"Assessment of genetic variability for high harvest index in summer groundnut" (*Arachis hypogaea* L.)

by

Mr. BAGAL KAILAS NEMINATH
(Reg. No. 014 /051)

A Thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI - 413 722, DIST. AHMEDNAGAR, MAHARASHTRA (INDIA)

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE
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MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722**
2016

CANDIDATE'S DECLARATION

I here by declare that this thesis or a part

There of has not been submitted

by me or any other person

to any other University

or Institute for

a Degree or

Diploma.

Place : M.P.K.V. Rahuri

Date : / / 2016 **(BAGAL K. N.)**

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CERTIFICATE

This is to certify that the thesis entitled, **"Assessment of genetic variability for high harvest index in summer groundnut (*Arachis hypogaea* L.)"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr.BAGAL KAILAS NEMINATH** under my guidance and supervision and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : M.P.K.V. Rahuri **(Dr.V.L.Amolic)**
Date : / /2016.

Dr. B.R. Ulmek,
Associate Dean,
Post Graduate Institute,
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Rahuri - 413 722, Dist. Ahmednagar,
Maharashtra State (India).

CERTIFICATE

This is to certify that the thesis entitled, submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr. BAGAL KAILAS NEMINATH** under the guidance and supervision of **Dr. V.L. AMOLIC,** Groundnut Breeder, AICRP on Groundnut, M.P.K.V., Rahuri, and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : M.P.K.V. Rahuri **(Dr.B.R. Ulmek)**
Date : / /2016.

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Place : M,P.K.V. Rahuri

Date : / /2016 (BAGAL K. N.)

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ABSTRACT

"Assessment of genetic variability for high harvest index in summer groundnut" (*Arachis hypogaea* L.)"

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MAHATMA PHULE KRISHI VIDYAPEETH,

RAHURI – 413 722

2016

Research Guide : Dr. V.L. Amolic

Major discipline : Genetics and Plant Breeding

The present investigation entitled "Assessment of genetic variability for high harvest index in summer groundnut" (*Arachis hypogaea* L.)" was undertaken to estimate the genetic variability for nine F_2 crosses in summer groundnut.

Total nine F_2 crosses were evaluated during summer, 2015 season in a randomized block design with three replications at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.). Observations were recorded on the traits *viz.*, Days to 50% flowering, Days to maturity, Plant height(cm), Number of branches per plant, Number of mature pods per plant, , Dry haulm yield per plant(gm), Number of immature pods per plant(gm), Dry pod yield per plant(gm), Hundred kernel weight%, Shelling percentage, Harvest index%, Oil content%, Protein content% & Sound mature kernel%. The treatment differences were statistically significant for majority of the characters and

also the magnitude of genotypic and phenotypic coefficients of variations indicated the presence of good amount of variability.

The character Dry haulm yield per plant, Plant height, Number of immature pods per plant, Number of mature pods per plant,, Harvest index have high heritability with high genetic advance. Dry pod yield per plant & oil % have high heritability with medium genetic advance. Days to maturity show low heritability with low genetic advance.

The estimates of phenotypic coefficient of variation (PCV) were magnitudinally higher than the estimates of genotypic coefficient of variation (GCV) for all the characters studied indicating the influence of environment on these traits.

Heritability is used to predict the resemblance between parents and their progeny. Where as, the genetic advance provides the knowledge about expected gain for a particular character after selection.

Transgressive segregation

Transgressive segregants in desirable direction were observed for all characters in each of the three crosses in F_2 generation. In general the highest proportion of transgressive segregants were recorded for Dry pod yield per plant (gm), followed by Harvest index%, Number of mature pods per plant, Days to 50% flowering, 100 kernel wt, Sound mature kernel% and Shelling%. On the basis of performance of transgressive segregants, it was concluded that, when the desired intensity of a character is not available in the parents, transgressive breeding can be successfully be used to extend the limit of expression of character. This could be possible by accumulation of favourable plus genes, in a hybrid derivatives from both parents, involved in hybridization.

In most of the transgressive segregants, in each of the three crosses, better parent yield was transgressed simultaneously with transgression of one or several other characters. Simultaneous transgression of Dry pod yield per plant (gm)in association with number of mature pods per plant, Harvest index%, Days to 50% flowering was observed more frequently. It was concluded that either Dry pod yield per plant (gm) is dependent on this character or there may be linkage drag so that genes responsible for these characters move together.

The most promising transgressive segregants *viz.,* plant No.45 of Phule Unnati x TPG 41, plant No.222 of Phule 6021 x RHRG 6110, plant No.111 of Phule Unnati x SB XI transgressed grain yield per plant in addition to the higher expression of other three or four characters than the increasing parent. They produced 76.79 (Phule 6021 x RHRG 6110) 66.52 (Phule Unnati x SB XI) and 46.77 (Phule Unnati x TPG 41) per cent more Dry pod yield per plant(gm) than their respective increasing parents. These transgressant needs to be evaluated further for maintaining consistency in their performance. If they found superior in further generations, they may be identified as improved varieties after adequate evaluation or used in further breeding programme for amulgamation of genetic constellations.

1. INTRODUCTION

Groundnut (*Arachis hypogaea L.*) is a major oilseed crop in India. The crop accounts for near about 45.00 per cent of total area under oilseed and 55.00 per cent of the oilseed produced in the country. Groundnut seeds contain about 50.00 per cent edible oil and 25.00 per cent protein. The haulms are used as valuable nutritious fodder. Groundnut oil cake is an important cattle feed and a good soil amendment.

Major groundnut producing countries of the world are China, USA, India, Senegal, Brazil and West Africa. The India is second in production of groundnut after China. The total area in India under groundnut cultivation was 5.505 million hectares in the year 2015-16with production of 5.106 million tonnes and productivity of 1078 kilogram per hectare (Source: Department of agriculture cooperation govt. of India, 2015).

In Maharashtra, total area under groundnut cultivation was 0.315 million hectare with production 0.167 million tonnes and productivity of 1080 kg per hectare during year 2015-16. (Source: Department of Economics and Statistics, Dept. of Agriculture and Cooperation, 2015).

The word groundnut (*Arachis hypogaea* L.) is derived from the Greek word “Arachis” meaning legume and “hypogaea” meaning below ground. It is commonly known as peanut, monkeynut and goobernut. Groundnut is self pollinated, tetraploid with chromosome number 2n=40.

Table No 1 :-Area, Production and Productivity of Groundnut in major producing states (2015-16).

State	Area (M.ha.)	Production (M.T.)	Productivity (Kg/ha.)
Gujarat	1.84	2.20	1563
Andhra Pradesh	1.38	0.48	361
Tamil Nadu	0.36	0.906	2202
Rajasthan	0.462	0.889	1931
Karnataka	0.655	0.21	650
Maharashtra	0.315	0.167	1080
Madhya Pradesh	0.19	0.38	1618
Orissa	0.059	0.028	830
Uttar Pradesh	0.09	0.093	1000
Others	0.11	0.12	---
All India	5.505	5.106	1078

(Source: Ministry of agriculture, Govt. of India, 2015 and Department of Economics and Statistics, Dept. of Agriculture and Cooperation, 2015).

The genus *Arachis* is a member of family Fabaceae (synonym: Leguminoseae), subfamily papillionoidae, tribe Aeschynomeneae and subtribestylosanthinae. It belongs to the section *Arachis*and series amphiploidies and the family Fabaceae (Gregory *et al.,* 1980). The species *Arachishypogaea* consists of two subspecies, *Hypogaea* sp. and *Fastigiata* sp. Each subspecies has two botanical varieties. Four cultivated types of groundnut according to Krapovickas and Rigoni (1957) are;

1. *Arachis hypogaea* Linn.
2. *Arachis hirsute* Kohler.
3. *Arachis fastigiata* Waldron.
4. *Arachis fastigiata vulgaris* Harz.

Cultivated groundnut can be botanically classified into two subspecies differing in branching pattern viz, subspecies *hypogaea* with alternate branching and subspecies *fastigiata* with sequential branching. Each subspecies is again divided into two botanical varieties, *subsp.Hypogaea* into variety *hypogaea* (Virginia) and *var.hirsuta*; and subsp. *Fastigiata* into *var. Fastigiata* (Valencia), *var.Vulgaris* (Spanish), *var.*peruviana, and *var.*aequatoriana in trade. The bold seeded types are referred as *Virginia*, the small seeded as Spanish and a third type runner is also recognized.

Groundnut belongs to C_3 plant, it needs good sunshine and high temperature to produce more pods.

Therefore summer is the ideal season for groundnut cultivation wherever irrigation facilities are available. The average total dry matter produced per plant in bunch groundnut at harvest is 25.7% in summer season (Ong, 1986).

Diseases are major constraints to groundnut production throughout the country during *kharif.* However, during *Summer* attack of diseases and pests are very less than *Kharif* season. In summer, bud necrosis disease is the major cause of poor yield.

Some of the reasons for low productivity of groundnut in the country are,

i) Optimum sowing time is not followed.
ii) Use of uncertified seeds.
iii) Recommended dose of fertilizer is not applied at proper time.
iv) Irrigation schedule is not followed properly.
v) Foliar diseases.

The use of uncertified seed and local types is one of the causes of poor groundnut yield in India. Groundnut needs good sunshine and high temperature to produce more pods (Cox, 1978 and Ong, 1984) leading to higher productivity. Now, looking to the most favourable condition and high productivity of summer crop, it is essential to develop a genotype with fairly high yield potential than the existing ones to boost up productivity of groundnut substantially. The primary aim of plant breeder is to evolve the variety which will be superior to the existing one in respect of yield and quality. This may be achieved by selecting the promising types from naturally existing variation or by hybridization followed by selection of the good recombinants.

In formulating any hybridization programme, it is prerequisite to have genotype with higher yield potential i.e. high *per se* performance. In groundnut with this it is also important to have divergent parents with good performance for yield as well as other quantitative characters for hybridization, to obtain desirable segregants through selection in advanced generations. It is already proved in many crops that by using divergent parents, heterotic hybrids can be obtained than those between closely related.

The magnitude of variability and the knowledge of extent to which desirable characters are heritable is a pre-requisite for crop improvement. The inbuilt variability in the breeding material is very important for selection of superior plant types, where selection of superior plant is based not only on yield alone but also on the yield contributing characters. For the reliable field selection, it becomes necessary to partition the relative amounts of heritable and non-heritable variability exhibited by yield contributing characters.

Production of transgressive segregants for yield and its components like Dry pod yield, harvest index and mature pod number, plays a vital role in breeding programme. Although transgressive segregants includes lines which fall outside the range of performance of either parents, but only those being superior to better parents in desirable direction are of practical value. Therefore, a breeder is more concerned with obtaining higher frequency of transgressive segregants in segregating population, as it provides him a better scope for exercising selection to improve productivity

The present study was undertaken to access variability and transgressive segregants in a set of groundnut genotypes irrespective of their growth habit for yield and other component characters.

Keeping in view, in the above important aspects, the present investigation was carried out with the following objectives.

1. To study genetic variability for high harvest index in summer groundnut.
2. To study the genetic variability for different traits in summer groundnut.
3. To identify transgressive segregants for yield and yield contributing character in summer groundnut.

2. REVIEW OF LITERATURE

Attempts have been made to review the published literature on variability and transgressive segregants for important economic characters related to yield in groundnut. The review of literature is presented below under different subheadings.

2.1 Variability in groundnut

2.2 Identification of transgressive segregants in groundnut.

2.1 Variability in groundnut

Ganeshan and Sudhakar (1995) reported high PCV and GCV for pods per plant followed by primary branches. This difference between PCV and GCV was minimum (0.08) for oil percentage, suggesting that this trait was least affected by the environment. This was supported by very high value of heritability (95.77 %) for the character. The plant height, on the other hand, exhibited high gap (6.04) between PCV and GCV indicating role of high environmental influence on the character expression.

Reddy (1995) reported genetic variation and heritability derived from data on 12 yield-related traits in 48 spanish bunch groundnut (*Arachis hypogaea L.*) genotypes grown at Tirupati during *kharif* 1990. percentage, sound mature kernel weight and pod yield per plant. High heritability coupled with moderate genetic advance as percent of mean (GAM) was recorded for protein and sound mature kernel weight. Oil content showed high heritability with low GAM. It was also observed that variability and heritability for chlorophyll content and yield in 40 peanut genotypes and reported wide variability and moderate heritability values for chlorophyll content and seed weight per plant. High GCV, PCV and heritability and genetic advance were noticed for harvest index and its component traits viz., pod yield per plant, number of branches per plant and sound mature kernel percentage.

Reddy *et al.* (1995) estimated heritability values for 12 yield components using F_3, F_4 and F_5 progenies, involving parents. Heritability values varied between generations, but were consistently high for secondary branches per plant, plant height and shelling percentage. The influence of environment was evident for number of pods, number of mature pods and pod yield per plant in the F_3 and F_4 generations, as these characters recorded negligible heritability estimates.

Uddin *et al.* (1995) studied variability, correlation and path coefficient analysis for seven yield components in 23 divergent groundnut genotypes during 1988-89. High genotypic coefficients of variation were observed for seed yield/plant, seeds/plant, primary branches/plant, plant height and 100 seed weight. Heritability estimates were high for all of the traits studied. All the characters, except days to maturity and shelling percentage had moderate to high genetic advance.

Gowda *et al.* (1996) studied variability available for all selection, the nature and magnitude of the association with productivity and pod morphology. High levels of variability were recorded for leaf area affected by the disease, pod yield and pod number. High productivity was associated with larger pods and thick shells and low disease resistance. The frequency of desirable recombinants for pod yield, shelling percentage, sound mature kernel percentage and shell thickness was very low.

Singh *et al.* (1996) in seven selections of F_4 generation lines derived from three crosses in HPS groundnut observed an exploitable amount of genetic variability for days to first flowering, length of main axis, mature pods, 100 seeds weight, shelling percentage and dry pod yield.

Khader and Gowda (1997) studied three-way back and double crosses of Virginia and Valencia bunch type varieties of groundnut with RMPL and P-1393516 and they were evaluated in the S_1 during *kharif* 1991 for yield components. Variability was greater between families than within families for most of the characters. Family selection in S_1 was recommended.

Naik and Nadaf (1997) generated variability for various quantitative characters in *A. hypogaea.* Dharwad Early Runner (DER), a growth habit variant, was treated with ethyl methane sulphonate (EMS) and resulting six mutant lines further treated with EMS (0.5 %). Seed of treated plants were grown for 2 generations during 1993-95 and evaluated for five yield components. Out of seven genotypes treated, DER, 124-5 and 225-1 were the most sensitive to treatment. Number of pods per plant and 100 seed weight were the most sensitive yield components to mutagenic treatment.

Chandran *et al.* (1998) collected 23 samples of *Arachis hypogaea* cv. TMV-2, released in 1940, from Karnataka, Andhra Pradesh, Tamil Nadu and Kerala and evaluated at Junagadh during 1994-95. Variations were found mainly in branching pattern, stem hairiness and leaflet hairiness, while most other characters, including seed storage proteins, had maintained their homogeneity.

Islam and Rasul (1998) reported high magnitude of GCV for pods per plant and seed yield.

Jayalakshmi *et al.* (1998) studied genotypic and phenotypic coefficients of variation, heritability and genetic advance to specific leaf area, total dry matter, pod weight per plant and harvest index in seven F_4 progenies in each of eight groundnut crosses grown during *rabi* 1996-97 at Tirupati. ICGV 86031 x JL-24 was the best for harvest index.

Ramesh Kumar *et al.* (1998) In twenty-seven M_7 groundnut mutants along with parent (AK-12-24) and two checks, observed high genotypic and phenotypic coefficient of variation for length of main axis, number of kernels per pod, kernel yield per plant and oil yield per plant.

Khurram *et al.* (1998) studied 12 elite genotypes of groundnut in 1993-94. Estimates of variability were worked out for ten characters. The differences among the genotypes were significant for all the characters studied except for oil content where the differences were non-significant.

Salara and Gowda (1998) studied sufficient variability existed in the crosses for selection to be effective for various characters. Pod yield and pod number exhibited high coefficient of variation values and genetic advance compared to test weight, shelling percentage and sound mature kernel percentage. Germination percentage exhibited the maximum variability.

Vasanthi *et al.* (1998) studied interrelationships among yield and its attributes and late leaf spot sensitivity in

11 elite lines and three varieties. A significant and positive association of shelling percentage and haulm weight per plant was reported.

Yadav *et al.* (1998) derived information on genetic variability, heritability and genetic advance from the data on seven yield and quality related traits in 34 strains/varieties of Spanish bunch groundnut (*Arachis hypogaea L.*) grown at Kanpur. High genotypic and phenotypic coefficients of variability were observed for pod yield and 100 pod weight. Heritability was high for all the characters under study. Genetic advance was highest for pod yield per plot followed by 100 pod weight and 100 kernel weight.

Rudraswamy *et al.* (1999) derived information on genetic variability, heritability and inbreeding depression from data on parental, F_1, F_2 and F_3 generations of six crosses of groundnut, grown at Banglore during *kharif* 1989. For Number of secondary branches, number of immature pods, pod yield per plant and shelling percentage, the genetic advance was moderate because of high heritability and variability in some of the crosses. None of the other characters in any cross showed substantial genetic advance, pod yield and other characters showed moderate to high genetic advance.

Singh and Singh (1999) derived information on heritability and genetic advance from data on high yield components in 44 lines grown during *kharif* 1994, 1995 and 1996. High values for heritability (78.00 %) were shown by days to maturity, plant height, primary branches per plant, pods per plant, pod weight per plant, shelling percentage and 100 kernel weight.

Gimenes *et al.* (2000) studied genetic variation and phylogenetic relationship based on RAPD analysis in section caulorrhizae, genus, Arachis (Leguminoseae). They studied many new accessions of the two species (*Arachis repens* and *A. pintoi*) and found that these accessions harbour significant genetic variability beyond that available in the few older accessions, previously available. Therefore, these new accession need to be conserved, documented and considered in terms of their potential for crop improvement and direct commercial use.

Kale and Murty (2000) by crossing a selection TG-19 having large pods low yield and dormancy with high yielding cultivars TAG-24 and TG-26, true breeding selection with large kernels, designated as TGLPS-1-8 were established in F_5 generation. For four seasons, they showed superior yield over the large kernel checks, TKG-19A and BAU-13. Among the eight selections, TGRPS-2, 3 and 7 were found to have desirable traits such as early maturity, high yield and large kernels (> 80 g 100-kernel weight) and lacked dormancy. Due to lower oil content, they may suit for table purpose.

The findings of Prakash *et al.* (2000) in 91 genotypes of spreading groundnut for eight characters revealed a broad range of phenotypic variability for all characters except for days to 50 per cent flowering. GCV ranged from 3.68 (oil percentage) to 18.72 (pods per plant). The highest PCV (31.13) and GCV (29.20) were noticed for yield per plant followed by pods per plant.

Shoba *et al.* (2009) made crosses to develop a foliar disease resistant groundnut lines with acceptable pod and kernel traits using TMV-2 and three foliar disease resistant parents. Three F_2 cross derivatives and their four parents were used to study their mean performance, genetic variability, heritability and genetic advance as percentage of mean for yield and contributing characters. Among the crosses, TMV-2 x COG-0437 had higher mean performance for all the characters followed by TMV2 x COG 438. Higher PCV and GCV values were also recorded by this cross. The cross TMV-2 x COG-0437 had high heritability and high to moderate GAM for most of characters followed by TMV-2 x COG-0438. Hence, based on mean and variability parameters, TMV-2 x COG-437 is adjudged as best cross combination for further selection programme to evolve a promising progeny.

John *et al.* (2009) studied that High heritability along with high GAM was observed for number of secondary branches per plant, number of immature pods per plant, shelling percentage, 100-kernel weight, SMK weight,total number of pods, total number of gynophores, maturity index, reproductive efficiency and pod yield. This showed additive type of gene action plays an important role. It indicates that phenotypic selection for these characters will be effective. Pod and kernel yields per plant showed significant and positive association with number of secondary branches per plant, number of mature pods per plant, SMK weight, SMK number, 100-kernel weight. So these characters have been considered as selection indices for the improvement of kernel and pod yields per plant.

Korat *et al.* (2009) evaluated eighty diverse genotypes of bunch groundnut during summer 2006 for genetic parameters *viz.*, variability, heritability and genetic advance. The estimates of PCV and GCV were high for number of secondary branches per plant and number of aerial pegs per plant. High heritability along with high genetic advance as per cent of mean was observed for number of secondary branches per plant and number of aerial pegs per plant indicating that these traits are mainly governed by additive gene action and responsive to selection for further improvement of these traits.

Malave (2009) estimated the genetic variability, correlation between dry pod yield and other yield contributing characters and genetic divergence on one hundred germplasm lines and two checks of summer groundnut. A wide range of variability was observed in respect of days to flower intiation (27.50-45.50), plant height (20.50-50 cm). Number of filled pods per plant (9.90-35.50),fresh pod yield per plant (8.01-29.32 gm).the fresh haulm yield per plant showed the highest heritability followed by harvest index, dry haulm yield per plant, plant height, days to flower intiation, number of filled pods per plant.Total 102 genotypes were evaluated during summer 2009, in a randomized block design with two replications at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, District Ahmednagar (M.S).

Cholin *et al.* (2010) studied that the groundnut (*Arachis hypogaea* L.) is the world's third most important source of oil and fourth most important source of vegetable protein. Oil content, protein content and fatty acid composition (O/L ratio) are the most important quality attributes of groundnut. A mapping population segregating for these traits was evaluated for genetic variability and correlation among the traits. The population exhibited significant variation among the genotypes, seasons and G x E interaction. Moderate magnitude of variability followed by higher heritability was observed for most of the quality traits. Negative correlation between oil and protein content, oleic and linoleic acid indicated their antagonistic nature. All the eight fatty acids were correlated with each other either positively or negatively. Superior RILs were identified for higher protein content, oil content, oleic acid and O/L ratio from the population.

Aghav (2010) evaluated fifty five genotypes of summer groundnut for variability, path analysis and genetic diversity during summer 2010, at Rahuri. Appreciable amount of variability was observed for all characters studied. The magnitudes of genotypic and phenotypic coefficient of variation indicated the presence of good amount of variability. The number of mature pods showed highest heritability followed by harvest index, oil content, dry pod yield and fresh pod yield per plant. The number of mature pods showed highest genetic advance, while other characters recorded moderate genetic advance.

Singh *et al.*(2010) evaluated thirty two groundnut genotypes of both spreading and bunch types for their yield, yield attributes, seed protein and oil content to analyse the degree of genetic variability in quantitative and qualitative traits. This degree of variation in seed yield and quality traits offer an opportunity to further evolve the promising groundnut varieties to boost both the seed and oil production in the country.

K. John & P. Raghava Reddy et.al (2011) Twenty eight F_2 populations were evaluated for genetic parameters of 23 characters of morphological, physiological, yield and yield attributes during *rabi* 2009. TPT-4 x ICGV-91114 was distinct for its lowest mean value for days to maturity and highest mean values for number of well-filled and mature pods per plant, shelling per cent, 100- kernel weight. The F_2 involving JL-220 as one of the parents *viz.*, JL-220 x ICGV 99029 for SCMR, JL-220 x TCGS- 647 for SMK per cent, protein per cent, kernel yield per plant and pod yield per plant showed the highest *per se* performance High genotypic coefficient of variation was observed for number of secondary branches per plant. High heritability and high GAM was recorded for number of secondary branches per plant, high heritability and moderate GAM observed for days to 50% flowering. Moderate heritability and high GAM was showed for leaf area index, number of well filled and mature pods per plant, dry haulms yield per plant and harvest index. This indicates that these characters are under additive genetic control and selection for genetic improvement will be worthwhile and may rapidly contribute yield

Kamble (2013) estimated the amount and nature of variability and association among dry pod yield and yield contributing characters and direct and indirect contribution of component characters to the dry pod yield and nature and magnitude of divergence on 55 germplasm lines and five checks of summer groundnut. total 60 germplasm lines evaluated in 2013, in randomized block design with two replication at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi vidyapeeth, Rahuri, Dist Ahmednagar (M.S)

Dhage (2013) estimated the amount and nature of variability and association among dry pod yield and yield contributing characters and direct and indirect contribution of component characters to the dry pod yield and nature and magnitude of divergence on 55 germplasm lines and one checks (Phule unnati) of summer groundnut. the character percent oil content showed the highest heritability followed percent protein content, dry pod yield per plant, fresh pod yield per plant, number of mature pods per plant, days to maturity and days to 50% flowering other characters recorded moderate to low heritability, the fresh pod yield per plant showed the highest genetic advance. Total 56 germplasm lines evaluated in 2013, in randomized block design with two replication at All India Co-ordinated Research Project on Groundnut,Mahatma Phule Krishi vidyapeeth, Rahuri, Dist Ahmednagar (M.S)

Ajay *et al* (2014), study F_2 and F_3 generations were evaluated for yield and yield contributing traits to understand genetic variability and to identify transgressive segregants in three pigeonpea crosses. High variance, high heritability and high genetic advance were recorded for secondary branches per plant, number of pods per plant and seed yield in F_2 and F_3 generations. There was decrease in variability from F_2 to F_3 generation for some traits. High heritability and high genetic advances indicates that traits are under the control of additive gene action and selection will be effective. Among the three crosses transgressive segregants were high in the cross TTB 7 x ICPL 87119 indicating the superiority of this cross over the others.

Atak S. M. (2014) study the variability for twenty different characters among 31 genotypes, genetic divergence among all genotypes. entitled “Genetic diversity in F_4 generation of groundnut (*Arachis hypogaea L.*)”. The treatment differences were statistically significant for majority of the characters and also the magnitude of genotypic and phenotypic coefficients of variations indicated the presence of good amount of variability. The character number of pegs per plant showed the highest heritability followed by dry haulm yield per plant, number of immature pods per plant, number of mature pods per plant, plant height, specific leaf area, oil content, dry pod yield per plant, days to 50% flowering, photosynthetic rate, shelling percentage, harvest index, protein content, days to maturity, 100 kernal weight, total chlorophyll, leaf temperature. Other characters recorded moderate to low heritability. The number of pegs per plant showed the highest genetic advance followed by dry haulm yield per plant, number of mature pods per plant, plant height and dry pod yield. Other characters showed moderate to low genetic advance.

2.2 To identify transgressive segregants for yield and yield contributing character in summer groundnut.

Briggs and Allard (1953) reported that backcrossing is successful and precise method of adding simply inherited traits to an existing plant cultivar. Backcrossing is more effective in getting recombination between linked alleles, because more opportunity for meaningful crossing over (heterozygosity) occurs and thus useful for obtaining desirable transgressive segregants.

Langham (1961) reported that high-low method of crop improvement in which he explained the basis of transgressive segregation. According to him there are upper (high) and lower (low) limits for the expression of character the highest frequency of individuals having average expression which are favoured by natural selection. It is postulated that the genes responsible for high performance are associated with modifiers or buffers which will not allow expression of characters beyond a certain higher limit. When crosses where made between high performing lines, they would be associated with negative buffer only and hence could not transgress a threshold limit. Similar situation would occur when crosses made between low performing lines. However, when cross made between high and low performing parents, there is a maximum possibility of getting transgressive segregation from F_2 generation onwards, since the segregating high genes will be buffered or linked with positive modifiers. Similar procedure can be continued in future generation also for accumulation of more positive buffers with more high genes.

Improvement has been shown by him in Sesamum for certain characters by these procedure.

Auckland and singh (1976) reported transgressive segregation in respect of plant height, seed size, pod number and seed yield in F_2 generation of Kabuli x Deshi cross in Chickpea.

Bahl (1979) initiated the work on Kabuli-Deshi introgression in 1976 and reported the encouraging results from this line of work. He could isolate early maturing types with determinant in growth habit and better harvest index as compared to standard check variety. He also suggested that three way instead of single crosses are more useful for introgression of new germplasm into the breeding population.

Haddad (1979) isolated transgressive segregants in term of earliness, tallness, erectness, high pod number and high yield in Lentil.

Hawtin and Singh (1979) suggested that the introgression of Deshi germplasm is necessary if quantum yield increases are to be realized for Kabuli type in West Asia. The reverse would be the case for improvement of Deshi type in East Asia.

Ugale S.D. and Bhal P.N. (1980) studied three crosses in chickpea and recorded transgressive segregants in all the crosses for nine characters. In case of plant spread, the highest proportion of individuals (30.77%) transgressed the increasing parent. He observed transgressive segregants in respect of days to flowering, pod number, fruiting branches, seed yield per plant, seeds per pod, 100-seed weight and plant height in descending order.

Jaiswal and singh (1986) observed large variation in F_2 generation of four crosses for yield and yield contributing characters. They observed segregants for yield per plant, pods per plant, plant height, branching and 100-seed weight. Further they believed the possibilities of introgressing desirable genes from *C. reticulatum* into cultivated Chickpea.

Gowda *et al.*(1987) studied utility of Deshi x Kabuli crosses in Chickpea improvement and observed wide range of segregants in F_2 for seed shape, seed size, and seed colour with seed of Deshi type predominating. They further observed Kabuli type segregants predominated in F_2 of second cycle and reduced variability in comparison with the original F_2 generation.

Reddy and Singh (1989) obtained superior transgressive segregants in the BC_1F_2 population for all the important character *viz.*, pods per plant, pod per cluster, seed weight and yield per plant. This reveals the introgression of wild germplasm created large amount of genetic variability and ultimately the frequency of transgressive segregants for yield increased. These results suggested that only one backcross with the recurrent parent may be enough to achieve higher proportion of transgressive segregation in the wide crosses of Blackgram.

Reddy and Singh (1990) reported that high mean and large variance where exhibited in the F_2 generation of T 44 x PLN 15 for yield per plant and pod per plant, in ML 5 x LM 293 (BC_1F_2) for pod per plant and in T 44 x ML 5 (F_2) for days to first flower. The F_2 generation of T 44 x PLN 15 showed transgression for seeds per pod, yield per plant and pods per plant. ML 5 x LM 293 (F_2) and T44 x ML 5 (BC_2 F_2) expressed significantly higher transgressive for days to first flower and seed weight, respectively.

Singh and Singh (1999) effected Interspecific hybrid involving four genotypes of Mungbean (*Vigna radiata* L.) as female and three genotypes of Urdbean (*Vigna mungo* L.) as male parent. They reported that genotypes influenced cross ability, germination, survival and fertility of F_1s.The crossed seeds were shrivelled and the F_1s were partially fertile, late maturing and intermediate in morphology. Purple colour of stem was dominant over green colour. Only 2 out of 6 hybrids, namely, BHUM 1 x Pant U30 and T44 x T9 resulted in fertile F_1s which reached maturity. Fertility of the progenies improved from F_2 to F_4 generation. Desirable transgressive segregates incase of plant height, numbers of branches per plant, pods per plant, pod length, seeds per pod, yield per plant observed in the advanced generations open up new avenues for amelioration of these crops.

Kant and Singh (1998) reported that in Lentil the experimental material consisted of 13 diverse parents and 30 F_2 and F_3 bulk population. In general exotic x indigenous crosses had higher frequency of transgressive segregants for plant height, where as indigenous x indigenous crosses exhibited higher frequency of transgressive segregants for primary and secondary branches per plant in both the generation. None of the crosses showed transgressive segregates for 100-seed weight in F_2 generation.

Mitra and Mehra (1998) advanced F_2 generation of two crosses of Grasspea by single seed descent, random bulk and pedigree method of breeding and observed transgressant in F_5 generation. They observed transgressant for pods per plant, seeds per pod, 100-seed weight and yield per plant, more or less by all three methods.

Jayalakshmi (2000) studied the frequency of transgressive segregates in 21 crosses in F_2 and F_3 generations for physiological and yield attributes.Cross ICG 2716 x ICGV 86031 exhibited higher frequency of transgressive segregants for majority of the attributes in addition to kernel yield. Among others, ICG 2716 x TAG 24, ICG 2716 x TG 26, ICG 86031 x TG 26, TAG 24 x TG 26 x TMV2-NLM expressed transgressive segregates for kernel yield and other attributes like harvest index and pod number per plant.

Rajavindran *et al.* (2000) studied the six cross combinations of sesame. Among the mean values of the six crosses, SO 338 x Paiyur 1 and EC 132836 x TMV4 exhibited low mean values for days to flowering. For the plant height, a high level of significant transgressive segregants (STS) (16.88%) was noticed in EC 132836 x TMV4. This cross also exhibited high mean values and high STS (62.33%) for the primary branches. Among the crosses, Si 833 x CO1 recorded a high STS value (13.92%) for seed yield. For oil content, the cross Si 833 x CO 1 also recorded a high range with a maximum oil content of 69.17% in one of the segregants. The crosses Si 833 x CO 1 and EC 132836 x TMV4, gave a high frequency of transgressive segregants for seed yield per plant, primary branches per plant and capsule number per plant, may be preferred over the other crosses.

Girase and Deshmukh (2002) observed the transgressive segregation for all the seven characters in three crosses of Chickpea. They observed the highest transgressive segregation for plant height (27%) followed by pods per plant, fruiting branches per plant and yield per plant in both F_2 and F_3 generation of all the three crosses, except F_3 generation of JG-62 x Vijay. They also reported the simultaneous transgressive segregation for yield in combination with other characters. They reported that the proportion of transgressive segregants were more in backcross population with increasing parent than straight F_2 population.

Rahman *et al.* (2002) studied transgressive segregation in the backcross populations, involving three crosses in Longbean [*Vigna sesquipedalis* (L.) Fruw]. Trends were different for different crosses. In Cross 1, high mean variance and significant transgressive segregation (STS) pattern were exhibited by BC_2F_1 generation for shelf life, pod yield per plant and pod weight. In Cross 2, high means were shown by BC_1F_1 generations for shelf life and pod yield per plant, but high STS were observed in BC_2F_1 generation for shelf life, BC_1F_1 for pod yield per plant and BC_1F_2 for pod weight. In Cross 3, BC_1F_2 generation revealed high variances for shelf life, pod yield per plant and number of pods per plant, but highest STS values were revealed in BC_1F_3 (selected) for shelf life and pod yield per plant, BC_2F_1 for number of pods per plant, and BC_1F_2 for pod weight. In general, shelf life was exhibited high mean and STS in the BC_2F_1 generation.

Rio *et al.* (2003) reported that two Ethiopian Mustard (*Brassica carinata* A. Braun) lines with low (about10%) and zero erucic acid (C22:1) have been obtained. The low C22:1 mutant line L-2890 was isolated after a chemical-mutagen treatment of C-101 seeds (about 40% C22:1). The zero C22:1 line L-25X-1 was obtained by interspecific crossing. Reciprocal crosses between L-2890,L-25X-1 and high C22:1 lines, and between L-2890 and L-25 X-1,were made. The F_1, F_2 and BC_1F_1 generations were obtained. The F_1 and segregating generations of the crosses L-2890 x L-25X-1 showed a strong transgressive segregation with C22:1 values of up to 50.0%, four-fold higher than those of L-2890. The analyses of the F_2, BC_1F_1 and F_3 generations indicated that the combination of alleles at four loci, M_1 and M_2 in L-2890 and E_1 and E_2 in L-25X-1, controlled the transgressive segregation for C22:1.

Kotzamanidis. S. T. (2006), The first peanut crosses ever tried in Greece were performed over two growing seasons. The 13 successful crosses in 1985 belong to the following crossing schemes: Virginia x Spanish, Virginia x Valencia, Valencia x Virginia, Virginia x Virginia, Valencia x Valencia and Valencia x Spanish. The 7 successful crosses in 1986 belong to 2 crossing schemes: Virginia x Valencia and Virginia x Virginia. It resulted that in the climatic conditions of Greece a higher percentage of success can be achieved (16%), when the crosses are realized as early as possible so that the high summer temperatures can be avoided. Also, the transgressive segregation for yield characteristics of 100-pod weight and 100-seed weight was studied during the years 1985-1990 in the Cotton Research Institute. Pedigree selection was applied from the F_3 to F_5

generation and segregated materials together with the parental varieties were evaluated. Most of the selections that showed transgressive segregation belonged to the cross type Virginia x Spanish. Data indicated that yield and quality of peanuts could be improved by exploiting the phenomenon of transgressive variation occurring principally in crosses between varieties that belong to peanut types Virginia and Spanish.

Lema *et al.* (2006) studied that in F_2 phenotypes with a transgressive glucosinate (GSL) content lower than the parents were identified in all crosses involving the line S2–1241, suggesting that this line carries alleles for reduced GSL content not present in the other lines. F_3 and F_4 lines from transgressive F_2 phenotypes were evaluated for two years, which resulted in the selection of an F_3 and F_4 line with an average GSL content of 58 and 46 μmol/gm seed

Chahota *et al.* (2007) reported that the prediction of expected transgressive segregants in F_1 generation obtained as a ratio of additive genetic effect [d] and additive variance (D) i.e. $[d]/\sqrt{D}$ was studied in 28 crosses of Lentil generated in a diallel fashion involving four parents each of macrosperma (exotic) and microsperma (Indian) types, respectively, resulting in three hybridization groups. The seed material advanced to F_2, F_3 and F_4 generations through single seed descent method was evaluated to determine the observed transgressive segregants for seed yield per plant. The observed frequency of crosses showing more than 20% transgressive segregants in F_2

to F_4 generations were exhibited in 9 (32%) crosses, of which 7(77%) crosses were of macrosperma x microsperma type.

Dhole and Reddy (2011) reported that total of eight transgressive segregants (2.56%) was recorded in the cross-I of Mungbean, which ranged from 8.52 to 9.29 g for 100 seed weight. No transgressive segregants were obtained in cross-II and cross-III for 100 seed weight. Among the F_2 populations, the mean seed yield per plant was the highest in the cross-I (3.89 gm) followed by the cross-III (2.74 gm) and the cross-II (1.88 gm). For seed yield per plant, fifteen (4.79%) and one (0.0027%) transgressive segregants were recorded in the cross-I (range 7.95 to 11.93gm) and the cross-III (15.01gm) respectively. Transgressive segregants were also reported in Mungbean for various characters (Kataraki and Kajjidoni, 2006 and Sarwar *et. al.*, 2004). Changes in mean value were closely followed by alteration in variances.

Shivani *et al.* (2011) studied twenty-four crosses of line x tester set in Safflower and observed maximum number of positive transgressive segregants for seed yield, number of capitula per plant, number of seeds per capitulum in TSF-1 x SFS 9920, TSF-1 x SSF 658, TSF-2 x ASD-0710,Sagarmutyalu x SFS 9920 and Manjira x SSF 998 crosses.

K. John & P. Raghava Reddy (2011) Twenty eight F2 populations were evaluated for genetic parameters of 23 characters of morphological, physiological, yield and yield attributes during spring 2009. TPT-4 x ICGV-91114 was distinct for its lowest mean value for days to maturity and highest mean values for number of well-filled and mature pods per plant, shelling percentage, 100- kernel weight. The F_2 involving JL-220 as one of the parents viz., JL-220 x ICGV-99029 for SCMR, JL-220 x TCGS-647 for SMK percentage, protein percentage, kernel yield per plant and pod yield per plant showed the highest *per se* performance. High genotypic coefficient of variation was observed for the number of secondary branches per plant. High heritability and high GAM was recorded for the number of secondary branches per plant, high heritability and moderate GAM were observed for days to 50% flowering. The leaf area index, number of well-filled and mature pods per plant, dry haulms yield per plant and harvest index showed moderate heritability and high GAM. This indicates that these characters are under additive genetic control and selection for genetic improvement will be worthwhile and may rapidly contribute to pod-and kernel yields.

Ajay *et al* (2014), study F_2 and F_3 generations were evaluated for yield and yield contributing traits to understand genetic variability and to identify transgressive segregants in three pigeonpea crosses. High variance, high heritability and high genetic advance were recorded for secondary branches per plant, number of pods per plant and seed yield in F_2 and F_3 generations. There was decrease in variability from F_2 to F_3 generation for some traits. High heritability and high genetic advances indicates that traits are under the control of additive gene action and selection will be effective. Among the three crosses transgressive segregants were high in the cross TTB 7 x ICPL 87119 indicating the superiority of this cross over the others.

E.Jambormias,(2015). The success of selection in self-pollinated crops depends on the extent to which breeders can fix transgressive segregation in early generations. The objectives of this research were to predict the heritabilities of quantitative traits and the mixing variance, and to detect the multiple traits transgressive segregant families of the early generation of mungbean. Material genetics were the F_3 generation progeny of a cross *Gelatik* × *Mamasa Lere Butsiw* variety. The experiment design used 1-stage nested-augmented randomized incomplete block design. Recovery of the phenotypes and the breeding values use a transformed linear mixed model with logarithm natural transformation. Analysis of heritabilities is expressed by the proportion of additive variance to the phenotypic variance, and mixing variance by the value of the within-control variance minus the within-check variance. Furthermore, analysis of transgressive segregation used BLUPWFT and BLUPFT bi plot. The results showed that the mixed models produce BLUP with an accuracy of the breeding values of quantitative traits ranged from moderate to high (0.36-0.95); the narrow sense heritability is low to high (0.13-0.91), and the presence of the mixing variance. There were at least 18.90% families of multiple traits transgressive segregant for selection characters with seed weight and simultaneous harvest index ranged between 11-18 g and 0.56-0.65, respectively. Most of these families were better or at least equal to the superior variety Gelatik as the best varieties.

3. MATERIAL AND METHODS

The field experiment related to the present investigation entitled"Assessment of genetic variability for high harvest index in summer groundnut (*Arachis hypogaea* L.)" was conducted at All India Co-ordinated Research Project on Groundnut, Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.), during summer, 2015. The details of material used and methods adopted during the course of the investigation are given below.

3.1 Material

The material used in the present study consisted of nine crosses of groundnut. The crosses were obtained from the Groundnut Breeder, All India Co-ordinated Research Project, on Groundnut, M.P.K.V.Rahuri.

3.2 Methods

3.2.1 Experimental design

The experiment was conducted in a randomized block design with three replications. Each plot consisted of a single row of 5 m length with a spacing of 30 cm between rows and 10 cm between plants. One border row was sown at both the sides of block to reduce the border effect.

The parents and F_2 generations of three crosses for the transgressive segregation & Nine crosses for genetic variability were used for conducting an experiment during summer-2015.

Table 2. Details of three F_2 crosses of groundnut for transgressive segregation.

Generation	Cross-1	Cross-2	Cross-3
P_1	Phule Unnati	Phule 6021	Phule Unnati
P_2	TPG -41	RHRG-6110	SB XI
F_2	Phule Unnati x TPG -41	Phule 6021 x RHRG-6110	Phule Unnati x SB XI

Source of parent & F_2 is All India Co-ordinated Research Project, on Groundnut, M.P.K.V., Rahuri.

Table 3. Details of Nine F_2 crosses of groundnut for assessment of genetic variability.

Sr. No.	Name of crosses	Source
1.	Phule Unnati x TPG 41	MPKV, RAHURI
2.	WRGS 15 x SB XI	MPKV, RAHURI
3.	Phule 6021 x RHRG6110	MPKV, RAHURI
4.	TAG 24 x SB XI	MPKV, RAHURI
5.	Phule 6021 x Phule Unnati	MPKV, RAHURI
6.	Phule Unnati x SB XI	MPKV, RAHURI
7.	TAG 24 x Phule Unnati	MPKV, RAHURI
8.	WRGS 15 x R8808	MPKV, RAHURI
9.	Phule 6021 x ICGV-0350	MPKV, RAHURI

3.2.2 Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowing. The seeds were sown on 28th Jan 2015 by dibbling single seed per hill at 30 x 10 cm^2 distance (between rows and between plants). During the growth period the usual cultural practices like weeding, irrigation and plant protection measures were followed as and when required.

3.2.3 Manures and fertilizers

The chemical fertilizers were applied @ 25 kg N and 50 kg P_2O_5 per ha. at the time of sowing in the form of ammonium phosphate and single super phosphate, respectively.

3.2.4 Harvesting

The pods were picked after attaining their physiological maturity to avoid germination of kernels within pods in soil. The following symptoms were considered for the physiological maturity of groundnut.

a. Yellowing of foliage and dropping of older leaves.

b. The mature pod becomes hard and tough. The inside shell surface becomes rough with visible net venation with a dark brown colour.

c. The seed becomes smooth and testa develops colour typical of the variety.

3.2.5 Observations recorded

Following observations were recorded on ten randomly selected plants from each treatment in each replication and averages were worked out.

3.2.5.1 Days to 50% flowering

Number of days required from sowing to day on which 50 per cent of the plants flowered was recorded as days to 50% flowering.

3.2.5.2 Days to maturity

The number of days from the date of sowing till the date when at least eighty per cent plants were matured in each replication was recorded.

3.2.5.3 Plant height at maturity (cm)

Plant height measured from ground level to uppermost tip of main branch of the plant in centimeters at physiological maturity on randomly height was selected plants.

3.2.5.4 Number of branches per plant

The number of branches produced on the main stem of observational plants was counted as branches at the time of harvesting.

3.2.5.5 Number of immature pods per plant

The number of immature pods per plant were counted at the time of harvest.

3.2.5.6 Number of mature pods per plant

The number of mature pods per plant were counted at the time of harvest.

3.2.5.7 Dry haulm yield / plant (gm)

The haulm of randomly selected plant was dried and the weight was recorded.

3.2.5.8 Dry pod yield per plant (gm)

The pods harvested from ten randomly select l plants in each replication were cleaned and dried under shade for one month after harvest. The weight of pods after drying was recorded and averaged.

3.2.5.9 Hundred kernel weight (gm)

The weight of randomly selected hundred mature kernels taken from observational plants were considered as hundred kernel weight.

3.2.5.10 Shelling percentage (%)

Weights of mature pods of selected plants were recorded. After shelling, weight of kernel was also recorded. Shelling percentage was calculated using following formula.

$$\text{Shelling percentage} = \frac{\text{Weight of kernels (gm)}}{\text{Weight of pods (gm)}} \times 100$$

3.2.5.11 Harvest index (%) on dry weight basis

The ratio economic yield i.e pod yield to the biological yield was taken as harvest index.

3.2.5.12 Sound of mature kernel percentage

Total pods harvested from ten experimental plants in each replication, fully matured kernels were counted and SMK (%) was calculated as follows.

$$\text{SMK (\%)} = \frac{\text{No. of fully matured, wrinkle free kernels}}{\text{Total number of kernels}} \times 100$$

3.2.5.13 Protein percentage

Percent crude protein content of the groundnut sample was estimated by NIR Spectro photo Analyzer machine.

3.2.5.14 Oil content percentage

The oil percentage was estimated by NIR Spectro photo Analyzer machine.

3.3 Statistical analysis

The mean values of ten randomly selected observational plants for fourteen different characters were used for statistical analysis for calculate genetic variability & for transgressive segregation seven yield contributing character are taken.

The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.3.1 Analysis of variance (ANOVA)

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1967). Statistical analysis will be performed by using the methods proposed by Dewey and Lu (1959) and Mahalnobis (1936) as described by Rao (1952).

The genotypic mean squares (GMS) were tested for their significance against error mean squares (EMS) by 'F' test for n_1 = (g-1) and n_2 = (r-1) (g-1) degrees of freedom

Where,

g = Number of genotypes

r = Number of replications

The characters showing significant differences were only subjected to further analysis

3.3.2 Estimates of components of variability

a. Mean

The mean values for all the characters were worked out by dividing total corresponding number of observations.

$$\overline{X} = \frac{\sum xi}{n}$$

Where,

$\overline{X}$ = Mean

$\sum xi$ = Total of all observations

n = Number of observations

b. Range

The lowest and the highest values of mean for each character represented the range.

c. Estimation of coefficient of variation

The genotypic and phenotypic coefficient of variation was calculated by using the following formula given by Burton (1952).

i. Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\overline{x}$ = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$ = Mean of character

The high, medium and low estimates of coefficient of variation were classified as

Low = 0 to 10 %

Medium = 10 to 20 %

High = 20 % and above

d. Heritability (b.s.)

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.*(1956).

$$h^2_{(b)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The high, medium and low heritability estimates were classified as;

Low = 0 to 30 %

Medium = 30 to 60 %

High = 60 % and above

e. Genetic advance (GA)

Genetic advance (at 5 % selection intensity) was calculated using formula cited by Allard (1960).

$$GA = K \times \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

K = Selection differential

(At 5 % selection intensity the value of K = 2.06)

f. GA as percentage of mean

$$= \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean of corresponding Character

The estimates of genetic advance as percentage of mean were classified as below;

Low = 0 to 10 %

Medium = 10 to 20 %

High = 20 % and above

3.3.3 Transgressive segregation

The data on individual plants for each character were pooled together and means, standard deviations, standard error of means, variances and standard variates were obtained as given below.

$$\text{Mean } (\bar{X}) = \frac{\Sigma (X_i)}{\quad}$$

$i=1$ N

Where,

N= Number of individuals observed for particular

Xi= Value of an individual from the sample.

$$\text{Standard deviation } (б) = \sqrt{\frac{\Sigma (X_i - \overline{X})^2}{N}}$$

$$= \sqrt{\frac{\Sigma (X_i)^2}{N}}$$

Where,

Xi = $(X1-\overline{X})$ = An individual deviation.

$\overline{X}$ = Mean of sample.

$$\text{Standard error of mean} = \frac{б}{\sqrt{n}}$$

Where,

б= Standard deviation of a sample as a whole.

n= Number in the sample.

$$\text{Variance } (б^2) = \frac{\Sigma (X_i)^2}{N-1}$$

Where,

Xi = $(X1-\overline{X})$ = An individual deviation

$$\text{Standard variate} = \frac{X1 - \bar{X}}{б}$$

Where,

Xi = Variate value of i^{th} individual

$\bar{X}$ = Mean of sample.

б = Standard deviation.

Normal deviation (Limiting value):

The limiting value of standard variates corresponding to range of parental means at 5 per cent probability level was calculated. So that the segregants showing deviation beyond this limiting value would be the transgressant. Transgressive segregants showing significant deviation only in desirable direction were considered for drawing inferences about transgression. The limiting value/ normal deviation value was calculated as per the formula given below.

$$\text{N. D. value} = \frac{\bar{P}_{(+)} + 1.96 \times б\, P_{(+)} - \bar{X}}{б}$$

Where,

$\bar{P}_{(+)}$ = Mean of increasing parent.

$бP_{(+)}$ = Standard deviation of increasing parent.

$\bar{X}$ = Mean of segregating generation.

б = Standard deviation of respective segregating generation.

4. EXPERIMENTAL RESULTS

The results obtained in the present investigation entitled "Assessment of genetic variability for high harvest index in summer groundnut (*Arachis hypogaea* L.)"conducted at AICRP, Groundnut, Cotton Improvement Project, M.P.K.V., Rahuri are presented in this chapter under different sub-heading

4.1 Range and mean performance

The data on mean performance for fourteen characters of Nine F_2 crosses of summer groundnut is presented in Table 4.

4.1.1 Days to 50% flowering

Thevariation for days to 50% flowering ranged between 42.26 to 47.26 days. The population mean for this character was 44.31 days. Five out of nine F_2 crosses flowered significantly earlier than the population mean. The F_2 crosses cross-5 (P.6021 x P.Unnati) (42.26) was the earliest followed bycross 3 (P.6021 x RHRG 6110) (42.60), cross-7 (TAG-24 x P.Unnati) (42.80). The cross-4 (TAG-24 x SB- XI) (47.26), cross-9 (P.6021 x ICGV 0350) (46.46) were comparatively late in days to 50% flowering.

4.1.2 Days to maturity

Five out of nine F_2 crosses showed significantly early maturity when compared with the population mean of 122.40 days. The variation for this character ranged between115.66 to to 130 days. cross-7 (TAG-24 x P.Unnati) recorded the lowest days to maturity 115.66 followed by cross-3 (P.6021 x RHRG 6110) (119).The cross-9 (P.6021 x ICGV 0350) 130, cross-5 (P.6021 x P.Unnati) (128.33) were comparatively late in maturity.

4.1.3 Plant height (cm)

The variation for plant height ranged between 20.93 to 30.00 cross9 (P.6021 x ICGV 0350) was the tallest F_2 cross having maximum plant height of 30.00 cm followed by cross-7 (TAG-24 x P.Unnati) (28.06) and cross-1 (P.Unnati x TPG 41) (27.76). The F_2 cross cross-4 (20.93) was dwarfest followed by cross-2 (WRGS 15 x SB XI) (21.90).

4.1.4 Number of branches per plant

The variation for number branches per plant ranged between 4.33 to 5.86. Looking to the population mean of 5.15 branches per plant, five F_2 crosses showed higher branches than population mean.Cross-3 (P.6021 x RHRG 6110) (5.86),cross-4 (TAG-24 x SB- XI) (5.70),cross-2 (WRGS 15 x SB XI) (5.56),were the F_2 crosses possessing high number of branches per plant.

4.1.5 Number of mature pods per plant

The variation for the character ranged between 28.98 to 47.10. The population mean for this character was 36.95 four F_2 crosses showed higher number of mature pods per plant over population mean of which cross-6 (P.Unnati x SB XI) (47.10), cross-1 (P.Unnati x TPG 41) (41.66), cross4 (TAG-24 x SB-XI) (38.33) and cross-5 (P.6021 x P.Unnati) (28.98) produced the lowest number of mature pods per plant.

4.1.6 Number of immature pods per plant

The number of immature pods per plant ranged between 7 to 13.46 while the population mean was 10.86. SixF_2 crosses showed higher number of immature pods per plant than population mean. Cross-4 (TAG-24 x SB-XI) (7.00) produced lowest number ofimmature pods per plant.

4.1.7 Dry haulm yield per plant (gm)

The Dry haulm yield per plant (gm) ranged between 18.33 to 54.36while the population mean was 10.86.The F_2 cross cross-3 (P.6021 x RHRG 6110) produced the higher dry haulm yield per plant (gm) (54.36) followed by cross-6 (P.Unnati x SB XI)(43.20). The F_2 cross-4 (TAG-24 x SB-XI) (18.33) produced the lowest dry haulm yield per plant followed by cross-2 (WRGS 15 x SB XI) (22.66)). The population mean was 36.06.

4.1.8 Dry pod yield per plant (g)

The Dry pod yield per plant (gm) ranged between 32 to 38 while population mean for dry pod yield per plant was 35.22 gm. The cross-4 (TAG-24 x SB-XI) (38.00) and cross-9 (P.6021 x ICGV 0350)(38.00) recorded the highest dry pod yield per plant followed by cross-6 (P.Unnati x SB XI) (36.21).The cross-7 (TAG-24 x P.Unnati) (32.00) recorded low yield. Four out of nine F_2 crosses showed higher mean values for this character than population mean.

4.1.9 100 kernel weight (g)

The variation for this character ranged between 32.66 to 41.48. Five out of nine F_2 crosses showed numerically high hundred kernel weight when compared with population mean of 35.92 g. The F_2 cross-1 (P.Unnati x TPG 41), cross-6 (P.Unnati x SB XI) (38.33), cross-8 (WRGS15 x R 8808) (36.63) showed higher hundred kernel weight.Cross-2 (WRGS 15 x SB XI) show lowest 100 Kernel wt (32.66).

4.1.10 Shelling percentage

The population mean for this trait was 67.91. The variation ranged between 65.48 to 72.56. Numerically highest shelling percentage was recorded by cross-4 (TAG-24 x SB-XI) (72.56) followed by cross-5 (P.6021 xP.Unnati) (69.40), cross-6(P.Unnati x SB XI) (69.00). The lowest value for shelling percentage was recorded by cross-8 (WRGS15 x R 8808) (65.48) followed by cross-1 (P.Unnati x TPG 41)(66.20).

4.1.11 Harvest index (%)

Four F_2 crosses recorded significantly higher harvest index over the population mean of 36.24. The range observed for this character was between 29.33 to 42.54 The cross-5 (P.6021 x P.Unnati) had the highest harvest index (42.54) followed by cross-1 (P.Unnati x TPG 41) (41.83), cross-6 (P.Unnati x SB XI) (41.80)).The lowest value for harvest index was recorded by cross-4 (TAG-24 x SB-XI) (29.33) followed by cross-9 (P.6021 x ICGV 0350) (30.73).

4.1.12 Oil content (%)

The population mean for this character was 48.73 per cent. The F_2 crosses cross-8 (WRGS15 x R 8808)(45.15) recorded the lowest oil content while the F_2 crosses cross-6 (P.Unnati x SB XI) (52.15) recorded highest oil content followed by cross-5 (P.6021 x P.Unnati) (52.06), cross-3 (P.6021 x RHRG 6110) (49.76).Six F_2 crosses recorded high value for oil content as compared to population mean.

4.1.13 Protein content (%)

The protein content in nine summer F_2 crosses ranged between 21.19 to 26.42 with a population mean of 23.68 percent. The F_2 crosses cross-5 (P.6021 x P.Unnati) (26.42), cross-2 (WRGS 15 x SB XI) (24.99), cross-7 (TAG 24 x P.Unnati) (24.15)) recorded the highest amount of percent protein. In contrast the F_2 crosses cross-3(P.6021 x RHRG 6110) (21.19) recorded lowest values for protein content.

4.1.14 Sound mature kernel (%)

The range observed for sound mature kernel percentage was between 84.13 to 87.06 .The population mean for this character was 85.86. The highest sound mature kernel percentage was observed for F_2 crosses cross-9 (P.6021 x ICGV 0350) (87.06) followed by cross-1 (P.Unnati x TPG 41) (86.93) and cross-6 (P.Unnati x SB XI) (86.63).lowest sound mature kernel value observed in cross-7 (TAG-24 x P.Unnati) (84.13).

4.2 Analysis of variance

Analysis of variance (Table 6) revealed highly significant differences among the F_2 crosses for the characters studied except No. of branches per plant, Days to maturity, sound mature kernel, 100 kernel weight, indicating appreciable amount of diversity among the genotypes.

4.3 Parameters of genetic variability and heritability

Estimates of range, variability heritability (b.s) and genetic advance are presented in Table 5.

4.3.1 Coefficient of genotypic and phenotypic variation

It was observed that the estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the characters.

Dry haulm yield/plantrecorded the highest estimate of GCV (28.91) followed by No. of immature pods per plan (gm)(22.50),harvest index % wt basis (13.95),No. of mature pods per plant (13.46),plant height at maturity (cm) (11.57).

The highest value of PCV were observed Dry haulm yield per plant(gm) (31.29) followed by no. of immaturepods per plant (25.81),harvest index % wt basis (17.85), no. of mature pods per plant (gm)(16.00),plant height at maturity (cm)(13.25).Low GCV and PCV value were recorded by character sound of mature kernel % (1.00 & 1.57), shelling percentage % (2.52 & 4.27).given in Tab. No 5.

4.3.2 Heritability (b.s.)

The heritability (b.s.) estimates were high in case of characters *viz.*, Dry haulm yield/plant (gm) (85.41), Dry pod yield per plant (gm)(81.00), Oil % (79.94),plant height(cm) (76.28), Numberof immature pods per plant(76.03), Number of mature pods per plant(70.76), Days to 50% flowering (64.58),Protein % content (61.90),Harvest index % (59.83),Days to maturity (54.76),Hundred kernel weight (53.71), no of branches plant (51.01),sound mature kernel (41.23), Shelling % (34.86).given in Tab. No 5.

4.3.3 Genetic advance

The highest magnitude of genetic advance was observed for Dry haulm yield per plant (gm) (19.85) followed by Number of mature pods per plant (8.62), Oil %(8.17), Harvest index % (7.90), Days to maturity (7.40), Plant height (cm) (5.33), Number of immature pods per plant (4.39).Dry pod yield per plant (gm) (4.10). The lowest value of genetic advance was observed for number of Branches per plant (0.7), sound mature kernel %(1.14).

Genetic advance as a percent of mean was the highest for Dry haulm yield per plant (gm) (55.05) Number of immature pods per plant (40.42) followed by Number of mature pods per plant (23.33), Harvest index % (22.01) and In contrast, Sound mature kernel % (1.33) recorded lowest value followed by Shelling percentage % (3.07).

4.4 Transgressive Segregation:

Frequency distribution and proportion of desirable transgressive segregants for seven agronomic characters, individually and for combination of characters along with Dry pod yield per plant, have been reported separately for each of the three crosses namely, Phule Unnati x TPG 41 (Cross 1), Phule 6021 x RHRG 6110 (Cross 2), Phule Unnati x SB XI (Cross 3).The result of each cross are reported separately.

4.4.1. Phule Unnati x TPG 41 (Cross I)

4.4.1.1 Means, standard deviations, frequency distribution and proportion of desirable transgressive segregants for seven characters in F_2 generation

Days of 50% flowering

Data presented in table 7, shows that the increasing parent TPG 41(45.27) had higher number of days for 50% flowering of F_2 generation 43.97. In F_2 generation the percentagetransgressantfor this trait was 27.15 per cent. The range in number of days for 50% flowering among the transgressant was 48.77-55.80.While the threshold value was 45.27.(Table 11).

Number of mature pods per plant

Data presented in Table 7 shows that, the increasing parent, Phule Unnati (43.07) had higher number of pods per plant and F_2 generation had 48.75. The widest (among the characters studied) range of number of mature pods per plant (53.73 to 85.74) was observed in F_2 generation. In F_2 generation the percentage transgressant for this trait was 22.33 per cent. Threshold value for number of pods per plant was 43.07 (Table 11).

Dry pod yield / plant (gm)

Data presented in Table 8 shows that, The dry pod yield/plant (gm) increasing parent TPG-41 (40.47) and F_2 generation 40.77. In F_2 generation the percentage of transgressant for this trait was 17.01 per cent. The range in Dry pod yield/plant (gm), among transgressant was 45.20-59.40. The threshold value for Dry pod yield/plant(gm) was 40.47(Table 11).

Hundred kernel weight (gm)

Data presented in Table 8 shows that,The 100 kernel weight (gm) in increasing parent TPG-41 was 48.07 and in F_2generation was 45.52 (Table 8). In F_2 generation the percentage of transgressant for this trait was 4.00 per cent. The range in 100 kernel wt (gm) in F_2 generation was 55.26-69.66. The threshold value for 100 kernel weight (gm) was 48.07 (Table 11).

Shelling %

Data presented in Table 9, shows that mean for shelling% of increasing parent TPG-41 (67.23) and F_2 generation was 65.79. The range in F_2 generation for shelling% was 72.83-78.44. The percentage of transgressant in F_2 generation for this trait was 4.00 per cent. The shelling% threshold value was 67.23 (Table 11).

Harvest index %

Data presented in Table 9 shows that,The harvest index in TPG 41 increasing parent 37.93 and F_2 generation was 38.73 (Table 9). The percentage of transgressant for Harvest index was 22.33 per cent. The threshold value for Harvest index% was 37.93. The range in F_2, among transgressant was 44.19 to 50.45 (Table 11).

Sound mature kernel (%)

Data presented in Table 10 shows that,The SMK % P.Unnati increasing parent 86.00 and F_2 generation was 86.64 (Table 10). The percentage of transgressant for SMK was 7.67 per cent. The threshold value for SMK % was 87.00. The range in F_2, among transgressant was 91.96 to 96.93 (Table 11).

4.4.1.2 Frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combination of characters along with Dry pod yield/plant (gm) in F_2 generation.

Data on frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combinations of characters along with Dry pod yield/plant(gm) are summerised in Table 12.

The transgression of Dry pod yield/plant (gm)along with five other characters took place in one case only. The Dry pod yield/plant (gm)was transgressed, simultaneously with mature pod perplant, 50 % flowering,shelling%, 100 kernel wt(gm),sound mature kernel and harvest index in F_2 generation.

These combinations along with the frequencies of transgressive segregants in F_2 generation are given below.

1. Dry pod weight/plant(gm)+Mature pod per plant + 50% Flowering +Harvest index % (1.66)
2. Dry pod weight/plant(gm)+Mature pod per plant + 50% Flowering+ Shelling%+ 100 kernel wt+ SMK (2.00)
3. Dry pod weight/plant(gm)+ Mature pod per plant + 50% Flowering + Harvest index%+ Shelling%+SMK%(1.66)
4. Dry pod weight/plant(gm)+Mature pod per plant + SMK% +Harvest index %(2.00)
5. Dry pod weight/plant(gm) alone(1.33)

Transgressive segregants for Dry pod weight/plant (gm) alone were observed in F_2generation to the extent of 1.33 per cent.

4.4.2. Phule 6021 x RHRG 6110

4.4.2.1 Means, standard deviations, frequency distributions and proportion of desirable transgressive segregants for seven characters in F_2 generation.

Days of 50% flowering

Data Data presented in Table 13 shows that,the increasing parent Phule 6021(43.87) had higher number of days for 50% flowering of F_2 generation (41.91). In F_2 generation the percentage transgressant for this trait was

29.00 per cent. The range in number of days for 50% flowering among the transgressant was 47.08 to 53.51.While the threshold value was 43.87 (table17.)

Number of mature pods per plant

Data presented in Table 13 shows that,the increasing parent, Phule-6021 (38.67) had higher number of pods per plant and F_2 generation had 43.86. The range of number of mature pods per plant (46.63 to 70.53) was observed in F_2 generation. In F_2 generation the percentage transgressant for this trait was 29.67 per cent. Threshold value for number of mature pods per plant was 38.67 (Table 17).

Dry pod yield / plant(gm)

Data presented in Table 14 shows that,The Dry pod yield/plant(gm) increasing parent Phule 6021 (36.33) and F_2 generation 37.92.In F_2 generation the percentage of transgressant for this trait was 14.33 per cent. The range in among transgressant was 43.30 to 64.23The threshold value for Dry pod yield/plant (gm) was36.33 (Table 17).

Hundred kernel weight (gm)

Data presented in Table 14 shows that,The 100 kernel weight (gm) in increasing parent Phule 6021was 40.80 and in F_2 generation was 39.99. In F_2 generation the percentage of transgressant for this trait was 17.33 per cent. The range in 100 kernel weight (gm) in F_2 generation was 49.38 to 57.96. The threshold value for number of seeds per pod was 40.80(Table 17).

Shelling %

Data presented in Table 15 shows that,mean for shelling% of increasing parent Phule 6021 (65.40) and F_2 generation was 66.45. The range in F_2 generation for shelling% was 70.64 to 74.88. The percentage of transgressant in F_2 generation for this trait was 5.00 per cent. The shelling% threshold value was 66.40 (Table 17).

Harvest index %

Data presented in Table 15 shows that,The harvest index% Phule 6021 increasing parent 42.80 and F_2 generation was 46.08(Table 15). The percentage of transgressant for Harvest index % was 21.93per cent. The threshold value for Harvest index % was 42.80. The range in F_2, among transgressant was 49.87 to 64.02 (Table 17).

Sound mature kernel%

Data presented in Table 16 shows that,The SMK% P.6021 increasing parent 83.60 and F_2 generation was 84.21(Table 16). The percentage of transgressant for SMK% was 18.54 per cent. The threshold value for SMK% was 83.60. The range in F_2, among transgressant was 86.89 to 93.48 (Table 17).

4.4.2.2 Frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combination of characters along with Dry pod yield/plant (gm) in F_2 generation.

Data on frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combinations of characters along with Dry pod yield/plant (gm) are summerised in Table 18.

The transgression of Dry pod yield/plant (gm) along with five other characters took place in one case only. The Dry pod yield/plant (gm) was transgressed, simultaneously withMature pod perplant, 50% flowering,Shelling%, 100 kernel wt(gm),Sound mature kernel and harvest index in F_2 generation.

These combinations along with the frequencies of transgressive segregants in F_2 generation are given below.

1. Dry pod weight/plant(gm) + Mature pod per plant + 50% flowering +Harvest index (2.00)

2. Dry pod weight/plant(gm) + Mature pod per plant + 50% Flowering+ Shelling%+ 100 kernel wt+ SMK% (1.66)

3 .Dry pod weight/plant(gm)+ mature pod per plant + 50% Flowering + Harvest index + Shelling%+SMK%(1.66)

4. Dry pod weight/plant(gm)+ Mature pod per plant + SMK% + Harvest index (2.00)

5. Dry pod weight/plant(gm) alone(1.66)

Transgressive segregants for Dry pod weight/plant(gm) alone were observed in F_2 generation to the extent of (1.66)%.

4.4.3. Phule Unnati x SB XI

4.4.3.1 Means, standard deviations, frequency distributions and proportion of desirable transgressive segregants for seven characters in F_2 generation.

Days of 50 %flowering

Data presented in Table 19 shows that,the increasing parent SB XI (40.47) had higher number of days for 50% flowering of F_2 generation (40.59). In F_2 generation the percentagetransgressant for this trait was 12.33 per cent. The range in number of days for 50% flowering among the transgressant was 44.96 to 53.96. While the threshold value was 40.47 (Table 23)

Number of mature pods per plant

Data presented in Table 19 shows that, the increasing parent Phule Unnati (43.07) had higher number of pods per plant and F_2 generation had 41.55. Therange of number of mature pods per plant (53.73 to 85.74) was observed in F_2 generation. In F_2 generation the percentage transgressant for this trait was 12.00 per cent. Threshold value for number of pods per plant was 43.07 (Table 23).

Dry pod yield / plant (gm)

Data presented in Table 20 shows that, The Dry pod yield/plant(gm) increasing parent Phule Unnati (35.67) and F_2 generation 43.09. In F_2 generation the percentage of transgressant for this trait was 24.67 per cent. The range in among transgressant was 47.51to 83.04.The threshold value for Dry pod yield per plant (gm) was 35.67(Table 23).

Hundred kernel weight (gm)

Data presented in Table 20 shows that,The 100 kernel weight (gm) in increasing parent Phule Unnati was 42.20 and in F_2 generation was 43.61 (Table 20). In F_2 generation the percentage of transgressant for this trait was 22.26 per cent. The range in 100 kernel weight (gm) in F_2generation was 46.3 to 58.75. The threshold value for 100 kernel weight (gm) was 42.20(Table 23).

Shelling %

Data presented in Table 21, shows that mean for shelling% of increasing parent Phule Unnati (65.07) and F_2 generation was 65.83. The range in F_2 generation for shelling% was 70.43 to 81.16. The percentage of transgressant in F_2 generation for this trait was 4.97 per cent. The shelling% threshold value was 65.07 (Table 23).

Harvest index %

Data presented in Table 21 shows that, The harvest index% in Phule Unnati increasing parent 35.93 and F_2 generation was 37.89. The percentage of transgressant for Harvest indexwas 14.33 per cent. The threshold value for Harvest index%was 35.93. The range in F_2, among transgressant was 43.28 to 50.63 (Table 23).

Sound mature kernel%

Data presented in Table 22 shows that,The SMK% SB XI increasing parent 86.80 and F_2 generation was 86.80.The percentage of transgressant for SMK% was 8.00 per cent. The threshold value for SMK was 83.40. The range in F_2, among transgressant was 90.38 to 97.36 (Table 23).

4.4.3.2 Frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combination of characters along with Dry pod yield/plant (gm) in F_2 generation.

Data on frequency and percentage of transgressive segregants for Dry pod yield/plant (gm) and for combinations of characters along with Dry pod yield/plant (gm) are summerised in Table 24.

The transgression of Dry pod yield/plant (gm)along with five other characters took place in one case only. The Dry pod yield/plant (gm) was transgressed, simultaneously with mature pod perplant, 50 % flowering, shelling%, 100 kernel wt(gm), sound mature kernel% and harvest index% the in F_2 generation.

These combinations along with the frequencies of transgressive segregants in F_2 generation are given below.

1. Dry pod weight/plant(gm) + Mature pod per plant + 50% Flowering +Harvest index (2.00)

2. Dry pod weight/plant(gm) + Mature pod per plant + 50% Flowering+ shelling%+ 100 kernel wt(gm) + SMK% (1.66)

3. Dry pod weight/plant(gm) + Mature pod per plant + 50% Flowering + Harvest index%+ shelling%+SMK%(2.33)

4. Dry pod weight/plant (gm)+mature pod per plant + SMK% +Harvest index(1.66)

5. Dry pod weight/plant (gm) alone(1.66)

Transgressive segregants for Dry pod weight/plant(gm) alone were observed in F_2 generation to the extent of 1.66%

5. DISCUSSION

Success of any plant breeding programme depends on selection of elite genotypes which ultimately depends on knowledge of variability and genetic diversity of the germplasm. Therefore, to assess the extent of variability present in the population for particular characters, genotypic and phenotypic coefficients of variation were studied. The heritability which gives the relative role of genetic factors in the expression of phenotypes and also acts as an index of inheritance of a particular character to its offspring was also studied. The genetic advance measures the expected genetic gain from the selection applied in a population. Heritability along with genetic advance will help to fix the possible genetic control for any particular characters.

5.1 In the present investigation, entitled "Assessment of genetic variability for high harvest index in summer groundnut (*Arachis hypogaea L.*)" attempts were made to study the variability for fourteen different characters among nine F_2 crosses, transgressive segregation for three F_2 crosses. The following sub-heads are taken into consideration, while discussing the results on various aspects.

5.2 Genetic variability

5.3 Genotypic and phenotypic coefficient of variation

5.4 Heritability (b.s.) and genetic advance

5.5 Transgressive segregation

5.1 Genetic variability

A wide range of variability was observed in respect of Dry haulm yield per plant (gm) (18.33 to 54.36),, Number of mature pods per plant (28.98 to 47.10),), Harvest index% (29.33 to 42.54), Days to maturity (115.66 to 130), Number of immature pods per plant (7.00 to 13.46).

This indicated a great scope for exploitation of these traits. The findings of Reddy *et al.* (1995), Gowda *et al.* (1996), Singh *et al.* (1996), Khurram *et al.* (1998), Gimenes *et al.* (2000) were similar to the results of the present research. The rest of the characters exhibited comparatively less variability.

5.2 Genotypic and phenotypic coefficient of variation

The estimates of phenotypic coefficient of variation (PCV) were magnitudinally higher than the estimates of genotypic coefficient of variation (GCV) for all the characters studied (Fig. 1) indicating the influence of environment on these traits.

The PCV estimates were higher for Number of immature pods per plant, Harvest index%, Dry haulm yield per plant (gm) , Number of mature pods per plant, Plant height (cm) ,Number of branches per plant, Oil%,100 kernel wt (gm). These results confirmed earlier findings of Ganeshan and Sudhakar (1995), Jayalakshmi *et al.* (1998), Ramesh Kumar *et al.* (1998), Yadav *et al.* (1998), Prakash *et al.* (2000), Aghav (2010) and John *et al.* (2009).

The GCV estimates were higher for Number of immature pods per plant, Harvest index%, Number of mature pods per plant, Plant height (cm), Oil%, Number of branches per plant, Dry haulm yield per plant (gm), Dry pod yield per plant (gm). This confirmed the earlier results of Reddy *et al.* (1995), Jayalakshmi *et al.* (1998), Islam and Rasul (1998), Yadav *et al.* (1998), Ramesh Kumar *et al.* (1998) and John *et al.* (2009).

Low GCV and PCV values were observed for character sound mature kernel, shelling percentage, Days to maturity indicating hardly any scope for improvement of these traits by selection. These results are in confirmity with the earlier findings of Korat *et al.* (2009).

5.3 Heritability and genetic advances

Heritability is used to predict the resemblance between parents and their progeny. Where as, the genetic advance provides the knowledge about expected gain for a particular character after selection.

In general, in self-pollinated crops, characters with high heritability possess high genetic advance which is said to be governed by additive gene action suggesting direct selection for traits. In contrast, high heritability with low genetic advance or low heritability with high genetic advance are the results of non-additive gene action and selection for such traits may not be rewarding.

In the present investigation, plant height, number of mature pods per plant, number of immature pods per plant, dry haulm yield per plant, harvest index had high heritability along with high genetic advance indicating that these traits were governed by additive gene action and simple selection would be effective.

Similar results were observed by Ganeshan and Sudhakar (1995), Jayalakshmi *et al.* (1998), Islam and Rasul (1998), Vasanthi *et al.* (1998), Yadav *et al.* (1998), Singh and Singh (1999), Prakash *et al.* (2000) and John *et al.* (2009).

The traits *viz.* Days to 50% flowering, photosynthetic rate, Days to maturity, percent oil content, percent protein content exhibited high heritability coupled with low genetic advance indicating importance of non-additive gene action in the inheritance of these traits. Heterosis breeding may be useful in such characters. Similar results were obtained by Rudraswamy *et al.* (1999), Uddin *et al.* (1995) and Korat *et al.* (2009).

5.4 Transgressive segregation

The conventional idea of hybridization is to recombine the desirable characteristics in a new hybrid derivative, already observed in two parents involved in hybridization. The occurrence of transgressive segregants in segregating generation suggests that, transgressive breeding can be used as positive tool in plant breeding. The studies on transgressive segregation in the segregating generation, suggest that parent do not represent the extremes in terms of intensities of desired characters. If some genes for enhanced expression of a character are lacking in the genotype of the increasing parent but are present in donar parent, some individuals among the hybrid derivatives, emanating from the cross of these parents, might receive a fortuitous gene combination showing a larger effect than produced by either of the parents (Gardner, 1968). Smith (1966) suggested that in order to have reasonable chance of getting transgressive segregants, parents should have favorable expressions of the desirable characters and they should be rather distantly related so that desired character in the two parents may be controlled by differing set of genes.

Not much information is available on this aspect in groundnut. Hence, some research reports on pulses and oilseeds are discussed here. Auckland and Singh (1976) were the first to report transgressive segregants in this crop. Hence present study was carried out to provide information on transgressive segregation in straight F_2 originating from three groundnut crosses made among the five genotypes namely, Phule Unnati x TPG-41 (Cross1), Phule 6021 x RHRG 6110 (Cross2), Phule Unnati x SB XI (Cross3).

5.4.1 Transgressive segregants

Transgressive segregation is considered as an important tool by the plant breeder to bring about crop improvement. Due to segregation and recombination, in certain cases transgressive segregants are produced in F_2 or latter generations by accumulation of favourable genes from the parents involved in hybridization. Bahl (1979) initiated the work on Kabuli-Deshi introgression and reported encouraging results from this line of work. He could isolate early maturing types with determinant growth habit and better harvest index as compared to standard check variety. He also suggested that three ways instead of single cross are more useful for introgression of new germplasm in to breeding population.

It is interesting to note that, in the present study, transgressants were recorded in each of the three crosses in F_2

generation for all the seven characters (Table 7 to 24). In case of Dry pod yield per plant (gm), the highest proportion of individuals 14.33 to 24.67 percent transgressed beyond the increasing parent in total the three crosses, followed by Harvest index% 14.33 to 22.33, No of mature pod per plant 12.00 to 29.67 and Days of 50% flowering in which 12.33 to 29.00 per cent individuals were transgressed beyond the increasing parents. Rest of the characters in order of decreasing proportion of transgressive segregants were 100 Kernel weight (gm) 4.00 to 22.26 ,Sound mature Kernel% 7.67 to 18.54 and Shelling % 4.00 to 5.00.

Auckland and Singh (1976) reported transgressive segregants in respect of plant height (cm), number of seeds per pod, pod number and grain yield per plant (gm) in F_2 generation. Haddad (1979) isolated transgessants in Lentil in term of earliness, tallness, erectness, high pod number and high yield. Ugale (1980) reported transgressants for all these characters except pod length and cluster per plant with the highest proportion of individuals for plant spread (30.77 %). Kant and Singh (1998) observed transgressive segregants for plant height, yield per plant, primary branches per plant, secondary branches per plant, pods per plant, seed per pod and 100-seed weight. Girase and Deshmukh (2002) reported transgressive segregants for all seven characters like plant height, plant spread, fruiting branches per plant, pods per plant, seeds per pod and 100-seed weight, yield per plant. They observed the highest transgressive segregation for plant height (27%) followed by pods per plant, fruiting branches per plant and yield per plant in both F_2 and F_3 generation of all the three crosses.

If we consider ranking based on the proportion of transgressive segregants in F_2 generation, we find that top ranks for majority of the characters were shared by cross 2 depending on the involvement of increasing parent. The first rank appeared for three characters in Phule 6021 x RHRG 6110 (Table 25), whereas it was for one characters in Phule Unnati x TPG-41 and three character in Phule Unnati x SB XI.

In general Phule Unnati x TPG-41 secured second rank for majority of the characters, which indicated relatively lesser number of transgressive segregants.

Apart from the frequency of transgressants, it will be of great interest to examine the intensities of the characters achieved in the transgressants in each of the crosses. This will provide an insight into the extended limits and intensities of desired characters achieved by transgressive breeding. In the present investigation, the highest yielding transgressants in crosses 1, 2, and 3 produced 59.40, 64.23, and 59.40 Dry pod yield per plant (gm), respectively as against 40.47, 36.33 and 35.67 g per plant, produced by their respective increasing parents. These intensities for Dry pod yield per plant were 76.79 (Phule 6021 x RHRG 6110), 66.52 (Phule Unnati x SB XI) & 46.77 (Phule Unnati x TPG-41), per cent higher than those of their respective increasing parents.

Table 25: Ranking of F_2 generation based on proportion of the transgressive segregants for different characters in three crosses

Characters	Cross No.	Increasing parent	F_2	Rank
Days to 50% flowering	1	TPG-41(+)	43.97	1
	2	Phule 6021(+)	41.91	2
	3	SB XI (+)	40.59	3
No of mature pod/plant	1	Phule Unnati(+)	48.75	1
	2	Phule 6021(+)	43.86	2
	3	Phule Unnati(+)	41.55	3
Dry pod yield/plant(gm)	1	TPG-41(+)	40.77	2
	2	Phule 6021(+)	37.92	3
	3	Phule Unnati(+)	43.09	1
Hundred kernel wt(gm)	1	TPG-41(+)	45.52	1
	2	Phule 6021(+)	39.99	3
	3	Phule Unnati(+)	43.61	2
Shelling %.	1	TPG-41(+)	65.79	3
	2	RHRG 6110(+)	66.45	1
	3	Phule Unnati(+)	65.83	2
Harvest index% wt basis	1	TPG -41(+)	38.37	2
	2	Phule 6021(+)	46.08	1
	3	Phule Unnati(+)	37.89	3
Sound mature kernel%	1	Phule Unnati(+)	86.64	2
	2	Phule 6021(+)	84.21	3
	3	SB XI(+)	86.80	1

(+) = increasing parent

Table no 26: The uppermost limits achieved by transgressive segregants in respect of various characters in three F_2 crosses.

Characters	Highest intensity of character expression in three crosses		
	Cross 1	Cross 2	Cross 3
Days to 50% flowering	48.77 (45.27)	47.08 (43.87)	44.96 (40.47)
No of mature pod/plant	85.74 (43.07)	70.53 (38.67)	85.74 (43.07)
Dry pod yield/plant(g	59.40 (40.47)	64.23 (36.33)	83.04 (35.67)
100kernel wt(g)	69.66 (48.07)	57.96 (40.80)	58.75 (42.20)
Shelling %.	78.44 (67.23)	74.88 (66.40)	81.16 (65.07)
Harvest index weight basis	50.45 (37.93)	64.02 (42.80)	50.63 (35.93)
Sound mature kernel	96.93 (87.00)	93.48 (83.60)	90.38 (83.40)

* Figures in the bracket are the mean values of increasing parent for respective characters are as follows.

From this data it is evident that when the desired intensity of a character is not available in the parents, transgressive breeding can be employed to extend the limit of expression of character. It is therefore, concluded that transgressive breeding is effective for extending the limit of character expression, if plant breeder is interested in isolating the rare genotypes. In this method we impose more selection pressure which result in the highest recovery of characters than that of other breeding approaches.

5.4.2 Simultaneous transgressive segregation for two or more characters

In each of the three crosses under study in many transgressants, the Dry pod yield per plant (gm) of increasing parent was transgressed simultaneously with one or several other characters. Six characters in addition to Dry pod yield per plant (gm) considered for this purpose were, Days to 50% flowering, Number of mature pods per plant,100 Kernel weight (gm), shelling%, Harvest index% and sound mature Kernel%. It is interesting to note that some important and rare transgressive segregants, though low in frequency, were picked up in each of the three crosses. There were several such combinations of characters in which Dry pod yield per plant (gm) was transgressed in conjugation with transgression with other agronomic characters. The details of these rare and important transgressive segregants are as follow.

Table 27.Rare and important transgressants

Cross No.	Frequency of transgressant (%)	Characters for which transgression was simultaneous
1. 2. 3.	1.66 2.00 2.00	Dry pod yield /pl(gm) + No of Mature pod/pl + Days to 50% flowering + Harvest index%
1. 2. 3.	2.00 1.66 1.66	Dry pod yield /pl(gm) + No of Mature pod/pl + Days to 50% flowering + Shelling% + 100 Kernel weight (gm) + sound mature Kernel%
1. 2. 3.	1.66 1.66 2.33	Dry pod yield /pl(gm) + No of Mature pod/pl + Days to 50% flowering+ Harvest index% + Shelling% + sound mature Kernel%
1. 2. 3.	2.00 2.00 1.66	Dry pod yield /pl(gm) + No of Mature pod/pl + sound mature Kernel% + Harvest index%
1. 2. 3.	1.33 1.66 1.66	Dry pod yield /plant (gm) alone

Table 28.Number of transgressive segregation in all three F_2 crosses generation in summer groundnut.

Name of cross / character	Phule Unnati X TPG-41	Phule 6021 X RHRG 6110	Phule Unnati X SB XI
Days to 50% flowering	47	35	62
No of mature pod/plant	67	59	36
Dry pod yield/plant(g)	53	43	74
100kernel wt(gm)	16	52	67
Shelling %.	40	15	17
Harvest index wt basis	67	70	43
Sound mature kernel%	23	56	24

From this data it is clear that in majority of the individuals, whenever increasing parent Dry pod yield per plant was transgressed, there was simultaneous transgression for one or more other yield contributing characters like harvest index, number of mature pods per plant, Days to 50% flowering, 100 kernel wt, sound mature kernel and shelling%. There could be two possible explanations for this situation. The obvious reason for this could be that Dry pod yield per plant(gm) has been dependent on harvest index, Number of mature pods per plant, Days to 50% flowering, 100 kernel wt(gm), Sound mature kernel and shelling %. Alternatively there may be linkage drag so that genes responsible for these characters move together. Ugale and bahl (1980) suggested that there was a linkage drag among the plant spread, pod number, fruiting branches, seeds per pod and grain yield genes and concluded that genes of these characters are linked to each other. Whether it is linkage drag or dependency of grain yield per plant on some of the yield components, it could be safely inferred that selection of transgressive segregants for number of clusters per plant, number of pods per plant, pod length, number of seeds per pod will automatically lead to increase in grain yield per plant.

Promising transgressive segregants having combination of desirable attributes in F_2 generation of three crosses.

If we consider transgressive segregants for grain yield per plant in the cross Phule Unnati x TPG-41, plant No.45 was found to be most promising as it has given 46.77 per cent more Dry pod yield per plant (gm) in addition to higher expression of Shelling%, Number of mature pods per plant and 100-kernel weight (gm) than the increasing parent (Table 29). Besides, this transgressant had higher intensity of expression than the increasing parent for one character and also higher value for all characters than decreasing parents.. The transgressive segregants No.222 was most promising in cross Phule 6021 x RHRG 6110 which out yielded the increasing parent by 76.79 per cent and transgressed three other yield attributes. This segregants had higher values for all other traits than the decreasing parents.

In the cross Phule Unnati x SB XI the transgressive segregants No.111 was transgressed beyond the increasing parents with 66.52 per cent more Dry pod yield per plant (gm). It also produced more number of mature pods per plant, Shelling%, Harvest index%, and Sound mature kernel% than the increasing parent and higher values than decreasing parent for 100 kernel wt. From this study it can be suggested that the most promising transgressive segregants listed in (Table 29) need to be evaluated further. If they confirm their superiority in further generations may be considered for multi location evaluation for release as a variety or may be used as a parent in further breeding programme.

Table 29. Promising transgressive segregants having combinations of desirable attributes.

Generation	Plant no. 1	50% F 2	NMP 3	DPY 4	100 K 5	SH % 6	HI 7	SMK% 8	percentage of yield increased over the increasing parent
Cross-1 Phule Unnati x TPG-41									
F_2	45	55.80	85.74*	59.40*	69.6*	78.44*	50.45*	96.93*	46.77
P.Unnati	-	47.80	43.07	40.27	47.40	64.53	35.93	86.00	-
TPG-41	-	45.27	35.80	40.47	48.07	67.23	37.93	84.67	-
Cross-2 Phule 6021 x RHRG 6110									
F_2	222	53.51*	70.53*	64.23*	57.96*	74.88*	64.02*	93.48*	76.79
P.6021	-	43.87	38.67	36.33	40.80	66.40	42.80	83.60	-
RHRG-61110	-	44.33	36.47	36.20	39.00	65.40	39.67	82.80	-
Cross-3 Phule Unnati x SB XI									
F_2	111	53.96	85.74*	83.04*	58.7*	81.16*	50.63*	97.36*	66.52
P.Unnati	-	47.80	43.07	35.67	42.20	65.07	35.93	82.73	-
SB XI	-	40.47	38.20	33.47	40.67	63.93	35.73	86.80	-

1. 50% F = Days to 50% flowering
2. NMP = Number of mature pods per plant
3. DPY = Dry pod yield /plant (g)
4. 100K = 100 Kernel wt (g)
5. SH% = Shelling%
6. HI = Harvest index
7. SMK = Sound mature kernel

∗Intensity of expression of character higher than the increasing parent

6. SUMMARY AND CONCLUSION

The present investigation on "Assessment of genetic variability for high harvest index in summer groundnut (*Arachis hypogaea L.*)" was undertaken to study genetic advance, heritability, GCV, PCV for fourteen characters in Nine crosses of summer groundnut. The crosses were evaluated during summer, 2015, in a randomized block design with two replications. Observations were recorded on Days to 50% flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of mature pods per plant (gm), Dry haulm yield per plant (gm), number of immature pods per plant, Dry pod yield per plant(gm), Hundred kernel weight (gm), Shelling percentage, Harvest index%, Oil% content, Protein% content, Sound mature kernel%.

6.1 Genetic Variability

The treatment differences were statistically significant for majority of the characters and also the magnitude of genotypic and phenotypic coefficients of variations indicated the presence of good amount of variability. The character Dry haulm yield per plant (gm), Dry pod yield per plant (gm), Oil%, Plant height (cm), Number of immature pods per plant, Number of mature pods per plant, Oil content, Dry pod yield per plant (gm), Days to 50% flowering, Harvest index%, protein% content exihibited high heritability. Other characters recorded moderate to low heritability.The Dry haulm yield per plant highest genetic advance followed by Number of immature pods per plant Number of mature pods per plant, Harvest index%, Plant height (cm). Other characters showed moderate to low genetic advance.

6.2 Transgressive segregation

Transgressive segregation means a production of plants in the segregating generations,that are superior to both the parents for one or more characters by accumulation of favourable genes from both the parents, as a consequence of segregation and recombination.

1. Transgressive segregants in desirable direction were observed for all characters in F_2 generation of all three crosses.
2. In general the highest proportion of transgressive segregants were recorded for Dry pod yield per plant (gm), followed by Harvest index%, Number of mature pods per plant, Days to 50% flowering, 100 kernel wt (gm), Sound mature kernel% and shelling%.
3. On the basis of performance of transgressive segregants, it was concluded that, when the desired intensity of a character is not available in the parents, transgressive breeding can be successfully be used to extend the limit of expression of character. This could be possible by accumulation of favourable plus genes, in a hybrid derivatives from both parents involved in hybridization.
4. In most of the transgressive segregants, in each of the three crosses, better parent yield was transgressed simultaneously with transgression of one or several other characters. Simultaneous transgression of Dry pod yield per plant (gm) in association with number of mature

pods per plant, Harvest index%, Days to 50% flowering was observed more frequently. It was concluded that either Dry pod yield per plant (gm) is dependent on this character or there may be linkage drag so that genes responsible for these characters move together.

5. The most promising transgressive segregants *viz.,* plant No.45 of Phule Unnati x TPG 41, plant No.222 of Phule 6021 x RHRG 6110, plant No.111 of Phule 6021 x SB XI transgressed Dry pod yield per plant (gm) in addition to the higher expression of other three or four characters than the increasing parent. They produced 46.77 (Phule Unnati x TPG 41,), 76.79 (Phule 6021 x RHRG 6110) and 66.52 (Phule Unnati x SB XI) per cent more Dry pod yield per plant (gm) than their respective increasing parents. These transgressants needs to be evaluated further for maintaining consistency in their performance. If they found superior in further generations, they may be identified as improved varieties after adequate evaluation or used in future breeding programme for amulgamation of desired genetic constellations

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8. VITA

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of

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in

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

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