely linked to the diversification in floral morphology and function and this effect is particularly pronounced in animal-pollinated lineage (Scott Armbruster, 2014). Specifically, floral characters contribute to species separation much more often among animal-pollinated taxa than among wind- and water-pollinated taxa. Progress in our understanding of floral diversification has been mainly based on examination of phylogenetic and ecological correlation of floral variation at the species level, above and studies of phenotypic selection at the within-population (Agbolade and Komolafe, 2016).

African Yam Bean (Sphenostylis stenocarpa Hocbest ex. A. Rich) harms is an underutilized tropical African tuberous legume (Adewale et al., 2013) The crop belongs to the class Magnoliopsida; order Fabales; Family Fabaceae; subfamily Papilionoideae; and genus Sphenostylis (Nnamani et al., 2017) There are seven species in the genus Sphenostylis but African yam bean (AYB) is the most valuable (Adewale et al., 2013). The arable tuberous legume is important in most indigenous African food cultures and in peasant agriculture (Nnamani et al., 2017). The center of diversity, according to the Genetic Resources Information Network (GRIN) spreads from the west through to the east and southern parts of Africa (Adewale et al., 2013) and these areas are suspected to host the genetic resources of AYB. The utilization of AYB has links with sociocultural values in the cultures of some ethnic groups within the area (Adewale et al., 2013; Nnamani et al., 2017). The vegetative growing stage of AYB is characterized with the profuse production of trifoliate leaves. It possesses large and attractive flowers which seem to exhibit self-pollination (Popoola et al., 2017). Most legumes including AYB have remarkably low susceptibility to most field and storage leguminous pests with high nitrogen fixing-ability (Okeola and Machuka, 2001; Rajni and Vikas, 2018; Singh et al., 2018). In addition, AYB is used extensively in various dietary preparations and has potential for supplementing the protein requirement of many families throughout the year (Nnamani et al., 2017).

¹Corresponding author’s e-mail: oludareagbolade@gmail.com
²Department of Biodiversity and Conservation, Cape Peninsula University of Technology, Cape Town, South Africa.
³Department of Plant Science and Biotechnology, Federal University, Oye Ekiti.
⁴Department of Biological Sciences, Covenant University, Ota, Ogun State.
Pigeon pea \([\text{Cajanus cajan (L.) Millsp.}]\) is an erect perennial, warm-season crop that is widely grown in the tropics and subtropics for food, feed, forage and fuel wood (Pundir and Singh, 1985). Globally, it is grown in 7.03 mha with a total production of 4.89 mha from tropical and subtropical regions of the world (FAOSTAT, 2014). The crop may reach 4-5 metres in height, but usually 1-2 metres only, woody at the base, with a variable habit, but usually erect, deep and quick growing tap root with an angular stem resulting from three ribs starting from the base of each petiole. Leaves are trifoliate, alternate set in a spiral along the stem and leaflets are oblong- lanceolate; 5-10 cm long x 2-4 cm wide, pubescent likewise the stem (Agbolade and Komolafe, 2016). In spite of the economic and agronomic importance of both species as resource base for food, feed and forage rich in protein, they are underutilized and neglected and deserves consistent evaluation of their genetic resources toward enhancing the narrow gene pool and diversity. The main goal of this paper is to compare the levels of phenotypic variability in floral and vegetative characters among the accessions of the two minor legumes \((\text{Sphenostylis stenocarpa and Cajanus cajan})\) and to evaluate the contribution of both types of traits to the variability proportion between the two species.

**MATERIALS AND METHODS**

The experiment was carried out with five accessions each of Pigeon pea and African yam bean obtained from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Oyo-State, Nigeria, at the Teaching and Research Farm of the Department of Plant Science and Biotechnology, Federal University, Oye - Ekiti, Ekiti State, Nigeria, during the academic year 2017/2018 session. All other protocols are in accordance with Popoola et al., (2011 & 2017).

**RESULTS AND DISCUSSION**

**Observeable attributes:** Genetic data is important in selecting suitable genotypes for crop improvement and conservation (Narasimhulu et al., 2018). Variations observed in the qualitative and quantitative characters depicted different genetic basis for the phenotypic expressions of each trait among the two minor legumes species and accessions. The species studied varied in their growth habit; \(\text{Cajanus cajan}\) accessions were perennial while those of \(\text{Sphenostylis stenocarpa}\) were annual. Considerable variability in vegetative characters was expressed in pigmentation on stem, branch and petiole, leaflet size, stem texture and leaf shape. In spite of the observable morphological differences expressed by the two minor legumes studied, some traits were observed to be common to all the accessions which could be regarded as common diagnostic features. Such traits were reflected mostly in their leaf and flower type. These similarities further lend credence to the fact that the species belong to the same subfamily ‘\text{Pappilionacea}’. Variations

---

Table 1: Passport data and descriptive statistics of the ten accessions of African Yam Bean and Pigeon pea studied.

| Accession | Scientific name | Variance Component |
|-----------|----------------|--------------------|
| NGB01348 | \(\text{Cajanus}\) cajan | Pigeon pea |
| NGB01464 | \(\text{Cajanus}\) cajan | Pigeon pea |
| NGB01468 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |
| NGB01351 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |
| NGB00001 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |
| NGB00002 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |
| NGB00003 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |
| NGB00004 | \(\text{Sphenostylis}\) stenocarpa | Pigeon pea |

Legend: N.S. Non-Significant, P = 0.05, Max = Maximum, Min = Minimum, TLL – Terminal Leaflet Length, TLW – Terminal Leaflet Width, SL – Stipule Length, SW – Stipule Width, DSE – Days from Sowing to emergence, PL – Petiole Length, RL – Rachis Length, IL – Internode Length, NSP – Number of stems per plant, NMB – Number of main branches.
among accessions of the same species were very uncommon, indicative of a closer genetic relatedness.

**Measurable attributes:** Table 1 shows that two accessions (NG/AT/APR/09/014 and 93-IA&T) of the *Sphenostylis stenocarpa* were identified as early maturing accessions which recorded 54 days to 50% flowering compared to other accessions. Both could be utilized as parental accessions for breeding or crossing for early maturity days for AYB while only accession NGB01468 can be regarded as early maturing accession among the five accessions of *Cajanus cajan* (Table 1). This is in agreement with the studies of Popoola et al (2011) and Ojuderie et al. (2015). As presented in Table 2, all accessions of the minor legumes showed high degree of relatedness and variability in their floral and vegetative traits which can be linked to narrow genetic base and plasticity of many underutilized legume species. Number of flowers per peduncle which is a measure of pod and seed yield was observed to be prominent among the accessions with *Sphenostylis stenocarpa* accessions producing more flowers than the *Cajanus cajan*.

However, accessions with higher values for number of stems per plant, main branches per plant and internode length are expected in most cases to produce higher total number of pods per plant and consequently higher number of seeds per plant (Agbolade et al. 2017: Popoola et al., 2011). In addition, the prolific flower production in *Sphenostylis stenocarpa* has been reported by Adewale et al., (2013), supporting the potential capacity of the species for high seed yield. Among the *Sphenostylis stenocarpa* accessions, days from sowing to emergence was the minimum in accession NGB01348 which also recorded moderate days to 50% flowering (63 days)(Tables 1 & 2), this can be used as early maturing accessions in breeding program, conservation and utilization strategies.

**Correlation indices:** Correlation matrices between vegetative quantitative traits indicated that terminal leaflet length and width, stipule length and width, and days from sowing to emergence are important characters of choice that can be integrated into breeding programs of the two species. This is in perfect harmony with the previous studies (Adewale et al., 2010; Popoola et al., 2011; Ojuderie et al., 2015) particularly among the accessions of *Sphenostylis stenocarpa*.

Broad sense heritability for the ten vegetative traits in Table 3 were very high (> 95%) ranging from 95% (Stipule width) to 99.95% (Petiole length). El Soury et al. (2016), obtained such very high (> 95%) broad sense heritability for plant height in *Sesamum indicum*. However, further study to identify the additive component of the broad sense heritability for the ten traits is suggested. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV); this seems to indicate environmental influence in the expression of the studied vegetative traits. Our present report on the PCV and GCV follows the norm reported by many authors: Adewale et al., (2010), Ahsan et al. (2015). But for the >100% PCV and GCV observed in stipule length (Table 3), PCV and GCV of the other traits were lesser than 60%; the least PCV and GCV occurred in terminal leaflet length.

The Principal Component Analysis (PCA) identified terminal leaflet length and width, days from sowing to emergence, petiole length and internode length as vegetative characters that have contributed significantly to the variations expressed in this study (Table 4).

However, all the quantitative floral characters recorded ≥ 0.2 (0.25 – 0.53); indicating the consistency, stability and heritability of floral characters above the vegetative characters in the determination of the genetic variation.

**Table 2:** Descriptive statistics of six quantitative floral characters of the two minor legumes studied.

| Scientific name | Common name | Accession no | SPL | SPW | PDL | CLL | D50% | NFP |
|-----------------|-------------|--------------|-----|-----|-----|-----|------|-----|
| *Sphenostylis stenocarpa* | African | NG/AT/APR/09/014 | 2.11 | 0.93 | 9.13 | 0.17 | 54 | 10.5<sup>Max</sup> |
| | | NG/OA/09/11/058 | 2.62 | 1.11 | 6.18 | 0.81 | 63 | 15 |
| | | NGB01351 | 1.43 | 0.4<sup>Min</sup> | 8.04 | 0.2 | 78 | 9 |
| | | NGB01348 | 1.65 | 0.7 | 8.03 | 0.15 | 63 | 7.5 |
| | | 93-IA&T | 2.71<sup>Max</sup> | 1.43<sup>Min</sup> | 5.5<sup>Min</sup> | 0.1<sup>Min</sup> | 54 | 6.1 |
| *Cajanus cajan* | Pigeon pea | NGB01456 | 1.57 | 0.72 | 12.04 | 0.99<sup>Max</sup> | 78 | 2<sup>Min</sup> |
| | | NGB01462 | 1.74 | 0.48 | 10.35 | 0.16 | 60 | 5.5 |
| | | NGB01464 | 1.42<sup>Min</sup> | 0.51 | 12.61<sup>Max</sup> | 0.13 | 81<sup>Max</sup> | 3 |
| | | NGB01466 | 1.81 | 0.62 | 7.63 | 0.17 | 67 | 3.5 |
| | | NGB01468 | 2.51 | 0.51 | 10.54 | 0.14 | 45<sup>Min</sup> | 4.51 |
| Mean | | | 1.96 | 0.74 | 9.01 | 0.30 | 64.3 | 6.66 |
| S.E | | | 0.16 | 0.10 | 0.75 | 0.10 | 3.75 | 1.26 |
| Variance | | | 0.25 | 0.11 | 5.60 | 0.10 | 140.90 | 15.76 |
| Coef. Variation | | | 25.35 | 43.95 | 26.29 | 105.23 | 18.46 | 59.60 |

Legend: SPL – Standard Petal Length, SPW – Standard Petal Width, PDL – Peduncle Length, CLL – Calyx Lobe Length, D50% - Days to 50% flowering, NFP – Number of flowers per peduncle. Min - Minimum, Max – Maximum.
Table 3: Estimates of the broad sense heritability, phenotypic and genotypic coefficient of variations for the vegetative characters.

| Traits                          | Heritability (%) | PCV (%) | GCV (%) |
|---------------------------------|------------------|---------|---------|
| Terminal Leaflet Length         | 99.03            | 20.24   | 20.14   |
| Terminal Leaflet Width          | 97.48            | 37.44   | 36.97   |
| Stipule Length                  | 99.66            | 105.47  | 105.29  |
| Stipule Width                   | 95.09            | 35.99   | 35.10   |
| Days from Sowing to emergence   | 99.05            | 44.54   | 44.32   |
| Petiole Length                  | 99.95            | 59.25   | 59.23   |
| Rachis Length                   | 98.01            | 45.14   | 44.69   |
| Internode Length                | 99.53            | 24.78   | 24.72   |
| Number of Stems per plant       | 99.50            | 35.30   | 35.21   |
| Number of Main Branches         | 99.75            | 28.17   | 28.14   |

Table 4: Eigen values and contribution of the first five principal component axes (PCA) to variation in AYB/Pigeon pea accessions studied based on 10 vegetative quantitative traits.

| Variables                          | PC1     | PC2     | PC3     | PC4     | PC5     |
|------------------------------------|---------|---------|---------|---------|---------|
| Terminal Leaflet Length            | 0.41    | -0.297  | -0.041  | 0.007   | -0.012  |
| Terminal Leaflet Width             | 0.424   | 0.118   | 0.311   | 0.117   | -0.01   |
| Stipule Length                     | -0.426  | 0.024   | 0.215   | 0.16    | 0.429   |
| Stipule Width                      | 0.193   | -0.395  | -0.402  | 0.511   | 0.038   |
| Days from Sowing to emergence      | 0.467   | -0.119  | 0.051   | 0.169   | 0.044   |
| Petiole Length                     | 0.234   | 0.345   | -0.394  | -0.423  | -0.142  |
| Rachis Length                      | -0.169  | -0.488  | -0.156  | -0.476  | -0.369  |
| Internode Length                   | 0.324   | 0.132   | 0.496   | -0.288  | 0.04    |
| Number of Stems per plant          | -0.145  | -0.304  | 0.501   | 0.15    | -0.558  |
| Number of Main Branches            | -0.07   | 0.51    | -0.119  | 0.4     | -0.586  |
| Eigen values                       | 4.098   | 2.455   | 1.7792  | 0.643   | 0.523   |
| Percent variation                  | 0.41    | 0.246   | 0.178   | 0.064   | 0.052   |
| Cumulative Proportion              | 0.41    | 0.655   | 0.833   | 0.898   | 0.95    |

PC = Principal Component, Eigenvectors with values ≥ 0.20 used as cut off point.

Table 5: Eigen values, variance proportion of five PC-Axes and Eigen vector of five floral characters.

| Character                          | PC1     | PC2     | PC3     | PC4     | PC5     |
|------------------------------------|---------|---------|---------|---------|---------|
| Standard petal length              | 0.53    | -0.3    | -0.07   | -0.65   | -0.54   |
| Standard petal width               | 0.43    | 0.28    | -0.73   | 0.45    | -0.02   |
| Peduncle length                    | 0.47    | 0.28    | 0.53    | 0.58    | -0.29   |
| Calyx lobe length                  | 0.49    | -0.29   | -0.01   | -0.22   | 0.75    |
| Number of flower per Peduncle      | 0.25    | -0.39   | 0.43    | -0.06   | 0.25    |
| Eigen Values                       | 3.23    | 1       | 0.54    | 0.13    | 0.08    |
| % Variance Per PC-axes             | 0.6466  | 0.21    | 0.11    | 0.03    | 0.02    |
| % Cumulative variance across PC axes| 0.6466  | 0.85    | 0.96    | 0.98    | 1       |

NB: Eigen vectors ≥0.2 are in bold

Fig 1: Cluster analysis of the two minor legumes (AYB/Pigeon pea) based on vegetative quantitative characters.
variability among the studied taxa (Table 5). This result partly
agrees with the result of Popoola et al. (2017).

In accordance with Figs 1&2, the cluster analysis of the
quantitative vegetative and floral characters generated
different outcomes. The comparative cluster analysis of the
vegetative characters showed that cluster group I consisted
of five accessions of *Sphenostylis stenocarpa* and were
associated with terminal leaflet length and width, rachis
length, stipule length and width, days from sowing to
emergence and number of main branches per plant (Fig 1).
Similar trends was observed for cluster group II which also
consisted of five accessions of *Cajanus cajan* associated with
stipule length and width, days from sowing to emergence,
petiole length, number of stem per plant and internode
length (Fig 1). Contrarily, the floral cluster generated
interrelation of the accessions (Fig 2).

High degree of relatedness and similarity recorded
supports the narrow gene pool or genetic diversity reported
among minor legumes (McKee and Latner, 2000). The
clustering observed is indicative of taxonomic classification
of these legumes in the family *Fabaceae* with similar diploid
genome of 11 pairs of chromosome (2n=2x=22) (Popoola
et al. 2011). The narrow gene pool among minor legumes
has been connected to fewer genotypes with high degree of
relatedness usually used in heterosis or breeding programmes
for the development of new cultivars which leads to
narrowing down the genetic base of the species (Yang
et al., 2011; Yadav et al., 2012). Recently, studies using evidences
from other genetic markers such as RAPD, RFLP, AFLP,
Dart, ISR, SSR and SNP supported the narrow genetic bases
of the domesticated Pigeon pea and African yam bean
(Ammar et al., 2015; Shitta et al., 2016).

CONCLUSION
Understanding variation and its pattern among crop’s
germplasm is an essential material for crop improvement.
This study investigated levels of morphological variation
in floral and vegetative characters and also evaluated the
relative importance of each trait in contributing to the
variability of the two minor legume species evaluated. Result
obtained is useful for maintenance of diversity and future
breeding work, the variability data vis-a-vis the correlation
indices of traits’ performance is a pointer to selecting suitable
traits for crop improvement and conservation.

REFERENCES
Adewale, B.D., Kehinde, O.B., Aremu, C.O., Popoola, J.O. and Dumet, D.J. (2010a). Seed Metric for genetic and shape determinations
in african yam bean [Fabaceae] (Sphenostylis stenocarpa Hochst. Ex. A. Rich) Harms). Afr. J. Plant Sci. 4:107-115.
Adewale, B.D., Okonji, C., Oyekanmi, A. A., Akintoni, D. A. C. and Aremu, C. O. (2010b). Genotypic variability and stability of some
grain yield components of cowpea. *African Journal of Agricultural Research* 5:874-880.
Adewale, B.D. and Odoh, N.C. (2013). A review on genetic resources, diversity and agronomy of african yam bean (Sphenostylis
stenocarpa) (Hochst, Ex A. Rich.) Harms): a potential future food crop. *Sustainable Agr. Res.* 5:32-38.
Agbolade, J.O. and Komolafe, R.J. (2016). Genetic diversity and phylogenetic behaviour of some minor legumes. *Inter. J. Plant Biol.*
7:15 - 21
Agbolade, J.O., Adekoya, M.A., David, O.A., Chukuma, D.M., Komolafe, R.J. and Olaya, A.E. (2017). Genetic diversity in pigeon
pea (Cajanus cajan L. Millspaugh) germplasm revealed by gel electrophoresis of the seed proteins. *J. Plant Sci.* 6: 48 - 55.
Ahsan, M.Z., Majidano, M.S., Bhutto, H., Soomro, A.W., Panhwar, F.H., Channa, A.R. and Sial. K.B. (2015). Genetic variability,
coefficient of variance, heritability and genetic advance of some *gossypium hirsutum* l. accessions. *J. Agr. Sci.* 7: 147 – 151.
Ammar, M.H., Alghamdi, SS.., Migdadi, H.M., Khan, M.A., El-Harty, E.H. and Al-Faifi, S.A. (2015). Assessment of genetic
diversity among faba bean genotypes using agro-morphological and molecular markers. *Saudi J. Biol. Sci.* 22: 340-50.
El Soury, H.F., El Bashir, G and Ginaro, M.K. (2016). Phenotypic and genotypic coefficients of variation and other growth attributes
in sesame genotype under rain-fed conditions. *Advances in Agr. and Agr. Sci.* 2079 – 084.
FAOSTAT (2014). Food and agricultural organization of the united nations.http://faostat.fao.org/site/567/default.aspx#anchor (Accessed
on 25/05/2018).
McKee, L.H. and Latner, T.A. (2000). Underutilized sources of dietary fiber: a review: *Plant Foods Hum. Nutr.* 55 : 285-304.
Narasimhulu, R., Naidu, N.V. and Ready, K.H.P. (2018). Genetic analysis for yield and yield attributes in green gram [*Vigna radiata* (L.)
Wilczek]. *Legume Res.* 41:349-355.
Nnamani, C.V., Ajayi, S.A., Oselebe, H.O., Atkinson, C.J., Igboabuchi, A.N. and Ezigbo, E.C. (2017). *Sphenostylis stenocarpa* (ex. A. Rich.) Harms., a fading genetic resource in a changing climate: prerequisite for conservation and sustainability. *Plants* (Basel) **6**:30

Ojuederie, O.M., Balogun, M.O., Akande, S.R., Korie, S. and Omodele, T. (2015). Intraspecific variability in agro-morphological traits of African yam bean *Sphenostylis stenocarpa* (Hochst ex. A. Rich) Harms. *J. Crop Sci. Biotech.* **18**: 53 - 62

Okeola, O. G. and Machuka, J. (2001). Biological effects of african yam bean lectins on clavigralla tomentosicollis (Hemiptera: Coreidae). *J. Econ. Entomol.* **94**: 724-9.

Popoola, J. O., Adebayo, M.B., Adebibite, A.E., Omonhinmin, A.C. and Adebale, B.D. (2017). Fruit morphometric and RAPD intraspecific variability in african yam bean (*Sphenostylis stenocarpa* Hochst. ex. A. Rich. Harms). Annual Res. and Rev. in Biol. **14**:1-10.

Popoola, J. O., Adebibite, A.E., Obembe, O.O. and Agbolade, J.O. (2011). Reproductive mechanisms and pollen characterization in some accessions of an underutilized legume: (*Sphenostylis stenocarpa* Hochst Ex. A. Rich) harms, *Int. J. Biodiversity and Conservation*, **6**:185-192.

Pundir, R. P. and Singh, R.B. (1985). Biosystematic relationships among *Cajanus*, *Atylosia*, and *Rhynchosia* species and evolution of pigeonpea (*Cajanus cajan* (L.) Millsp.): *Theor Appl Genet.* **69**: 531-4.

Rajni, K. and Vikas, N. (2018). Proximate composition, nutritional profile and health benefits of legumes-a review. *Legume Res.* **41**:325-332.

Roman, R.M., Wilcox, C.J. and Martin F.G. (2000). Estimate of repeatability and heritability of productive and reproductive traits in a herd of jersey cattle. *Genet. Mol. Biol.* 23:113-119.

Scott Armbruster, W. (2014). Floral specialisation and angiosperm diversity: Phenotypic divergence, fitness trade-offs and realized pollination accuracy. *AoB Plants*. 6https://doi.org/10.1093/aobpla/plu003.

Shitta, N.S., Abberton, M.T., Adesoye, A.I., Adewale, D.B. and Oyatomi, O. (2016). Analysis of genetic diversity of african yam bean using SSR markers derived from cowpea. *Plant Genet. resources* **14**:50-56.

Singh, S.P., Yadav, R.S., Amit, K. and Jakhar, R.R. (2018). Productivity augmentation of green gram(*Vigna radiata*) through weed management. *Legume Res.* **41**:410-415.

Yadav, K., Yadav, S.K., Yadav, A., Pandey, V.P. and Dwivedi, U.N. (2012). Genetic diversity of pigeon pea cultivars and its wild relatives using randomly amplified polymorphic DNA (RAPD) markers. *Amer. J. Plant Sci.* **3**:322-330.

Yang, S. Y., Saxena, R. K., Kulwal, P. L., Ash, G. J., Dubey, A., Harper, J.D., Upadhyaya, H.D., Gothwal, R., Kilian, A. and Varshney, R.K. (2011). The first genetic map of pigeon pea based on diversity arrays technology (DArT) markers. *J. Genet.* **90**: 103-9.