RVSKVV/2168

Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut genotypes (*Arachis hypogea* L.)

THESIS

Submitted to the

Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya

In partial fulfilment of the requirement for the degree of

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In

AGRICULTURE

(GENETICS AND PLANT BREEDING)

By

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2020

RVSKVV/2168

CERTIFICATE – I

This is to certify that the thesis entitled **"Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut genotypes (*Arachis hypogea* L)"** submitted in partial fulfilment of the requirement for the Degree of **MASTER OF SCIENCE** in **AGRICULTURE (Genetics and Plant Breeding)** of **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior** is a record of the bona-fied research work carried out by Mr. **RAMCHARAN AHIRWAR** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation has been acknowledged by the scholar.

Signature

(Dr. R.S. Sikarwar)
Chairman of the Advisory Committee

MEMBER OF STUDENT'S ADVISORY COMMITTEE

Co Advisor	(Dr. Shushma Tiwari)	…………………….………………..
Member	(Dr. V. B. Singh)	………………………………………
Member	(Dr. Rajni Singh Sasode)	………………………………………
Member	(Dr. Ekta Joshi)	……………………………………….

RVSKVV/2168

CERTIFICATE – II

This is to certify that thesis the entitled **"Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut genotypes (*Arachis hypogea* L.)"** submitted by Mr. **RAMCHARAN AHIRWAR** to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE** in **AGRICULTURE** in the department of **Genetics and Plant Breeding, College of Agriculture, Gwalior** has been accepted after evaluation by the External Examiner and approved by the Student's Advisory Committee after an oral examination of the same.

Signature

(Dr. R.S. Sikarwar)

Chairman of the Advisory Committee

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Member (Dr. Rajni Singh Sasode) ……………………………………...

Member (Dr. Ekta Joshi) …………………………………………….

Head of the Department ………………………...……….

Dean, Collage of Agriculture, Gwalior ………………………………….

Director of Instruction ………………………………….

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Everyone is not mentioned, but no one is forgotten.
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Place: Gwalior
Date:

(Ramcharan Ahirwar)

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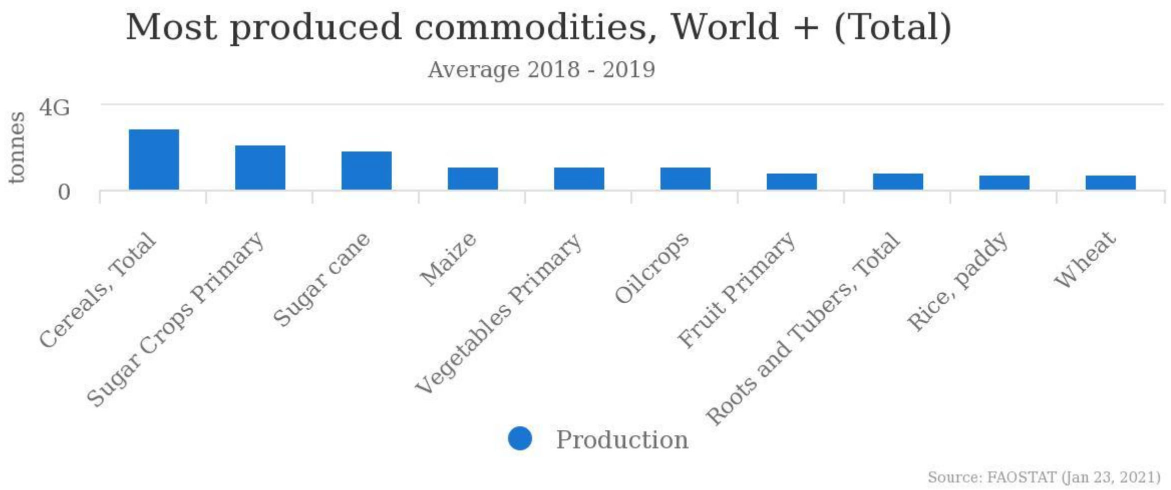
Abbreviations/ Acronyms	Meaning
Ag.	Agriculture
a.i.	Active ingredient
&	And
et al.	And co-workers
@	At the rate of
BCR	Benefit: cost ratio
AGR	Absolute growth rate
CD	Critical difference
CGR	Crop growth rate
Cm	Centi meter
DAS	Days after sowing
DAT	Days after transplanting
dSm^{-1}	Deci Siemens per meter
^{o}C	Degree centigrade
Dist.	District
E	East
ELS	Early leaf spot
EC	Electrical conductivity
F	Fertility
Fig.	Figure
FYM	Farm yard manure
G	Gram
Ha	Hectare
H. I.	Harvest index
HW	Hand weeding
i.e.	In reference to; that is
INM	Integrated nutrient management
Kg	Kilogram
kg ha^{-1}	Kilogram per hectare
LAI	Leaf area index
LAR	Leaf area ratio

Max.	Maximum
Mg m^{-3}	Mega gram per cubic meter
M	Meter
mg kg^{-1}	Milli gram per kilogram
Min	Minimum
Mm	Milli meter
M.P.	Madhya Pradesh
Mt	Metric tones
Viz	Namely
N	Nitrogen
No.	Number
OC	Organic carbon
O.M.	Organic manure
%	Per cent
K	Potassium
LLS	Late leaf spot
P	Phosphorus
PE	Pre-emergence
PoE	Post emergence
PSB	Phosphorus Solubilizing Bacteria
RDF	Recommended dose of fertilizer
RGR	Relative growth rate
RH	Relative humidity
Rs.	Rupees
R.V.S.K.V.V.	Rajmata Vijayaraje Scindia Krishi Vishwa Vidhyalaya
pH	Soil reaction
Q	Quintal
S	Sulphur
S.E.m (d)	Standard error mean of difference
SL	Shivpuri-local
Sy.	Symbol
Temp.	Temperature
t ha^{-1}	Tonnes per hectare
U.P.	Uttar Pradesh
VC	Vermicompost
Wt.	Weight

CHAPTER- I

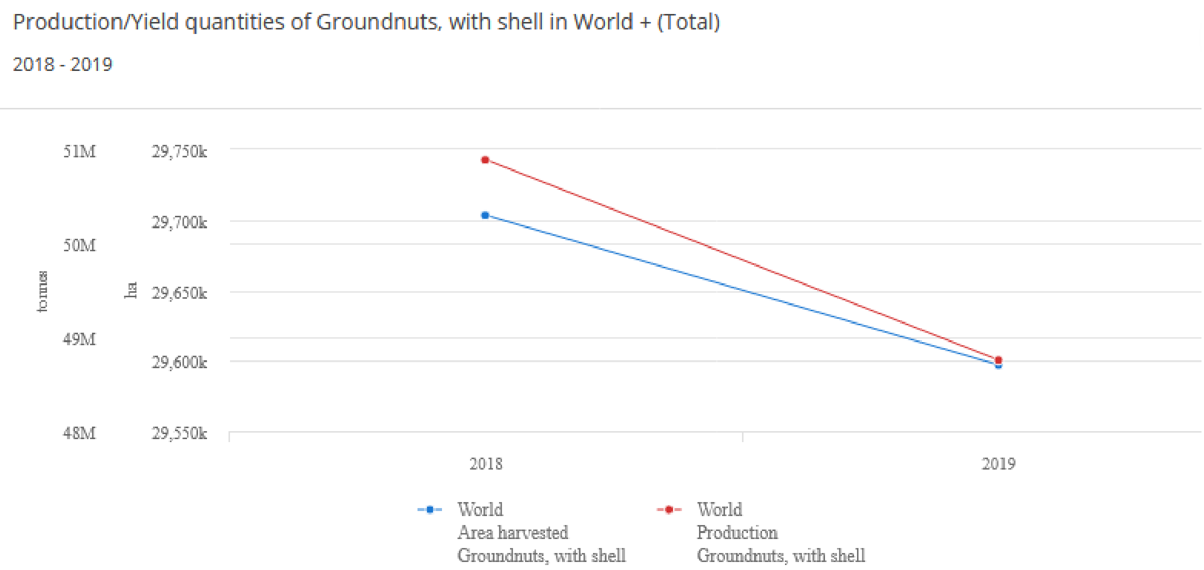
INTRODUCTION

Groundnut (*Arachis hypogaea* L.), conjointly called peanut and belongs to the family leguminous. It's one amongst the world's principal oil seed crops that is originated from South America. Now, groundnut is wide cultivated crop throughout the tropical, sub-tropical and therefore the heat temperate environmental condition zones. It's in the main autogamous crop. Groundnut kernel could be a made supply of edible oil (45-55%). Haulms and groundnut cake square measure vital sources of animal feed. It contains resveratrol, a polyphenol inhibitor, that has been found to supply protecting operate against cancer, heart condition, virus infection and chronic nerve malady. It's the most important seed crop mature in tropical, sub-tropical and heat temperate regions of the planet. It contains 22-36% macromolecule and 36-54% to grease that is made in essential unsaturated fatty acids i.e. omega-6 and linoleic acids. Groundnut, thus, referred as 'King of seed crops'. Presence of genetic variability is pre-requisite to upgrade a crop as per demand by providing adequate scope for choice. Yield, being a quantitative attribute, has low heritability and additional influenced by environmental effects. Therefore, direct choice primarily based upon the composition is dishonest. Hence, correct understanding of nee nature of variation is vital before makingchoice.

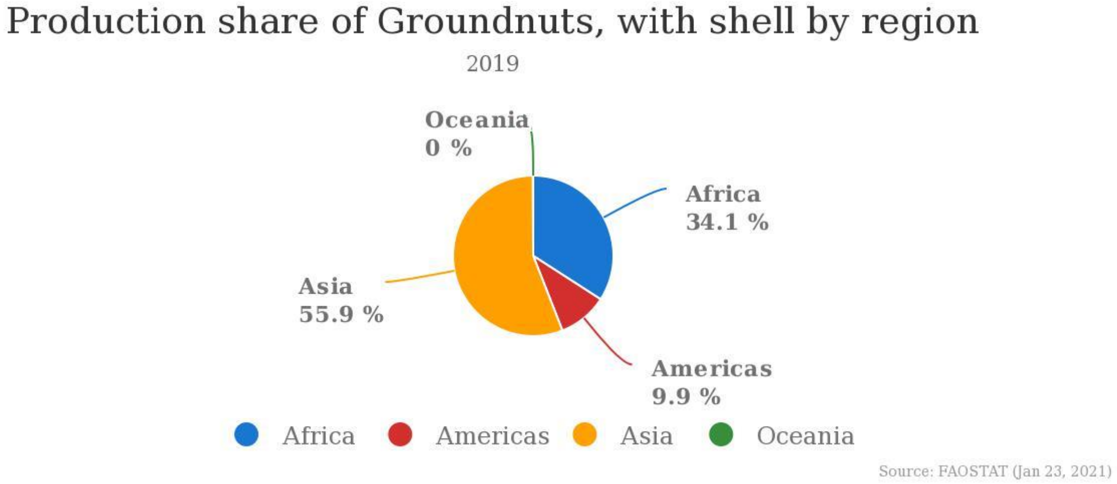


India occupies the second position in production and initial position in space within the world. In India, groundnut area harvested is 4.73 million hectare with a production of 6.72 millon tonnes and with a median yield of 14220 hg/ha (FAOSTAT 2019). According to the all Bharat kharif crop coverage report, Government of Bharat, as on

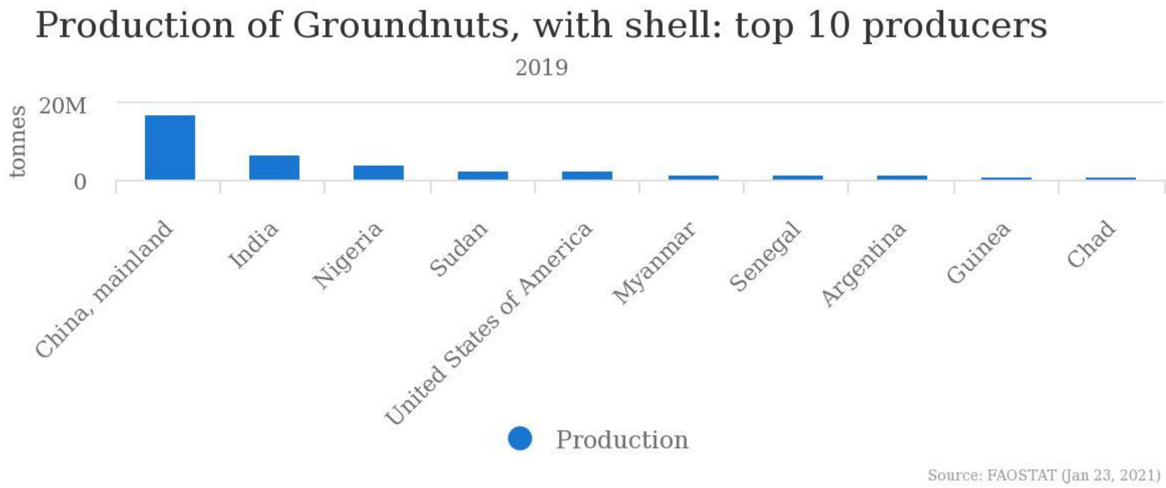
26thSeptember 2019, groundnut was seeded in around thirty-nine. 31 100000 hectares as compared to last year (40.19 100000 ha) and Madhya Pradesh (2.21 100000ha). Source: agricrop. Cultivated species of groundnut is an allotetraploid (AABB, 2n= 4x=40) having terriblyslim genetic diversity. Contrastingly, the diploid wild-type ancestors square measure inherently heterogeneous and ideally chosen for cumulating stress resistant genes throughout adaptation to severe environments (Kochert*et al*., 1996; Gimenes*et al*., 2002). The least level of variation in cultivated peanut has been authorized to 3 reasons or to combos of these obstructions to sequencebe due associated diploid species to domesticated peanut as a results of the polyploidization issue. contemporary polyploidization, from one or atiny low variety of individual(s) of every diploid parental species, combined with pollination (Halward *et al*., 1991). Utilization of few leading breeding lines and few exotic germplasms in breeding programs, succeeding in an exceedingly restricted genetic base (Isleib and Wynne 1992).



Majority of the economically vital characters together with pod yield and its yield attributing traits square measure amenable for genetic improvement through intense breeding among genetically various oldsters. Genetic divergence among oldstersis important since the crossing programme involving genetically various oldstersis probably going to supply high heterotic effects and conjointly additional variability can be expected within the segregating generations. Genetic diversity between populations or genotypes indicates the variations in sequence frequencies. Mahalanobis (1928) planned D2 statistics as live of cluster distance on multiple characters. D^2 measures the degree of diversification and determines the relative proportion of everyelement character to the whole divergence by partitioning intra-cluster and inter- cluster levels. As Genetic divergence, the presence of genetic variability is additionally a pre-requisite for the success of plant breeding programmes. Seed dormancy has been outlined because the failure of an intact, viable seed to complete germination underneath favorable conditions (Bewley, 1997).



Considerable dormancy discovered within the contemporary harvested seeds of many bunch groundnut cultivars is termed fresh seed dormancy. In groundnut, seed dormancy has been reportable to be controlled by 2 hormones: abscisic acid that inhibits development and olefin that is accumulated in storage to interrupt dormancy to permit germination (Ketring and Morgan, 1971, 1972).The aim of groundnut breeding programs across the planet is to develop new varieties that meet the wants of growers, processors, and customers.



Thus, for improvement in groundnut to full fill the wants of growers, processors, and consumers' genetic variability and divergence is incredibly vital. the trail constant analysis is one amongst the impactive technique to sought-after out bury relationship among completely different yield characters and their direct and indirect effect on yield through correlation values. Path constants important to accumulate optimum combination of yield contributory characters and to understand the implication of the inter relationships of varied characters in an exceedingly single genotype. Keeping in sight of the on top of genetic variability and divergence aspects, the current investigation are going to be meted out to understand the character and magnitude of genetic divergence in thirty groundnut genotypes for his or her incorporation in future union program that might eventually facilitate in development of groundnut varieties with higher pod yield.

Objectives of investigation:

1. To study the genetic variability, heritability and genetic advance for yield and its attributes.
2. To study the association and path coefficient analysis for yield and its attributes.
3. To estimate genetic divergence using D^2 analysis under study.
4. To estimate fresh seed dormancy of genotypes under study.

Chapter-II

REVIEW OF LITERATURE

The relevant literatures related to various aspects of present study are reviewed under the following heads:

2.1 Genetic variability, Heritability and Genetic advance

2.2 Path analysis and correlation coefficient

2.3 Genetic divergence (D^2 analysis)

2.4 Fresh seed dormancy

2.1 Genetic variability, Heritability and Genetic advance:

Meta *et al*. (2010) reported that high GCV and PCV for pods per plant, kernel yield per plant and pod yield per plant indicated large extent of genetic variability for these traits in the material. High heritability was accompanied by high genetic advance for plant height and 100-pod weight, whereas, moderate heritability was associated with high genetic advance and high GCV for pods per plant and kernel yield per plant, indicating involvement of additive gene action for these traits. Pod yield per plant expressed high genetic advance with low heritability, however, its high magnitude of GCV suggested the scope of pod yield improvement.

Cholin *et al.* (2010) analyzed 2 Spanish bunch groundnut genotypes for variability parameters and results revealed that magnitude of variation (PCV, GCV) was low to moderate. For the protein content, genetic advance as per cent of mean was moderate with high heritability indicating the role of additive gene action in controlling these traits and for oil content, lower magnitude of variation with higher heritability and lower genetic advance was reported.

Zaman *et al*. (2011) reported high genetic coefficient of variation for kernel yield per hectare, followed by kernel yield per plant, branches per plant, immature and mature nuts per plant, 100 kernel weight and plant height. The highest heritability was observed in kernel yield per pant (95.08%), followed by kernel yield per hectare (94.38%), 100 kernel weight (87.01%), immature and mature nuts per plant (82.24%, 80.32%), branches per plant (79.54%) and 100 nut weight (78.98%), while high values of genetic advance were obtained in all the characters except days to maturity and days to 50 per cent flowering.

Vishnuvardhan *et al*. (2012) studied the genetic parameters and recorded observations on 16 characters. Analysis of variance revealed highly significant differences among the genotypes for all the characters except number of mature pods per plant and pod yield per plant. High GCV accompanied by high heritability were obtained for number of immature pods per plant indicating predominant role of additive gene action and amenability for phenotypic selection in early generations. Moderate GCV and heritability were registered for plant height at harvest, number of primary branches per plant, number of leaves per plant at harvest, number of mature pods per plant, kernel weight per plant indicating that additive and non-additive gene actions have a role in their inheritance and phenotypic selection would be effective to some extent. For days to 50 per cent flowering and days to maturity, GCV was low and heritability was high.

Terkimbi *et al*. (2014) analyzed variability for basal stem diameter, biological yield, days to first and 50 per cent flowering, plant height, number of leaves per plant, branches per plant and 100-seed weight showing a wide scope for improvement through selection. Coefficient of variation at phenotypic and genotypic levels were close in magnitude for number of branches per plant, plant height, days to first flowering and grain yield suggesting the presence of additive gene effects. High heritability estimates coupled with genetic advance were noted for number of branches per plant, plant height, days to first flowering and grain yield.

Yadav *et al*. (2014) observed that magnitude of GCV, PCV, heritability and genetic advance as percentage of mean were recorded high for various characters like pod yield per plant, hundred seed mass, harvest index, plant height and shelling per cent. High broad sense heritability estimates were recorded for hundred seed mass, days to maturity, shelling per cent, pod yield per plant, harvest index, protein per cent indicating that these traits were less influenced by the environment.

Dewangan *et al*. (2015) studied the genetic variability among 50 groundnut genotypes with K-6 as a check. The analysis of variance was significant for all characters days to 50% flowering, plant height (cm), number of branches per plant, days to maturity, number of pods per plant, number of grain per pod (g), seed index (100 seed weight), pod yield per plant (g), sound matured kernel (%) and shelling (%). Based on the mean performance among 50 genotypes, ICG-10185 followed by ICG-10092 were found to the best genotypes for pod yield per plant indicating the presence of amount of variation for these characters and indicating these traits could be used for selection for crop improvement. High heritability was observed for plant height (99%), seed index (94%) and pod yield/ plant (83%). High value of genetic advance was observed for plant height (21.92), while moderate value of genetic advance was observed for seed index (18.07), followed by shelling (%) (12.67).

Rao *et al.* (2015) studied genetic variability, heritability and genetic advance in 39 groundnut genotypes. Analysis of variance revealed significant difference among genotypes for all the seven characters. The magnitude of PCV and GCV was moderate to high for dry pod yield and kernel yield. High heritability was recorded for hundred kernel weight, dry pod yield and kernel yield. High heritability combined with high genetic advance was recorded for dry pod yield and kernel yield indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Bhargavi *et al*.(2017) evaluated 20 Spanish bunch groundnut genotypes along with the check TMV 2 were used to study their variability, heritability and genetic advance as per cent of mean for nineteen characters viz., days to 50% flowering, SPAD chlorophyll meter reading (SCMR) at 40, 50, 60, 70 DAS and at maturity, days to maturity, number of mature pods per plant, biological yield per plant (g), pod yield per plant (g), biological yield per hectare (q), pod yield per hectare (q), harvest index, 100 kernel weight (g), shelling percentage, kernel yield per plant (g), kernel yield per hectare (q), oil content (%) and oil yield per hectare (q) during summer 2013. The results revealed that the highest PCV and GCV were observed for number of mature pods per plant. High heritability accompanied with high genetic advance as per cent of mean was recorded for number of mature pods per plant, biological yield per plant (g), pod yield per plant (g), biological yield per hectare (q), pod yield per hectare (q), kernel yield per plant (g), kernel yield per hectare (q), 100 kernel weight (g) and oil yield per hectare (q) indicating the preponderance of additive gene action which might be exploited through simple selection procedures. The study revealed that the genotypes Abhaya and JCG 88 were better for further breeding from yield point of view.

Bhargavi *et al*. (2017) an investigation was carried out in 10 Virginia bunch groundnut genotypes to assess the variability, heritability and genetic advance as per cent of mean for 19 characters. Analysis of variance revealed highly significant differences among the genotypes for all the characters studied. The PCV was generally higher than the GCV for all the characters studied, which indicate that the variation was not only due to genotypes but also due to influence of environment on the trait. The results revealed that high PCV and GCV was observed for oil yield per hectare (q). High heritability accompanied with high genetic advance as per cent of mean was recorded for biological yield per plant (g), pod yield per plant, kernel yield per plant (g) and 100 kernel weight (g) indicating the preponderance of additive gene action which may be exploited through simple selection procedures.

Reddy *et al*. (2017) evaluated 30 drought tolerant groundnut genotypes for variability with regards to yield, physiological and quality traits. Estimates of heritability, genetic advance and genetic advance as per cent mean were also obtained for the above traits. The results revealed high to moderate GCV and PCV in addition to high heritability and high genetic advance as per cent mean for haulm yield per plant and free proline content.

Wadikar *et al*.(2018) studied 40 diverse genotype of groundnut were raised to measure genetic variability and character association for *viz.,* Days to 50 percent flowering, Days to maturity, Plant height (cm), No. of primary branches per plant, Shelling percentage (%), Strong Mature Kernel (%), Test weight (g), Harvest Index (%), Oil content (%), No. of seeds per pod, No. of pods per plant, Kernel yield per plant (g), Pod Yield Per plant(g) at Oilseeds research station, latur. It is essential to know the association and variability among yield and yield related traits in the material generated for effectual selection. Analysis of variances recorded significant differences among genotypes for all the characters indicating the presence of considerable amount of variability. Higher PCV and GCV values observed for kernel yield per plant followed by pod yield per plant, no. of pods per plant indicating good amount of variation for these characters. High heritability coupled with high genetic advance as per cent of mean has been noticed for kernel yield per plant, no. of pods per plant, pod yield per plant. The character association studies indicated that the highly significant positive association kernel yield per plant followed by harvest index, no. of pod per plant and test weight with pod yield at both genotypic and phenotypic level.

Mahesh R *et al*. (2018) reported that genetic parameters of variability and heritability of different 13 characters were studied in 40 genotypes of groundnut. The analysis of variance revealed the existence of significant differences among the genotypes for all the traits studied. The genotypes *viz.*, K-6, K-1696, TCGS-1157 and Dharani showed high mean performance for pod yield and its component traits *viz.*, number of primary branches per plant, hundred seed weight (g) and kernel yield per plant (g). High heritability coupled with high genetic advance as per cent of mean was recorded by kernel yield per plant, hundred seed weight, pod yield per plant, number of primary branches per plant, number of pods per plant, shelling percent, harvest index, plant height and number of seeds per pod indicating that these characters are under additive genetic control and selection of these traits for improvement will be worthwhile and may rapidly contribute to increased pod yield in groundnut cultivars.

Hampannavar *et al.* (2018) studied genetic parameters like variability, heritability and genetic advance as the percent of meanamong 144 groundnut genotypes. In all genotypes recorded the 13 different characters out of that plant height (cm), number of primary branches per plant, number of mature and immature pods per plant, kernel yield per plant, hundred kernel weight (g), haulm yield per plant and dry pod yield per plant had high GCV, PCV, heritability and genetic advance as the percent of mean. The high GCV, PCV, heritability in addition to genetic advance as per cent of mean for most of the characters was observed indicating the presence of considerable genetic variation and additive gene effects.

Selvakumar *et al.* (2019) found high GCV, PCV values were recorded for the number of pods per plant, 100 pod weight, 100 kernel weight, shelling percent and number of mature kernels in the present study. This indicates the presence of ample variability for these traits. Hence these traits can be opted for selection as they contribute more towards variability with least influence of environment over it.

Khan *et al.* (2020) observed a highly significant variation for all the traits evaluated. There was a substantial variation (7.27 to 41.21%) coefficient value, and 14 out of the 27 numerical traits noted. Yield (kg/ha) disclosed positively strong to perfect high significant correlation (to 1.00) with traits like fresh pod weight, dry pod weight, and dry seed weight. The topmost PCV and GCV values were estimated for biomass dry (41.09%) and fresh (40.53%) weight with high heritability (Hb) and genetic advance (GA) %, % and %, %, respectively. The topmost heritability was recorded for fresh pod weight (99.89%) followed by yield (99.75%) with genetic advance 67.95% and 62.03%, respectively. The traits with and suggested the least influenced by the environment as well as governed by the additive genes and direct selection for improvement of such traits can be beneficial.

2.2 Path analysis and correlation coefficient:

Shobha *et al*. (2012) observed that kernel yield was significant and positively correlated with number of pods per plant, pod yield per plant, shelling per cent and hundred kernel weight for all the crosses. Among the nine traits studied, pod yield per plant exerted maximum positive direct effect on kernel yield per plant for all the three crosses. When both direct and indirect positive contributions were considered, number of pods per plant and pod yield per plant influenced kernel yield per plant. Thus, on the basis of correlations and direct and indirect effects, number of pods per plant, pod yield per plant, hundred kernel weight and shelling percentage were proved to be the outstanding characters influencing kernel yield in groundnut and need to be given importance in selection to achieve higher kernel yield.

Thakur *et al.* (2013) observed that pod yield per ha showed highly significant and positive association with days to maturity, sound mature kernel per cent, pod length, pod width and kernel length but the highly significant and negative association was shown with days to flowering, pod per plant, shoots length, shelling per cent and specific leaf area. Partitioning the total yield contributions into individual and combined effect showed that days to maturity, root length, pod width, pod length and kernel length made individual high positive direct contribution to pod yield per ha. Days to flowering, shoot length, shelling per cent, SMK per cent and 100 kernel weights had direct negative contribution with pod yield per ha. Therefore, days to maturity, root length, pod width, pod length and kernel length were identified to be the important traits which could be used in selection for yield.

Yadlapalli (2014) reported that pod yield exhibited significant and positive genotypic correlations with all the characters except with plant height. Number of pods per plant showed positive direct effect on pod yield per plant followed by 100 seed weight, no. of branches per plant and days to 50 per cent flowering. Selection for characters showing high significant correlation and showing high direct effects will be helpful in the improvement of yield in the groundnut.

Terkimbi and Terkula (2014) studied path analysis and observed that grain yield was correlated positively with all the character except the phenological traits. The path analysis implicated biological yield, failed pegs per plant, number of leaves per plant and basal stem diameter as having substantial influence on grain yield in groundnut. Thus, selection of breeding lines based on the biological yield, failed pegs, number of leaves per plant and basal stem diameter could give a better scope for maximum grain yield in groundnut.

Bharagavi *et al*. (2015) repotted that days to maturity, number of mature pods per plant, biological yield per plant, biological yield per hectare, harvest index, 100 kernel weight, kernel yield per plant, kernel yield per hectare, oil yield per hectare and pod yield per hectare showed significant positive association with pod yield per plant both at phenotypic and genotypic levels. Path analysis studies revealed that 100 kernel weight, kernel yield per plant and biological yield per hectare exerted maximum positive direct effect on pod yield per plant.

Gupta *et al*. (2015) evaluated correlation and path analysis of 60 genotypes of Virginia groundnut. The magnitudes of genotypic correlation coefficients were higher as compared to the corresponding phenotypic correlation coefficients. The pod yield per plant had highly significant and positive correlations at phenotypic levels with number of mature pods per plant, 100-pod weight, shelling out-turn, kernel yield per plant, biological yield per plant and harvest index. Path analysis revealed that the biological yield per plant and harvest index had high and positive direct effects on pod yield per plant.

Raghuwanshi *et al*. (2016) analyzed 50 diverse groundnut genotypes for associations among various agronomic characters and also path analysis for pod yield per plant. The magnitudes of genotypic correlation coefficients were generally higher compared to the corresponding phenotypic correlation coefficients for most of the traits. The pod yield per plant showed highly significant and positive correlations at both genotypic and phenotypic level with kernel yield per plant, number of mature pods per plant, harvest index, biological yield per plant, 100-kernel weight, days to 50% flowering, and shelling out-turn. Path analysis revealed high and positive direct effects of kernel yield per plant, while moderate and positive direct effects of number of mature pods per plant and harvest index on pod yield per plant. Days to 50% flowering and shelling out-turn contributed moderate and negative direct effects, but significant indirect effects along with 100-kernel weight for pod yield per plant. These results suggest kernel yield per plant, number of mature pods per plant, harvest index, 100-kernel weight, days to 50% flowering and shelling out-turn as useful traits for developing high yielding groundnut varieties.

Chavadhari *et al*. (2017) evaluated variability parameters of 70 groundnut genotypes for yield and yield components. A wide range of variation was observed for important yield components. High estimates of the genotypic coefficient of variation (GCV) were observed for kernel yield per plant followed by the number of branches per plant, harvest index and biological yield per plant. The estimates of heritability were observed to be high for harvest index followed by biological yield per plant, kernel yield per plant, 100-kernel weight, plant height, 100-pod weight and number of branches per plant indicated that these characters were less influenced by the environmental fluctuations. High heritability along with high genetic advance was observed for 100-pod weight. High heritability along with moderate genetic advance was observed for biological yield per plant, 100-kernel weight and harvest index indicating that these traits were mainly governed by additive gene action and responsive for further improvement of these traits.

Dhakar *et al*. (2017) studied correction and path coefficient analysis of 90 groundnut genotypes along with three check varieties viz., JL TG37A, PM-2 and UG-5. Association estimates revealed that dry pod yield per plant showed positive and significant correlation at both genotypic and phenotypic levels with kernel yield per plant, 100 -kernel weight, sound mature kernels and biological yield per plant. Correlation for dry pod yield per plant was divided into direct and indirect effects of different characters. Highest positive direct effect on dry pod yield was exhibited by kernel yield per plant (2.28) followed by days to maturity (0.57), oil content (0.31) and days to 50% flowering (0.22). This indicates that increase in kernel yield per plant, 100-kernel weight and sound mature kernels would improve the dry pod yield per plant of groundnut.

Kamdi *et al*. (2017) conducted experiment with 18 local collections of groundnut, along with checks (TAG-24 and Kopergoan-3). The analysis of variance revealed significant differences among the genotypes for all characters, indicating genetic variability. For all the traits, phenotypic coefficients of variations were higher than the genotypic coefficient of variations. The small differences observed between genotypic and phenotypic variability for number of mature pods plant^{-1}, weight of dry haulm plant^{-1} and weight of dry pods in kg ha^{-1} suggested that these characters were less influenced by environment. Positive and significant genotypic and phenotypic correlations between number of mature pods plant^{-1} and weight of dry pods in kg ha^{-1} was observed. Path co-efficient analysis also indicated that number of mature pods plant^{-1}, number of primary branches plant^{-1} and days to 50% flowering had positive direct effect on yield of dry pods. Improvement in yield of groundnut can thus be achieved by improving number of mature pods plant^{-1}.

Reddy *et al*. (2017) evaluated 30 drought tolerant groundnut genotypes. Pods per plant, pod yield per plant, and 100 kernel weights were observed with high positive direct effects and strong positive associations with kernel yield per plant. Consequently, these attributes are identified as effective selection criteria for kernel yield improvement in groundnut.

Singh *et al*. (2017) studied genetic characterization character association direct and indirect effects by path analysis for pod yield per plant and its components by using 15 groundnut genotypes. Dry pod yield per plant shown to have maximum genotypic coefficient of variation followed by kernel per plant suggesting substantial amount of genetic variability. Dry pod yield per plant, kernel yield per plant, 100-kernel weight, and days to maturity was observed high heritability and high genetic advance these traits were controlled by additive genes and can easily be transferred to succeeding generations. Dry pods per plant registered positive and significant genotypic and phenotypic correlations with kernel yield per plant and 100-kernel weight. It indicated that the selection for increased dry pods per plant may give higher kernel yield per plant and 100-kernel weight and thus, may contribute in increasing the dry pods per plant. The path coefficient analysis revealed that the kernel yield per plant, oil content and shelling percentage exhibited high and positive direct effect on dry pod yield per plant.

Uikey *et al*. (2017) studied the correlation and path coefficient among 38 local groundnut genotypes with 2 checks.The results on correlation studies showed that dry pod yield plant^{-1} was significant and positively correlated with number of mature pods plant^{-1} at both genotypic and phenotypic levels. Whereas, genotypic positive significant correlation of dry pod yield plant^{-1} was observed with number of primary branches plant^{-1} and mature kernels per cent. The partitioning of positive genotypic correlation of dry pod yield plant^{-1} with different traits into direct and indirect effects revealed that days to 50 per cent flowering (1.014) contributed highest positive direct effect to dry pod yield plant^{-1} followed by hundred kernel weight (0.664), number mature pods plant^{-1} (0.606), mature kernel per cent (0.395), plant height (0.254), oil content (0.108) and number of immature pods plant^{-1} (0.001). The major contributors to the indirect effect were number of mature pod plant^{-1} and mature kernel per cent.

Aparna *et al*. (2018) conducted an experiment with 168 germplasm lines and five checks of groundnut were used to study the correlation and path coefficient analysis for yield and yield contributing characters. Correlation studies revealed that kernel yield per plant exhibited highly significant and positive relationship with pod yield per plant followed by number of pods per plant, number of mature pods per plant, harvest index, 100 kernel weight, number of pegs per plant, shelling percentage, number of immature pods per plant, plant height and number of primary branches per plant. Path coefficient analysis indicated that that the number of pods per plant and kernel yield per plant exhibited very high positive direct effects on pod yield per plant. Thus, these characters turned-out to be the major components of pod yield in groundnut.

Mohammad Raza *et al*. (2018) reported path analysis which was carried with 40 genotypes of groundnut for yield and its component traits. Path coefficient analysis indicated that kernel yield per plant exerted the highest positive direct effect on pod yield per plant. It was also revealed that plant height, days to maturity, seed calcium uptake and seed iron uptake contributed indirectly to pod yield per plant through kernel yield per plant. These characters also exhibited highly significant and desirable association with pod yield and among themselves. This information could be utilised in formulating a sound selection criterion in groundnut breeding programmes for genetic improvement of high yield potential genotypes with high nutrient uptake ability.

Saritha *et al*. (2018) studied Correlation and path co-efficient analysis were carried out for physiological, yield and yield contributing characters in 32 genotypes of groundnut. The genotypic correlation co-efficients were found to be of relatively higher magnitude than the corresponding phenotypic correlation co-efficients indicating strong inherent association between the characters. Pod yield displayed significant positive association with number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index. Path co-efficient analysis revealed high direct effects of these characters on pod yield.

Nagaveni *et al*. (2019)assessed genotypes for various characters and also path analysis for pod yield per plant. The magnitudes of genotypic correlation coefficients were generally higher compared to the corresponding phenotypic correlation coefficients for most of the traits. The highly significant positive association recorded for kernel yield, haulm yield, and root diameter and root dry weight with pod yield per plant at both phenotypic and genotypic levels under both control and terminal drought conditions. The path analysis study indicated that high positive direct effect by kernel yield per plant on pod yield.

Rao *et al*. (2019) estimated character association, direct and indirect effects by path analysis for pod yield and its components by using 39 groundnut genotypes. The genotypic correlation coefficients were found to be relatively closer to the corresponding phenotypic correlations coefficients, representing strong inherent association between the traits. Pod yield was significant positively correlated with Kernel yield, Shelling percent and hundred kernel weight and significant negative association with day to 50% flowering, days to maturity and dry haulm yield. Path coefficient analysis revealed that the direct positive effect of kernel yield followed by days to maturity.

2.3 Genetic divergence (D^2 analysis):

Lakshmidevamma *et al*. (2006) studied the genetic diversity among 81 genotypes of groundnut. The genotypes were grouped into 16 clusters Of the 16 clusters formed, cluster I was the largest with 47 accessions followed by cluster II with 10 accessions. Test weight, days to maturity and oil content were the most potential traits contributing to the total divergence. Cluster XI and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII has genotype with most favorable characters and hence can be involved as potential parent for development of superior genotypes.

Korat *et al.* (2009) repotted maximum inter cluster distances between clusters I and VIII followed by clusters IV and VIII, clusters III and VIII and clusters II and VIII. The cluster VII showed high mean in respect to pod yield per plant, number of secondary branches per plant, number of aerial pegs per plant, number of kernels per pod, 100-kernel weight and harvest index. The cluster I had desirable value for days to 50 per cent flowering and days to maturity. While higher number of primary branches were found in cluster V. The cluster VII was the best for plant height and biological yield per plant. The cluster IV and III had desirable values for shelling percentage and oil content, respectively. The cluster IX was the best for number of underground pegs per plant. It will be advisable to intercross among the genotypes from clusters I, II, III, IV and VIII for generation of transgressive segregants and wide spectrum genetic variability for improvement of pod yield in groundnut.

Dolma *et al.* (2010) analyzed genetic divergence in among 33 genotypes of groundnut and observed that 33 genotypes were grouped into six clusters, where a cluster I was the largest containing 18 genotypes followed by cluster II with 10 genotypes. The inter cluster distance was maximum between cluster IV and V followed by cluster III and V.

Vekariya *et al*. (2010) studied genetic divergence analysis among 50 groundnut genotypes was carried out using Mahalanobis's D^2 statistic. The genotypes were grouped into 13 clusters. The maximum inter-cluster distance (D=327.33) was found between clusters III and XIII followed by clusters III and IX (D=267.26) and III and V (D=253.94) indicated that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters.

Zaman *et al*. (2010) conducted a study in 34 groundnut genotypes were studied for genetic divergence using Mahalanobis D^2 statistics. The genotypes were grouped into five clusters. Cluster III contained the highest number of genotypes (12) and the cluster II contained the lowest (2)**.** The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity is present among the genotypes of distant grouped. The highest intra cluster distance was observed in cluster V and the lowest in II. The highest inter cluster distance was observed between the cluster IV and III followed by V and III and the lowest between cluster V and I. Days to 50% flowering, days to maturity, number of branches per plant, number of matured nuts per plant and karnel size were the most important contributors based on the latent vector. But the highest cluster means for matured nuts per plant, 100 karnel weight, 100 nuts weight and yield per plant were obtained from the cluster II. With moderate yield but early maturity varieties were found in cluster IV. Therefore, more emphasis should be given on cluster VI for selecting genotypes as parents for crossing with the genotypes of cluster II and III for getting new recombinants with early maturity and higher yield.

Nirmala *et al.* (2013) studied 30 genotypes and grouped into 14 clusters. Among the various traits, the highest contribution towards divergence was found for number of secondary branches per plant, followed by crop growth rate (CGR) at 75 days after sowing (DAS) to harvest, CGR at 30-75 DAS, 100-seed weight, plant height, SPAD chlorophyll meter reading and harvest index.

Yadav *et al.* (2014) analyzed 60 genotypes for the study of genetic divergence. D^2 analysis indicated existence of wider genetic variability in the population of 60 genotypes which were grouped in 12 clusters, based on their inter clusters distance. The maximum inter-cluster distance (D = 7.044) was found between cluster III and X carrying one and two genotypes from each cluster, respectively followed by that between V and X (D = 6.447) and cluster III and XII (D = 5.943). The minimum inter cluster distance was observed between cluster VII and XI (D = 2.770). The intra-cluster distance (D) ranged from 1.909 to 2.863, the maximum being in cluster V (2.863). The minimum intra-cluster distance (D) was found in cluster II (1.909) which includes eight genotypes. Cluster III showed high genetic divergence with cluster X followed by cluster V.

Gupta *et al*. (2015) studied the genetic divergence among 60 groundnut genotypes of groundnut. The genotypes were grouped into thirteen clusters. The maximum inter-cluster distance (D=36.51) was found between clusters III and V followed by clusters IV and V (D=32.67) and II and IV (D=24.21) indicated that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters from ideal parents for yield improvement in groundnut.

Vivekananda *et al*. (2015) studied genetic diversity among 31 genotypes of groundnut were estimated using Mahalanobis D^2 statistic for five agro-morphological characters. The analysis of variance revealed significant differences among the genotypes for all characters. Based on Tocher's method, 31 genotypes were grouped into seven clusters, where cluster I was the largest containing 11 genotypes followed by cluster II and III with 7 genotypes each. The inter-cluster distance was maximum between clusters I and cluster VI followed by cluster I and cluster V, cluster III and VI and cluster I and IV. Considering the cluster distances and cluster means the genotypes from cluster I, III, V and VI could be selected for hybridization programme.

Bhakal *et al.* (2016) reported genetic divergence using D2 analysis of 40 genotypes of groundnut (*Arachis hypogaea* L.) of different geographic origins revealed existence of considerable diversity for eleven quantitative and qualitative characters. The genotypes were grouped into 7 clusters. The clusters VI was the largest containing 12 genotypes each followed by cluster V consisted 7 genotypes, cluster I and cluster VII consisted 6 genotypes, cluster III consisted 4 genotypes, cluster II consisted 3 genotypes and cluster IV consisted 2 genotypes. The diversity among the genotypes measured by intra-cluster & inter-cluster distance was adequate for improvement of groundnut by hybridization and selection. The genotype included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better sergeants in groundnut.

Niveditha *et al*. (2017) evaluate genetic divergence of 50 groundnut genotypes. The genotypes were classified into eight clusters, based on Mahalanobis D^2 statistic. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster IV and VIII. Intra-cluster distance was highest for cluster VIII, indicating the existence of high variability within this cluster. A perusal of the results on cluster means revealed high for pod yield per plant, kernel yield per plant, haulm yield and 100 kernel weight for cluster II, while days to 50 per cent flowering, number of filled pods per plant, sound mature kernel per cent and protein content were more for cluster IV. Similarly, high SPAD Chlorophyll Meter Reading (SCMR) for cluster V indicated the desirability of genotypes from these clusters for improvement of kernel yield and disease resistance.

Chavadhari *et al*. (2018) evaluate genetic divergence among seventy groundnut genotypes grouped into eleven clusters. The maximum inter-cluster distance (D) was observed between clusters IV and XI (D=239.0) followed by clusters VIII and IX (D=235.65) and clusters II and VIII (D=228.02) indicating that the genotypes of these groups may be mire divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters form ideal parents for improvement in groundnut.

Hampannavar *et al*. (2018) worked on genetic diversity among 144 genotypes for 13 characters was measured by employing D^2 statistic. The 144 groundnut genotypes were grouped under 16 clusters. Among 16 clusters, cluster IV was the largest which comprising of 24 genotypes followed by clusters I and II with 22 genotypes in each, cluster III and VII comprising 15 genotypes, cluster IV (14), VI (12), VII (7) and X (6) genotypes. The rest of clusters had shown solitary in nature. The average D^2 values of inter cluster distances, showed maximum distance between Cluster-XI and XVI (241.24) followed by inter cluster distance (223.43) between IV and XVI. It indicates that crossing between these clusters helps in production of transgressive segregates or better recombinants. The clusters were ranked based on the overall score across 13 traits. Accordingly, cluster-V was superior which indicates the presence of most promising genotypes in them. Each character had their own contribution to total divergence where, the haulm yield and oil percentage had maximum contribution of 33.39% and 30.99% respectively to the divergence of genotypes.

Raza *et al*. (2018) analyzed 40 groundnut genotypes for nature of magnitude of genetic diversity. The genotypes were grouped into 8 clusters using Mahalanobis D^2 statistics. The maximum inter-cluster distance was found between clusters II and VIII (D=183.23) followed by cluster VI and VIII indicating that the genotypes of these groups were highly divergent from each other. Among all the characters, pod yield per plant contributed the maximum to the diversity followed by leaf iron content (ppm) at 60 DAS, seed iron content (ppm) at maturity, seed calcium uptake (Kg ha-1) and seed calcium content (%) at maturity. The genotypes of above clusters revealed a substantial difference in the means for important yield contributing characters and form ideal parents for genetic improvement in groundnut.

Saritha K *et al*. (2018) studied Genetic diversity among 32 genotypes of groundnut was estimated for six characters using Mahalanobis D^2 statistic. Based on Tocher's method of clustering, 32 genotypes were grouped into eight clusters, of which cluster II was the largest containing 10 genotypes followed by cluster I with seven genotypes. The inter-cluster distance was maximum between cluster II and cluster VIII (2031.75) followed by cluster V and cluster VIII (1768.25) and cluster VII and VIII (1702.17). Considering the cluster distances and cluster means, crossing between the genotypes of cluster II and cluster VIII, and cluster VIII and cluster V is suggested in order to get transgressive segregants for yield and yield parameters.

Rejeki *et al*. (2020) Analysed of means (ANOM) calculated to test differences between landraces in particular traits. Heritability of three pure lines calculated based on Mean Square Estimated of Analysis of Variance (ANOVA), as well as coefficient correlation, using Minitab 18. The result showed that S19-3 as an introduced landrace from Namibia has traits similarity to the two landraces, namely GHC and Gresik except days to 50% flowering time. Analysis of means shows that S19-3 has days to 50% flowering early compare to the others. The trait of 50% flowering time (dap) also shows a high heritability (0.58). First flowering time has a significant correlation with 50% flowering time in positive direction.

2.4 Fresh seed dormancy:

Sreeramulu and Rao (1968) reported that freshly harvested seeds of TMV 2 show only 50 per cent germination and this is due to high moisture content of the seeds which blocks oxygen diffusion. Occurrence of fresh seed dormancy, which disappeared after seven days of curing has been reported in several Spanish groundnut cultivar19.

Asibuo James Yaw *et al*. (2008) studied four Spanish groundnut genotypes during 2004 and 2005. The F1 progenies from crosses between dormant and non-dormant parents were dormant. The F2 progenies fitted the expected 3 dormant to 1 non-dormant ratio The study showed that fresh seed dormancy is controlled by monogenic inheritance with dormancy dominant over non-dormant. The 2 dormant parents would be used as parents to transfer fresh seed dormancy trait into the background of adapted lines in Ghana to reduce losses associated with *in situ* sprouting which would lead to higher productivity and adoption by farmers.

Faye *et al.* (2010) studied the inheritance of fresh seed dormancy in Spanish x Spanish crosses with two sets of segregating populations, in which an F2 population derived from true F1 hybrids identified with peanut micro satellites markers and other populations (F2, BC1, P1s and BC1P2s) from randomly selected F1 individuals are used. Here the results revealed that in the F2 population developed with true F1 hybrids, the chi-square test was not significant for the deviation from the expected 3:1 (dormant : non-dormant). In addition the bimodal frequency distribution curve with the

F2 population gave more evidence that fresh seed dormancy is controlled by single dominant gene. Therefore, fresh seed dormancy is Spanish varieties is qualitative in nature.

Kumar*et al.*(2018) studied 33 advanced breeding lines and two varieties during summer 2012 and 2013. Advanced breeding lines evaluated for fresh seed dormancy showed significant genetic variation for germination percent at weekly intervals, duration, intensity and degree of fresh seed dormancy in groundnut. It was concluded that three advanced breeding lines PBS-12171, PBS-12169 and PBS-18035 had more than four week duration of fresh seed dormancy, highest intensity of fresh seed dormancy and degree of fresh seed dormancy during 2012 and 2013. Therefore, these genotypes were identified as new sources of fresh seed dormancy in groundnut.

Kumar *et al*. (2019) evaluate eight promising Spanish bunch groundnut genotypes for fresh seed dormancy over the environmentalconditions. Based on the results of intensity and durationof dormancy and germination stability index, identified fourstable advanced breeding linesviz., PBS 12192, PBS 12187,PBS 12191 and PBS 12190 having high fresh seed dormancy of three week.

CHAPTER-III

MATERIAL AND METHODS

The experimental materials used and methods adopted during the present investigation entitled “Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut Genotypes (*Arachis hypogaea* L.).”

3.1 Location: Experiment was carried out during the *kharif* season 2018-19 at Research Farm, Department of Genetics and Plant Breeding, RVSKVV, College of Agriculture, Gwalior (M.P.). Gwalior is located in the Grid region (Agro climatic zone No. VI, wheat-pearl millet crop zone) and situated at an altitude of 211.52 mean sea levels, 26^0 13’ N Latitude and 78^0 14’ E Longitude. The soil is sandy loam which is low in available nitrogen, medium in phosphorus and high in potash with P^H of 8.5.

3.2 Experimental Material: Experimental material consists of 23 genotypes and 7 cultivar of groundnut received from different origations, which were obtained from the All India Coordinated Research Project (AICRP) on Groundnut, Department of Genetics and Plant Breeding, RVSKVV, COA, Gwalior.

Material for fresh seed dormancy:

Positive control parent: TG-26

Negative control parent: JGN-3

28 genotypes

Table 3.1 List of genotypes used in the present study

Genotypes	Source
PBS 22059	DGR, Junagadh
PBS 22062	DGR, Junagadh
PBS 22063	DGR, Junagadh
PBS 22066	DGR, Junagadh
PBS 22067	DGR, Junagadh
PBS 22080	DGR, Junagadh
PBS 22116	DGR, Junagadh
PBS 22122	DGR, Junagadh
PBS 22132	DGR, Junagadh
PBS 22196	DGR, Junagadh
PBS 22200	DGR, Junagadh
ICRISAT 1	ICRISAT, Hyderabad
ICRISAT 2	ICRISAT, Hyderabad
ICRISAT 3	ICRISAT, Hyderabad
ICRISAT 4	ICRISAT, Hyderabad
ICRISAT 5	ICRISAT, Hyderabad
ICRISAT 6	ICRISAT, Hyderabad

ICRISAT 7	ICRISAT, Hyderabad
ICRISAT 10	ICRISAT, Hyderabad
ICRISAT 11	ICRISAT, Hyderabad
ICRISAT 12	ICRISAT, Hyderabad
ICRISAT 13	ICRISAT, Hyderabad
ICRISAT 15	ICRISAT, Hyderabad

Table 3.2 List of cultivar used in study

Cultivar Name	Source
KDG 128	DGR, Junagadh
TG 26	DGR, Junagadh
Gangapuri	RVSKVV, Gwalior
Sunolic 95 R	DGR, Junagadh
ICGS 144	DGR, Junagadh
JGN 3	RVSKVV, Gwalior
GPBD 4	DGR, Junagadh

3.3 Experiment details: The experiment was laid out in a Randomized Block Design (RBD) with three replications. The material was planted on 12th July, 2019. In each replication every genotype was sown in one rows of 5m length with a spacing of 30 cm between the rows and 10 cm between the plants within the rows.

Experimental details for fresh seed dormancy: Each replication consisted of 20 fresh harvested seeds sown at 2 to 3cm deep foreach genotype. The seeds of each genotype were sown at 45 cm spacing between rows and 10 cm between plants.The soil moisture was maintained at field capacity duringthe growth periodof the test (30 DAS) by irrigation. The observations were recorded on number of seedsgerminated at every day until the end of experiment.

3.4 Observations recorded: The Observations will be recorded on 5 randomly selected plants of each genotype in each replication for various characters. The methodology used for recording observations on different characters is described below:

1. **Plant height (cm):** plant height was measured in centimeter from ground level to the tip of main axis at the time of maturity on each randomly selected five plants.
2. **Days to 50% flowering:** Number of days were counted from the date of sowing to date when at least 50% of the plants having at least one flower.
3. **Days to maturity:** The total numbers of days were calculated from the date of sowing to date when all the plants attained complete physiological maturity.

4. **Number of primary branches per plant:** Total number of primary branches originating from the main axis were counted at maturity.
5. **Number of secondary branches per plant:** Number of branches originating onprimary branches were counted at maturity.
6. **Number of pods per plant:** The numbers of mature pods were counted for each randomly selected five plants at the time of harvesting.
7. **Pod yield per plant (gm):** The fully developed dry pods were weighed in grams from each randomly selected five plant at the time of maturity and average weight per plant was calculated.
8. **100 pod weight (gm):** Hundred pods were counted from random sample from each genotype and weighed in grams.
9. **Kernel yield per plant (gm):** Kernel yield per plant was computed by multiplying the dry pod yield with shelling percentage and divided by hundred.
10. **Hundred kernel weight (gm):** Hundred kernels were counted from random sample from each plot and weighed in grams.
11. **Shelling percentage (%):** The 100 gm pods were weighed from each genotypes and shelled. The shelling percentage was calculated using the following formula:

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

12. **Sound mature kernel (%):**Fully matured kernels were counted from representative sample of 100 kernels obtained from each genotypes. The sound mature kernel was calculated using the formula:

$$\text{SMK (\%)} = \frac{\text{Number of sound mature kernels}}{\text{Total number of kernels}} \times 100$$

13. **Pod yield per hectare (kg):** Pod yield per hectare was computed by multiplying the pod yield per plant with plant population per hectare.
14. **Kernel yield per hectare (kg):** kernel yield per hectare was computed by multiplying the kernel yield per plant with plant population per hectare.

Plate 1. Field view of groundnut genotypes.

3.5 Statistical analysis:

The data recorded were subjected to following statistical analysis:

3.5.1. Analysis of variance (Panse and Sukhatme, 1954)

3.5.2. Estimation of phenotypic and genotypic coefficients of variation (Burton, 1952)

3.5.3. Estimation of heritability and genetic advance (Singh and Choudhary, 1977)

3.5.4. Estimation of correlation coefficient (Miller *et al*., 1958)

3.5.5. Estimation of path coefficient analysis (Wright, 1921 and Dewey and Lu, 1959).

3.5.6. Estimation of D^2 analysis (Mahalanobis, 1928 and Rao, 1952)

3.5.7. Estimation of fresh seed dormancy (Kumar *et al*., 1991)

Table 3.3: Weekly Metrological Data for the crop growing period.

Meteorological week	Weekly Metrological Data for the crop growing period					
	Date	Temperature (℃)		Humidity (%)		Rainfall (mm)
		Maximum	Minimum	Morning	Evening	
23	June 4-10	45.8	29.1	40.6	19.7	0
24	June 11 - 17	42.7	29.4	45.6	39.4	10.8
25	June 18 - 24	37.3	25.3	79.3	51.4	72.8
26	June July 25 - 1	40.4	27.9	66.3	36.4	10.2
27	July 2 - 8	35.3	24.8	39	63	128.6
28	July 9 - 15	34.5	26.4	79.4	59.3	48.2
29	July 16 - 22	37.7	26.4	75.4	45	2.4
30	July 23 - 29	35.1	25.7	85.1	65	38.6
31	July Aug. 30 - 5	33.2	25.9	91.3	64.3	9.2
32	Aug 6 - 12	32.9	24.9	89.1	66.1	22.4
33	Aug. 13 - 19	31.1	24.1	91.1	84	59.8
34	Aug. 20 - 26	32.3	24.4	89.9	72.1	117.8
35	Aug. Sep. 27 - 2	33.5	25.2	90.1	66.7	21.8
36	Sep. 3 - 9	33.7	25.1	90.3	67.6	68.4
37	Sep. 10 - 16	32	23	94.3	78.3	67.9

38	Sep. 17 - 23	29	22.2	94.1	77.1	123.8
39	Sep. 24 - 30	31.6	21.5	95.7	80	73.6
40	Oct. 1 – 7	33.2	18	90.8	60	31.4
41	Oct. 8 - 14	32.6	17.5	32.2	40.7	0
42	Oct. 15 - 21	31.5	14.1	90.5	44.4	0
43	Oct. 22 - 28	33.2	18	89.4	31.7	0
44	Oct. Nov. 29 - 4	32	16.4	89	42.28	0

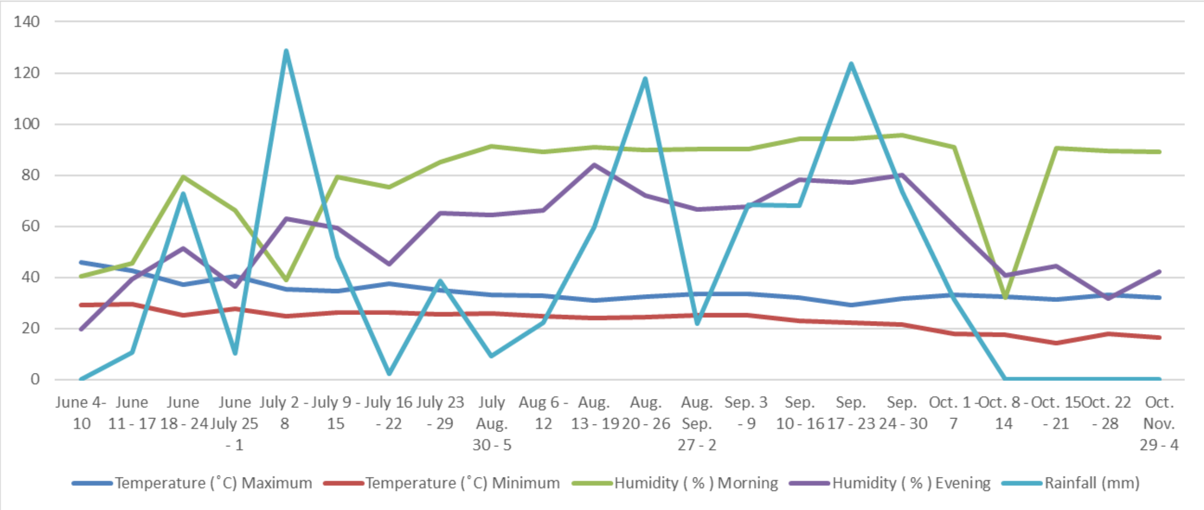


Fig 3.1 Weekly Metrological Data for the crop growing period.

3.5.1. Analysis of variance: The data were statistically analyzed on the basis of method described by Panse and Sukhatme (1954) using the mean values of five randomly selected plants in each treatment for each replication. The modal of analysis of variance table is below:

ANOVA table for the design of experiment

Source	Degree of freedom	Mean sum of square	Variance ratio
Replication	(r-1)	MSSr	MSSr/MSSe
Treatment	(t-1)	MSSt	MSSt/MSSe
Error	(r-1) (t-1)	MSSe	-
Total	rt-1	-	-

Where, r= Number of replications

t= Number of treatments,

MSSr = Mean square due to replication

MSSt = Mean square due to treatment

MSSe = Mean square due to error

Standard error of mean, critical difference and coefficient of variation:

(1) Standard error of mean: Standard error of mean was calculated using the following formula: $SE(m) = \sqrt{\frac{\text{MSSe}}{\text{r}}}$

Where, SE (m) =Standard error of mean, MSSe =Mean square due to error,
r= Number of replications

(2) Standard error of difference: Standard error of difference was calculated using the following formula: $SE(d) \pm = \sqrt{\frac{2\,\text{MSSe}}{\text{r}}}$

Where,

SE (d)± = Standard error of difference, MSSe = Mean square due to error,
r= Number of replications

(3) Critical difference: Critical difference was calculated using the following formula:

CD (5%) = SE (d) × t value at 5% level of significanceWhere, CD (5%) =Critical difference, SE (d) ± =Standard error of difference, 't' = Table value at error degree of freedom at 5%

(4) Coefficient of variation: The coefficient of variation as percentage of mean was estimated as mentioned bellow: $CV(\%) = \frac{S.D.}{Mean} \times 100$

Where, CV (%) = Coefficient of variation,

S.D. = standard deviation

(5) Mean: It was calculated by using following formula:

Mean $(\overline{X}) = \frac{\sum_{i=1}^{n} X_i}{n}$

Where,

$\sum x$ =sum of all observations

n =Number of observations

(6) Range: The range of variation was expressed by the limit of smallest and the largest value of each observation.

3.5.2. Estimation of phenotypic and genotypic coefficients of variation: The following genetic parameters were estimated for the character exhibiting significant mean squares due to the genotypes.

(a) Genotypic variance: It was calculated using following formula:

$$Vg = \frac{MSSt - MSSe}{r}$$

Where,

Vg = Genotypic variance, MSSt = Mean square due to treatment

MSSe = Error mean square, and r = Number of replications

(b) Phenotypic variance: It was calculated as follows:

$$V_p = V_g + V_e$$

Where,

V_p = Phenotypic variance, V_g = Genotypic variance, and

V_e = Error variance i.e. MSSe

(c) Genotypic coefficient of variation (GCV): It was calculated using the following formula as suggested by the Burton (1952).

$$GCV = \frac{\sqrt{V_g}}{\overline{X}} \times 100$$

Where,

V_g = Genotypic variance, and $\overline{X}$ = Population mean

(d) Phenotypic coefficient of variation (PCV): It was calculated using the following formula as suggested by Burton (1952).

$$PCV = \frac{\sqrt{V_p}}{\overline{X}} \times 100$$

Where,

V_p = Phenotypic variance and $\overline{X}$ = Population mean

3.5.3. Estimation of heritability and genetic advance: Heritability in percentage in broad sense was estimated by the following formula given by Sing and Choudhary (1977):

$$Heritanility\ (\text{h2}) = \frac{Genotypicvariance}{Phenotypicvariance} \times 100$$

$$\text{Genotypic variance (Vg)} = \frac{\text{MSSt - MSSe}}{\text{r}}$$

Phenotypic variance = genotypic variance + MSSe

Where, MSSt = Mean square due to treatment,

MSSe = Mean square due to error, r= Number of replications

Genetic advance from selection is calculated by the following formula suggested by Johnson*et al*. (1955).

$$G(s) = h^2 \times \sigma_p \times K$$

Where,

G(s) = Genetic advance

σ_p = Phenotypic standard deviation

h^2 = Heritability

K = Selection intensity at 5% level of significance i.e., 2.06

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al*. (1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as percentage of mean was classified as low, moderate and high (Johnson *et al*. ,1955) and values are given below:

0-10% - low

10-20% - Moderate

≥20% - High

3.5.4. Estimation of correlation coefficient: Correlation coefficient among the characters in all possible combination at phenotypic, genotypic and environmental level by the formula given by Miller *et al*. (1958).

(a) Genotypic correlation coefficient

$$r_{xy}(g) = \frac{Covxy(g)}{\sqrt{Vx(g).Vy(g)}}$$

(b) Phenotypic correlation coefficient

$$r_{xy}(p) = \frac{Covxy(p)}{\sqrt{Vx(p).Vy(p)}}$$

Where,

$r_{xy}(g)$ = Genotypic correlation coefficient between X and Y traits

$r_{xy}(p)$ = Phenotypic correlation coefficient between X and Y traits

$Cov_{xy}(g)$ = Genotypic covariance of X and Y traits

$Cov_{xy}(p)$ = Phenotypic covariance of X and Y traits

$V_x(g)$ = Genotypic variance for X trait

$V_y(g)$ = Genotypic variance for Y trait

$V_x(p)$ = Phenotypic variance for X trait

$V_y(p)$ = Phenotypic variance for Y trait

The significance of phenotypic and genotypic correlation coefficients were tested with estimated values compared with the tabulated values of Fisher and Yates (1938) at n-2 d.f. at two levels of probability viz., 5% and 1%.

3.5.5. Estimation of path coefficient analysis: The proportion of direct and indirect contributions of various characteristics to the total correlation coefficients with kernel yield was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1l}P_{ly}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2l}P_{ly}$

$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \ldots + P_{ly}$

Where,

r_{1y} to r_{ly}= Coefficient of correlation between causal factor 1 to l and Dependent character y,

r_{12} to $r_{l-1,l}$ = Coefficient of correlation among causal factors themselves,

P_{1y} to P_{Iy} = Direct effects of characters 1 to I on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

Where,

$$R^2 = \sum_{iy} P_i^2 Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} \; P_{jy} \; R_{ij}$$

R_2 is the coefficient of multiple determinations.

3.5.6. Estimation of D^2 analysis:

The data collected on different characters were analyzed through Mahalanobis's generalized distance D^2 (1928).

3.5.6.1 Computation of D^2 values: Mahalanobis's D^2 statistics (1928) was used for assessing the genetic divergence between populations the generalized distance between any two populations is defined as:

$$\Delta^2 = (\lambda ij)\ Di \times Dj$$

Where,

λij = Reciprocal matrix to the common dispersion matrix.

Di = Difference between the mean values of the two populations for the i^{th} character.

Dj = Difference between the mean values of the two populations for the j^{th} character.

The quantity is estimated by the D^2 statistic as

$$D^2 = (S^{ij})\ DiDj$$

Where,

S^{ij} = Sample estimate of ij^{th} character.

Since the formula for computation requires the inversion of the matrix of 14^{th} order, transformation of the original correlated unstandardized character means to standardized uncorrelated variables was done to simplify the computational procedure. This information was effected by pivotal condensation method (Rao, 1952).

3.5.6.2 Determination of group clusters: Grouping of the populations into various clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average, show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of the combinations of each genotype were arranged in ascending order of their magnitudes in a tabular form as described by Singh and Choudhary (1977). To start with, two populations having the smallest distance from each other were considered, to which a third population having the smaller D^2 value from the first two populations was added. Similarly next, the nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered in that cluster. The groups of the first cluster were then omitted and the rest were treated in a similar way. This process was continues till all the populations were included into one or the other cluster. After the formation of the clusters, the average inter and intra – cluster divergence (distance) were calculated. The square root of the D^2 values obtained from the above represents the distance (D) between and within clusters.

3.5.6.3. Average intra - cluster distance: For the measurement of intra – cluster distances, the formula used was

$$=\Sigma_i Di^2/n$$

Where,

$\Sigma_i Di^2$= was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.5.6.4. Average inter – cluster distance: Clusters are taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of the D^2 values between the members of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

3.5.6.5. Contribution of individual characters towards divergence: In all the combinations each cluster was ranked on the basis of its combination towards divergence between two entries ($di = Yi^i – Yj^j$). Rank one is given to the highest mean difference and rank 'P' to the lowest difference. Where 'P' is the total number of characters. Percentage contribution of each character (x) towards genetic divergence was calculated using the formula:

$$X = \frac{N}{M} \times 100$$

Where,

X=Percentage contribution of character

N = Number of genotype combinations where the character ranked first.

M = All possible combinations of number of genotypes

3.5.7. Estimation of fresh seed dormancy: Appreciable dormancy observed in the freshly harvested seeds of several bunch groundnut cultivars, which disappears after curing is called fresh seed dormancy. Fresh seed dormancy is characterized by its intensity and duration. Fresh seed dormancy parameters were estimated using the method suggested by Kumar *et al*. (1991).

(1) Germination percentage: The percentage of germinated seeds for entry at a given date was calculated by the following formula:

$$Germination\ (\%) = \frac{Number\ of\ germinated\ seeds}{Total\ number\ of\ seeds} \times 100$$

(2) Intensity of fresh seed dormancy: The intensity of dormancy was measured aspercentage of non-germinated seed at seven days aftersowing.

Intensity of dormancy (%) = 100- Germination percentage

(3) Duration of fresh seed dormancy: Duration of dormancy was measured by daystaken to attend 50 per cent germination by a genotype.

CHAPTER- IV

RESULTS

4.1. Experimental data were analyzed statistically and results described as under:

1. **Analysis of variance**
2. **Mean and Range performance**
3. **Genetic parameters*:*** Genotypic and phenotypic coefficient of variation, heritability and genetic advance
4. **Association analysis:** Genotypic and phenotypic correlation coefficient & path coefficient analysis.

4.1.1. Analysis of variance:

Analysis of variance for grain yield and its attributing characters is presented in Table 4.1. All the genotypes under study in this experiment showed significant variations for all the 12 characters under study *viz*: days to 50% flowering, days to maturity, plant height, numbers of primary branches per plant, numbers of pods per plant, 100-pod weight, 100 kernel weight, kernel yield per plant, shelling percentage, sound mature kernel, pod yield per/hectare and kernel yield/hectare. It indicates the presence of considerable amount of variability for all these traits.

4.2.1. Mean and Range performance:

Morphological traits observed are presented in Table 4.2 and mean and range data presented in Table 4.3 and described as under.

Days to 50% flowering

Days to 50% flowering showed ranges between 24-35 days (GPBD 4) and (PBS 22067) respectively with mean value of 28.56 days and CV as 0.793%. Genotypes ICRISAT1, PBS 22196, PBS 22200 and JGN 3 showed significantly early flowering.

Days to maturity (days)

Days to maturity showed range between 106 days (PBS 22132) and 116 days (ICRISAT12) with the mean value 111 days and CV as 2.096%. The genotypes ICRISAT 2, ICRISAT 11, ICGS 144 and ICRISAT 109 showed significantly early maturity.

Plant height (cm)

Plant height differed in range of 19. 30 cm (ICRISAT12) to 48.95 cm (KDG 128) with an average of 36.45 cm and CV was obtained 10.35%. Genotypes TG26, JGN3, GPBD-4 and ICRISAT 4 proved significantly taller than remaining genotypes.

Number of primary branches

Number of primary branches differed in range of 3.5 (PBS 22116) to 6.00 (Sunolic 95 R) with an average of 4.3 and CV was obtained 10.269%. Genotypes ICRISAT12, ICRISAT13, Gangapuri and ICGS 144 have more numbers of primary branches.

Pod yield per plant

Pod/plant ranged from 5.41gm (KDG 128) to 31.12 gm (GPBD 4) with a mean value of 16.05 gm and CV estimated as 3.311%. Genotypes JGN3, PBS 22080, PBS 22200, ICRISAT 1 and Sunoleic 95R showed significantly higher pod yield per plant.

Hundred pod weight

Hundred pod weight varied in range of 35.20 gm (JGN3) to 96.65 gm (PBS 22122) with an average value of 66.74 gm and CV as 0.585%. Genotypes PBS22122, PBS22122, PBS22059 and PBS22062. Showed significantly hundred pod weight.

Hundred kernel weight

Hundred kernel weight ranged between 14.93 gm (PBS 22122) to 45.59 gm (Gangapuri) with an average value of 29.76 gm and CV was obtained 10.887%. Genotypes GPBD 4, Sunoleic 95 R, ICRISAT10 and PBS 22059. Showed significantly higher hundred kernel weight.

Kernel yield/plant

Kernel yield/plant ranged between 1.76 gm (PBS22116) to 16.03 gm (GPBD 4) with a mean value of 7.78 gm and CV estimated as 6.766%. Genotypes Gangapuri, PBS 22200 and ICRISAT 1 Showed significantly higher kernel yield/plant.

Shelling percentage

Shelling% ranged from 15.51% (PBS 22122) to 94.69% (Gangapuri) with a mean value of 47.11% and CV as 7.431%. Genotypes PBS2206, ICRISAT1 and PBS22200 displayed higher shelling percentage.

Sound mature kernel

Sound mature kernel varied from 68.50 (JGN3) to 93.00 (PBS 22200) with an average of 81.48 and CV was obtained 0.506%. Genotypes PBS 22196, ICRISAT 10 and ICRISAT7 Showed significantly higher sound mature kernel.

Pod yield/hectare

Pod yield/hectare ranged from 1200.85 kg (KDG 128) to 6914. 45 kg (GPBD4) with a mean value of 3566.49 kg and CV estimated as 3.317%. GenotypesPBS 22080, Sunoliec 95 R and ICRISAT 10.Showed significantly higher pod yield kg/hectare.

Kernel yield/hectare

Kernel yield/hectare ranged from 389.70 kg (PBS 22122) to 3561.30 (GPBD4) with a men value of 1729.73 kg/hectare and CV was obtained 6.761%. Genotypes Gangapuri, PBS 22200 and ICRISAT 1 Showed significantly higher Kernel yield/hectare.

Table: 4.1 (a) Analysis of variance for yield and different attributing traits.

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	pod yield /plant	100 Pod weight (gm)
Replication	2	0.0085	0.0335	4.1115*	10.2085*	1.065	0.072
Treatment	29	14.879*	16.607*	81.391*	0.955	60.624*	487.373**
Error	29	0.051	5.48	17.265	0.486	0.277	0.153

Source of variation	DF	100 kernel weight (gm)	kernel yield/plant	Shelling %	sound mature kernel per 100 kernel	Pod yield per hec (Kg)	Kernel yield pre hectare (kg)
Replication	2	7.1765*	0.019	10.62*	0.0335	52652.4505**	949.1245**
Treatment	29	132.066**	33.612*	513.762**	92.825*	2993758.497**	1659629.707**
Error	29	10.475	0.272	11.98	0.17	13742.82	13420.07

*Significant at 5% **Significant at 1%

Table 4.2 Mean performances of different grains yielding characters.

Sr. No.	Name of Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	pod yield /plant	100 Pod weight (gm)	100 kernel weight (gm)	kernel yield/plant	Shelling %	sound mature kernel per 100 kernel	Pod yield per hec (Kg)	Kernel yield pre hectare (kg)
1	PBS 22059	26	114	38.2	4	12.455	80.125	36.85	5.73	45.99	79	2,767.80	1,273.10
2	PBS 22062	27	114.5	36.85	5	14.075	92.35	34.2	5.215	37.03	81.5	3,127.75	1,158.60
3	PBS 22063	29	112	38.15	4.5	19.005	60.55	34.75	10.9	57.39	78	4,222.90	2,422.85
4	PBS 22066	32	113.5	32.25	3.5	13.025	55.35	20.87	4.915	37.7	87	2,894.20	1,092.20
5	PBS 22067	34.5	116	29.55	4.5	16.9	48.9	36.68	12.68	75.01	71	3,755.55	2,817.45
6	PBS 22080	28	109.5	34.6	4	25.425	63.25	31.22	12.55	49.38	70	5,649.80	2,790.15
7	PBS 22116	30.5	108	35.75	3.5	7.47	86.3	20.96	1.815	24.29	87.5	1,659.55	403.15
8	PBS 22122	31	114	38.95	4	11.305	96.65	14.93	1.76	15.51	75	2,512.20	389.7
9	PBS 22132	32	106	31.75	3.5	15.505	94.4	32.97	5.415	34.925	79	3,445.15	1,203.25
10	PBS 22196	25	108.5	28.75	4	8.58	56.3	27.56	4.195	48.96	91	1,906.25	933.2
11	PBS 22200	25.5	106.5	37.95	3.5	20.925	62.3	40.81	13.71	65.515	93	4,649.55	3,046.65
12	ICRISAT 1	24	116	40.75	4	19.465	52.6	36.52	13.52	69.44	83	4,325.35	3,003.45
13	ICRISAT 2	29	107	28.25	4.5	12.46	60.3	34.85	7.205	57.8	91.5	2,769.10	1,600.45
14	ICRISAT 3	31	109.5	32.1	3.5	13.385	56.7	22.29	5.26	39.32	87	2,974.20	1,169.45
15	ICRISAT 4	32	111	46.7	3.5	16.44	56.2	28.99	8.49	51.595	76	3,653.55	1,887.30
16	ICRISAT 5	29	113	32.85	4.5	19.035	64.2	24.06	7.13	37.475	83	4,229.55	1,584.65
17	ICRISAT 6	25	110.5	37.8	4.5	18.345	74.6	30.99	7.615	41.545	80.5	4,076.90	1,692.25
18	ICRISAT 7	26	111	35.7	3.5	13.555	90.3	32.63	4.895	36.14	89	3,012.45	1,088.30
19	ICRISAT 10	28	114.5	33.6	5	19.365	76.2	40.705	10.35	53.42	90	4,303.15	2,299.05
20	ICRISAT 11	30	107	30.5	4.5	14.195	68.4	20.845	4.325	30.475	85.5	3,154.00	961.25
21	ICRISAT12	29	116	19.3	5	13.125	62.5	20.745	4.355	33.195	76	2,916.20	966.95
22	ICRISAT 13	29	111	41.75	5	12.37	76.5	22.795	3.69	29.795	79	2,749.15	819.85
23	ICRISAT 15	26	114	35.8	3.5	16.175	52.45	24.98	7.69	47.63	82	3,589.80	1,709.70
24	KDG 128	28	113	48.95	5.5	5.405	56.3	21.05	2.015	37.385	86	1,200.85	447.4
25	TG 26	31	113.5	47.3	4.5	13.515	50.45	30.8	8.245	61.05	71	3,002.90	1,832.45
26	Gangapuri	32	112.5	37.7	5	16.48	48.15	45.59	15.605	94.69	75	3,662.20	3,467.05
27	Sunolic 95 R	29	112.5	40.55	6	19.67	82.50	39.605	9.445	48.01	80	4,371.30	2,098.95
28	ICGS 144	27	108.5	36.8	5	11.67	66.40	27.15	4.77	40.885	82	2,593.60	1,060.05

29	JGN 3	26	114	44.75	4	26.655	35.20	15.57	11.79	44.235	68.50	5,922.90	2,620.20
30	GPBD 4	24	113	44.4	3.5	31.115	77.37	39.84	16.03	51.5	89.00	6,914.45	3,561.30
Mean		**29**	**111**	**36.45**	**4.31**	**16.05**	**66.74**	**29.76**	**7.78**	**47.11**	**81.48**	**3566.49**	**1729.73**
C.D.		**0.465**	**4.812**	**8.541**	**1.432**	**1.082**	**0.803**	**6.653**	**1.072**	**7.114**	**0.848**	**240.959**	**238.113**
SE(m)		**0.16**	**1.655**	**2.938**	**0.493**	**0.372**	**0.276**	**2.289**	**0.369**	**2.447**	**0.292**	**82.894**	**81.915**
SE(d)		**0.226**	**2.341**	**4.155**	**0.697**	**0.527**	**0.391**	**3.237**	**0.522**	**3.461**	**0.412**	**117.23**	**115.845**
C.V.		**0.793**	**2.096**	**10.35**	**10.269**	**3.311**	**0.585**	**10.887**	**6.766**	**7.431**	**0.506**	**3.317**	**6.761**

4.3.1. Genetic parameters

Genotypic and phenotypic coefficient of variation

The presence of genetic variability in the population is the fundamental requirement of plant breeding on which selection acts to evolve superior cultivar. Thus, higher the amount of variation present for a concerned character in the breeding materials, greater is the scope for its improvement through selection. During present investigation, genotypic coefficient of variation was lower than phenotypic coefficient of variation for all traits studied. (Table 4.3.)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were categorized as low (<10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). Kernel yield/plant has the highest GCV and PCV content (51.66, 51.81) pursued by Kernel yield/hectare (kg) (51.12, 51.39), Pod yield/hectare (kg) (34.69, 34.86), pod/plant (34.06, 34.23), shelling% (32.82, 32.87), hundred pod weight (23.44, 23.45) and moderate for plant height (14.59, 14.68), number of primary branches (14.24, 15.64), hundred kernel weight (13.14, 63.15) and low GCV and PCV for days to 50% flowering (9.47, 9.52), sound mature kernel (8.24, 8.28) and days to maturity (2.58, 2.59).

Heritability in Broad Sense (%)

Heritability in broad sense was presented in Table 4.3. Heritability estimates were classified as high (> 70%), moderate (50- 70%) and low (< 50%). All the 11 out of 12 characters have higher heritability estimates including hundred pod weight (99.91), shelling% (99.65), kernel yield/plant (99.42), days to maturity (99.13), sound mature kernel (99.12), pod/plant (99.0002), pod yield/hectare (kg) (99), kernel yield/hectare (kg) (98.96), days to 50% flowering (98.91), plant height (98.74) except hundred kernel weight which has low heritability (4.34).

Genetic advance as percentage of mean

Genetic advance as percentage of mean was estimated for all the characters under study. The genetic advance was classified as suggested by Johnson *et al.* (1955) *i.e.*, high (> 20%), moderate (10-20%) and low (< 10%). The high genetic advance as percentage of mean (at 5% selection intensity) was recorded for kernel yield/plant (106.12), kernel yield/plant (104.77), pod yield/hectare (kg) (71.11), pod/plant (69.81), shelling% (67.49), hundred pod weight (48.28), plant height (29.87) and number of primary branches (26.78) and moderate for days to 50% flowering (19.41) and sound mature kernel (16.90). Low for hundred kernel weight (5.64) and days to maturity (5.30).

4.4.1. Association analysis:

Genotypic and phenotypic correlation coefficient among grain yield and its contributing characters are presented in Table (4.4. a & b).

Genotypic correlation coefficient

Plant height

Plant height is negatively significant and correlated with days to 50% flowering (r = -0.207) at 5% significance level. It showed highly significant positive association with days to maturity (r = 0.494) at 1% significance level.

No of primary branches

No of primary branches is positively significant and association with days to 50% flowering (r = 0.234) and days to maturity (r = 0.265) at 5% significance level.

Pod/plant

Pod/plant is negatively significant and correlated with days to 50% flowering (r = -0.311) and number of primary branches (r = -0.230) at 5% significance level.

100 kernel weight

100 kernel weight is highly significant and positively associated with days to maturity (r = 0.431), no. of primary branches (r = 0.470) and pod/plant (r = 0.384) at 1% significance level. It is negatively significant and correlated with plant height (r = -0.230) at 5% significance level.

Kernel yield/plant

Kernel yield/plant is highly significant and positively associated with pod/plant (r = 0.831) and hundred kernel weight (r = 0.727) at 1% significance level. It is highly negatively significant and correlated with hundred pod weight (r = -0.404) at 1% significance level.

Shelling%

Shelling% is highly significant and positively associated with pod/plant (r = 0.344), hundred kernel weight (r = 0.800) and kernel yield/plant (r = 0.799) at 1% significance level. It is highly negatively significant and correlated with hundred pod weight (r = -0.546) at 1% significance level.

Sound mature kernel

Sound mature kernel is highly negatively significant and correlated with Days to 50% flowering (r = -0.368), days to maturity (r =-0.352) and plant height (r = -0.318) at 1% significance level. It is negatively significant and correlated with pod/plant (r = -0.211), 100 kernel weight (r = -0.260) and kernel yield/plant (r = - 0.216) at 5% significance level. It had significant and positively associated with 100 pod weight (r = 0.247) at 5% significance level.

Pod yield/hectare (kg)

Pod yield/hectare (kg) is highly significant and positively associated with pod/plant (r = 1.000), 100 kernel weight (r = 0.383), kernel yield/plant (r = 0.821) and shelling% (r = 0.330) at 1% significance level. It is highly negatively significant and correlated with days to 50% flowering (r = -0.316) at 1% significance level. It had negatively significant and correlated no. of primary branches (r = -0.237) and sound mature kernel (r = -0.215) at 5% significance level.

Kernel yield/hectare (kg)

Kernel yield/hectare (kg) is highly significant and positively associated with pod/plant (r = 0.827), 100 kernel weight (r = 0.743), kernel yield/plant (r = 1.000), shelling% (r = 0.804) and Pod yield/hectare (kg) (r = 0.817) at 1% significance level. It is highly negatively significant and correlated with 100 pod weight (r = -0.395) at 1% significance level.

Phenotypic correlation coefficient

Plant height

Plant height is highly significant and positively associated with days to maturity (r = 0.489) at 1% significance level.

No. of primary branches

No. of primary branches is significant and positively associated with days to maturity (r = 0.242) at 5% significance level.

Pod/plant

Pod/plant is highly negatively significant and correlated with days to 50% flowering (r = -0.308) at 1% significance level. It had negatively significance and associated with no. of primary branches (r = -0.216) at 5% significance level.

Kernel yield/plant

Kernel yield/plant is highly significant and positively associated with pod/plant (r = 0.828) at 1% significance level. It had highly negatively significance and associated with 100 pod weight (r = -0.402) at 1% significance level.

Shelling%

Shelling% is highly significant and positively associated with pod/plant (r = 0.341) and kernel yield/plant (r = 0.797) at 1% significance level. It had highly negatively significance and associated with 100 pod weight (r = -0.545) at 1% significance level.

Sound mature kernel

Sound mature kernel is highly negatively significant and correlated with days to 50% flowering (r = -0.365), days to maturity (r = -0.350) and plant height (r = -0.341) at 1% significance level. It had negatively significance and associated with pod/plant (r = -0.211) and kernel yield/plant (r = -0.214) at 5% significance level. It had significant and positively associated with 100 pod weight (r = 0.246) at 5% significance level.

Pod yield/hectare (kg)

Pod yield/hectare (kg) is highly significant and positively associated with pod/plant (r = 0.995), Kernel yield/plant (r = 0.819) and shelling% (r = 0.328) at 1% significance level. It had highly negatively significant and correlated with Days to 50% flowering at 1% significance level. It had negatively significant and correlated with No. of primary branches (r = -0.213) and sound mature kernel (r = -0.213) at 5% significance level.

Kernel yield/hectare (kg)

Kernel yield/hectare (kg) is highly significant and positively associated with pod/plant (r = 0.821), kernel yield/plant (r = 0.995), shelling% (r = 0.799) and pod yield/hectare (kg) (r = 0.811) at 1% significance level. It had negatively significant and correlated with 100 pod weight (r = -0.392) at 1% significance level.

Table 4.3. Parameters of genetic variability for yield traits and its attributing traits.

Characters	Mean	Range		Heritability (Percent)	GCV	PCV	Genetic Advance	Genetic Advance value % means
Days to 50% flowering	29	24	35	98.911	9.477	9.529	5.525	19.416
Day to maturity	111	106	116	99.138	2.586	2.597	5.92	5.303
Plant height	36.45	19.30	48.95	98.742	14.593	14.686	11.093	29.872
No. of primary branches	4.31	3.5.	6.00	82.918	14.243	15.642	0.971	26.718
Pod/plant	16.05	5.41	31.12	99.002	34.062	34.233	11.136	69.816
100 pod weight	66.74	35.20	96.65	99.911	23.447	23.458	32.188	48.28
100 kernel weight	29.76	14.93	45.59	4.34	13.148	63.115	1.816	5.642
Kernel yield/plant	7.78	1.76	16.03	99.427	51.664	51.812	8.252	106.122
Shelling%	47.11	15.51	94.69	99.653	32.822	32.879	31.678	67.496
Sound mature kernel	81.48	68.50	93.00	99.124	8.245	8.281	13.775	16.909
Pod yield/hectare (kg)	3566.49	1200.85	6914.45	99	34.694	34.869	2,504.76	71.112
Kernel yield/hectare (kg)	1729.73	389.70	3561.30	98.966	51.124	51.391	1,808.37	104.77

Table 4.4. (a) Genotypic correlation coefficient for seed yield and its 12 attributing characters in groundnut.

Characters	Days to 50% flowering	Day to maturity	Plant height	No. of primary branches	Pod/plant	100 pod weight	100 kernel weight	Kernel yield/plant	Shelling%	Sound mature kernel	Pod yield/hectare (kg)	Kernel yield/hectare (kg)
Days to 50% flowering												
Day to maturity	0.137^{NS}											
Plant height	-0.207^{*}	0.494^{**}										
No. of primary branches	0.234^{*}	0.265^{*}	0.143^{NS}									
Pod/plant	-0.311^{**}	0.129^{NS}	0.186^{NS}	-0.230^{*}								
100 pod weight	-0.062^{NS}	-0.077^{NS}	-0.107^{NS}	-0.082^{NS}	-0.173^{NS}							
100 kernel weight	-0.128^{NS}	0.431^{**}	-0.230^{*}	0.470^{**}	0.384^{**}	0.195^{NS}						
Kernel yield/plant	-0.166^{NS}	0.176^{NS}	0.173^{NS}	-0.111^{NS}	0.831^{**}	-0.404^{**}	0.727^{**}					
Shelling%	0.042^{NS}	0.177^{NS}	0.053^{NS}	0.120^{NS}	0.344^{**}	-0.546^{**}	0.800^{**}	0.799^{**}				
Sound mature kernel	-0.368^{**}	-0.352^{**}	-0.318^{**}	-0.035^{NS}	-0.211^{*}	0.247^{*}	-0.260^{*}	-0.216^{*}	-0.175^{NS}			
Pod yield/hectare (kg)	-0.316^{**}	0.117^{NS}	0.184^{NS}	-0.237^{*}	1.000^{**}	-0.162^{NS}	0.383^{**}	0.821^{**}	0.330^{**}	-0.215^{*}		
Kernel yield/hectare (kg)	-0.180^{NS}	0.182^{NS}	0.162^{NS}	-0.104^{NS}	0.827^{**}	-0.395^{**}	0.743^{**}	1.000^{**}	0.804^{**}	-0.205^{NS}	0.817^{**}	

*. Significant at the 0.05 level (2-tailed). **. Significant at the 0.01 level (2-tailed). NS = (non-significant).

Table 4.4. (b) Phenotypic correlation coefficient for seed yield and its 12 attributing characters in groundnut.

	Days to 50% flowering	Day to maturity	Plant height	No. of primary branches	Pod/plant	100 pod weight	100 kernel weight	Kernel yield/plant	Shelling%	Sound mature kernel	Pod yield/hectare (kg)	Kernel yield/hectare (kg)
Days to 50% flowering												
Day to maturity	0.137^{NS}											
Plant height	-0.205^{NS}	0.489**										
No. of primary branches	0.204^{NS}	0.242*	0.130^{NS}									
Pod/plant	-0.308**	0.126^{NS}	0.185^{NS}	-0.216*								
100 pod weight	-0.062^{NS}	-0.077^{NS}	-0.106^{NS}	-0.076^{NS}	-0.173^{NS}							
100 kernel weight	-0.019^{NS}	0.100^{NS}	-0.037^{NS}	-0.061^{NS}	0.085^{NS}	0.040^{NS}						
Kernel yield/plant	-0.165^{NS}	0.175^{NS}	0.172^{NS}	-0.099^{NS}	0.828**	-0.402**	0.146^{NS}					
Shelling%	0.042^{NS}	0.176^{NS}	0.052^{NS}	0.108^{NS}	0.341**	-0.545**	0.171^{NS}	0.797**				
Sound mature kernel	-0.365**	-0.350**	-0.314**	-0.025^{NS}	-0.211*	0.246*	-0.034^{NS}	-0.214*	-0.174^{NS}			
Pod yield/hectare (kg)	-0.315**	0.117^{NS}	0.184^{NS}	-0.213*	0.995**	-0.161^{NS}	0.073^{NS}	0.819**	0.328**	-0.213*		
Kernel yield/hectare (kg)	-0.177^{NS}	0.180^{NS}	0.161^{NS}	-0.095^{NS}	0.821**	-0.392**	0.154^{NS}	0.995**	0.799**	-0.204^{NS}	0.811**	

*. Significant at the 0.05 level (2-tailed). **. Significant at the 0.01 level (2-tailed). NS = (non-significant).

4.5. Path coefficient analysis

Path coefficient analysis measures direct and indirect contribution of various independent characters on the dependent character. Path analysis will indicate whether the association of the yield related traits with yield is due to their direct effect on yield or due to their indirect effect through some other traits. Path analysis is carried out using the estimates of correlation coefficient. Path coefficient analysis was carried out using phenotypic correlation and seed yield per plant as a dependent variable.

Genotypic path coefficient analysis

Direct effect on grain yield

The genotypic path coefficient analysis of different morpho-physiological and yield traits on Kernel yield/hectare (kg) [Table: 4.5(a)] illustrated that kernel yield/ plant had considerably higher estimates of positive direct effect on Kernel yield/hectare (kg)(0.9718).Substantial positive direct effect was also recorded for Podyield/hectare (kg) (0.0342),100 kernel weight (0.0152), shelling% (0.0145), days to maturity (0.0123), sound mature kernel (0.0072), whereas, negative direct effect onKernel yield/hectare (kg) observed by 100 pod weight (-0.0001), nubmber of primary branches per plant (-0.0010), plant height (-0.0114), days to 50% flowering (-0.0167) and pod/plant (-0.0290).

Indirect effects on grain yield

Days to 50% flowering

Days to 50% flowering demonstrated positively significant indirect effect on kernel yield/hectare (kg) *via*pod/plant (0.0090), pursued by plant height (0.0024), days to maturity and shelling% (0.0006)and negatively indirect effected byno. of primary branches/plant (-0.0002), 100 kernel weight (-0.0019), sound mature kernel (-0.0026), Pod yield/hectare (kg) (-0.0108) and Kernel yield/plant (-0.1613).

Day to maturity

Day to maturity showed significantly positive indirect effect onkernel yield/hectare (kg) *via*Kernel yield/plant (0.1710), 100 kernel weight (0.0065), pod yield/hectare (kg) (0.0040) and Shelling% (0.0026) and negatively indirect effect by No. of primary branches (-0.0003), sound mature kernel (-0.0025), days to 50% flowering (-0.0023), pod/plant (-0.0037) and plant height (-0.0056).

Plant height

Plant height demonstrated positively significant indirect effect on kernel yield/hectare (kg) kernel yield/plant (0.1681), pod yield/hectare (kg) (0.0063), day to maturity (0.0061), days to 50% flowering (0.0035) and shelling% (0.0008) and negatively indirect effected byno. of primary branches(-0.0002), sound mature kernel (-0.0023), 100 kernel weight (-0.0035) and pod/plant (-0.0054).

No. of primary branches

No. of primary branches showed significantly positive indirect effect on kernel yield/hectare (kg) *via*100 kernel weight (0.0071), pod/plant (0.0067), day to maturity (0.0033) and shelling% (0.0050)and negatively indirect effected by sound mature kernel (-0.0003), plant height (-0.0016), days to 50% flowering (-0.0039), pod yield/hectare (kg) (-0.0081) and kernel yield/plant (-0.1079).

Pod/plant

Pod/plants howed significantly positive indirect effect on kernel yield/hectare (kg) *via*kernel yield/plant (0.8076), pod yield/hectare (kg) (0.0342), 100 kernel weight (0.0058), days to 50% flowering (0.0052), shelling% (0.0050), day to maturity (0.0016) and no. of primary branches (0.0002) and negatively indirect effected bysound mature kernel (-0.0015) and plant height (-0.0021).

100 pod weight

100 pod weight showed significantly positive indirect effect on kernel yield/hectare (kg) pod/plant (0.0050),100 kernel weight (0.0030), sound mature kernel (0.0018), plant height (0.0012), days to 50% flowering (0.0010) and no. of primary branches (0.0001) and negatively indirect effected byday to maturity (-0.0009), pod yield/hectare (kg) (-0.0055), shelling% (-0.0079) and kernel yield/plant (-0.3926).

100 kernel weight

100 kernel weight showed significantly positive indirect effect on kernel yield/hectare (kg) kernel yield/plant (0.7065), pod yield/hectare (kg) (0.0131), shelling% (0.0116), day to maturity (0.0053), plant height (0.0026) and days to 50% flowering (0.0021)and negatively indirect effected by no. of primary branches (-0.0005), sound mature kernel (-0.0019) and pod/plant (-0.0111).

Kernel yield/plant

Kernel yield/plant showed significantly positive indirect effect on kernel yield/hectare (kg) pod yield/hectare (kg) (0.0281), shelling% (0.0116), 100 kernel weight(0.0110), days to 50% flowering (0.0028) and day to maturity (0.0022) and negatively indirect effected bysound mature kernel (-0.0015), plant height-0.0020) and pod/plant (-0.0241).

Shelling%

Shelling% demonstrated positively significant indirect effect on kernel yield/hectare (kg) kernel yield/plant (0.7765), 100 kernel weight (0.0122), pod yield/hectare (kg) (0.0113) andday to maturity (0.0022) and negatively indirect effected byno. of primary branches (-0.0001), plant height (-0.0006), days to 50% flowering (-0.0007), sound mature kernel (-0.0013) and pod/plant (-0.0100).

Sound mature kernel

Sound mature kernelshowed significantly positive indirect effect on kernel yield/hectare (kg) *via*days to 50% flowering (0.0062), pod/plant (0.0061) and plant height (0.0036) and negatively indirect effected by shelling% (-0.0025), 100 kernel weight (-0.0040), day to maturity (-0.0043), pod yield/hectare (kg) (-0.0073) and kernel yield/plant (-0.2099).

Pod yield/hectare (kg)

Pod yield/hectare (kg) howed significantly positive indirect effect on kernel yield/hectare (kg) kernel yield/plant (0.7979), 100 kernel weight (0.0058), days to 50% flowering (0.0053), shelling% (0.0048), day to maturity (0.0014) and no. of primary branches (0.0002) and negatively indirect effected bysound mature kernel (-0.0015), plant height (-0.0021) and pod/plant (-0.0290).

Phenotypic Path coefficient analysis

Direct effect on grain yield

The phenotypic path coefficient analysis of different morph-physiological and yield traits on kernel yield/hectare (kg) [Table4.5 (b)] revealed that kernel yield/plant (0.921) considerably higher estimates of positive direct effect on kernel yield/hectare (kg). Substantial positive direct effect was also recorded for pod/plant (0.135), shelling% (0.059), 100 pod weight (0.016), day to maturity (0.015), no. of primary branches (0.003) and 100 kernel weight (0.002).), where as negative direct effect on kernel yield/hectare (kg) was observed bysound mature kernel (-0.003), plant height (-0.019), days to 50% flowering (-0.024) and pod yield/hectare (kg) (-0.100).

Indirect Effects on kernel yield/hectare (kg)

Days to 50% flowering

Days to 50% floweringhave indirect positive effect onkernel yield/hectare (kg)*via*pod yield/hectare (kg) (0.032), plant height (0.004), day to maturity (0.002), shelling% (0.002), no. of primary branches (0.001) and sound mature kernel (0.001) and negatively indirect effected bypod/plant (-0.042) and kernel yield/plant (-0.152).

Day to maturity

Day to maturity have indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.161), pod/plant (0.017), shelling% (0.010), no. of primary branches (0.001) and sound mature kernel (0.001)and negatively indirect effected by 100 pod weight (-0.001), days to 50% flowering (-0.003), plant height (-0.009) and pod yield/hectare (kg) (-0.012).

Plant height

Plant height have indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.158), pod/plant (0.025), day to maturity (0.007), days to 50% flowering (0.005), shelling% (0.003) and sound mature kernel (0.001) and negatively indirect effected by100 pod weight (-0.002) and pod yield/hectare (kg) (-0.018).

No. of primary branches

No. of primary branches have indirect positive effect on kernel yield/hectare (kg) *via*pod yield/hectare (kg) (0.021), shelling% (0.006) and day to maturity (0.004) and negatively indirect effected by100 pod weight (-0.001), plant height (-0.002), days to 50% flowering (-0.005), pod/plant (-0.029) and kernel yield/plant (-0.091).

Pod/plant

Pod/plant have indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.763), shelling% (0.020), days to 50% flowering (0.007), day to maturity (0.002) and sound mature kernel (0.001) and negatively indirect effected byno. of primary branches (-0.001), plant height (-0.003), 100 pod weight (-0.003) and pod yield/hectare (kg) (-0.100).

100 pod weight

100 pod weighthave indirect positive effect on kernel yield/hectare (kg) *via*pod yield/hectare (kg) (0.016), plant height (0.002) and days to 50% flowering (0.001) and negatively indirect effected byday to maturity (-0.001), sound mature kernel(-0.001), pod/plant (-0.023), shelling% (-0.032) and kernel yield/plant (-0.370).

100 kernel weight

100 kernel weighthave indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.134), pod/plant (0.011), shelling% (0.010),day to maturity (0.002), plant height (0.001) and 100 pod weight (0.001) and negatively indirect effected by pod yield/hectare (kg) (-0.007).

Kernel yield/plant

Kernel yield/plant have indirect positive effect on kernel yield/hectare (kg) pod/plant (0.112), shelling% (0.047), days to 50% flowering (0.004), day to maturity (0.003) and sound mature kernel (0.001)and negatively indirect effected by plant height (-0.003), 100 pod weight (-0.006) and pod yield/hectare (kg) (-0.082).

Shelling%

Shelling% have indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.734), pod/plant (0.046) and day to maturity (0.003)and negatively indirect effected by days to 50% flowering (-0.001), plant height (-0.001), 100 pod weight (-0.009) and pod yield/hectare (kg) (-0.033).

Sound mature kernel

Sound mature kernel have indirect positive effect on kernel yield/hectare (kg) pod yield/hectare (kg) (0.021), days to 50% flowering (0.009), plant height (0.006) and 100 pod weight (0.004) and negatively indirect effected byday to maturity (-0.005), shelling% (-0.010), pod/plant (-0.028) and kernel yield/plant (-0.197) and negatively indirect effected byday to maturity (-0.005), shelling% (-0.010), pod/plant (-0.028) and kernel yield/plant (-0.197).

Pod yield/hectare (kg)

Pod yield/hectare (kg)have indirect positive effect on kernel yield/hectare (kg) kernel yield/plant (0.754), pod/plant (0.134), shelling% (0.019), days to 50% flowering (0.008), day to maturity (0.002) and sound mature kernel (0.001).

Table: 4.5(a) Genotypic path coefficients for yield and its attributing traits of groundnut genotypes.

Characters	days to 50% flowering	day to maturity	plant height	no. of primary branches	pod/plant	100 pod weight	100 kernel weight	kernel yield/plant	shelling%	sound mature kernel	pod yield/hectare (kg)	kernel yield/hectare (kg)
days to 50% flowering	**-0.0167**	0.0017	0.0024	-0.0002	0.0090	0.0000	-0.0019	-0.1613	0.0006	-0.0026	-0.0108	**-0.1800**
day to maturity	-0.0023	**0.0123**	-0.0056	-0.0003	-0.0037	0.0000	0.0065	0.1710	0.0026	-0.0025	0.0040	**0.1820**
plant height	0.0035	0.0061	**-0.0114**	-0.0002	-0.0054	0.0000	-0.0035	0.1681	0.0008	-0.0023	0.0063	**0.1620**
no. of primary branches	-0.0039	0.0033	-0.0016	**-0.0010**	0.0067	0.0000	0.0071	-0.1079	0.0017	-0.0003	-0.0081	**-0.1040**
pod/plant	0.0052	0.0016	-0.0021	0.0002	**-0.0290**	0.0000	0.0058	0.8076	0.0050	-0.0015	0.0342	**0.8270**
100 pod weight	0.0010	-0.0009	0.0012	0.0001	0.0050	**-0.0001**	0.0030	-0.3926	-0.0079	0.0018	-0.0055	**-0.3950**
100 kernel weight	0.0021	0.0053	0.0026	-0.0005	-0.0111	0.0000	**0.0152**	0.7065	0.0116	-0.0019	0.0131	**0.7430**
kernel yield/plant	0.0028	0.0022	-0.0020	0.0001	-0.0241	0.0000	0.0110	**0.9718**	0.0116	-0.0015	0.0281	**1.0000**
shelling%	-0.0007	0.0022	-0.0006	-0.0001	-0.0100	0.0000	0.0122	0.7765	**0.0145**	-0.0013	0.0113	**0.8040**
sound mature kernel	0.0062	-0.0043	0.0036	0.0000	0.0061	0.0000	-0.0040	-0.2099	-0.0025	**0.0072**	-0.0073	**-0.2050**
pod yield/hectare (kg)	0.0053	0.0014	-0.0021	0.0002	-0.0290	0.0000	0.0058	0.7979	0.0048	-0.0015	**0.0342**	**0.8170**

R SQUARE= 0.9876 **RESIDUAL EFFECT= 0. 1013**

Table: 4.5(b) Phenotypic path coefficients for yield and its attributing traits of groundnut genotypes.

Characters	days to 50% flowering	day to maturity	plant height	no. of primary branches	pod/plant	100 pod weight	100 kernel weight	kernel yield/plant	shelling%	sound mature kernel	pod yield/hectare (kg)	kernel yield/hectare (kg)
days to 50% flowering	**-0.024**	0.002	0.004	0.001	-0.042	-0.001	0.000	-0.152	0.002	0.001	0.032	**-0.177**
day to maturity	-0.003	**0.015**	-0.009	0.001	0.017	-0.001	0.000	0.161	0.010	0.001	-0.012	**0.180**
plant height	0.005	0.007	**-0.019**	0.000	0.025	-0.002	0.000	0.158	0.003	0.001	-0.018	**0.161**
no. of primary branches	-0.005	0.004	-0.002	**0.003**	-0.029	-0.001	0.000	-0.091	0.006	0.000	0.021	**-0.095**
pod/plant	0.007	0.002	-0.003	-0.001	**0.135**	-0.003	0.000	0.763	0.020	0.001	-0.100	**0.821**
100 pod weight	0.001	-0.001	0.002	0.000	-0.023	**0.016**	0.000	-0.370	-0.032	-0.001	0.016	**-0.392**
100 kernel weight	0.000	0.002	0.001	0.000	0.011	0.001	**0.002**	0.134	0.010	0.000	-0.007	**0.154**
kernel yield/plant	0.004	0.003	-0.003	0.000	0.112	-0.006	0.000	**0.921**	0.047	0.001	-0.082	**0.995**
shelling%	-0.001	0.003	-0.001	0.000	0.046	-0.009	0.000	0.734	**0.059**	0.000	-0.033	**0.799**
sound mature kernel	0.009	-0.005	0.006	0.000	-0.028	0.004	0.000	-0.197	-0.010	**-0.003**	0.021	**-0.204**
pod yield/hectare (kg)	0.008	0.002	-0.003	-0.001	0.134	-0.003	0.000	0.754	0.019	0.001	**-0.100**	**0.811**

R SQUARE= 0.6840 **RESIDUAL EFFECT= 0. 1324**

4.6. Mahalanobis generalize distance (D^2)

The analysis of variance showed highly significant differences among the population for the 12 characters investigated. The D^2 values corresponding to possible comparison among 30 genotypes taking two genotypes at a time were computed separately in the analysis.

Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by 8 characters is presented in Table 4.6. Character 100 pod weight (62.98%), shelling% (8.50%), sound mature kernel (7.58%), days to maturity (5.51%), pod/plant (5.28), contributed most towards genetic divergence followed by plant height (3.45%) and kernel yield/plant (2.75%).

Table: 4.6 Percent contribution of characters towards divergence

Sr. no.	Character	Contribution of various traits to divergence	Rank
1	Days to 50% flowering	3.908	17
2	Day to maturity	5.517	24
3	Plant height	3.448	15
4	No. of primary branches	0	0
5	Pod/plant	5.287	23
6	100 pod weight	62.988	274
7	100 kernel weight	0	0
8	Kernel yield/plant	2.758	12
9	Shelling%	8.505	37
10	Sound mature kernel	7.589	33
11	Pod yield/hectare (kg)	0	0
12	Kernel yield/hectare (kg)	0	0

Genetic Divergence:

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance between pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time. The genetic divergence has been studied using Mahalanobis' D^2 statistics on 30 genotypes over 12 yield and yield contributing characters. Results are presented as under:

Table: 4.7. Distribution of groundnut genotypes in different clusters.

Cluster	No.	Genotypes
I	10	PBS 22062, PBS 22122, PBS 22132, ICRISAT 7, Sunolic 95 R, PBS 22059, PBS 22116, ICRISAT6, ICRISAT10, ICRISAT13.
II	14	PBS 22063, PBS 22066, PBS 22196, ICRISAT 1, ICRISAT 2, ICRISAT3, ICRISAT 4, ICRISAT 5, ICRISAT 11, ICRISAT12, ICRISAT15, KDG 128, TG 26 and ICGS 144.
III	2	PBS 22067 and Gangapuri.
IV	2	PBS 22200 and PBS 22080
V	1	GPBD 4
VI	1	JGN 3

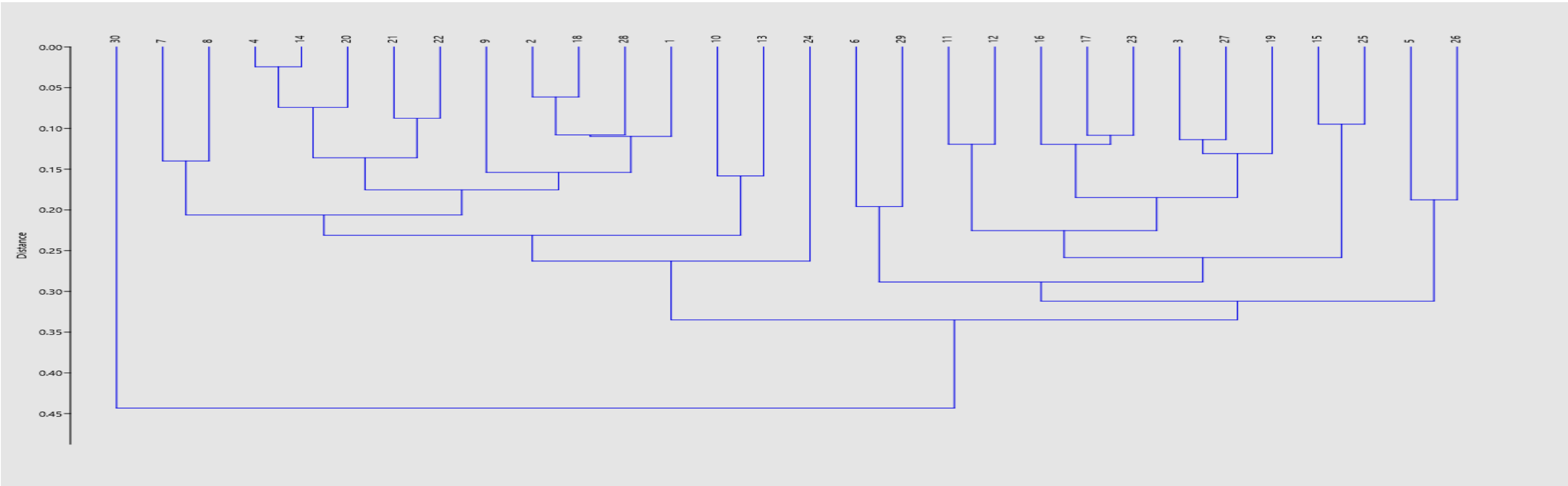


Fig.4.1. Cluster diagram of groundnut genotypes based on morpho-physiological data by tocher'smethods.

Grouping of genotypes into different clusters

The study comprised of 30 genotypes based on 12 morpho-physiological and yield related traits following Mahalanobis D^2 statistics. On the basis of D^2 values, the 30 genotypes were grouped into 6 clusters following Tocher's method. The cluster 2 was polygenotypic (14 genotypes) pursued by cluster 1 (10 genotypes), cluster 3 (2 genotypes), cluster 4 (2 genotypes), cluster 5 (1 genotype) and cluster 6 (1genotype). (Table 4.7)

Intra and inter cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979) (Table: 4.8 & 4.9) Cluster No 4 showed maximum intra cluster D^2 value (D^2 = 2017.945), chase by cluster 2 (D^2 = 1704.595), cluster 1 (D^2 = 1685.039), cluster 3 (D^2 = 829.423) cluster 5 and 6 were mono-genotypic with no intra cluster divergence. The highest inter cluster divergence was observed between genotypes of cluster 1 and 6 (D^2 = 15254.2193), pursued by cluster 5 *vs* 6 (D^2 = 12084.3505), cluster 1 *vs* 3 (D^2 = 11546.1879), cluster 3 *vs* 5 (D^2 = 10082.0643), cluster 4 *vs* 6 (D^2 = 6049.5146), cluster 2 *vs* 5 (D^2 = 5739.4374), cluster 1 *vs* 2 (D^2 = 5643.2397), cluster 1 *vs* 4 (D^2 = 4959.9375), cluster 2 *vs* 6 (D^2 = 4803.0884), cluster 3 *vs* 6 (D^2 = 4411.2430), cluster 3 *vs* 4 (D^2 = 4090.5072), cluster 2 *vs* 3 (D^2 = 4046.9287), cluster 4 *vs* 5 (D^2 = 3647.4257), cluster 1*vs* 5 (D^2 = 3439.7043) and cluster 2 *vs* 4 (D^2 = 2410.2722).

Cluster mean value

Cluster no. III showed highest cluster mean value for days to 50% flowering (33.16) and in cluster V (24). Cluster no. V showed highest cluster mean value for days to maturity (114 days) and least for cluster II (111 days). Cluster no. V showed highest cluster mean value for plant height (44.80cm) and least for cluster no. III (33.46cm). Cluster no. III showed highest cluster mean value for primary branches per plant (4) and least for cluster no. IV (3). Cluster no. V showed highest cluster mean value for pod per plant (31.53) and least for cluster no. II (14.08). Cluster no. I showed highest cluster mean value for hundred pod weight (84.95) and least for cluster no. V (35.33). Cluster no. III showed highest cluster mean value for hundred kernel weight (41) and least for cluster no. VI (15.70). Cluster no. V showed highest cluster mean value for kern yield/plant (15.96) and least for cluster no. I (5.77). Cluster no. III showed highest cluster mean value for shelling% (84.91) and least for cluster no. I (37.80). Cluster no. V showed highest cluster mean value for sound mature kernel (88.66) and least for cluster no. VI (69). Cluster no. V showed highest cluster mean value for pod yield/hectare (6889.63) and least for cluster no. II (3100.63). Cluster no. V showed highest cluster mean value for kernel yield/hectare (3532.20) and least for cluster no. I (1294.06). (Table 4.10).

Divergent genotype

On the basis of divergent trait showed in inter cluster distance, genotype PBS 22062, ICRISAT 7 and PBS 22122 (cluster no. 1), GPBD 4 (cluster no. 5) and PBS 22067 and Gangapuri (cluster no. 3) were found to be the most divergent and promising genotypes and will be employed as parents in future hybridization programmes.

Table: 4.8. Average intra cluster D^2 values of 30 genotypes of groundnut.

Clusters	Average Intra Cluster D2
Cluster1	1685.039
Cluster2	1704.595
Cluster3	829.423
Cluster4	2017.945
Cluster5	0
Cluster6	0

Table: 4.9. Average inter cluster D^2 values of 30 genotypes of groundnut.

AVERAGE INTER CLUSTER D^2	
BETWEEN CLUSTERS 1 2	5643.2397
BETWEEN CLUSTERS 1 3	11546.1879
BETWEEN CLUSTERS 1 4	4959.9375
BETWEEN CLUSTERS 1 5	3439.7043
BETWEEN CLUSTERS 1 6	15254.2193
BETWEEN CLUSTERS 2 3	4046.9287
BETWEEN CLUSTERS 2 4	2410.2722
BETWEEN CLUSTERS 2 5	5739.4374
BETWEEN CLUSTERS 2 6	4803.0884
BETWEEN CLUSTERS 3 4	4090.5072
BETWEEN CLUSTERS 3 5	10082.0643
BETWEEN CLUSTERS 3 6	4411.2430
BETWEEN CLUSTERS 4 5	3647.4257
BETWEEN CLUSTERS 4 6	6049.5146
BETWEEN CLUSTERS 5 6	12084.3505

Table: 4.10 Cluster means value for 12 different morpho-physiological traits.

Clusters	DF50%	DM	PH	PB	PPP	HPW	HKW	KYP	SH%	SMK	PY/H	KY/H
1	28.3000	111.7333	37.0833	3.6333	14.3633	84.9533	31.9100	5.7700	37.8067	82.1000	3195.8700	1294.0634
2	28.6429	111.5714	36.7262	3.7619	14.0810	58.3548	31.1976	6.6452	46.4238	82.6429	3100.6334	1476.7143
3	33.1667	113.8334	33.4667	4.0000	16.7667	48.1000	41.0500	14.0500	84.9167	72.8334	3583.3667	3123.4167
4	26.6667	107.5000	36.3500	3.0000	23.2500	62.6167	35.9333	13.2167	57.1833	81.3334	5170.1499	2893.5167
5	24.0000	114.0000	44.8000	3.0000	31.5333	76.8000	40.0000	15.9667	51.5000	88.6667	6889.6333	3532.2000
6	26.0000	113.0000	44.6667	3.0000	26.2000	35.3333	15.7000	12.0333	44.3000	69.0000	5904.5999	2600.3334

4.7. Fresh Seed Dormancy:

Analysis of variance for germination percentage at 7days after sowing is presented in Table: (4.11).

Duration of fresh seed dormancy:

Duration of fresh seed dormancy, intensity of dormancy and mean value of germination percentage is presented in Table: 4.12. Genotypes tested showed different durations of dormancy and it ranged from 7 to >35 days. Genotypes TG-26 had highest >35 days duration of dormancy followed by ICRISAT 3 and ICRISAT 13. PBS22132 and ICRISAT 6 had 21 days duration of dormancy. In contrast, non-dormant genotypes such as PBS22059,PBS 22063, PBS22066,PBS22196, PBS 22200, ICRISAT 1,ICRISAT 7, ICRISAT 10, ICRISAT 11, ICRISAT12,ICRISAT 15, KDG 128, Gangapuri, Sunolic 95 R, JGN-3 and GPBD4 had lowest 7 days dormancy duration.

Intensity of fresh seed dormancy:

Intensity of fresh seed dormancy ranged from 10 to 100 %.The highest (100%) intensity of dormancy was recorded inTG-26 followed by ICRISAT 13 and ICRISAT 3.While the lowest have recorded in ICRISAT1 (10%), JGN3 (10%), Gangapuri (10%) and GPBD 4 (10%).This large variation could be due to genetic variation among the genotypes.

Table 4.11. ANOVA for germination percentage at seven days after sowing

Source of Variation	DF	Sum of Squares	Mean Squares	F-Calculated	Significance
Replication	2	2.22			
Germination percentage	29	64,262.22	2,215.93**	55.134	0.00000
Error	58	2,331.11	40.19		
Total	89	66,595.55			

CV = 9.8, CD = 10.3.8, ** significant at 1%

Table 4.12. Duration of dormancy, intensity of dormancy and mean value of germination percentage in 30 groundnut genotypes.

Genotypes	Mean value of germination%	Duration of dormancy (days)	Intensity of fresh seed dormancy %
PBS 22059	80.8	7	20
PBS 22062	70.7	10	30
PBS 22063	80.8	7	20
PBS 22066	90.8	7	15
PBS 22067	70.2	10	55
PBS 22080	50.6	10	45
PBS 22116	40.5	10	55
PBS 22122	60.7	10	35
PBS 22132	10.2	21	85
PBS 22196	70.7	7	30
PBS 22200	80.8	7	20
ICRISAT 1	90.9	7	10
ICRISAT 2	70.7	10	30
ICRISAT 3	10	>28	95
ICRISAT 4	60.6	10	40
ICRISAT 5	50.6	10	45
ICRISAT 6	20.2	21	80
ICRISAT 7	80.8	7	20
ICRISAT 10	90.9	7	10
ICRISAT 11	80.8	7	20
ICRISAT 12	90.9	7	10
ICRISAT 13	10.1	>28	90
ICRISAT 15	80.8	7	20
KDG 128	70.8	7	25
TG 26	0	>28	100
Gangapuri	90.9	7	10
Sunolic 95 R	80.8	7	20
ICGS 144	70.8	10	25
JGN 3	90.9	7	10
GPBD 4	90.9	7	10

CHAPTER- V
DISCUSSION

The future objective of most plant breeding programmes is to extend yield potential of a crop with top quality, which is achieved by manipulating genes for its yield components. The choice of suitable parents for specific characters may be a pre requisite for the successful hybridization programme in groundnut. The knowledge of genetic parameters like genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance, genetic divergence also as correlation and path coefficient analysis are essential for creating effective selections from the breeding material either for direct advancement or to formulate efficient crossing programme.

This investigation was administered to guage 30 genotypes of groundnut to get the knowledge on mean performance, variability, heritability, genetic advance, genetic divergence, character associations, path coefficient analysis and fresh seed dormancy. The findings of this investigation are interpreted and discussed within the chapter within the light of the similar research work administered by other research workers.

Analysis of variance and Mean performance:

Analysis of variance revealed that genotypes were highly significant for 10 characters *viz.*plant height (cm), days to 50% flowering, number of pod per plant, pod yield per plant (gm), 100 pod weight (gm), kernel yield per plant (gm), 100 kernel weight (gm), shelling percentage (%), sound mature kernel (%), pod yield per hectare (kg) and kernel yield per hectare (kg). Similarly (Ragimekula *et al.* 2012, Savemore *et al.* 2017)Found highly significant differences among the genotypes for all the traits indicating thereby sufficient variability present in the material studied.

Mean performance revealed that four genotypes showed significantly higher kernel yield per hectare compared to other genotypes. Genotype gangapuri showed significantly higher kernel weight with kernel yield/plant, shelling%.Similarly, Genotype GPBD4 showed higher value for pod per plant,pod yield/hectare and kernel yield/hectare. The increased kernel yield in genotypes GPBD4 was due to higher number of primary branches per plant, number of pods per plant, kernel yield per plant, pod yield per plant and pod yield per hectare. Similarly, PBS 22122 also observed the higher value for hundred pod weight. Genotype PBS 22200 showed higher sound mature value.

These result suggested that the Gangapuri and PBS22200 could be used as donors for kernel yield improvement in groundnut.

Phenotypic and genotypic coefficient of variation:

In present investigation among all the characters studied, Kernel yield/plant recorded the highest PCV and GCV pursued by Kernel yield/hectare (kg) (51.12, 51.39), Pod yield/hectare (kg) (34.69, 34.86), pod/plant (34.06, 34.23), shelling% (32.82, 32.87), hundred pod weight (23.44, 23.45) the pod/plant result are in confirmation withZaman *et al*. (2011) and Mahatma *et al.*(2019) and plant height observed as moderate estimates of PCV and GCV values which suggested that these characters were least affect by environment. High proportion of GCV to PCV is desirable in process because it depicts that traits are much under the genetic control rather than the environment. The results are in confirmation with Zaman *et al*. (2011) and Bhargavi *et al*. (2017).

The minimum GCV and PCV was exhibited by the characters days to 50% flowering (9.47, 9.52), sound mature kernel (8.24, 8.28) and days to maturity (2.58, 2.59) which indicates that selection for these characters is less effective, these result were in agreement with Rao *et al*. (2015) , Zaman *et al*. (2011) and Bhargavi *et al*. (2017).

Heritability (broad sense) and genetic advance:

Estimation of high heritability value coupled with high genetic advance was recorded for hundred pod weight (99.91), shelling% (99.65), kernel yield/plant (99.42), pod/plant (99.0002), pod yield/hectare (kg) (99), kernel yield/hectare (kg) (98.96), indicating that the inheritance of these characters were most likely due to additive gene effects. Similar result finding has been reported Zamen *et al*. (2011), Bharagavi *et al*. (2017), Chavadhari *et al*. (2017), Hampamnawa *et al*. (2018) and Mahatma *et al*.(2019).

High heritability with moderate genetic advance was observed for plant height (14.59, 14.68), number of primary branches (14.24, 15.64), hundred kernel weight (13.14, 63.15), indicating that the inheritance of these trait were likely due to non-additive gene effect and further limited scope of improvement for this traits.

Correlation analysis:

Correlation analysis revealed that kernel yield per hectare was positively and significantly correlated at both genotypic as well as phenotypic level with pod/plant, kernel yield/plant, shelling% and pod yield/hectare (kg)at 1% significance level.

These findings in accordance with Shobha *et al*. (2012), Terkimbi and Terkula (2014), Bharagavi *et al*. (2015), Reddy *et al*. (2017), Aparna *et al*. (2018) andMahatma *et al*.(2019).

Path analysis:

Direct indirect effect of various traits on kernel yield per hectare (kg) revealed that kernel yield per plant followed by 100 kernel weight, shelling%and days to maturity, exhibited highest positive direct effect on kernel yield per hectare at both genotypic as well as phenotypic path analysis.Whereas, negative direct effect on Kernel yield/hectare (kg) observed by plant height and days to 50% flowering at both genotypic as well as phenotypic path analysis.

The residual effect values was showed very low (-0.001) and (0.009) genotypic and phenotypic level respectively thus, indicated majority of the factors influencing the kernel yield per hectare was considered in the present study. Present finding are in confirmation with Raghuwanshi *et al*. (2016), Dhakar *et al*. (2017), Reddy *et al*. (2017), Aparna *et al*. (2018) and Saritha *et al*. (2018), Rao *et al* (2019), kumar el al. (2019) and Mohapatra *et al*. (2020)

Genetic divergence:

Using Tocher's methods as suggested by Rao (1952), 3 genotypes were groups into 6 clusters. The Cluster II was incorporated maximum 14 genotypes followed by Cluster I was incorporated 10 genotypes which is pursued by III and IV clusters having two genotypes each and remaining clusters have only one genotype. From the inter cluster D^2 values of 6 clusters, it can be seen that the highest divergence occurred between cluster 1 and 6 (D^2 = 15254.2193), pursued by cluster 5 *vs* 6 (D^2 = 12084.3505), cluster 1 *vs* 3 (D^2 = 11546.1879), cluster 3 *vs* 5 (D^2 = 10082.0643), cluster 4 *vs* 6 (D^2 = 6049.5146) etc. suggested wide diversity between them and indicated that the genotypes in these clusters could be used as parents in hybridization programme for getting transgressive segregants.

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The utility of D^2 statistics is enhanced by its applicability to estimates relative contribution of various characters to genetic divergence. Relative contribution of Character 100 pod weight (62.98%) has maximum contribution in genetic divergence followed byshelling% (8.50%), sound mature kernel (7.58%), and days to maturity (5.51%), pod yield per plant (5.28) and plant height (3.45%) whereas, magnitude of genetic divergence was less than 3% per cent for kernel yield/plant (2.75%). No. of primary branches, Pod yield/hectare (kg)and Kernel yield/hectare (kg)have no contribution towards divergence.Similar result earlier reported by Zaman *et al*. (2010), Nirmami *et al*. (2013), Gantait*et al*. (2017) Mohammod *et al*. (2018).

Fresh seed dormancy:

Fresh seed dormancy in bunch type groundnut has a significant influence on kernel yield and quality. It is required to avoid economic loss in the form of in-situ germination during unpredictable rainfall at maturity. Genotypes evaluated for fresh seed dormancy showed significant genetic variation for germination percentage at seven days after sowing. It was concluded that genotypes TG-26 had more than four week duration of dormancy, highest intensity of fresh seed dormancy. There for these genotypes were identified as new sources of fresh seed dormancy in groundnut. Kumar *et al*. (2018) reported similar result in their experiment.

It is concluded from experiment that genotypes was significant different for 10 out of 12 characters. Estimation of high heritability values coupled with high genetic advances was recorded hundred pod weight (99.91), shelling% (99.65), kernel yield/plant (99.42), pod/plant (99.0002), pod yield/hectare (kg) (99), and kernel yield/hectare (kg) (98.96). Genotypic and phenotypic correlation analysis revealed that only four characters viz. pod/plant, kernel yield/plant, shelling percentage and pod yield/hectare (kg) exhibited positive and significant association with kernel yield per hectare.

Path analysis revealed that that kernel yield per plant followed by 100 kernel weight, shelling%and days to maturity, exhibited highest positive direct effect on kernel yield per hectare (kg) at both genotypic as well as phenotypic path analysis. On the basis of divergent trait showed in inter cluster distance, genotype PBS 22062, ICRISAT 7 and PBS 22122 (cluster no. 1), GPBD 4 (cluster no. 5) and PBS 22067 and Gangapuri (cluster no. 3) were found to be the most divergent and promising genotypes and will be employed as parents in future hybridization programmes for getting transgressive segregants.On the basis of fresh seed dormancy analysis genotypes TG-26, ICRISAT13 and ICRISAT3 were identified as new sources of fresh seed dormancy in groundnut.

CHAPTER- VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

6.1. SUMMARY

The present investigation "Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut genotypes (*Arachis hypogea* L.)" was undertaken to understand phenotypic and genotypic coefficient of variation, heritability, genetic advance, correlation coefficient, path coefficient analysis, genetic divergence analysis and find out fresh seed dormancy among the genotypes**.** Experiment was conducted with 3 replication during the season 2019-20 at Research Farm, Department of Genetics and Plant Breeding, RVSKVV, College of Agriculture, Gwalior (M.P.). The Observations will be recorded on 5 randomly selected plants of each genotype in each replication for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pod per plant, pod yield per plant (gm), 100 pod weight (gm), kernel yield per plant (gm), 100 kernel weight (gm), shelling percentage (%), sound mature kernel (%), pod yield per hectare (kg) and kernel yield per hectare (kg).

The analysis of variance revealed genotypes were significantly differed for 10 characters, thereby, indicating variability for the characters.Kernel yield/plant has the highest GCV and PCV content pursued by Kernel yield/hectare (kg), Pod yield/hectare (kg), pod/plant, shelling%, hundred pod weight and moderate for plant height, number of primary branches, hundred kernel weight and low GCV and PCV for days to 50% flowering, sound mature kernel and days to maturity.All the 11 out of 12 characters have higher heritability estimates including hundred pod weight, shelling%, kernel yield/plant, days to maturity, sound mature kernel, pod/plant, pod yield/hectare (kg), kernel yield/hectare (kg), days to 50% flowering, plant height except hundred kernel weight which has low heritability.The high genetic advance as percentage of mean (at 5% selection intensity) was recorded for kernel yield/plant, kernel yield/plant, pod yield/hectare (kg), pod/plant, shelling%, hundred pod weight, plant height and number of primary branches and moderate for days to 50% flowering and sound mature kernel. Low for hundred kernel weight and days to maturity.Correlation analysis revealed that kernel yield per hectare was positively and significantly correlated at both genotypic as well as phenotypic level with four characters pod/plant, kernel yield/plant, shelling% and pod yield/hectare (kg) at 1% significance level.

Direct indirect effect of various traits on kernel yield per hectare (kg) revealed that kernel yield per plant followed by 100 kernel weight, shelling%and days to maturity, exhibited highest positive direct effect on kernel yield per hectare at both genotypic as well as phenotypic path analysis. Whereas, negative direct effect on Kernel yield/hectare (kg) observed by plant height and days to 50% flowering at both genotypic as well as phenotypic path analysis.Whereas, negative direct effect on Kernel yield/hectare (kg) observed by plant height and days to 50% flowering at both genotypic as well as phenotypic path analysis.From the inter cluster D^2 values of 6 clusters, it can be seen that the highest divergence occurred between cluster 1 and 6 (D^2 = 15254.2193), pursued by cluster 5 vs 6 (D^2 = 12084.3505), cluster 1 vs 3 (D^2 = 11546.1879), cluster 3 vs 5 (D^2 = 10082.0643), cluster 4 vs 6 (D^2 = 6049.5146) etc. suggested wide diversity between them and indicated that the genotypes in these clusters could be used as parents in hybridization programme for getting transgressive segregants.

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The utility of D^2 statistics is enhanced by its applicability to estimates relative contribution of various characters to genetic divergence. Relative contribution of Character 100 pod weight (62.98%) has maximum contribution in genetic divergence followed by shelling% (8.50%), sound mature kernel (7.58%), and days to maturity (5.51%), pod yield per plant (5.28) and plant height (3.45%) whereas, magnitude of genetic divergence was less than 3% per cent for kernel yield/plant (2.75%). No. of primary branches, Pod yield/hectare (kg) and Kernel yield/hectare (kg) have no contribution towards divergenceIntensity of fresh seed dormancy ranged from 10 to 100 %. The highest (100%) intensity of dormancy was recorded in TG-26 followed by ICRISAT 13 and ICRISAT 3. While the lowest have recorded in ICRISAT1 (10%), JGN3 (10%), Gangapuri (10%) and GPBD 4 (10%). This large variation could be due to genetic variation among the genotypes.

6.2. Conclusion

The following relevant conclusions could be drawn from the present study:

- Estimation of high heritability value coupled with high genetic advance was recorded for hundred pod weight, shelling%, kernel yield/plant, pod/plant, pod yield/hectare (kg), kernel yield/hectare (kg), indicating that the inheritance of these characters were most likely due to additive gene effects. Indicating that the inheritance of these characters were most likely due to additive gene effects and direct selection for these traits would be more effective for desired genetic improvement.
- Kernel yield per hectare showed positively and significantly correlated at both genotypic as well as phenotypic level with with four characters pod/plant, kernel yield/plant, shelling% and pod yield/hectare (kg) at 1% significance level indicated that direct selection for these traits may lead increase in genetic potential of kernel yield.
- Path analysis revealed that some traits viz., kernel yield per plant followed by 100 kernel weight, shelling%and days to maturity, exhibited highest positive direct effect on kernel yield per hectare at both genotypic as well as phenotypic path analysis and some traits have indirect positive effect on kernel yield per hectare and each traits be given preference in selecting the superior types.
- On the basis of divergent trait showed in inter cluster distance, genotype PBS 22062, ICRISAT 7 and PBS 22122 (cluster no. 1), GPBD 4 (cluster no. 5) and PBS 22067 and Gangapuri (cluster no. 3) were found to be the most divergent and promising genotypes and will be employed as parents in future hybridization programmes.
- On the basis of fresh seed dormancy analysis genotypes TG-26 followed by ICRISAT 13 and ICRISAT 3. While the lowest have recorded in ICRISAT1 were identified as new sources of fresh seed dormancy in groundnut.

6.3. Suggestions for further work

- The genetic variability reported for different characters in relation in kernel yield should be exploited.
- Characters showing high heritability with high genetic advance should be utilized in selection.
- Selection should be more effective for the characters viz., pod/plant, kernel yield/plant, shelling% and pod yield/hectare (kg), these traits were under the influence of additive gene action and they highly significant and positive correlation with kernel yield per hectare.
- Direct selection should be done for characters such as kernel yield per plant followed by pod yield per hectare, days to maturity, 100 pod weight, 100 kernel weight, plant height, number of primary branches per plant, number of pods per plant and sound mature kernel.
- Highly diverse genotypes viz., PBS 22062, ICRISAT 7 and PBS 22122 (cluster no. 1), GPBD 4 (cluster no. 5) and PBS 22067 and Gangapuri (cluster no. 3) may be used for future hybridization program for further kernel yield improvement in groundnut.

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THESIS ABSTRACT

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ABSTRACT

The present investigation entitled, "Study of Genetic Divergence and Fresh Seed Dormancy in Groundnut genotypes (*Arachis hypogea* L.)Was conducted during *Kharif* season of 2018-19 at Research Farm, RVSKVV, College of Agriculture; Gwalior (M.P.). Groundnut is one of the most important food and oilseed crop cultivated and consumed in most parts of the world. Main constrants in groundnut productions are foliar fungal diseases and high oleic acid containing peanut is in demand for industrial purpose. In groundnut, seed dormancy has been reportable to be controlled by 2 hormones: abscisic acid that inhibits development and olefin that is accumulated in storage to interrupt dormancy to permit germination.The aim of groundnut breeding programs across the planet is to develop new varieties that meet the wants of growers, processors, and customers.The analysis of variance revealed genotypes were significantly differed for 10 characters, thereby, indicating variability for the characters. Kernel yield/plant has the highest GCV and PCV content pursued by Kernel yield/hectare (kg), Pod yield/hectare (kg), pod/plant, shelling%, hundred pod weight and moderate for plant height, number of primary branches, hundred kernel weight and low GCV and PCV for days to 50% flowering, sound mature kernel and days to maturity.All the 11 out of 12 characters have higher heritability estimates including hundred pod weight, shelling%, kernel yield/plant, days to maturity, sound mature kernel, pod/plant, pod yield/hectare (kg), kernel yield/hectare (kg), days to 50% flowering, plant height except hundred kernel weight which has low heritability.

Direct indirect effect of various traits on kernel yield per hectare (kg) revealed that kernel yield per plant followed by 100 kernel weight, shelling%and days to maturity, exhibited highest positive direct effect on kernel yield per hectare at both genotypic as well as phenotypic path analysis. Whereas, negative direct effect on Kernel yield/hectare (kg) observed by plant height and days to 50% flowering at both genotypic as well as phenotypic path analysis.The high genetic advance as percentage of mean (at 5% selection intensity) was recorded for kernel yield/plant, kernel yield/plant, pod yield/hectare (kg), pod/plant, shelling%, hundred pod weight, plant height and number of primary branches and moderate for days to 50% flowering and sound mature kernel. Low for hundred kernel weight and days to maturity. Correlation analysis revealed that kernel yield per hectare was positively and significantly correlated at both genotypic as well as phenotypic level with four

characters pod/plant, kernel yield/plant, shelling% and pod yield/hectare (kg) at 1% significance level.From the inter cluster D2 values of 6 clusters, it can be seen that the highest divergence occurred between cluster 1 and 6 (D2 = 15254.2193), pursued by cluster 5 vs 6 (D2 = 12084.3505), cluster 1 vs 3 (D2 = 11546.1879), cluster 3 vs 5 (D2 = 10082.0643), cluster 4 vs 6 (D2 = 6049.5146) etc. suggested wide diversity between them and indicated that the genotypes in these clusters could be used as parents in hybridization programme for getting transgressive segregants.

APPENDIX

Mean performance of 12 characters in 30 groundnut genotypes.

Sr. No.	Name of Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	pod yield /plant	100 Pod weight (gm)	100 kernel weight (gm)	kernel yield/plant	Shelling %	sound mature kernel per 100 kernel	Pod yield per hec (Kg)	Kernel yield pre hectare (kg)
1	PBS 22059	26	114	38.2	4	12.455	80.125	36.855	5.73	45.995	79	2,767.80	1,273.10
2	PBS 22062	27	114.5	36.85	5	14.075	92.35	34.2	5.215	37.035	81.5	3,127.75	1,158.60
3	PBS 22063	29	112	38.15	4.5	19.005	60.55	34.75	10.9	57.395	78	4,222.90	2,422.85
4	PBS 22066	32	113.5	32.25	3.5	13.025	55.35	20.87	4.915	37.7	87	2,894.20	1,092.20
5	PBS 22067	34.5	116	29.55	4.5	16.9	48.9	36.68	12.68	75.01	71	3,755.55	2,817.45
6	PBS 22080	28	109.5	34.6	4	25.425	63.25	31.225	12.555	49.38	70	5,649.80	2,790.15
7	PBS 22116	30.5	108	35.75	3.5	7.47	86.3	20.965	1.815	24.29	87.5	1,659.55	403.15
8	PBS 22122	31	114	38.95	4	11.305	96.65	14.93	1.755	15.51	75	2,512.20	389.7
9	PBS 22132	32	107	31.75	3.5	15.505	94.4	32.97	5.415	34.925	79	3,445.15	1,203.25
10	PBS 22196	25	108.5	28.75	4	8.58	56.3	27.565	4.195	48.96	91	1,906.25	933.2
11	PBS 22200	25.5	106.5	37.95	3.5	20.925	62.3	40.815	13.71	65.515	93	4,649.55	3,046.65
12	ICRISAT 1	24	116	40.75	4	19.465	52.6	36.525	13.52	69.44	83	4,325.35	3,003.45
13	ICRISAT 2	29	107	28.25	4.5	12.46	60.3	34.85	7.205	57.8	91.5	2,769.10	1,600.45
14	ICRISAT 3	31	109.5	32.1	3.5	13.385	56.7	22.295	5.26	39.32	87	2,974.20	1,169.45

15	ICRISAT 4	32	111	46.7	3.5	16.44	56.2	28.995	8.49	51.595	76	3,653.55	1,887.30
16	ICRISAT 5	29	113	32.85	4.5	19.035	64.2	24.06	7.13	37.475	83	4,229.55	1,584.65
17	ICRISAT 6	25	110.5	37.8	4.5	18.345	74.6	30.99	7.615	41.545	80.5	4,076.90	1,692.25
18	ICRISAT 7	26	111	35.7	3.5	13.555	90.3	32.63	4.895	36.14	89	3,012.45	1,088.30
19	ICRISAT 10	28	114.5	33.6	5	19.365	76.2	40.705	10.35	53.42	90	4,303.15	2,299.05
20	ICRISAT 11	30	107	30.5	4.5	14.195	68.4	20.845	4.325	30.475	85.5	3,154.00	961.25
21	ICRISAT12	29	115.5	19.3	5	13.125	62.5	20.745	4.355	33.195	76	2,916.20	966.95
22	ICRISAT 13	29	111.5	41.75	5	12.37	76.5	22.795	3.69	29.795	79	2,749.15	819.85
23	ICRISAT 15	26	114	35.8	3.5	16.175	52.45	24.98	7.69	47.63	82	3,589.80	1,709.70
24	KDG 128	28	113	48.95	5.5	5.405	56.3	21.05	2.015	37.385	86	1,200.85	447.4
25	TG 26	31	113.5	47.3	4.5	13.515	50.45	30.8	8.245	61.05	71	3,002.90	1,832.45
26	Gangapuri	32	112.5	37.7	5	16.48	48.15	45.59	15.605	94.685	75	3,662.20	3,467.05
27	Sunolic 95 R	29	112.5	40.55	6	19.67	82.5	39.605	9.445	48.01	80	4,371.30	2,098.95
28	ICGS 144	27	108.5	36.8	5	11.67	66.4	27.15	4.77	40.885	82	2,593.60	1,060.05
29	JGN 3	26	114	44.75	4	26.655	35.2	15.57	11.79	44.235	68.5	5,922.90	2,620.20
30	GPBD 4	24	113	44.4	3.5	31.115	77.37	39.84	16.025	51.5	89	6,914.45	3,561.30
	C.D.	**0.465**	**4.812**	**8.541**	**1.432**	**1.082**	**0.803**	**6.653**	**1.072**	**7.114**	**0.848**	**240.959**	**238.113**
	SE(m)	**0.16**	**1.655**	**2.938**	**0.493**	**0.372**	**0.276**	**2.289**	**0.369**	**2.447**	**0.292**	**82.894**	**81.915**
	SE(d)	**0.226**	**2.341**	**4.155**	**0.697**	**0.527**	**0.391**	**3.237**	**0.522**	**3.461**	**0.412**	**117.23**	**115.845**
	C.V.	**0.793**	**2.096**	**10.35**	**10.269**	**3.311**	**0.585**	**10.887**	**6.766**	**7.431**	**0.506**	**3.317**	**6.761**

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