Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)

Lifu'k xPNk eaxQyh esa fofo/krk vkj iFk fo'ys"k.k ¼,jfdl gkbikft;k ,y-½

ANUSHKA KUNTAL

Thesis

Master of Science in Agriculture

(Genetics and Plant Breeding)

2024

DEPARTMENT OF GENETICS AND PLANT BREEDING
RAJASTHAN COLLEGE OF AGRICULTURE
MAHARANA PRATAP UNIVERSITY OF AGRICULTURE AND TECHNOLOGY
UDAIPUR – 313 001 (RAJASTHAN)

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Submitted to the

Maharana Pratap University of Agriculture and Technology, Udaipur

In partial fulfillment of the requirements for the Degree of

Master of Science in Agriculture

(Genetics and Plant Breeding)

By

ANUSHKA KUNTAL

2024

RAJASTHAN COLLEGE OF AGRICULTURE
MAHARANA PRATAP UNIVERSITY OF AGRICULTURE AND TECHNOLOGY, UDAIPUR

CERTIFICATE - I

CERTIFICATE OF ORIGINALITY

The research work embodied in the thesis titled **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)"** submitted for the award of degree of Master of Science in Agriculture in the subject of Genetics and Plant Breeding to Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan), is original and bonafide record of research work carried out by me under the supervision of **Dr. Pratap Bhan Singh**, Assistant Professor, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur. The contents of the thesis, either partially or fully, have not been submitted or will not be submitted to any other institute or university for the award of any degree or diploma.

The work embodied in the thesis represents my ideas in my own words and where others' ideas or words have been included. I have adequately cited and referenced the original sources. I also declare that I have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in my submission. I understand that any violation of the above will be cause for disciplinary action by the university and can also evoke panel action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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CERTIFICATE – II

Date: / /2024

This is to certify that the thesis entitled **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L)"** submitted for the degree of Master of Science in Agriculture in the subject of Genetics and Plant Breeding, embodies bonafide research work carried out by **Ms. ANUSHKA KUNTAL** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on / /2024.

The manuscript has been subjected to plagiarism check by software- **DrillBit.** It is certified that as per the check, the similarity index of the content is **8%** and is within permission limit as per the MPUAT guideline on checking plagiarism.

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This is to certify that the thesis **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L)"** submitted by **Ms. Anushka Kuntal** to the Maharana Pratap University of Agriculture and Technology, Udaipur in partial fulfillment of the requirement for the degree of **Master of Science in Agriculture** in the subject of **Genetics and Plant Breeding** after recommendation by the external examiner was defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination held on / /2024 was found satisfactory, we therefore, recommend that the thesis be approved.

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This is to certify that **Ms. Anushka Kuntal** student of Master of Science in Agriculture, **Department of Genetics and Plant Breeding** has made all the corrections/modifications in the **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L)"** which were suggested by the external examiner and the advisory committee in the oral examination held on …./…./2024. The final copies of the thesis duly bound and corrected were submitted on …./…./2024 are enclosed here with for approval.

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ACRONYMS & ABBREVIATIONS

%	:	Per cent
AICRP	:	All India Coordinated Research Project
ANOVA	:	Analysis of variance
cm	:	Centimeter
^{o}C	:	Degree Celsius
d.f.	:	Degree of Freedom
^{o}N	:	Degree north
DAS	:	Days after sowing
et al.	:	And else where
Fig.	:	Figure
g	:	Gram
ha	:	Hectare
ha^{-1}	:	Per hectare
HI	:	Harvest index
Hrs.	:	Hours
i.e.	:	that is
Kg	:	Kilogram
M	:	Million
m^2	:	Square meter
Max.	:	Maximum
mg	:	Milligram
Min.	:	Minimum
MPUAT	:	Maharana Pratap University of Agriculture and Technology
MSS	:	Mean sum of square
NS	:	Non-Significant
q	:	Quintal
r	:	Correlation Coefficient
RBD	:	Randomized block design
RH	:	Relative humidity
SEm	:	Standard error of mean

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an important crop among oilseeds. It is self-pollinated, annual, herbaceous legume having cleistogamous flower, belongs to fabaceae family and chromosome number (2n= 4x = 40) (x=10 basic chromosome number), grown in tropical and sub-tropical regions of the world. The term *Arachis* is derived from the Greek word "arachos", meaning a weed and *hypogaea*, meaning underground chamber *i.e.,* in botanical terms, a weed with fruits produced below the soil surface. Groundnut was originated from Brazil and it was popularly known as groundnut, an annual legume crop, which is responsible to supply edible oil for human consumption and recognized as peanut in America and several other names such as it is well known as Mungphali in India. Groundnut has other synonyms such as peanut, earthnut, monkeynut, goober, panda and manilanut. It accounts for 30 per cent of total domestic vegetable oil supply. Groundnut is one of the most important cash crops of our country.

Groundnut is a member of the Leguminosae family and genus *Arachis*. It is thought to have originated in the South American region spanning from southern Bolivia to northern Argentina. Of the 80 species in the genus *Arachis*, only two are allotetraploid, and the majority are diploid (2n = 2x = 20). The cultivated groundnut is allotetraploid (AABB, 2n = 4x = 40), which is thought to be the outcome of chromosome doubling following hybridization between two wild species, *Arachis duranensis* (AA-genome, 2n = 2x = 20), known as the "A-genome ancestor," and *Arachis ipaensis* (BB-genome, 2n = 2x = 20), known as the "B-genome ancestor." The two cultivated subspecies of the species *A. hypogaea* subsp. *fastigiata* and *A. hypogaea* subsp. *Hypogaea* are separated by patterns of reproductive and vegetative branching as well as pod morphology. Botanical varieties are further classifications for the subspecies. There are two subspecies of the subsp. *hypogaea*: *hypogaea* (Virginia) and *hirsuta*, and there are four subspecies of the subsp. *fastigiata*: *fastigiata* (Valencia), *vulgaris* (Spanish), *peruviana*, and *aequatoriana* (Desmae *et al*. 2019).

It is widely grown as an oilseed and food crop in more than 144 countries worldwide, where commercial production mostly confined between 40°S and 40°N latitudes. Groundnut is presumed to be domesticated in South America about 6

thousand years ago followed by widely distribution in post Columbian times. Major groundnut producing countries in the world are China, India, Nigeria, USA, Indonesia and Sudan. It is grown in an area of 25.44 million hectares worldwide with a total production of 45.22 million tonnes and productivity of 1777.33 kg/ha. In India, groundnut is cultivated on an area of 49.61 lakh ha with a production of 102.97 lakh tonnes and productivity is 2075 kg/ha during 2022-23 (Anonymous, 2023). In India, groundnut cultivation is mostly confined to the southern states *viz.*, Gujarat, Karnataka, Andhra Pradesh, Tamil Nadu and Maharashtra. Some other important groundnut growing states are Madhya Pradesh, Rajasthan, Uttar Pradesh and Punjab. In Rajasthan, it is cultivated on an area of 8.05 lakh ha with a production of 19.32 lakh tonnes and productivity is 2400 kg/ha (Anonymous, 2023). Under present scenario, the major area of groundnut in Rajasthan is represented by Chittorgarh, Bhilwara, Jaipur, Tonk, Sawai Madhopur, Dausa, Bikaner and Hanumangarh.

Groundnut, also known as "The king of oilseeds" because of the presence of poly unsaturated fatty acids (PUFA) (40-50%) and monounsaturated fatty acids (MUFA) like linoleic acid (25-35%) in right proportion which makes groundnut oil stable and nutritive. It is used for a variety of purposes. The kernels can be eaten raw, roasted, boiled, or processed into confections and peanut flour to enhance flavour. They can also be crushed to make oil for use in industry and food. High-quality edible oil (44–56%), protein (22–30%) from dry seeds, carbohydrates (10–25%), vitamins (E, K, and B complex), minerals (Ca, P, Mg, Zn, and Fe), and fibre are among the nutritional benefits of groundnuts. Haulm is used as manure or animal feed; legume roots enrich soil with organic matter and nitrogen (100–152 kg ha–1); shell is used as fuel and animal feed, cattle litter, and filler in the feed and fertiliser industry. (Hampannavar *et al.* 2018). Groundnut used as a rich source of seed oil and protein, it has great potential to cope with the problem of malnutrition and to ensure food security. Groundnut is widely known as poor man's almonds due to its high nutritional contents as well as fat and protein level, making up 80% of seeds contents. Moreover, groundnut is also a vibrant ingredient in numerous delicious commercial products (Pandey *et al*. 2012 and Pandey and Varshney 2018).

Groundnut is relatively day length insensitive crop. Therefore, most of the varieties developed anywhere in the world can be evaluated at any latitude, where favorable temperature exists. In addition to this, groundnut is relatively well adapted

to semi-arid region as it has inherent drought tolerance capacity. The productivity of groundnut is low in India as compared to other countries. It is generally grown as rainfed crop. Its seed multiplication ratio is low leading to no availability of sufficient seed of improved variety to the farmers. Therefore, for increasing its production it is necessary to develop cultivars with high genetic potential under rainfed conditions.

The progress of any breeding programme depends upon the extent of genetic variability present in the population. The genetic variability along with the heritability gives a reliable picture of the genetic advance to be expected from selection while the heritability coupled with genetic advance aids in predicting the valuable conclusion for effective selection based on phenotypic performance. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its components and also among various components. To exploit optimum combination of yield contributing characters in a single genotype, it is essential to entail the implication of the interrelationships of various characters along with path coefficients. Through correlation and path analysis, the nature and extent of association between different characters influencing yield and causes of association can be better understood which helps in formulation of selection criteria for improvement of yield.

In view of the above facts, the present investigation entitled "**Variability and Path analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)**" was carried out in Randomized Block Design during *Kharif*, 2023 to obtain the information on following aspects:

(1) To find out the variability parameters for yield and yield attributing characters in spanish bunch groundnut.

(2) To find out the genotypic and phenotypic correlation between yield and other yield contributing characters in groundnut.

(3) To find out the direct and indirect effects of different characters on yield using path analysis.

2. REVIEW OF LITERATURE

The present research was undertaken to study the magnitude of genetic variability and path analysis for various quantitative and qualitative traits in 30 genotypes of spanish bunch groundnut. The literature pertaining to objectives of this investigation have been reviewed briefly under the following sub-heads:

2.1 Variability parameters

2.2 correlation coefficient analysis

2.3 Path analysis

2.1 VARIABILITY PARAMETERS

Genetic variability is necessary for any programme aimed at improving crops, but locally adapted variable material has been rapidly disappearing, so it needs to be conserved. Free variability is the variation between homozygous genotypes/ populations, which can be used to develop genetically through selection. An effective breeding programme may benefit from selection as well as knowledge of genetic advancement and heritability. Crop improvement programmes require genetic variability in order to estimate various genetic parameters, such as components of variances, genotypic and phenotypic coefficients of variability, heritability, and genetic advance, and ultimately produce high-yielding varieties.

The heritable portion of phenotypic variance, or heritability, is a reliable indicator of how much a character is inherited from parents to progeny. In a broad sense, heritability is the ratio of genotypic variance to phenotypic variance. Because it establishes the expressivity of genes transmitted by a genotype, its estimation is important. Breeders can base their selection on phenotypic performance when a character's heritability is high because the phenotypic value gives them an accurate representation of the genotypic value. Therefore, understanding heritability aids the plant breeder in predicting the outcomes of selection for a specific character. Heritability estimates combined with genetic advance, however, are more helpful for determining the effect of selection than the heritability estimates alone.

Patil *et al.* (2014) investigated 58 spanish bunch groundnut genotypes for analysis of variability in 16 plant characters. Analysis of variance revealed significant

differences among the genotypes for all the characters studied. The analyses of variances for 16 characters in each environment revealed that the mean squares due to genotypes were significant indicating the presence of sufficient amount of variability in the material studied. Maximum broad sense heritability was recorded for days to 50 per cent flowering followed by plant height and 100- kernels weight. In general, moderate to high heritability along with moderate to high genetic advance for days to 50 per cent flowering, plant height, 100-kernels weight, 100-pods weight, shelling per cent and harvest index, designated the involvement of additive gene action and scope of improvement in these traits through selection.

Dewangan *et al.* (2015) examined 50 genotypes of groundnut and manifest that the analysis of variance was significant for most of the characters studied. Based on the mean performance among 50 genotypes, ICG-10185 followed by ICG-10092 were found to be the best genotypes for pod yield per plant indicating that the presence of amount of variation for these characters and indicating that these traits could be used for selection for crop improvement. High heritability was observed for plant height, seed index and pod yield per plant.

Padmaja *et al*. (2015) evaluated the variability in F_2 population of JL 24 x ICG 13919 in groundnut and reported high variability in the form of PCV, GCV, heritability in the form of mean for mature pods per plant, total pods per plant indicating selection for these traits would be helpful in the genetic improvements.

Bhargavi *et al*. (2017) conducted an experiment to evaluate genetic variation among 20 Spanish bunch groundnut genotypes along with check TMV 2 for SPAD chlorophyll meter reading (SCMR) at 40, 50, 60, 70 DAS and other yield attributing characters. For number of mature pods per plant, highest PCV and GCV were reported. For number of mature pods per plant, biological yield per plant, biological yield per hectare, pod yield per plant, pod yield per hectare, kernel yield per plant, kernel yield per hectare, 100-kernel weight and oil yield per hectare, high heritability along with high genetic advance as percent mean were observed which revealed prevalence of additive gene action. The experiment concluded that the genotypes Abhaya and JCG 88 were better for used in breeding programmes in order to increase yield.

Rajarathinam *et al*. (2017) conducted an experiment for 9 quantitative characters in four F_3 population viz., CO 7 × VRI Gn 6, TMV 2 × VRI Gn 6, TMV Gn 13 × VRI Gn 6 and VRI 2 × VRI Gn 6. Considering the mean performance, the cross derivative TMV Gn 13 × VRI Gn 6 found superiority for the characters viz., 100-pod weight (g), 100-kernel weight and sound mature kernel. High percentage of PCV, GCV, heritability coupled with high GAM values were recorded by number of pods per plant, pod yield per plant, kernel yield per plant, late leaf spot score and rust score in varied crosses. Regarding the population distribution, significant and negative skewness were observed in all the four crosses for shelling (%) and sound mature kernel (%). Hence, based on mean performance and various genetic parameters, the cross CO 7 × VRI Gn 6 was found superior for late leaf spot and rust resistance in groundnut.

Singh *et al*. (2017) studied 15 groundnut genotypes and revealed that dry pod yield per plant indicate 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, days to maturity was observed to have high heritability and high genetic advance. These traits were controlled by additive genes and can be easily transferred to succeeding generations.

Zongo *et al.* (2017) studied genetic variability using two F_3 populations from crosses QH243C × NAMA and TS32-1 × NAMA. For cross QH243C × NAMA, GCV and PCV showed high value for pod yield, kernel yield and ELS score at 60 and 80 days after sowing and for the remaining traits low to moderate GCV and PCV were obtained. High heritability values along with high genetic advance as per cent mean recorded for ELS-II, defoliation per cent, pod yield in cross QH243C × NAMA, shelling per cent for cross TS32-1 × NAMA, plant height, kernel yield in both crosses, showed important role of additive gene action for inheritance of these traits.

Roy *et al*. (2018) evaluated 33 genotypes of groundnut for the estimation of genetic variability, heritability and genetic advance. The results revealed presence of significant difference in the characters which are taken into consideration. For traits *viz*. days to 50 per cent flowering, SCMR 70 DAS, harvest index and 100-kernel weight, moderate PCV and GCV along with high heritability and high genetic advance as per cent of mean were reported. Moderate GCV and high PCV with high heritability and high genetic advance as per cent mean were reported for kernel yield

per plant. These traits can be upgraded by simple selection procedure due to presence of additive gene action.

Tirkey *et al*. (2018) studied 15 advanced genotypes including three checks *viz*. Birsa Bold ICGS 76 and Kaushal to assess the genetic variability for six yield attributing and quality characters in both the years and then evaluated. The analysis of variance designate the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes for various traits. High estimate of genotypic and phenotypic coefficient of variation were observed for pod yield per plot, kernel yield per plot and 100-kernel weights indicated wider genetic variation for these traits. High value of heritability along with high expected genetic advance were also observed for these characters.

Kumar *et al*. (2019) evaluated 20 groundnut genotypes for 14 characters to study the genetic variability parameters. Analysis of variance showed highly significant differences among genotypes for all the characters indicating that sufficient variability was found among the genotypes studied for these characters. Days to 50 per cent flowering, number of pods per plant, 100 pod weight, 100 sound mature kernel and sound mature kernel had high heritability along with high genetic advance as per cent of mean and medium to high GCV specify selection would be rewarding for improving these traits because of greater control of additive gene effects, while the traits like primary branches per plant, pod yield and kernel yield had moderate GCV and heritability along with high genetic advance as per cent of mean revealed heritable component of genetic variance playing greater role in expression of these traits and selection would be effective. For seed size and quality related traits, medium heritability along with low genetic advance as per cent of mean was observed protein content, oil content and sugar content indicating high influence of environment on expression of these traits.

Vinithashri *et al*. (2019) studied to examine the variability of prominent yield and yield attributing traits in groundnut. They recorded high GCV, PCV values for the number of pods per plant, 100-pod weight, 100-kernel weight, shelling per cent and number of mature kernels. Thisi indicate the presence of high variability for these traits. These traits can be choosen for selection as they contribute more towards variability with least influence of environment on it.

Venkataravana *et al.* (2020) investigated the extent of genetic variability for pod yield and its attributing characters. They conducted their experiment using three different F_2 populations of three cross combinations *viz.*, TAG 24 × ICGV 00350, TMV 2 × ICGV 86031 and JL 42 × ICGV 91114. The estimates of PCV and GCV were high for number of branches per plant, pod yield per plant, kernel yield per plant, and oil yield per plant in all the three crosses. It will be more significant if the yield is estimated through its component rather than directly because there may not be any gene for yield as such but it operates only through its component characters.

Mitra *et al*. (2021) investigated 31 groundnut accessions and higher level of coefficient of variation both at phenotypic and genotypic level expressed by number of pods/plant, secondary branches, kernel width and pod yield.

Kannappan *et al*. (2022) studied two crosses in F_3 generation to assess variability. For cross VRI 8 X K6, better mean performance in all traits along with very good pod and kernel yield per plant compared to cross BSR2 X K6 were observed. High heritability for pod and kernel yield were found for cross VRI 8 X K6 while low and moderate GAM for pod and kernel yield for cross BSR 2 X K6. Low to moderate PCV and GCV were found for both the crosses except for kernel yield in BSR 2 X K6 and pod yield in both the crosses with higher PCV and GCV values.

Pachauri and Sikarwar (2022) evaluated 32 groundnut genotypes in Randomized Block Design with three replications. Analysis of variance showed that there were positive and highly significant differences for all attributes studied among 32 genotypes.

Sridevi *et al*. (2022) evaluated genetic variability using 30 groundnut genotypes. The values of PCV and GCV were higher for the characters *viz.,* number of branches, total biomass, 100 kernel weight, leaf area ratio and leaf area index. Total number of branches, total biomass and 100 kernel weight exhibited high heritability and high genetic advance as per cent of mean.

Khaniya *et al*. (2023) evaluated fifty-eight genotypes of bunch groundnut for fourteen agro-morphological characters. Characters such as the number of primary branches per plant, the plant height, the days to flowering, the days to maturity, the 100 pods weight, the 100 kernels weight, the number of mature pods per plant, the kernel yield per plant, the pod yield per plant, the shelling out turn, the sound mature

kernel, the biological yield per plant, the harvest index, and the oil content. Analysis of variance indicated extremely significant genetic differences for all the characters under study except shelling out turn. PCV is greater than GCV for almost all characters. The biological yield per plant, harvest index, and number of mature pods per plant showed the greatest values, but days to maturity, number of primary branches per plant, and oil content showed the lowest values. The number of mature pods per plant, pod yield per plant, 100 pod weight, kernel yield per plant, 100 kernel weight, and biological yield per plant all manifested higher heritability and genetic advance of percent mean, indicating the consequence of additive gene action and the great potential for improvement in these genotypes through simple selection. Pod yield per plant was highly affected by harvest index, biological yield per plant, and kernel yield per plant.

Yadav *et al*. (2023) conducted an experiment using 45 groundnut genotypes. The analysis of variance indicate presence of substantial difference in genotypes for all the characters. High heritability along with high genetic advance and GCV was reported for biological yield per plant, 100-kernel weight, kernel yield per plant, dry pod yield per plant and pods per plant making sure that these characters are under additive genetic control and consideration of these traits for the improvement will be lucrative and may rapidly contribute to increase yield.

2.2 CORRELATION COEFFICIENT ANALYSIS

Main objective of almost all plant breeders is yield. Therefore, the main focus in plant breeding is given on increasing the yield. Yield is a quantitative character and it depends upon various component characters. Association between the characters are studied by the correlation coefficient. Correlation studies help in determining the direction and the magnitude of selection of various component traits for overall crop improvement. Galton (1889) has given the concept of correlation, which was further explained by Fisher (1918), in order to initiate effective crop improvement programme.

Rao (2016) studied under drought stress condition on 30 groundnut genotypes and evaluated that dry pod yield was significantly correlated with kernel yield, no of pods per plant, 100-kernel weight and SPAD chlorophyll meter reading (SCMR).

Singh *et al*. (2017) evaluated 15 groundnut genotypes and revealed that dry pods per plant have positive and significant genotypic and phenotypic correlations with kernel yield per plant and 100-kernel weight. It indicates that the selection for increased dry pods per plant may give higher kernel yield per plant and 100-kernel weight and thus, it may contribute in increasing the dry pods per plant.

Zongo *et al.* (2017) studied correlation analysis and showed significant positive correlation for pod and kernel yield with 100-kernel weight and shelling percent for cross QH243C X NAMA while insignificant correlation for cross TS32-1 X NAMA. Early generation selection found effective for days to first flowering, days to 50 per cent flowering, plant height, pod yield, kernel yield, 100-kernel weight and early leaf spot resistance which recorded higher value of heritability in the two crosses.

Kadam *et al*. (2018) analysed 30 genotypes of groundnut for 15 characters and revealed that significant and positive correlation between dry pod yield per plant and other quantitative characters with number of mature pods per plant, dry biomass, number of pegs per plant, fresh pod yield per plant, fresh biomass, fresh fodder yield per plant and immature pods per plant.

Sab *et al*. (2018) assessed 9 characters of 34 advanced breeding lines of groundnut for the estimation of correlation for WUE and yield related traits during summer 2015 and revealed that SLA showed strong negative correlation with pod yield per plant whereas SCMR and yield contributing characters show strong positive correlation with pod yield per plant.

Tirkey *et al.* (2018) evaluated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for most of the traits. Significant correlation coefficient was existed for pod yield along with the characters like shelling per centage, kernel yield and 100-kernel weight.

Rao and Venkanna (2019) investigated 39 groundnut genotypes and evaluated that pod yield was significant positively correlated with kernel yield, shelling per cent and 100-kernel weight and there was significant negative association with day to 50 per cent flowering, days to maturity and dry haulm yield.

Godhani *et al*. (2020) analysed nine crosses *viz.* TLG 45 x ICGV-05155, JL – 501 x KDG 128, K-1641 x ALR-3, SG-99 x R-8808, ALG-234 x ICGV-00350, AG-

24 x ICGV-6110, JSSPLS-58 x CS-19, TPG-41 x GG-16 and J-89 x ISK-I-16-13 in F_3 generation and observed that pod yield per plant had significant and positive correlation with plant height, number of mature pods per plant, number of immature pods per plant, kernel yield per plant and harvest index. Selection of these traits give rise to higher yield3.

Venkataravana *et al.* (2020) conducted an experiment using three different F_2 populations of three cross combinations *viz*., TAG 24 × ICGV 00350, TMV 2 × ICGV 86031 and JL 42 × ICGV 91114 to study the extent of genetic variability and correlation of pod yield and its attributing characters. Phenotypic correlation coefficient analysis for yield and its attributing traits for all the three crosses were carried out and characters which showed significant correlation with pod yield per plant were subjected to path analysis in order to partition the correlation coefficients in to direct and indirect effects of component traits on pod yield.

Shrotri *et al*. (2021) conducted an experiment using 30 groundnut genotypes and observed that genotypic coefficient of correlation was higher as compared to phenotypic coefficient of correlation. The pod yield per plant indicated highly significant positive correlation with number of mature pods per plant, kernel yield per plant, hundred kernel weight and sound mature kernel.

Sudhishna *et al*. (2021) investigated 40 groundnut genotypes and revealed that significant and negative association of dry pod yield per plant with number of immature pods per plant and 100 kernel weight. While, significant and positive association was noticed for the trait with plant height, mature pods per plant and fresh pod yield per plant.

Kannappan *et al*. (2022) studied correlation analysis among two crosses VRI 8 X K6 and BSR 2 X K6 in F_3 generation. High significant positive correlation between kernel yield and number of mature pods, number of pods, 100-pod weight, 100-kernel weight, pod yield and shelling percentage in both the crosses were observed. High significant correlation was found between shelling percentage and days to flowering in VRI 8 x K 6 while in BSR 2 X K 6, shelling percentage and 100-kernel weight were highly significantly correlated.

Pachauri and Sikarwar (2022) estimate 32 groundnut genotypes and indicates that genotypic and phenotypic correlation coefficient analysis revealed that the kernel

yield per plant showed significant and positive correlation with pod yield per plant, harvest index, 100-pod weight, number of pods per plant, shelling outturn and 100-kernel weight.

Sridevi *et al*. (2022) evaluated correlation coefficient using 30 groundnut genotypes and observed that kernel yield showed significant positive correlation with pod yield, mature pods, number of pods and shelling percentage.

Reddy *et al*. (2023) conducted an experiment using 26 genotypes of groundnut for the estimation of character association among yield contributing characters. Significant differences were found in days to maturity, test weight, sound mature kernels, harvest index, protein content and pod yield per plant. Days to maturity, test weight, harvest index and protein content had positive association with pod yield for both genotypic and phenotypic correlation coefficient.

Yadav *et al* (2023) conducted an experiment using randomized complete block design for the assessment of correlation among 45 groundnut genotypes with three replications. They concluded that there was significant positive association between kernel yield per plant, pods per plant and biological yield per plant with dry pod yield per plant both at genotypic and phenotypic levels whereas shelling percentage show association only at genotypic level.

2.3 PATH ANALYSIS

The concept of path analysis was given by Wright (1921) and expanded for crop plants by Dewey and Lu (1959). The path coefficient analysis is one of the effective techniques to sought out inter relationship between different yield characters and their direct and indirect effect on yield through correlation values. (Rao *et al*. 2014). It determines the relationship between major yield attributing characters with yield and among them with their direct and indirect effects on yield for making the selection more efficient.

Babariya and Dobariya (2012) evaluated 100-genotypes of spanish bunch groundnut and indicate biological yield per plant and harvest index exhibited high and positive direct effects on pod yield per plant. Kernel yield per plant, number of pods per plant and days to maturity had moderate and positive direct effects on pod yield per plant.

Rao (2016) evaluated 30 groundnut genotypes under drought conditions and observed that path coefficient analysis indicates that number of pods per plant and hundred kernel weight were essential traits to be considered for realizing the improvement in yield.

Kamdi *et al*. (2017) evaluated 18 local collections of groundnut for estimation of path analysis. Path coefficient analysis indicate that number of mature pods per plant, number of primary branches per plant, and days to 50 per cent flowering had positive direct effect on yield of dry pods. Increase in number of mature pods per plant reflects increase in yield of groundnut.

Singh *et al.* (2017) investigated 15 groundnut genotypes and the path coefficient analysis revealed that the kernel yield per plant, oil content and shelling per centage exhibited high and positive direct effect on dry pod yield per plant. Thus, these characters turned out to be the major components of pod yield and direct selection for these traits may be advantageous for yield improvement.

Tirkey *et al.* (2018) observed 15 advanced genotypes of groundnut and revealed the direct effect of path analysis for shelling per centage. He found that this character may be effective for selection of high pod yield. Emphasis should be given in selection of characters such as sound mature kernel, kernel yield, shelling per centage and 100 kernel weight to maximize pod yield per plant and for further improvement in groundnut crop.

Memon *et al*. (2019) analysed four crosses *viz*. JL-24 x GJG-22(Cross-1), ICGV-05155 x R-33-1(Cross-2), AK-343 x TPG-41(Cross-3) and JL-501 x TG-36 (Cross-4) in F_2 generation and observed that kernel yield per plant, biological yield per plant and harvest index had high positive and significant direct effect on pod yield per plant in all the crosses. Number of mature pods per plant and shelling outturn had high indirect effect on pod yield per plant through kernel yield per plant.

Rao and Venkanna (2019) worked on 39 groundnut genotypes and evaluated that path coefficient analysis revealed that the direct positive effect of kernel yield followed by days to maturity.

Bodke *et al*. (2020) studied 30 genotypes of groundnut to assess correlation and path analysis in groundnut and revealed proline content showed positive direct effect on pod yield per plant followed by pod per plant 100 kernel weight, days to 50

per cent flowering, SCMR reading, harvest index and plant height. Therefore, for improvement of groundnut under stress condition some weightage should be given to these characters.

Godhani *et al*. (2020) analysed 9 crosses in F_3 generation. Observations were recorded for 13 characters. Path analysis studies revealed direct positive effect of kernel yield per plant and harvest index on pod yield per plant. Harvest index showed higher indirect effect through kernel yield per plant.

Mohapatra and Khan (2020) assessed four F_3 crosses of groundnut genotypes to investigate the interrelationship among the yield attributing traits and physiological traits. Path analysis study indicated a high positive direct effect by kernel yield per plant in two crosses *viz.,* Kadri-9 × GPBD-4 and ICGV-00351 × Sunoleic-95R. This association indicates that these yield related parameters can be used as preliminary screening tools for selecting high yielding genotypes for the next generation.

Mitra *et al*. (2021) observed 31 groundnut genotypes and path coefficient analysis exerts high positive direct effects on pod yield through pod length, kernel width and number of pods per plant.

Patel *et al*. (2021) conducted an experiment on six crosses in F_2 generation during summer 2016. Observation on nine yield and yield contributing characters were recorded and concluded that high positive direct effect of kernel yield per plant on pod yield per plant whereas high negative direct effect of shelling out-turn on pod yield per plant in cross 6 was observed but it showed high indirect effect through kernel yield per plant.

Shrotri *et al*. (2021) conducted an experiment using 30 groundnut genotypes to assess path analysis and observed that the number of mature pods per plant had high positive direct effect on pod yield per plant.

Sudhishna *et al*. (2021) assessed 40 groundnut genotypes for character association among yield, yield contributing characters and quality traits in addition to path effects of the yield contributing characters and quality characters for dry pod yield. Path analysis revealed high and positive direct effect of mature pods per plant and fresh pod yield per plant, indicating their effectiveness as important selection criteria for dry pod yield improvement in groundnut.

Kannappan *et al*. (2022) studied path analysis among two crosses VRI 8 X K6 and BSR 2 X K6 in F_3 generation. High positive direct effect on kernel yield by 100 kernel weight and pod yield in both the crosses whereas shelling percentage in VRI 8 × K 6 had negligible positive direct effect on yield.

Pachauri and Sikarwar (2022) analysed genotypic and phenotypic path coefficient and revealed that shelling outturn, harvest index and pod yield per plant exerted highest positive and significant direct effect on kernel yield per plant. Therefore, it would be useful for the selection of these traits for fast improvement in kernel yield of groundnut.

Reddy *et al*. (2023) conducted an experiment using 26 genotypes of groundnut for the estimation of path analysis and revealed that harvest index, days to 50 per cent flowering, protein content and test weight had direct positive effect on pod yield per plant.

Yadav *et al*. (2023) conducted an experiment using 45 groundnut genotypes. The analysis revealed that kernel yield per plant, pods per plant and biological yield per plant had positive direct effect on dry pod yield per plant. These characters were identified as direct selection parameters for improvement in yield.

3. MATERIAL AND METHODS

The present investigation entitled **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)"** was conducted to assess the genetic variability, correlation coefficient and path analysis in groundnut at Instructional Farm College of Technology and Engineering, MPUAT, Udaipur (Rajasthan). The 30 spanish bunch genotypes along with 3 checks of groundnut were evaluated during *kharif* 2023. The details of the materials used and methods adopted during the investigation are discussed under the following heads.

3.1 SITE OF EXPERIMENT

Geographically, Udaipur is situated at an elevation of 579.5 meter above the mean sea level on latitude of 24º35' North and longitude of 73°42' East. The climate of Udaipur is tropical, summer is tolerably hot and winters are quite pleasant. The region experiences scanty rainfall in monsoon season. The meteorological data during which experiment was conducted is presented in Appendix-I

3.2 EXPERIMENTAL MATERIALS

The experimental materials used in the present investigation was consisted of the 30 diverse spanish bunch genotypes including 3 checks groundnut genotypes representing diversity in adaptability and variability in characters and geographical origin. The experimental materials were evaluated for genetic variability, correlation coefficient and path analysis for 14 economically important traits during *Kharif*, 2023 at CTAE Instructional Farm, MPUAT, Udaipur. The experimental materials were collected from All India Coordinated Research Project (AICRP) on Groundnut, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur. The details of the genotypes and their parentage used in this study are presented in Table 3.1

Table 3.1 Name and pedigree of 30 spanish bunch type groundnut

Sr. No.	Name of Genotypes	Parentage
1.	UG-3	Selection from ICGV98281
2.	UG-4	Selection from ICGV98221
3.	UG-5	Selection from ICGV98223
4.	UG-6	ICGV-93373 x ICGV-92224
5.	UG-7	ICGV-92267 x ICGV-93222
6.	UG-8	ICGV-95245 x ICGV-96352
7.	UG-9	ICGV-95322 x ICGV-96398
8.	UG-10	ICGV-96352 x ICGV-95006
9.	UG-11	Gajah-(NU x ICGS-44) x LI x ICGS-44)
10.	UG-12	Gajah x (NU x ICGS-44) x LI x ICGS-44)
11.	UG-13	Gajah x (NU x ICGS-44) x LI x ICGS-44)
12.	UG-14	ICGV-93134 x (LI x ICGS-44)
13.	UG-15	ICGV-93134 x (LI x ICGS-44)
14.	UG-16	ICGV-93143 x (LI x ICGS-44)
15.	UG-17	Gajah x (NU x ICGS-44) x (LI x ICGS-44)
16.	UG-18	{[(ICGV-86347 x ICGV-86031) x JL-24]x Gajah x (NU x ICGV-87883)]}
17.	UG-19	{[(ICGV-86347 x ICGV-8031) x JL-24]x Gajah x (NU x ICGV-87883)]}
18.	UG-20	[(ICGV-2411 x ICGV-7637) x (Gajah x ICGV-88315)]
19.	UG-21	(TAG-24 x ICGV-8666)
20.	UG-22	ICGV-87290 x ICGV-87846
21.	UG-23	ICGV-90054 x Gangapuri

Sr. No.	Name of Genotypes	Parentage
22.	UG-264	UG-5 x GPBD-4
23.	UG-265	PM-1 x GPBD-4
24.	UG-266	TG 37 A x GPBD-4
25.	UG-267	GG 20 x GPBD-4
26.	UG-268	TG 37A x PBS13037
27.	UG-269	GG 7 x KDG 128
28.	TG37A	TG 25 x TG 26
29.	JL501	Selection from TAG 24
30.	GG7	S206 x FESR8

3.3 EXPERIMENTAL DESIGN

The experiment was laid out in Randomized Block Design with three replications during *Kharif*, 2023. Two rows per genotype were sown in a plot of 5.0 m x 0.60 m with inter and intra row spacing 30 x 10 cm. All the recommended package of practice was followed to raise a good and healthy crop.

3.4 OBSERVATIONS RECORDED

Observations were recorded on plant basis, 5 individual plants were randomly selected for all the genotypes in each replication except for days to 50 per cent flowering and days to maturity,where observations were recorded on whole plot basis. The methodology used for recording observations for different characters are described as under:

3.4.1 Days to 50 per cent Flowering

It was recorded as the number of days from the date of sowing to the date when 50 per cent of the plants in a plot produced at least one flower.

3.4.2 Days to Maturity

The total number of days were calculated from the date of sowing to date when all the plants attained complete physiological maturity.

3.4.3 Number of Branches per Plant

The branches arising on main axis were counted on each randomly selected five plants at the time of maturity.

3.4.4 Plant Height (cm)

It was recorded in centimeters from the ground level to the top of the plant at the time of maturity.

3.4.5 Pods per Plant

The total number of pods from sampled plant was counted at the time of harvesting.

3.4.6 Shelling Percentage (%)

A sample of 100g mature pods taken per plot randomly and kernel yield obtained from this sample and calculated shelling percentage using following formula:

$$\text{Shelling percentage} = \frac{\text{Kernel yield(g)}}{\text{Total dry pod yield(g)}} \times 100$$

3.4.7 100-kernels weight (g)

Hundred kernels were counted from random sample from each plot and weighed in grams.

3.4.8 Kernels per Pod

It was recorded from five randomly selected pods from each of the randomly selected plant and after shelling average was worked out.

3.4.9 Sound Mature Kernel (%)

In random sample of hundred kernels, the number of well-developed kernels were separated and counted for calculating SMK (%) as per following formula:

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

3.4.10 Dry Pod Yield per Plant (g)

The fully developed dry pods were weighed in grams from each randomly selected five plants at the time of maturity and average weight per plant was calculated**.**

3.4.11 Biological Yield per Plant (g)

It was determined by weighing a single plant sample including pods after complete sun drying and recorded the weight in grams.

3.4.12 Harvest Index (%)

The harvest index was calculated as per the formula given below:

$$\text{Harvest index (\%)} = \frac{\text{Dry pod yield(g)}}{\text{Biological yield(g)}} \times 100$$

3.4.13 Oil content (%)

Oil content was determined by the Soxhlet's method as given by Appendix II.

3.4.14 Protein Content (%)

Protein content was determined as per the method suggested by Linder (1944) (Given in Appendix-III).

3.5 STATISTICAL ANALYSIS

The observed values of each character for each genotype were subjected to the following standard statistical procedure:

3.5.1 Analysis of variance for experimental design (ANOVA)

3.5.2 Variability parameters

- 3.5.2.1 Analysis of variance components
- 3.5.2.2 Broad sense heritability
- 3.5.2.3 Genetic Advance
- 3.5.2.4 Genetic Advance as percent of mean

3.5.3 Correlation coefficient analysis

3.5.4 Path coefficient analysis

3.5.1 Analysis of variance for experimental design

The mean values of different genotypes for all the characters were subjected to analysisof variance to determine the difference between thirty genotypes for different characters were tested for significance by using analysis of variance technique as per the procedure proposed by Panse and Sukhatme (1985).

$$y_{ij} = \mu + r_i + t_j + e_{ij}$$

Where,

y_{ij} = Phenotypic observation on i^{th} genotype in j^{th} replication.

μ = General mean

r_i = The effect of i^{th} replication

t_j = The effect of j^{th} genotype

e_{ij} = Uncontrolled random error associated with j^{th} genotype in i^{th} replication

The assumptions of the model are:

1. All the observations should be independent.
2. The different effects in the model should be additive.
3. Error involved in the population should be normally and independently distributed with mean zero and variance ($\sigma^2 e$). Covariance and variance between two traits, say X and Y necessary for calculating genotypic and phenotypic correlation coefficients were obtained from the mean sum of squares.

Analysis of variance tables for all the characters under study were constructed as follows:

Table 3.2 Analysis of Variance for experimental design

Source	**Degree of Freedom**	**Mean sum of square**	**Expected mean sum of square**	**F**
Replications	(r-1)	MSr	$\sigma^2 e + g\sigma^2 r$	MSg/MSe
Genotypes	(g-1)	MSg	$\sigma^2 e + r\sigma^2 g$	
Error	(r-1) (g-1)	MSe	$\sigma^2 e$	
Total	(N-1)			

Where,

r = Number of replications

g = Number of genotypes

N = Total number of observations (r × g)

MSr = Mean sum of square due to replication

MSg = Mean sum of square due to genotypes

MSe = Mean sum of square due to error

$\sigma^2 g$ = Genotypic variance

$\sigma^2 r$ = Variance due to replications

$\sigma^2 e$ = Error (environmental) variance

The genotypic, phenotypic and error variances were estimated using the following formulaproposed by Burton (1952) and Johnson *et al.* (1955):

Genotypic variance ($\sigma^2 g$) = $\frac{MSg - MSe}{r}$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Environmental variance ($\sigma^2 e$) = MSe

3.5.2 Variability Parameters

3.5.2.1 Analysis of variance components

(i) Mean ($\bar{X}$)

The mean value of each character was worked out by dividing the sum of all observations by corresponding number of observations.

$$\bar{X} = \frac{\sum Xij}{N}$$

Where,

X_{ij} = Observation of i^{th} genotypes and j^{th} replication

N = Total number of observations

(ii) Range

The lowest and the highest values for each character were recorded.

(iii) Standard error of mean (SEM)

Standard error of mean was calculated with help of error mean square from the analysis of variance.

$$SEm = \sqrt{\frac{MSe}{r}}$$

$$SEd = \sqrt{\frac{2MSe}{r}}$$

Where,

MS_e = Error mean square

SEm = Standard error of mean

(iv) Standard Error of Difference (SED)

$$SEd = \sqrt{\frac{2MSe}{r}}$$

Where,

MS_e = Error mean square

SEd = Standard error of difference

r = Number of replications

(v) Critical difference (CD)

For all the characters, critical difference was calculated to compare the genotype means. Critical difference is calculated to test the difference between two means at error degree of freedom using the following formula:

$$CD = \sqrt{\frac{2MSe}{r}} \text{ x "t" at 5 \% or 1 \% level of significance and error d.f.}$$

(vi) Coefficient of variation (CV)

Genotypic and phenotypic coefficients of variation were estimated by formula suggested by Burton and De vane (1953) for each character, as given below:

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{X}} \text{ x } 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{X}} \text{ x } 100$$

3.5.2.2 Heritability (h^2)

Broad sense heritability is the ratio of genotypic variance to the phenotypic variance and was calculated according to formula suggested by Hanson *et al.* (1956) for each character:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \text{ x } 100$$

As suggested by Johnson *et al.*(1955) heritability values were categorized as follows:

Low : Less than 30%

Moderate : 30-60 %

High : More than 60%

3.5.2.3 Genetic advance (GA)

The improvement in mean genotypic value of selected plants over the parental population is known as genetic advance. The expected genetic advance under selection was estimated as per the formula described by Johnson *et al.* (1955).

$$GA = k \times \sigma_p \times h^2$$

Where,

K = Selection differential (value of k at 5% selection intensity = 2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

3.5.2.4 Genetic advance expressed as percentage of mean (Genetic Gain)

The genetic advance expressed as percentage of mean was calculated by using the following formula suggested by Johnson *et al.* (1955) and is expressed in percentage.

$$\text{Genetic advance (as percentage of mean)} = \frac{GA}{\overline{X}} \times 100$$

Where,

GA = Expected genetic advance under selection

$\overline{X}$ = General mean of a character

Genetic advance as percentage of mean values were categorized as follows:

Low	:	Less than 10 %
Moderate	:	10-20 %
High	:	More than 20 %

3.5.3 Correlation Coefficient Analysis

To determine the degree of association of various characters with yield and also among the yield components, the correlation coefficients were calculated. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while the phenotypic correlation coefficient includes both genotypic as well as environmental influences.

The genotypic and phenotypic correlation coefficients were calculated from the genotypic and phenotypic components of variance and covariance as described by Singh and Choudhary (1985) and as per formula given by Jibouri *et al*. (1958):

Expectations of mean sum of cross products

Source	d.f.	M.S.P.	Expectations of mean sum of cross products
Replications	(r-1)	MSP_r	$COV_e(xy)+ gCOV_r(xy)$
Genotypes	(g-1)	MSP_g	$COV_e(xy)+ rCOV_g(xy)$
Error	(r-1) (g-1)	MSP_e	$COV_e(xy)$
Total	(rg-1)		

Genotypic correlation between characters X and Y

$$r_g(xy) = \frac{COV_g(xy)}{\sqrt{\sigma_g^2(x).\sigma_g^2(y)}}$$

Phenotypic correlation between characters X and Y

$$r_p(xy) = \frac{COV_p(xy)}{\sqrt{\sigma_p^2(x).\sigma_p^2(y)}}$$

Environmental correlation between characters X and Y

$$r_e(xy) = \frac{COV_e(xy)}{\sqrt{\sigma_e^2(x).\sigma_e^2(y)}}$$

Where,

$r_g(xy)$, $r_p(xy)$ and $r_e(xy)$ are the genotypic, phenotypic and environmental correlation coefficients between character x and y, respectively.

$COV_g(xy)$, COV_p (xy)and COV_e (xy) are the genotypic, phenotypic and environmental covariance'sbetween character x and y, respectively.

$\sigma_g^2(x)$, $\sigma_p^2(x)$ and $\sigma_e^2(x)$are the genotypic, phenotypic an environmental variance for x character, respectively.

$\sigma_g^2(y)$, $\sigma_p^2(y)$ and $\sigma_e^2(y)$are the genotypic, phenotypic and environmental variances for y character, respectively.

The calculated value of ''r'' was compared with table value of ''r'' (Fisher and Yates, 1938) at n-2 degrees of freedom at 5 per cent and 1 per cent level of significance, where n refers to number of pairs of observation.

3.5.4 Path Coefficient Analysis

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influence of one variable upon another thereby permitting the separation of the correlation coefficient into the component of direct and indirect effects. Path coefficient is the ratio of the standard deviation of the effect due to a given cause of the total standard deviation of the effects. The concept of the partitioning of correlation into direct and indirect effects through path analysis was originally developed by Wright (1921), but the technique was first used for plant selection by Dewey and Lu (1959) which operates on the principles of solving the simultaneous equations.

The direct and indirect effects of 14 characters on dry pod yield per plant (Y1) were obtained as per procedure given below:

r1Y1	r11 r12…….. r1 11	P1Y1
r2Y1	r21 r22…….. r2 11	P2Y1
”	”	”
”	”	”
”	”	”
”	”	”
r14Y	r14 14 r14 14…….. r14 14	P14Y
A	B	C

Where,

r_1Y, r_2Y, r_3Y,…., r_4Y are the genotypic correlations of Days to 50 percent flowering, Days to maturity, Plant height (cm), Number of branches per plant, Sound mature kernels (%), 100-kernel weight (g), Shelling percentage (%), Kernels per pod, Biological yield per plant (g), Harvest index (%), Protein content (%) and Oil content (%) on Dry pod yield per plant (g) (Y1), respectively.

P_1Y, P_2Y, P_3Y,……., $P_{14}Y$ are the direct effects of Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of branches per plant, Sound mature kernels (%), 100-kernel weight (g), Shelling percentage (%), Kernels per pod, Biological yield per plant (g), Harvest index (%), Oil content (%) and Protein content (%) on Dry pod yield per plant (g) (Y1), respectively.

$$\text{Or } A = BC$$

Values of 'C' vector were obtained as:

$$C = B\text{-}1A$$

Where,

A is the vector of direct correlations of twelve characters with seed yield Y1.

B^{-1} is the inverse of mutual correlation matrix of characters.

C is the vector of direct effects.

The inverse of this matrix was carried out by Pivotal Condensation Method.

To obtain indirect effect, B matrix was multiplied with vector C as follows:

Where,

D is the matrix of direct and indirect effect

B is the matrix of correlation among twelve characters.

Residual Factor

Residual factor which measures the contribution of the characters of causal scheme was obtained by using the following formula:

Residual factor (R) =

$$\sqrt{1 - (r1Y1P1Y1 + r2Y1P2Y1 + r3Y1P3Y1 + \ \ldots\ \ldots\ldots\ldots + r14Y1P14Y1)}$$

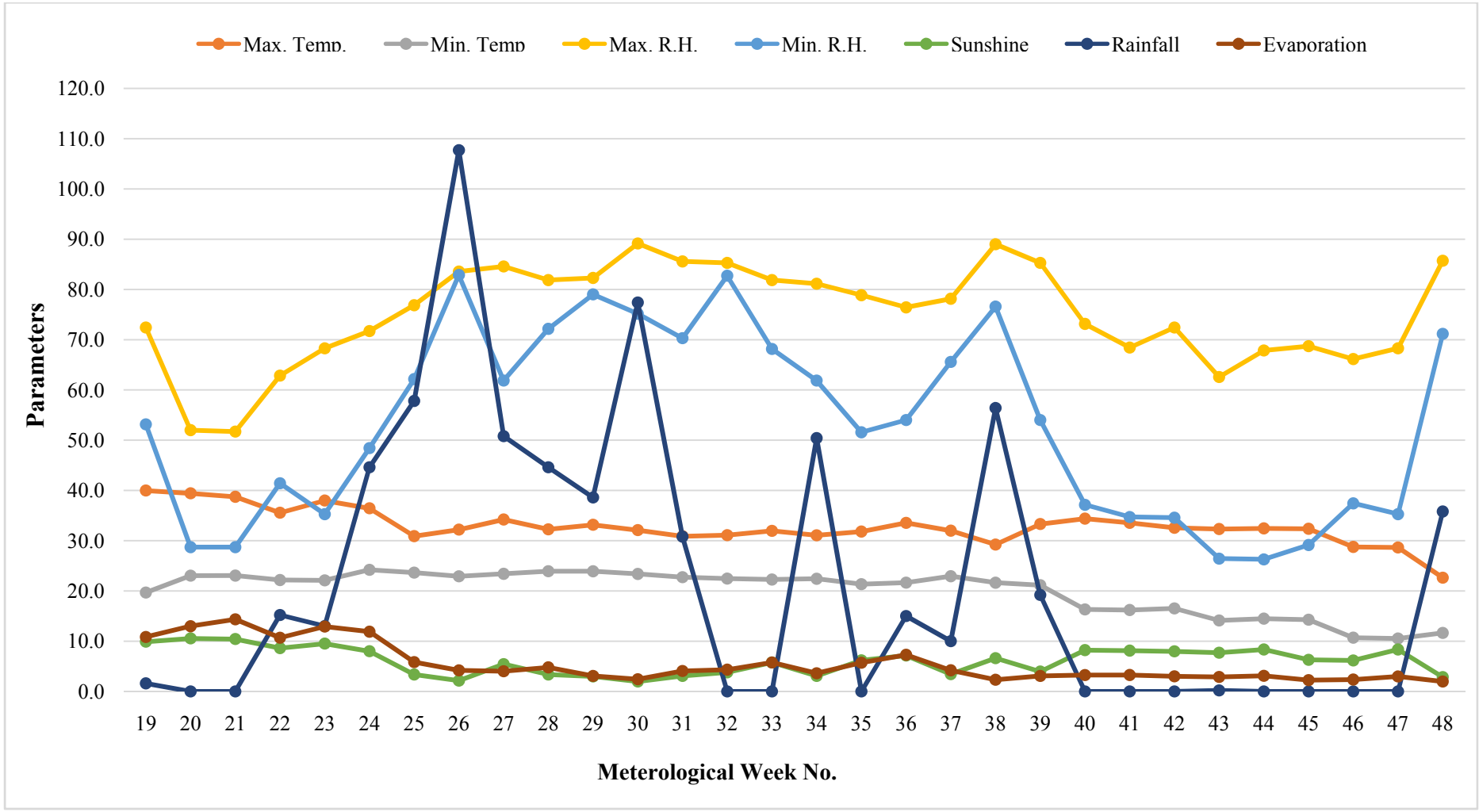

Fig.3.1 Mean weekly data on meteorological parameter during the crop growth period for *Kharif*, 2023

Plate I: General view of experimental field

Plate II: Cultural operation

1. Sowing of groundnut 2. Tagging

Plate III: Recording observation

1. Days to 50% flowering 2. Weighing of pods 3. Shelling

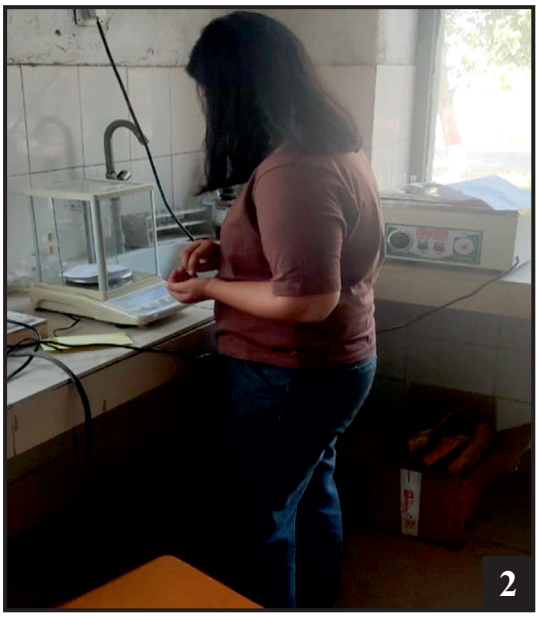

Plate IV: Analysis of protein and oil content

1. Grinding of groundnut kernels **2. Weighing**
3. Digestion **4. Taking reading**

4. RESULTS AND DISCUSSION

The goal of this research, **" Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.),"** was to determine the form and degree of genetic variability, character associations and path analysis for the characters under study among 30 genotypes including three checks. The experimental results obtained on various aspects in the present study were statistically analysed and have been presented under the following heads:

4.1 Analysis of variance

4.2 Genetic variability

4.3 Correlation coefficients

4.4 Path coefficient analysis

4.1 ANALYSIS OF VARIANCE

The mean squares due to genotype were highly significant with regards to different traits *viz.,* yield and component traits for groundnut are presented in Table 4.1. In the analysis of variance each genotype was highly significant for all the characters *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, pods per plant, shelling percentage (%), 100-kernels weight (g), kernels per pod, sound mature kernel (%), dry pod yield per plant (g), biological yield per plant (g), harvest index (%), oil content (%) and protein content (%).

Similar to the present findings, Kumar *et al.*(2019) and Khaniya *et al.*(2023) reported that the mean sum of squares was significant for all the characters under the study and found the significant difference among groundnut genotypes. This showed that the genotypes chosen for the current study had a significant degree of variability. This allows basis for these characters to be improved through hybridization and selection.

4.2 GENETIC VARIABILITY

The first step in any breeding programme and a requirement for any crop improvement programme is the assessment of genetic variability in the base population since it provides wider scope for selection. Estimates of the genotypic and phenotypic coefficients of variation (PCV and GCV) showed that there was a

significant amount of genetic variation for all the examined traits. Genotypic coefficient of variation (GCV) quantifies the degree of variation existing for a certain trait and shows the possibility for a specific characteristic to adapt to selection pressures on a specific population. It does not, however, quantify the percentage of heritable variation in the total variation present in each character. Heritability expresses the percentage of total phenotypic variance that can be attributed to the average effects of genes, which in turn defines how related are to one another. Heritability and the outcome of selection, or "genetic advance", are directly correlated. The most effective conditions for selection are those that combine high genetic advance with high heritability estimates (Larik *et al.*, 2000).

The estimates of various variability parameters *viz*., mean values, range, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (h^2bs), genetic advance (GA) and genetic advance expressed as percentage of mean (genetic gain) and character wise results of all the parameters are presented below.

Table 4.1: Analysis of Variance (ANOVA) for yield and its related traits in groundnut

S. No.	Characters	Replication [2]	Genotype [29]	Error [58]
1	Days to 50%flowering	1.21	8.31**	0.65
2	Days to maturity	0.95	7.61**	0.34
3	Plant height (cm)	1.02	5.90**	0.41
4	No. of branches/plant	0.19	9.47**	0.17
5	Pods per plant	3.17	44.75**	1.78
6	Shelling %	2.02	14.13**	1.24
7	100-Kernel weight (g)	1.03	16.68**	0.39
8	Kernels per pod	0.04	0.90**	0.05
9	Sound mature kernel (%)	1.87	20.78**	0.69
10	Dry pod yield per plant (g)	2.46	31.08**	1.80
11	Biological yield per plant (g)	2.03	48.61**	4.98
12	Harvest index (%)	40.24	116.91**	32.66
13	Oil content (%)	0.84	8.90**	0.29
14	Protein content (%)	0.44	3.94**	0.28

*, ** Significant at 5% and 1% respectively
[ ] Figure in parenthesis in degree of freedom

4.2.1 Mean Values and Range

A study of the results showed that majority of the characters had ranges that were noticeably high, indicating sufficient variability for selection and application in genetic improvement. The appendices IV and V contain the data on mean performance for fourteen characters across thirty groundnut genotypes.

4.2.1.1 Days to 50 percent flowering

The variation for days to 50 per cent flowering ranged between 30.13 to 35.69 days. The general mean recorded for days to 50 per cent flowering was 33.01 days. Out of thirty genotypes, sixteen genotypes flowered significantly earlier than general mean. Genotype UG-265 (30.13 days) was the earliest to 50 per cent flowering which was followed by UG-16 (30.17 days). The genotype UG-269 (35.69), UG-12 (35.37), UG-19 (35.20), and UG-8 (35.16) were comparatively late in days to 50 per cent flowering.

4.2.1.2 Days to Maturity

With respect to days to maturity, variation ranged between 100.68 (UG-13) to 105.90 (UG-12) days. Eighteen out of thirty genotypes showed significantly early maturity when compared with the general mean of 103.21 days. The genotype UG-13 (100.68 days) was earliest in maturity. The genotype UG-12 (105.90) was late in maturity.

4.2.1.3 Plant height

The range for the plant height was 40.80cm (UG-264) to 46.02cm (UG-16), highly significant variation is observed for this trait. The general mean 43.06 cm was found for this character. Fourteen genotypes among thirty showed greater height when compared to general mean. Genotypes UG-16 (46.02cm) and UG-264 (40.80 cm) had maximum and the minimum plant height, respectively.

4.2.1.4 Number of branches per plant

Number of branches per plant varied from 5.25 (UG-17) to 11.70 (TG37A). Most of the genotypes were in the range of 5 to 9 branches per plant except UG-7, UG-23, TG37A, JL501 and GG-7. The overall mean recorded for the number of branches per plant was 8.07. Maximum number of branches per plant was found in

genotype TG37A while the minimum number of branches was found in genotype UG-17.

4.2.1.5 Pods per plant

Mean value for the number of pods per plant ranged from 9.55 (UG-21) to 23.65 (UG-23). Maximum number of pods per plant was found in UG-23 (23.65), while minimum was found in UG-21 (9.55). The overall mean observed for number of pods per plant was 15.75.

4.2.1.6 Shelling percentage (%)

With an average of 71.05 per cent, the values of shelling percentage ranged from 65.23 per cent (UG-9) to 74.65 per cent (UG-16). Fifteen genotypes out of thirty had more shelling percentage than the general mean (71.05%). The genotype UG-16 (74.65%) showed maximum shelling percentage and the genotypes UG-265 (74.48), UG-20 (74.29), UG-17 (73.37), UG-6 (73.10), and UG-3 (72.87) had more shelling percentage.

4.2.1.7 100-kernels weight (g)

The variation for 100-kernel weight ranged between 38.23 g (UG-17) to 47.26 g (UG-23). The general mean of 100-kernel weight was 42.36 g. Genotype UG-23 (47.26 g) had the highest 100-kernel weight, whereas UG-17 (38.23 g) had the lowest.

4.2.1.8 Kernels per pod

Mean value for the kernels per pod ranged from 1.30 (UG-11) to 3.23 (UG-21). Maximum number of kernels per pod was found in UG-21(3.23), while minimum was found in UG-11(1.30). The overall mean observed for kernels per pod was 2.28.

4.2.1.9 Sound Mature Kernel (%)

The percentage of sound mature kernels was observed to range from 82.41% (UG-264) to 92.80%. (UG-6). The genotype UG-6 (92.80%) demonstrated the highest sound mature kernel percentage, while the average value for the characteristic was 88.91%. When compared to the average, seventeen genotypes out of thirty genotypes exhibited greater sound mature kernel percentages.

4.2.1.10 Dry pod yield per plant (g)

Dry pod yield per plant varied from 7.45g (UG-17) to 18.13g (UG-23). When compared to the overall mean dry pod yield per plant of 11.82g, fourteen out of the thirty genotypes recorded higher dry pod yield per plant. Higher dry pod yield per plant was obtained by the genotype UG-23 (18.13g), followed by UG-7 (17.94g), JL-501 (16.19g), and UG-12 (15.42g).

4.2.1.11 Biological yield per plant (g)

The range of biological yield per plant was 21.83g (UG-17) to 35.61g (UG-23) with a mean value of 28.30g.

4.2.1.12 Harvest index (%)

The overall average observed for harvest index was 41.32%. The mean for harvest index varied from 27.13% (UG-269) to 52.79% (UG-7).

4.2.1.13 Oil content (%)

The genotype UG-23 (47.01%) had the highest oil content, followed by TG37A (46.42%) and lowest was observed in the genotype UG-17 (40.24%). The average oil content was 43.97%.

4.2.1.14 Protein content (%)

The mean value for protein content was 22.08%. The highest protein content was found in genotype GG-7 (23.93%) and UG-23 (23.93%) followed by genotype TG37A (23.51%), while the lowest protein content was found in genotype UG-17 (20.14%).

Based on variability analysed in present study and that reported by earlier workers Patil *et.al* (2014), Dewangan *et al.*(2015),Bhargavi *et al.*(2017), Rajarathinam *et al.*(2017), Roy *et al.*(2018), Tirkey *et al.*(2018), Kumar *et al.*(2019), Vinithashri *et al.*(2019), Venkatravana *et al.*(2020), Mitra *et al.*(2021), Khaniya *et al.*(2023) and Yadav *et al.*(2023) in groundnut, it may be stated that these characters have a wide range of variability that could be used to improve through the selection of the characters studied in the present study.

4.2.2 Genotypic Coefficient of Variation (GCV)

The highest genotypic coefficient of variation was recorded for dry pod yield per plant (26.43%) followed by pods per plant (24.03%), kernels per pod (23.38%), number of branches per plant (21.82%). High values of the genotypic coefficient of variation for most characters demonstrated the presence of substantial levels of genetic variability. The moderate values (10-20%) for GCV was found for harvest index (12.83%) and biological yield per plant (13.48%). The value of GCV was low (<10%) for days to maturity (1.51%), sound mature kernel (2.91%), shelling per centage (2.92%), plant height (3.14%), oil content (3.85%), days to 50% flowering (4.84%), protein content (5.00%) and 100-kernel weight (5.50%). Table 4.2 provides the genotypic coefficient of variation for each character.

Similar results have also been reported by Padmaja *et al*. (2015), Bhargavi *et al*. (2017), Rajarathinam *et al*. (2017), Singh *et al*. (2017), Tirkey *et al*. (2018), Venkataravana *et al*. (2020), Mitra *et al.* (2021) and Yadav *et al*. (2023**)**

4.2.3 Phenotypic Coefficient of Variation (PCV)

For all the investigated traits, it was observed that the phenotypic coefficient of variation (PCV) was larger than the genotypic coefficient of variance. The highest values for phenotypic coefficient of variation were recorded for dry pod yield per plant (28.77%) followed by pods per plant (25.48%), kernels per pod (25.30%) and number of branches per plant (22.39%). Moderate value of PCV (10-20%) was recorded for harvest index (18.86%) and biological yield per plant (15.61%). The characters *viz*., days to maturity (1.61%), sound mature kernel (3.06%), shelling per centage (3.31%), plant height (3.48%), oil content (4.04%), days to 50% flowering (5.42%), protein content (5.54%) and 100-kernel weight (5.70%) showed low value (<10%) of phenotypic coefficient of variation. Phenotypic coefficients of variation were worked out for yield and quality attributes and are presented in Table 4.2.

Tirkey *et al*. (2018), Kumar *et al*. (2019), Mitra *et al.* (2021), Venkataravana *et al.* (2020) Yadav *et al*. (2023) were also observed similar findings.

4.2.4 Heritability (h^2)

The heritability estimates in broad sense were worked out and presented in Table 4.2. All the characters under investigation exhibited high level of heritability

except harvest index (46.23%). Highest value of heritability was found for number of branches per plant (94.91%) while the lowest value of heritability was found for harvest index (46.23%). High value (>60%) for heritability was found for most of the characters *viz.* biological yield per plant(74.50%), shelling per centage (77.56%),days to 50% flowering (79.76%), protein content(81.45%), plant height (81.54%), dry pod yield per plant (84.40%), kernels per pod (85.35%), days to maturity (87.63%), pods per plant (88.95%), sound mature kernel (90.63%), oil content (90.83%), 100-kernel weight (93.26%) and number of branches per plant (94.91%). However, harvest index (46.23%) exhibited moderate broad sense heritability values (30-60%).

Patil *et al.* (2014), Bhargavi *et al.* (2017), Rajarathinam *et al*. (2017), Singh *et al*. (2017), Zongo *et al.* (2017), Roy *et al.* (2018), Tirkey *et al.* (2018), Kumar *et al.* (2019), Vinithashri *et al.* (2019), Khaniya *et al.* (2023) and Yadav *et al*. (2023) also recorded similar finding.

4.2.5 Genetic Advance

Low values (<10%) for genetic advance was found for most of the characters such as kernels per pod (1.02%), protein content (2.05%),plant height (2.52%) days to 50% flowering (2.94%), days to maturity (3.00%), oil content(3.33%), number of branches per plant (3.53%), shelling per centage (3.76%), 100-kernel weight (4.63%), sound mature kernel (5.07%), dry pod yield per plant (5.91%),biological yield per plant (6.78%), pods per plant (7.35%) and harvest index (7.42%). Estimates for genetic advance are presented in Table 4.2.

Similar findings have also been reported by John *et al.* (2013).

4.2.6 Genetic Gain

The estimates of genetic advance are expressed as percentage of mean (Table 4.2) *i.e*., genetic gain was found high for dry pod yield per plant (50.03%), followed by pods per plant (46.69%), kernels per pod (44.49%), number of branches per plant (43.78%), biological yield per plant (23.96%) whereas moderate values (10-20%) were found for harvest index (17.96%) and 100-kernel weight (10.94%). The remaining characters showed low values (<10%) for genetic gain such as protein content (9.30%), days to 50% flowering (8.91%), oil content (7.57%), plant height (5.84%), sound mature kernel (5.71%), shelling per centage (5.29%) and days to maturity (2.91%).

Bhargavi *et al.* (2017), Rajarathinam et al. (2017), Kumar *et al.* (2019), Vinithashri *et al.* (2019), Khaniya *et al.* (2023) and Yadav *et al*. (2023) were also observed the similar results.

4.3 CORRELATION COEFFICIENTS

Correlation studies revealed the nature and extent of the relationship between two characters. Selecting the other pair will then allow you to achieve genetic advancement in one of the characters. Understanding the relationships between characters can obviously help in identifying the characters to select for higher dry pod yield as well as determining the degree and nature of the relationships that exist among dry pod yield contributing traits. It optimises the choice of a suitable breeding method as well as the contribution of parents to crop improvement. During the current study, the genotypic and phenotypic correlation coefficients for various traits, including dry pod yield, were calculated. In general, the genotypic correlation coefficient was greater than the phenotypic correlation coefficient (Upadhayay et al.,2020). reported similar findings. Lower phenotypic correlation may result from the environment's modifying effect on the genetic association of characters. The genotypic correlation coefficient represents a measure of genetic association between characters and thus aids in identifying the traits that are important and should be considered for yield improvement.

In order to explore the degree of relationship between yield and its component traits, correlation coefficient at the phenotypic and genotypic levels were computed using fourteen characters in thirty genotypes of groundnut. Some characters like days to maturity, plant height, shelling per centage, sound mature kernel was found non-significant with all the characters under study. Table 4.3 shows the genotypic and phenotypic correlations between various characters.

4.3.1 Days to 50 per cent Flowering

Days to 50 per cent flowering exhibited significant and positive correlation at genotypic and phenotypic levels with days to maturity (rg = 0.89* and rp = 0.76*).

4.3.2 Number of Branches per Plant

Number of branches per plant showed highly significant and positive correlation with pods per plant (rg = 0.83* and rp = 0.79*), 100-kernel weight (rg =

0.90** and rp = 0.84**) , dry pod yield per plant (rg = 0.93** and rp = 0.82**), biological yield per plant (rg = 0.91** and rp = 0.77**), harvest index (rg = 0.96** and rp = 0.62**), oil content (rg = 0.88** and rp = 0.83**) and protein content (rg = 0.99** and rp = 0.87**) at both genotypic and phenotypic level.

4.3.3 Pods per Plant

Pods per plant depicted highy positive and significantly correlation at genotypic and phenotypic levels with number of branches per plant (rg = 0.83* and rp = 0.79*), 100-kernel weight (rg = 0.97** and rp = 0.86**), dry pod yield per plant (rg = 0.96** and rp = 0.85**), biological yield per plant (rg = 0.90** and rp = 0.74**), harvest index (rg = 0.92** and rp = 0.68**), oil content (rg = 0.90** and rp = 0.82**) and protein content (rg = 0.94** and rp = 0.80**) while negative and significantly correlated at genotypic and phenotypic levels with kernels per pod (rg = -0.44** and rp = -0.39**).

4.3.4 100-kernels Weight

100-kernel weight exhibited highly significant and positive correlation with number of branches per plant (rg = 0.90* and rp = 0.84*), pods per plant(rg = 0.97* and rp = 0.86*), dry pod yield per plant (rg = 0.95** and rp = 0.85**), biological yield per plant (rg = 0.90** and rp = 0.75**), harvest index (rg = 0.89** and rp = 0.67**), oil content (rg = 0.92** and rp = 0.85**) and protein content (rg = 0.96** and rp = 0.83**) at both genotypic and phenotypic levels whereas negative and significantly correlated at genotypic and phenotypic levels with kernels per pod (rg = -0.36** and rp = -0.32**).

4.3.5 Kernels per Pod

Kernels per pod showed significant and negative correlation with pods per plant (rg = -0.44** and rp = -0.39**), 100-kernel weight (rg = -0.36** and rp = -0.32**), dry pod yield per plant (rg = -0.41** and rp = -0.34**), biological yield per plant (rg = 0.38** and rp = 0.31**) and significant negative correlation with harvest index (rg = 0.40**) at genotypic level only.

4.3.6 Biological Yield per Plant

Biological yield per plant showed positive and significant correlation with number of branches per plant (rg = 0.91*and rp = 0.97*), pods per plant (rg = 0.90**

and rp = 0.74**), 100-kernel weight (rg = 0.90** and rp = 0.75**), dry pod yield per plant (rg = 0.35** and rp = 0.79**), harvest index (rg = 0.69** and rp = 0.39**), oil content (rg = 0.84** and rp = 0.72**) and protein content (rg = 0.96** and rp = 0.73**) at both genotypic and phenotypic levels while negative and significantly correlated at genotypic and phenotypic levels with kernels per pod (rg = -0.38** and rp = -0.31**).

4.3.7 Harvest Index

Harvest index showed positive and significant correlation with number of branches per plant (rg = 0.96*and rp = 0.62*), pods per plant (rg = 0.92** and rp = 0.68**), 100-kernel weight (rg = 0.89** and rp = 0.67**), dry pod yield per plant (rg = 1.00** and rp = 0.87**), biological yield per plant (rg = 0.69** and rp = 0.39**), oil content (rg = 0.99** and rp = 0.61**) and protein content (rg = 0.73** and rp = 0.68**) at both genotypic and phenotypic levels and negative and significantly correlated at genotypic levels with kernels per pod (rg = -0.40**).

4.3.8 Oil Content

At both genotypic and phenotypic levels, oil content depicted highly significant and positive correlation with number of branches per plant (rg = 0.88*and rp = 0.83*), pods per plant (rg = 0.90** and rp = 0.82**), 100-kernel weight (rg = 0.92** and rp = 0.85**), dry pod yield per plant (rg = 0.89** and rp = 0.78**), biological yield per plant (rg = 0.84** and rp = 0.72**), harvest index (rg = 0.99** and rp = 0.61**) and protein content (rg = 0.56** and rp = 0.86**) at both genotypic and phenotypic levels.

4.3.9 Protein Content

Protein content was highly significant and positively correlated with number of branches per plant (rg = 0.99*and rp = 0.87*), pods per plant (rg = 0.94** and rp = 0.80**), 100-kernel weight (rg = 0.96** and rp = 0.83**), dry pod yield per plant (rg = 0.98** and rp = 0.84**), biological yield per plant (rg = 0.96** and rp = 0.73**), harvest index (rg = 0.73** and rp = 0.68**) and oil content (rg = 0.56** and rp = 0.86**) at both genotypic and phenotypic levels.

4.3.10 Dry Pod Yield per Plant

At both phenotypic and genotypic levels, dry pod yield per plant had highly significant and positive correlation with number of branches per plant (rg = 0.93*and rp = 0.82*), pods per plant (rg = 0.96** and rp = 0.85**), 100-kernel weight (rg = 0.95** and rp = 0.85**), biological yield per plant (rg = 0.35** and rp = 0.79**), harvest index (rg = 1.00** and rp = 0.87**), oil content (rg = 0.89** and rp = 0.78**) and protein content (rg = 0.98** and rp = 0.84**) and negative and significantly correlated at genotypic and phenotypic levels with kernels per pod (rg = -0.41** and rp = -0.34**).

Rao (2016), Singh *et al.* (2017), Kadam *et al*. (2018), Tirkey *et al.* (2018), Godhani *et al.* (2020), Pachauri and Sikarwar (2022), Reddy *et al.* (2023) and Yadav *et al*. (2023) also recorded similar finding.

4.4 PATH COEFFICIENT ANALYSIS

The relationship between yield attributes and their amount of association cannot be understood clearly through correlation studies alone. Path coefficient analysis was suggested by Wright (1921) and later Dewey and Lu (1959) to identify the direct and indirect impacts of traits by dividing the correlation into direct and indirect effects. In the current study, path coefficient analysis for dry pod yield per plant at the genotypic level was done.

4.4.1 Direct Effect

The maximum positive direct effect on dry pod yield per plant was exhibited by pods per plant (0.9136) followed by number of branches per plant (0.6681), protein content (0.3276), days to maturity (0.2375) and sound mature kernel per cent (0.0825). Similar findings were also reported by Babariya and Dobariya (2012), Tirkey *et al*. (2018), Mitra *et al*. (2021) and Shrotri *et al.* (2021).

Maximum negative direct effect on dry pod yield per plant was observed by 100-kernel weight (-0.6062) followed by days to 50 per cent flowering (-0.2721), oil content (-0.2664), plant height (-0.0765), shelling percentage (-0.0467) and kernels per pod (-0.0057). Similar findings were also reported by Patel *et al.* (2021) and Kannappan *et al*. (2022).

4.4.2 Indirect Effect

The indirect effect on dry pod yield per plant was analysed at genotypic level via different characters are presented in Table 4.4.

4.4.2.1 Positive Indirect Effect

The maximum positive indirect effect was noted by 100-kernel weight through pods per plant (0.8887) followed by protein content via pods per plant (0.8599), oil content through pods per plant (0.8235), number of branches per plant through pods per plant (0.7610) and protein content via number of branches per plant (0.6605).

Present findings are in accordance with the findings of Singh *et al*. (2017) and Tirkey *et al.* (2018).

4.4.2.2 Negative Indirect Effect

The high negative indirect effect was noted by pods per plant through 100-kernel weight (-0.5896) followed by protein content through 100-kernel weight (-0.5796), oil content through 100-kernel weight (-0.5604) and number of branches per plant through 100-kernel weight (-0.5466). Present findings are in accordance with the findings of Bodke *et al*. (2020) and Mitra *et al*. (2021)

Path coefficient analysis for dry pod yield per plant analysed for 11 traits at genotypic level out of them here only six traits are explained which showed significant correlation to dry pod yield per plant. Five traits *viz*., number of branches per plant, pods per plant, 100-kernel weight, oil content and protein content showed positive and significant correlation coefficients with dry pod yield per plant while kernels per pod showed significant and negative correlation with dry pod yield per plant.

Present findings are in accordance with Babariya and Dobariya (2012), Kamdi *et al.* (2017), Rao and Venkanna (2019), Patel *et al*. (2021), Shrotri *et al.* (2021), Sudhishna *et al*. (2021), Reddy *et al.* (2023), Yadav *et al.* (2023).

4.4.3 Number of Branches per Plant

Correlation between dry pod yield per plant and number of branches per plant was significant and positive, while it exerts positive direct effect (0.6681) on dry pod yield per plant. Positive indirect effect was shown by days to 50 per cent flowering (-

0.0200), pods per plant (0.5565), 100-kernels weight (0.6024), sound mature kernel per cent (0.0289), oil content (0.5902) and protein content (0.6605). Whereas negative indirect effect via days to maturity (-0.1246), plant height (-0.0149), shelling per cent (-0.0324), kernels per pod (-0.1936).

4.4.4 Pods per Plant

Correlation between dry pod yield per plant and pods per plant was highly significant and positive while it exhibits positive direct effect (0.9136) on dry pod yield per plant. Pods per plant show positive indirect effect on dry pod yield per plant through days to maturity (0.0195), number of branches per plant (0.7610), 100-kernels weight (0.8887), oil content (0.8235) and protein content (0.8599) whereas negative indirect effect via days to 50 per cent flowering (-0.0109), plant height (-0.0376), shelling per cent (-0.0970), kernels per pod (-0.3979) and sound mature kernel per cent (-0.0626).

4.4.5 100-Kernels Weight

Positive and highly significant correlation exist between dry pod yield and 100-kernel weight while it exerts negative direct effect (-0.6062) on dry pod yield per plant. 100-kernel weight shows positive indirect effect on dry pod yield per plant through days to 50 per cent flowering (0.0178), days to maturity (0.0295), plant height (0.0293), shelling % (0.0509), kernels per pod (0.2167), sound mature kernel % (0.0379) while negative indirect effect through number of branches per plant (-0.5466), pods per plant (-0.5896) and oil content (-0.5604) and protein content (-0.5796).

4.4.6 Kernels per Pod

Negative and significant correlation was found between dry pod yield per plant and kernels per pod while negative direct effect (-0.0057) of kernel per pod on dry pod yield per plant was noticed. Kernel per pod shows positive indirect effect on dry pod yield per plant through days to 50 per cent flowering (0.0003), days to maturity (0.0014), plant height (0.0018), number of branches per plant (0.0016), pods per plant (0.0025), shelling % (0.0015), 100-kernels weight (0.0020), oil content (0.0015) and protein content (0.0016) while negative indirect effect through sound mature kernel % (-0.0004).

4.4.7 Oil Content

Positive and highly significant correlation was recorded between dry pod yield per plant and oil content and shows negative direct effect (-0.2664) on dry pod yield per plant. Oil content exhibits positive indirect effect on dry pod yield per plant via days to maturity (0.0129), plant height (0.0168), shelling % (0.0146), kernels per pod (0.0682) and sound mature kernel % (0.0176) whereas negative indirect effect via days to 50 per cent flowering (-0.0145), number of branches per plant (-0.2353), pods per plant (-0.2401), 100-kernels weight (-0.2463) and protein content (-0.2687).

4.4.8 Protein Content

Correlation between dry pod yield per plant and protein content was observed positive and significant while it exhibits positive direct effect (0.3276) on dry pod yield per plant. Protein content exhibits positive indirect effect on dry pod yield per plant through days to 50 per cent flowering (0.0022), number of branches per plant (0.3239), pods per plant (0.3084), 100-kernels weight (0.3133) and oil content (0.3306) whereas negative indirect effect through days to maturity (-0.0380), plant height (-0.0407), shelling per cent (-0.0425), kernels per pod (-0.0913) and sound mature kernel per cent (-0.0110).

Residual Effect

The residual effect on dry pod yield per plant was high (0.7198), indicated that 28.02 per cent was controlled by the characters under investigation.

Table 4.2: Genetic variability parameters for yield and its contributing traits in groundnut

Characters	Range	Mean	GCV (%)	PCV (%)	h^2 (%)	GA	GG (%)
Days to 50% flowering	30.13-35.69	33.01	4.84	5.42	79.76	2.94	8.91
Days to maturity	100.68-105.90	103.21	1.51	1.61	87.63	3.00	2.91
Plant height	40.80-46.02	43.06	3.14	3.48	81.54	2.52	5.84
No. of branches per plant	5.25-11.70	8.07	21.82	22.39	94.91	3.53	43.78
Pods per plant	9.55-23.65	15.75	24.03	25.48	88.95	7.35	46.69
Shelling per cent	65.23-74.65	71.05	2.92	3.31	77.56	3.76	5.29
100-Kernel weight	38.23-47.26	42.36	5.50	5.70	93.26	4.63	10.94
Kernels per pod	1.30-3.23	2.28	23.38	25.30	85.35	1.02	44.49
Sound mature kernel	82.41-92.80	88.91	2.91	3.06	90.63	5.07	5.71
Dry pod yield per plant	7.45-18.13	11.82	26.43	28.77	84.40	5.91	50.03
Biological yield per plant	21.83-35.61	28.30	13.48	15.61	74.50	6.78	23.96
Harvest index	27.13-52.79	41.32	12.83	18.86	46.23	7.42	17.96
Oil content	40.24-47.01	43.97	3.85	4.04	90.83	3.33	7.57
Protein content	20.14-23.93	22.08	5.00	5.54	81.45	2.05	9.30

Table 4.3: Estimation of genotypic (rg) and phenotypic (rp) correlation coefficient for different characters in groundnut

S. No.	Character		Days to 50% flowering	Days to maturity	Plant height	No. of branches per plant	Pods per plant	Shelling per cent	100-kernel weight	Kernels per pod	Sound mature kernel	Biological yield per plant	Harvest index	Oil content	Protein content	Dry pod yield per plant
1.	Days to 50% flowering	rg		0.89**	-0.11	0.03	-0.01	-0.30	-0.03	-0.05	0.20	0.07	-0.08	0.05	0.01	-0.01
		rp		0.76**	-0.06	0.03	0.01	-0.22	-0.01	-0.03	0.19	0.06	-0.04	0.03	0.05	0.00
2.	Days to maturity	rg			-0.04	-0.19	0.02	-0.20	-0.05	-0.25	0.19	-0.06	-0.11	-0.05	-0.12	-0.08
		rp			-0.03	-0.16	0.03	-0.17	-0.03	-0.22	0.14	-0.06	-0.06	-0.06	-0.15	-0.06
3.	Plant height	rg				-0.02	-0.04	0.28	-0.05	-0.32	0.04	-0.08	-0.17	-0.06	-0.12	-0.11
		rp				-0.02	-0.03	0.23	-0.04	-0.27	0.04	-0.07	-0.08	-0.05	-0.09	-0.09
4.	No. of branches per plant	rg					0.83**	-0.05	0.90**	-0.29	0.04	0.91**	0.96**	0.88**	0.99**	0.93**
		rp					0.79**	-0.03	0.84**	-0.25	0.05	0.77**	0.62**	0.83**	0.87**	0.82**
5.	Pods per plant	rg						-0.11	0.97**	-0.44**	-0.07	0.90**	0.92**	0.90**	0.94**	0.96**
		rp						-0.05	0.86**	-0.39**	-0.04	0.74**	0.68**	0.82**	0.80**	0.85**
6.	Shelling per cent	rg							-0.08	-0.27	0.15	-0.14	-0.17	-0.05	-0.13	-0.13
		rp							-0.05	-0.22	0.10	-0.15	-0.05	-0.05	-0.09	-0.09
7.	100-kernel weight	rg								-0.36*	-0.06	0.90**	0.89**	0.92**	0.96**	0.95**
		rp								-0.32*	-0.07	0.75**	0.67**	0.85**	0.83**	0.85**
8.	Kernels per pod	rg									0.07	-0.38*	-0.40*	-0.26	-0.28	-0.41*
		rp									0.08	-0.31*	-0.24	-0.25	-0.20	-0.34*
9.	Sound mature kernel	rg										0.01	0.09	-0.07	-0.03	0.07
		rp										0.04	0.02	-0.04	-0.01	0.05
10.	Biological yield per plant	rg											0.69**	0.84**	0.96**	0.79**
		rp											0.39**	0.72**	0.73**	0.35**
11.	Harvest index	rg												0.99**	0.73**	0.87**
		rp												0.61**	0.68**	1.00**
12.	Oil content	rg													0.56**	0.89**
		rp													0.86**	0.78**
13.	Protein content	rg														0.98**
		rp														0.84**
14.	Dry pod yield per plant	rg														
		rp														

*,** Significant at 5% and 1% respectively.

Table 4.4: Genotypic path analysis for dry pod yield per plant in groundnut

S No.	Character	Days to 50% flowering	Days to maturity	Plant height	No. of branches per plant	Pods per plant	Shelling per cent	100-Kernel weight	Kernels per pod	Sound mature kernel	Oil content	Protein content	r with dry pod yield
1.	Days to 50% flowering	**-0.2721**	0.2121	0.0082	0.0200	-0.0109	0.0140	0.0178	0.0003	0.0167	-0.0145	0.0022	-0.0063
2.	Days to maturity	-0.2431	**0.2375**	0.0034	-0.1246	0.0195	0.0094	0.0295	0.0014	0.0157	0.0129	-0.0380	-0.0764
3.	Plant height	0.0291	-0.0106	**-0.0765**	-0.0149	-0.0376	-0.0130	0.0293	0.0018	0.0035	0.0168	-0.0407	-0.1129
4.	No. of branches per plant	-0.0081	-0.0443	0.0017	**0.6681**	0.7610	0.0023	-0.5466	0.0016	0.0036	-0.2353	0.3239	0.9280**
5.	Pods per plant	0.0033	0.0051	0.0032	0.5565	**0.9136**	0.0050	-0.5896	0.0025	-0.0057	-0.2401	0.3084	0.9620**
6.	Shelling per cent	0.0816	-0.0477	-0.0213	-0.0324	-0.0970	**-0.0467**	0.0509	0.0015	0.0124	0.0146	-0.0425	-0.1265
7.	100-Kernel weight	0.0080	-0.0116	0.0037	0.6024	0.8887	0.0039	**-0.6062**	0.0020	-0.0052	-0.2463	0.3133	0.9528**
8.	Kernels per pod	0.0140	-0.0600	0.0246	-0.1936	-0.3979	0.0127	0.2167	**-0.0057**	0.0054	0.0682	-0.0913	-0.4067*
9.	Sound mature kernel	-0.0550	0.0451	-0.0032	0.0289	-0.0626	-0.0070	0.0379	-0.0004	**0.0825**	0.0176	-0.0110	0.0728
10.	Oil content	-0.0148	-0.0115	0.0048	0.5902	0.8235	0.0026	-0.5604	0.0015	-0.0054	**-0.2664**	0.3306	0.8945**
11.	Protein content	-0.0018	-0.0276	0.0095	0.6605	0.8599	0.0061	-0.5796	0.0016	-0.0028	-0.2687	**0.3276**	0.9847**

Residual = 0.7198

*, ** Significant correlation with dependent char at 5% and 1% respectively.

5. SUMMARY AND CONCLUSION

The present investigation entitled " **Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)**" was carried out to estimate genetic variability parameters, heritability, genetic advance, correlation and path analysis for yield and it's contributing traits.

There were 30 genotypes in the experimental study, including 3 checks. In *Kharif* 2023 the groundnut genotypes were evaluated at the Instructional Farm of the College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan), using a randomized block design with three replications.

On five competitive plants, observations were taken regarding the number of branches per plant, plant height, pods per plant, shelling percentage (%), 100-kernels weight (g), sound mature kernel (%), dry pod yield per plant (g), biological yield per plant (g), harvest index (%), oil content (%) and protein content (%) whereas observations for kernels per pod were taken from five randomly selected pods from each of the five randomly selected plants and plot-based observations for days to 50 per cent flowering and days to maturity were taken.

The present study revealed the following important results:

- The findings of the analysis of variance revealed that the mean sum of squares resulting from genotypes were highly significant for each character, indicating a substantial amount of variability for every character and consequently, an excellent opportunity for precise phenotype-based selection.
- Genotypes varied greatly for a number of characteristics, including days to 50 per cent flowering, days to maturity, number of branches per plant, plant height, pods per plant, shelling percentage, 100-kernels weight, kernels per pod, sound mature kernel, dry pod yield per plant, biological yield per plant, harvest index, oil content and protein content.
- The magnitude of PCV in the investigation was higher than the magnitude of GCV for all characters. GCV pointing out the environment had minor effect on the expression of the different traits. GCV was found higher for the

character *viz.*, dry pod yield per plant, pods per plant, kernels per pod and number of branches per plant.

- The values of PCV was found to be high for the characters *viz*., dry pod yield per plant, pods per plant, kernels per pod and number of branches per plant.
- All the characters under investigation showed high levels of heritability, except for harvest index, which had moderate broad sense heritability values. The highest value of heritability was recorded for number of branches per plant followed by 100-kernel weight, oil content, sound mature kernel, pods per plant, days to maturity, kernels per pod, dry pod yield per plant, plant height.
- Genetic gain was highest for dry pod yield per plant followed by number of pods per plant, kernels per pod, number of branches per plant, biological yield per plant, harvest index and 100-kernel weight. In general, moderate to high heritability and moderate to high genetic gain suggested additive gene action and the potential for these qualities to be improved by selection. Number of branches per plant, pods per plant, kernels per pod, dry pod yield per plant and biological yield per plant exhibited high values for them thereby selection for these characters could be effective.
- Typically, the genotypic correlation estimates were greater or at par with the corresponding phenotypic correlation coefficient. At both the genotypic and phenotypic levels, there was a positive and significant association between the dry pod yield per plant and the number of branches per plant, number of pods per plant, 100-kernel weight, biological yield per plant, harvest index, oil content and protein content whereas negative significant correlation between dry pod yield per plant and kernels per pod.
- The path analysis showed that the number of pods per plant had the highest direct positive effect on dry pod yield per plant, followed by number of branches per plant , protein content, days to maturity, sound mature kernel per cent whereas 100-kernel weight had the highest direct negative impact on dry pod yield per plant followed by days to 50 per cent flowering, oil content, plant height, shelling percentage and kernels per pod. The highest positive

direct effect between the number of pods per plant and dry pod yield per plant was seen across all the parameters.

- The path analysis analysed at genotypic level for 11 traits out of which 5 traits *viz*., number of branches per plant, pods per plant, 100-kernel weight, oil content and protein content show significant and positive correlation with dry pod yield per plant while kernels per pod show significant and negative correlation with dry pod yield per plant.

According to the analysis of the experiment, the test genotypes UG- 5,UG-7, UG-12 and UG-23 were superior in terms of yield and desired yield component characters like number of branches per plant, pods per plant, 100-kernel weight and dry pod yield per plant. As a result, these genotypes appear to be promising and might be employed in groundnut breeding programmes in the future.

LITERATURE CITED

Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. 1958. Genotypic and environmental variances and covariance in an upland cotton cross of interspecific origin. *Agronomy Journal,* **50**: 632-636.

Anonymous 2023, Second advance estimates of production. Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare.

Babariya, C. A. and Dobariya, K.L. 2012. Correlation coefficient and path coefficient analysis for yield components in groundnut (*Arachis hypogaea* L.). *Electronic Journal of plant breeding*, **3**: 932-938.

Bhargavi, G., Rao, V. S. and Babu, D. R. 2017. Studies on variability, heritability and genetic advance as per cent of mean in Spanish bunch groundnut genotypes (*Arachis hypogaea* L.). *Legume Research-An International Journal*, **40**: 773-777.

Bodke, C. S., Dahat, D. V. and Deshmukh, M. P. 2020. Correlation and Path Analysis in Groundnut (*Arachis hypogaea* L.) Under Stress Condition. *Journal of Agriculture Research and Technology*, **45**: 162.

Burton, G. W. 1952. Quantitative inheritance in grasses. Proc. 6. *International Grassland Congress*, **1**: 277-283.

Burton, G.W. and De-Vane, E.M. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**: 478481.

Dewangan, H., Jaiswal, N. K., Gabrilal, M. L. and Rai, P.K. 2015. Study on genetic variability in groundnut (*Arachis hypogaea* L.) germplasm. *International Journal of Agricultural science and Research*, **5**: 2250-0057.

Desmae, H., Janila, P., Okori, P., Pandey, M. K., Motagi, B. N., Monyo, E. and Varshney, R. K. 2019. Genetics, genomics and breeding of groundnut (*Arachis hypogaea* L.). *Plant Breeding*, **138**: 425-444.

Dewey, D.R. and Lu, K.H. 1959. A Correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**: 515-518.

Fisher, R.A. 1918. The correlation amount relatives on the supposition of Mendelian Inheritance. *Trance Royal Society*, *Edinburg*, **52**: 399-433.

Fisher, R.A. and Yates, F. 1938. Statistical tables for biological agricultural and medical research, Oliver and Boyd, Edinburgh, 6th ed. pp. 63.

Galton, F. 1889. Natural Inheritance. McMillan, London.

Godhani, P. P., Jivani, L. L., Patel, B. M. and Raval, L. J. 2020. Character association and path coefficient analysis studies for quantitative traits in F_3 generation of groundnut (*Arachis hypogaea* L.). *Indian Journal of Pure and Applied Biosciences*, **8**: 190-199.

Hampannavar, M. R., Khan, H., Temburne, B. V., Janila, P., and Amaregouda, A. 2018. Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*, **7**: 870-874.

Hanson, G.H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies in segregating population of Korean lespedeza. *Agronomy Journal,* **48**: 268-272.

John. K., Vasanthi, R.P., Sireesha, K. and Giridhara, K.T. 2013. Genetic variability studies in different advanced breeding genotype of Spanish bunch groundnut (*Arachis* hypogaea L.). *Inter. J. Applied Bio. Pharma.Tech*.,**4**:55-60.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and Environmental variability in Soybeans, *Agronomy Journal,* **47**: 314-318.

Kadam, V. K., Chavan, B. H., Deshmukh, M. P. and Mali, A. R. 2018. Study on character association and path analysis in summer groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*, **7**: 3654-3657.

Kamdi, S. R., Patil, S. R., Kadu, P. R., Bhasme, S. P. and Kothikar, R. B. 2017. Genetic variability, correlation and path analysis in groundnut. *BIOINFOLET-A Quarterly Journal of Life Sciences*, **14**: 36-39.

Kannappan, P. A., Viswanathan, P. L., Manivannan, N. and Rajendran, L. 2022. Variability, correlation and path analyse in segregating population of

groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **13**: 1099-1104.

Khaniya, J., Talpada, M. M., Sapovadiya, M. H., Kulkarni, G. U. and Mehta, D. R. 2023. Spectrum of genetic variability, correlation and path analysis for yield and yield contributing traits in bunch groundnut (*Arachis hypogaea* L.). *The Pharma Innovation Journal*, **12**: 2850-2854.

Kumar, N., Ajay, B. C., Rathanakumar, A. L., Radhakrishnan, T., Mahatma, M. K., Kona, P. and Chikani, B. M. 2019. Assessment of genetic variability for yield and quality traits in groundnut genotypes. *Electronic Journal of Plant Breeding*, **10**: 196-206.

Larik, A. S., Malik, S. I., Kakar, A. A. and Naz, M. A. 2000. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. *Scientific Khyber*., **13**: 39-44.

Memon, J. T., Kachhadia, V. H., Dedaniya, A. P. and Patel, R. 2019. Character association and path coefficient analysis in F2 generation of groundnut (*Arachis hypogaea* L.). *International Journal of Chemical Studies*, **7**: 1329-1334.

Mitra, M., Gantait, S. and Kundu, R. 2021. Genetic variability, character association and genetic divergence in groundnut (*Arachis hypogaea* L.) accessions. *Legume Research-An International Journal*, **44**: 164-169.

Mohapatra, N. and Khan, H. 2020. Character association and path analysis in F3 segregating generations for yield and its component traits in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**: 794-799.

Pachauri, P. and Sikarwar, R.S. 2022. Correlation and path analysis of different environments for yield and component traits in groundnut (*Arachis hypogaea* L.). *The Pharma Innovation Journal*, **11**: 1181-1186.

Padmaja, D., Eswari, K. B., Rao, B. M. V. and Prasad, S. G. 2015. Genetic variability studies in F_2 population of groundnut (*Arachis hypogaea* L.). *Helix*, **2**: 668-672.

Pandey, M.K., Monyo, E., Ozias-Akins, P., Liang, X., Guimarães, P., Nigam, S.N., Upadhyaya, H.D., Janila, P., Zhang, X. and Guo, B., 2012. Advances in Arachis genomics for peanut improvement. Biotechnology Advances, **30**: 639-651.

Pandey, M.K. and Varshney, R.K., 2018. Groundnut entered post-genome sequencing era: opportunities and challenges in translating genomic information from genome to field. In: *Biotechnologies of Crop Improvement*, **3**: 199-209.

Panse, V. G. and Sukhatme, P. V. 1985. Statistical Methods for Agricultural Workers, ICAR New Delhi.

Patel, C. K., Vachhani, J. H., Kachadiya, V. H., Nayak, J. J. and Jalu, R. K. 2021. Studies on correlation and path analysis for important traits in F2 generations of groundnut (*Arachis hypogaea* L.). *International Journal of Plant Pathology and Microbiology*, **1**: 01-06.

Patil, A. S., Punewar, A. A., Nandanwar, H. R. and Shah, K. P. 2014. Estimation of variability parameters for yield and its component traits in groundnut (*Arachis hypogaea* L.). *The Bioscan*, **9**: 749-754.

Rajarathinam, P., Narayana, M., Alagirisamy, M. and Moshin, I. S. 2017. Variability, Correlation and Path Coefficient Analysis in Groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **5**: 824-827.

Rao, V. T., Venkanna, V., Bhadru, D. and Bharathi, D. 2014. Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *International Journal of Pure and Applied Bioscience*, **2**: 194-197.

Rao, V. T. 2016. Genetic variability, correlation and path coefficient analysis under drought in groundnut (*Arachis hypogaea* L). *Legume Research-An International Journal*, **39**: 319-322.

Rao, V. T. and Venkanna, V. 2019. Studies on character association and path analysis in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*, **8**: 76-78.

Reddy, P., Sabara, P., Padhiyar, S. M., Kulkarni, G. U., Sapara, G. K. and Tomar, R. S. 2023. Correlation and path analysis among agro-morphological traits in groundnut (*Arachis hypogaea* L.). *Annals of Arid Zone*, **62**: 227-234.

Roy, A., Lal Ahmed, M., Amaravathi, Y., Viswanath, K., Babu, J. D. P. and Sreekanth, B. 2018. Genetic Variability, Heritability and Genetic Advance of yield and yield attributes in Groundnut (*Arachis hypogaea* L.). *The Andhra Agric. J*, **65**: 88-91.

Sab, S., Shanthala, J., Savithramma, D. L. and Bhavya, M. R. 2018. Study of genetic variability and character association for water use efficiency (WUE) and yield related traits advance breeding lines of groundnut (*Arachis hypogaea* L.). *Int. J. Curr. Microbiol. App. Sci*, **7**: 3149-3157.

Shrotri, S. M., Dhuppe, M. V., Gavade, S. S. and Sargar, P. R. 2021. Character association and path analysis for yield and yield contributing traits and in Groundnut (*Arachis hypogaea* L.). *The Pharma Innovation Journal*, **10**: 979-981.

Singh, R.K. and Chaudhary, B.D. 1985. Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers, New Delhi.

Singh, P. B., Bharti, B., Kumar, A., Singh, R., Kumar, N. and Rathnakumar, A. L. 2017. Genetic characterization, character association for yield and yield component traits in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **8**: 1229-1235.

Sridevi, S., Meenakumari, B., Manivannan, N. and Ravichandran, V. 2022. Assessment of genetic variability, character association and path analysis of kernel yield and yield components in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **13**: 476-481.

Sudhishna, E., Naik, K. S. S., Srinivas, T. and Ramesh, D. 2021. Studies on Character Association and Path Analysis in Groundnut. *The Andhra Agricultural Journal*, **68**: 182-188.

Tirkey, S. K., Ahmad, E. and Mahto, C. S. 2018. Genetic variability and character association for yield and related attributes in groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry*, **7**: 2487-2489.

Venkataravana, P., Pushpa, H. D., Priyadarshini, S. K. and Dudagi, S. V. 2020. Genetic variability, correlation and path analysis studies in segregating generation of three crosses for pod yield and its attributing characters in

groundnut (*Arachis hypogaea* L.). *Journal of Pharmacognosy and Phytochemistry,* **9**: 771-776.

Vinithashri, G., Manivannan, N., Viswanathan, P. L. and Selvakumar, T. 2019. Genetic variability, heritability and genetic advance of yield and related traits in F_3 generation of groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **10**: 1292-1297.

Wright, S. 1921. Correlation and Causation. *Journal of Agricultural Research*, **20**: 555-586.

Yadav, G. L., Rajput, S. S., Gothwal, D. K. and Jakhar, M. L. 2023. Genetic variability, character association and path analysis for pod yield and its component characters in groundnut [*Arachis hypogaea* L.]. *Legume Research-An International Journal*, **46**: 678-683.

Zongo, A., Nana, A. T., Sawadogo, M., Konate, A. K., Sankara, P., Ntare, B. R. and Desmae, H. 2017. Variability and correlations among groundnut populations for early leaf spot, pod yield, and agronomic traits. *Agronomy*, **7**: 52

Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)

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ABSTRACT

In the present study entitled **"Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)"** was conducted during *Kharif* 2023 at Instructional Farm College of Technology and Engineering, MPUAT, Udaipur. The experimental material consisted of 30 genotypes including 3 checks, evaluated under Randomized Block Design with three replication. Two rows per genotype were sown in a plot of 5.0 m x 0.60 m with inter and intra row spacing 30 x 10 cm.

The observations were recorded on five randomly selected competitive plants for characters, *viz.,* number of branches per plant, plant height(cm), pods per plant, shelling percentage (%), 100-kernels weight (g), sound mature kernel (%), dry pod yield per plant (g), biological yield per plant (g), harvest index (%), oil content (%) and protein content (%) whereas the observation for days to 50 per cent flowering and days to maturity was taken on whole plot basis.

The mean sum of square due to genotypes was found significant for all of the characters under this investigation showing that there is enough variability among genotypes for different traits.

The estimates of Phenotypic Coefficient of Variation (PCV) were a little higher than their corresponding Genotypic Coefficient of Variation (GCV) pointing out that the environment had minor effect on the expression of the different traits.

The characters had high heritability along with high genetic gain were number of branches per plant, pods per plant, kernels per pod, dry pod yield per plant and biological yield per plant. Thus, selection for these traits will be effective.

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Association study revealed that the dry pod yield per plant had a positive and significant correlation with the number of branches per plant, number of pods per plant, 100-kernel weight, biological yield per plant, harvest index, oil content and protein content at both genotypic and phenotypic level.

The path coefficient analysis showed that the maximum positive direct effect on dry pod yield per plant was exerted by pods per plant, followed by number of branches per plant , protein content, days to maturity, sound mature kernel per cent. So these characters can be considered as selection criteria in improving the grain yield.

Thus, the test genotypes UG- 5, UG-7, UG-12 and UG-23 were superior in terms of yield and desired yield component characters like number of branches per plant, pods per plant, 100-kernel weight and dry pod yield per plant. As a result, these genotypes appear to be promising and might be employed in groundnut breeding programmes in the future.

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वर्तमान अध्ययन में ''स्पेनिश गुच्छा मूंगफली (एरेकिस हाइपोजिया एल.) में विविधता और पथ विश्लेषण'' शीर्षक से इंस्ट्रक्शनल फार्म कॉलेज ऑफ टेक्नोलॉजी एंड इंजीनियरिंग, एमपीयूएटी, उदयपुर में खरीफ 2023 के दौरान किया गया था। प्रायोगिक सामग्री में 3 चेक सहित 30 जीनोटाइप शामिल थे, जिनका मूल्यांकन तीन प्रतिकृति के साथ यादृच्छिक ब्लॉक डिजाइन के तहत किया गया था। प्रति जीनोटाइप दो पंक्तियों को 5.0 मीटर x 0.60 मीटर के प्लॉट में इंटर और इंट्रा पंक्ति की दूरी 30 x 10 सेमी के साथ बोया गया था।

लक्षणों के लिए पाँच यादृच्छिक रूप से चयनित प्रतिस्पर्धी पौधों पर अवलोकन दर्ज किए गए, जैसे, प्रति पौधा शाखाओं की संख्या, पौधे की ऊँचाई, प्रति पौधा फलियाँ, छिलका प्रतिशत (%), 100–कर्नेल वजन (ग्राम), ध्वनि परिपक्व गिरी (%), प्रति पौधा सूखी फली उपज (ग्राम), प्रति पौधा जैविक उपज (ग्राम), फसल सूचकांक (%), तेल सामग्री (%) और प्रोटीन सामग्री (%) जबकि पांच बेतरतीब ढंग से चुने गए पौधों और 50 प्रतिशत फूल आने के दिनों और परिपक्वता के दिनों का प्लॉट–आधारित अवलोकन किया गया।

इस जांच के तहत सभी लक्षणों के लिए जीनोटाइप के कारण वर्ग का औसत योग महत्वपूर्ण पाया गया, जिससे पता चला कि विभिन्न लक्षणों के लिए जीनोटाइप के बीच पर्याप्त परिवर्तनशीलता है।

फेनोटाइपिक वेरिएशन गुणांक (पीसीवी) का अनुमान उनके संबंधित जीनोटाइपिक वेरिएशन गुणांक (जीसीवी) से थोड़ा अधिक था, जो दर्शाता है कि विभिन्न लक्षणों की अभिव्यक्ति पर पर्यावरण का मामूली प्रभाव था।

उच्च आनुवांशिक लाभ के साथ–साथ उच्च आनुवंशिकता वाले लक्षण थे, प्रति पौधा शाखाओं की संख्या, प्रति पौधा फली, प्रति फली गुठली, प्रति पौधा सूखी फली की उपज और प्रति पौधा जैविक उपज। इस प्रकार, इन लक्षणों का चयन प्रभावी होगा।

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* स्नातकोत्तर छात्रा, आनुवंशिकी एवं पादप प्रजनन विभाग, राजस्थान कृषि महाविद्यालय, एमपीयूएटी, उदयपुर

** सहायक आचार्यए आनुवंशिकी एवं पादप प्रजनन विभाग, राजस्थान कृषि महाविद्यालय, एमपीयूएटी, उदयपुर

एसोसिएशन के अध्ययन से पता चला कि प्रति पौधा सूखी फली की उपज का प्रति पौधा शाखाओं की संख्या, प्रति पौधा फली की संख्या, 100–कर्नेल वजन, प्रति पौधा जैविक उपज, फसल सूचकांक, तेल सामग्री और दोनों में प्रोटीन सामग्री के साथ सकारात्मक और महत्वपूर्ण संबंध था।

पथ गुणांक विश्लेषण से पता चला कि प्रति पौधा सूखी फली की उपज पर अधिकतम सकारात्मक प्रत्यक्ष प्रभाव प्रति पौधा फली द्वारा डाला गया था, इसके बाद प्रति पौधा शाखाओं की संख्या, प्रोटीन सामग्री, परिपक्वता के दिन, ध्वनि परिपक्व गिरी प्रतिशत। इसलिए इन लक्षणों को अनाज की उपज में सुधार के लिए चयन मानदंड माना जा सकता है।

इस प्रकार, परीक्षण जीनोटाइप यूजी–5, यूजी–7, यूजी–12 और यूजी–23 उपज और वांछित उपज घटक विशेषताओं जैसे प्रति पौधा शाखाओं की संख्या, प्रति पौधा फली, 100–कर्नेल वजन और सूखी फली उपज के मामले में बेहतर थे। प्रति पौधा. परिणामस्वरूप, ये जीनोटाइप आशाजनक प्रतीत होते हैं और भविष्य में मूंगफली प्रजनन कार्यक्रमों में नियोजित किए जा सकते हैं।

APPENDIX-I

Mean weekly meteorological parameters during the crop growth period for *Kharif*, 2023

Standard week	Time Period	Temperature (^{0}C)		Relative Humidity		Sun-shine	Rain-fall	Evapo-ration
		Max.	Min	Max.	Min.			
19	7 May-13 May	40.0	19.7	72.4	53.1	9.9	1.6	10.8
20	14 May-20 May	39.4	23.0	52.0	28.7	10.5	0.0	13.0
21	21 May-27 May	38.7	23.0	51.7	28.7	10.4	0.0	14.3
22	28 May-3 June	35.6	22.2	62.9	41.4	8.6	15.2	10.7
23	4 June-10 June	38.0	22.1	68.3	35.3	9.5	13.0	12.9
24	11 June-17 June	36.4	24.2	71.7	48.4	8.0	44.6	11.9
25	18 June-24 June	30.9	23.6	76.9	62.1	3.4	57.8	5.8
26	25 June-1 July	32.2	22.9	83.6	82.9	2.1	107.7	4.2
27	2 July-8 July	34.2	23.4	84.6	61.9	5.4	50.8	4.0
28	9 July-15 July	32.3	23.9	81.9	72.1	3.4	44.6	4.8
29	16 July-22 July	33.2	23.9	82.3	79.0	3.0	38.6	3.1
30	23 July- 29 July	32.1	23.4	89.1	75.1	2.0	77.4	2.4
31	30 July-5 Aug	30.9	22.7	85.6	70.3	3.1	30.8	4.1
32	6 Aug-12 Aug	31.1	22.4	85.3	82.7	3.8	0.0	4.3
33	13 Aug-19 Aug	32.0	22.3	81.9	68.1	5.8	0.0	5.8
34	20 Aug-26 Aug	31.1	22.4	81.1	61.9	3.1	50.4	3.6
35	27 Aug-2 Sep	31.8	21.3	78.9	51.6	6.2	0.0	5.7
36	3 Sep-9 Sep	33.5	21.6	76.4	54.0	7.1	15.0	7.3
37	10 Sep-16 Sep	32.0	22.9	78.1	65.6	3.4	10.0	4.2
38	17 Sep- 23 Sep	29.2	21.6	89.0	76.6	6.6	56.4	2.3
39	24 Sep-30 Sep	33.3	21.1	85.3	54.0	3.9	19.2	3.1
40	1 Oct-7 Oct	34.4	16.3	73.1	37.1	8.2	0.0	3.3
41	8 Oct-14 Oct	33.6	16.2	68.4	34.7	8.1	0.0	3.3
42	15 Oct-21 Oct	32.6	16.5	72.4	34.6	8.0	0.0	3.0
43	22 Oct-28 Oct	32.3	14.1	62.6	26.4	7.7	0.2	2.9
44	29 Oct-4 Nov	32.4	14.5	67.9	26.3	8.3	0.0	3.1
45	5 Nov-11 Nov	32.4	14.3	68.7	29.1	6.3	0.0	2.2
46	12 Nov-18 Nov	28.8	10.7	66.1	37.4	6.2	0.0	2.4
47	19 Nov-25 Nov	28.6	10.5	68.3	35.3	8.3	0.0	3.0
48	26 Nov-2 Dec	22.6	11.6	85.7	71.1	2.9	35.8	2.0

APPENDIX-II

Estimation of seed oil content (Soxhlet's Ether Extraction Method A.O.A.C., 1984).

1. Grind 500 mg of pre dried seed material and transfer it in thimble, plug the mouth of the thimble with tallow free absorbent cotton.
2. Take the clean, dry receiver flask from the soxhlet assembly and weight it accurately.
3. Introduce the thimbles with sample into the soxhlet.
4. Assemble the apparatus and fill soxhlet with petroleum ether (boiling point 40-60°C) by pouring it through the condenser at the top. The amount of solvent is taken about 1.5 times the capacity of the soxhlet.
5. Place the apparatus on a water bath at 60°C and start cold water circulation in the condenser.
6. Extract for 8 hours.
7. After extraction is over, remove the thimble with the material from soxhlet.
8. Assemble the apparatus again and heat it on water bath to recover all the ether from the receiver flask. The flask now contains only the crude fat.
9. Disconnect the receiver flask, wipe the outside of the flask thoroughly with a clean dry cloth to remove the film of moisture and dust and dry it in a hot air oven at 100°C for 1 hour.
10. Cool in a desicator and weight (W1)

    Per cent oil content (%) is determined by the following formula:

$$\text{Oil content (\%)} = (W1-W) / M \times 100$$

Where:

W1 = Weight of oil flask after extraction

W = Weight of empty flask

M = Weight of dried material taken

APPENDIX-III

Estimation of protein content by micro kjeldahl's method, Linder (1944)

Principle

Samples are digested with H_2SO_4 and then with H_2O_2 till it become colorless. The intensity of the color developed by Nessler's reagent in the presence of sodium hydroxide (NaOH) and sodium silicate (Na_2SiO_3) is measured on a spectrophotometer at 420-650 nm.

Procedure

- Put 0.1g well ground and dried seed sample into a 100ml dry kjeldahl's flask.
- Add 2 ml of concentrated H_2SO_4 to the kjeldahl's flask, mix the contents of the flasks place on the digestion assembly (hot plate) and heat it till the sample is digested (for 1:30 hour).
- Cool the flask and add 0.5 ml (8-10 drops) of 30% H_2O_2 and again heat the contents till it become clear and colorless.
- Transfer the digested contents of kjeldahl's flask into 100 ml of volumetric flask by washing it 2-3 times with distilled water and make the volume.
- Take 5 ml of digested solution into 50 ml volumetric flask and add few ml distilled water. Then add 2 ml of 10% sodium hydroxide and 1 ml of 10% sodium silicate solutions respectively and then add some distilled water.
- Mix the contents and add 1.6 ml of Nessler's reagent to the flask while shaking. After this, make its volume and allow 10 minutes for color development.
- Take the reading of standard working solutions by adjusting the spectrophotometer at wave length of 420-650 nm. (In this experiment readings were taken at 420 nm)
- Plot the concentration of N on X- axis and the spectrophotometer reading on Y- axis and prepare a standard curve.
- Now take the reading of plant sample and calculate the ppm N with the help of standard curve.

Standard Curve

Dissolve 0.118 g of AR grade in water and make the volume one litre in volumetric flask. This solution contains 25 ppm N. For working standards take 1, 2, 3, 4, 5, 6, 7, 8 ml of 25 ppm N solution in 50 ml volumetric flasks. Add 2 ml 10% NaOH and 1 ml 10% sodium silicate solution in 50 ml volumetric flasks. Add some water and shake the contents. Now add 1.6 ml Nessler's reagent slowly drop while shaking and make the volume. The flasks will contain 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5 and 4.0 ppm N, respectively.

Estimation of Protein

Determine the nitrogen content using the standard curve. Then calculate the crude protein contents by multiplying the N contents with 6.25.

APPENDIX-IV

Mean values for Days to 50%flowering, Days to maturity, Plant height (cm), No. of branches/plant, Pods/plant, Shelling %, 100-Kernel weight (g)

S No.	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	Pods/ plant	Shelling %	100-Kernel weight (g)
1	UG-3	30.50	101.82	43.94	8.92	17.01	72.87	44.01
2	UG-4	32.81	102.85	41.95	8.48	18.80	71.76	43.81
3	UG-5	31.30	101.98	42.25	9.43	20.85	70.30	44.88
4	UG-6	33.65	103.69	41.31	8.33	17.25	73.10	43.17
5	UG-7	32.23	102.70	43.84	10.15	22.63	72.53	45.69
6	UG-8	35.16	105.72	44.26	8.97	19.59	71.48	44.39
7	UG-9	32.77	102.94	43.05	8.11	17.07	65.23	43.43
8	UG-10	34.89	104.23	44.04	7.13	13.79	72.61	40.73
9	UG-11	32.11	102.67	43.09	9.04	18.69	70.55	44.04
10	UG-12	35.37	105.90	44.71	9.97	22.91	68.67	45.62
11	UG-13	30.30	100.68	41.15	8.11	16.65	70.35	43.01
12	UG-14	32.84	102.68	42.57	7.37	14.15	70.40	42.02
13	UG-15	32.18	102.86	45.18	7.95	16.71	69.61	42.79
14	UG-16	30.17	100.89	46.02	7.10	13.78	74.65	40.75
15	UG-17	31.96	102.70	44.71	5.25	10.21	73.37	38.23
16	UG-18	33.76	103.88	44.97	6.77	12.79	71.52	39.92
17	UG-19	35.20	105.79	42.26	7.23	13.81	71.71	41.30
18	UG-20	34.73	105.77	43.94	6.23	11.05	74.29	39.84
19	UG-21	32.01	102.97	42.46	5.37	9.55	69.15	38.75
20	UG-22	31.84	101.80	43.97	6.87	13.93	71.51	40.62
21	UG-23	34.11	105.23	41.64	11.20	23.65	72.46	47.26
22	UG-264	34.63	103.55	40.80	7.53	15.43	70.87	42.42
23	UG-265	30.13	100.84	41.78	6.83	12.67	74.48	40.27
24	UG-266	31.95	102.97	43.16	7.86	15.37	70.93	42.17
25	UG-267	33.19	104.08	40.95	5.83	10.56	70.08	39.32
26	UG-268	34.81	105.10	41.86	7.20	14.07	67.37	41.73
27	UG-269	35.69	105.21	42.86	5.37	9.55	68.24	38.90
28	TG37A	33.31	100.92	44.71	11.70	14.67	72.97	45.06
29	JL501	32.07	101.82	42.50	10.74	18.62	69.37	45.30
30	GG7	34.71	102.15	41.75	11.11	16.61	68.96	41.33
	GM	33.01	103.21	43.06	8.07	15.75	71.05	42.36
	SE	0.46	0.34	0.37	0.24	0.77	0.64	0.36
	CD5	1.32	0.96	1.05	0.67	2.18	1.82	1.02
	CD1	1.75	1.27	1.40	0.89	2.90	2.42	1.36
	CV	2.44	0.57	1.49	5.05	8.47	1.57	1.48

APPENDIX-V

Mean values for Kernels/pod, Sound mature kernel (%), Dry pod yield/plant (g), Biological yield/plant (g), Harvest index (%), Oil content (%), Protein content (%)

S No.	Genotype	Kernels/ pod	Sound mature kernel (%)	Dry pod yield/plant (g)	Biological yield/plant (g)	Harvest index (%)	Oil content (%)	Protein content (%)
1	UG-3	2.33	88.86	14.35	30.86	46.78	45.34	22.88
2	UG-4	2.20	87.09	15.08	30.52	50.21	45.22	22.82
3	UG-5	2.70	85.00	12.61	29.24	42.99	45.84	23.09
4	UG-6	2.43	92.80	13.18	30.24	43.71	44.89	22.70
5	UG-7	1.67	90.84	17.94	34.21	52.79	46.08	23.38
6	UG-8	1.80	92.32	14.65	31.53	46.35	45.71	23.09
7	UG-9	2.77	87.35	13.69	29.78	46.28	44.56	22.62
8	UG-10	2.63	92.17	10.14	25.59	39.86	42.95	21.24
9	UG-11	1.30	90.63	14.88	31.06	47.87	45.42	23.00
10	UG-12	2.03	90.25	15.42	32.78	47.58	46.02	23.30
11	UG-13	2.70	87.98	13.44	29.70	45.77	44.41	22.60
12	UG-14	3.13	88.94	10.09	27.74	36.45	43.84	21.89
13	UG-15	2.30	85.12	11.47	28.98	39.55	44.39	22.25
14	UG-16	1.37	86.38	9.20	26.12	35.31	43.28	21.31
15	UG-17	2.63	86.12	7.45	21.83	34.41	40.24	20.14
16	UG-18	1.70	87.65	8.53	23.82	35.93	41.98	20.76
17	UG-19	2.53	89.32	9.21	26.66	34.76	43.29	21.63
18	UG-20	1.60	91.72	8.13	23.03	35.22	41.97	20.68
19	UG-21	3.23	93.33	7.53	21.92	34.52	41.31	20.24
20	UG-22	2.67	91.86	8.77	24.76	35.18	42.76	21.13
21	UG-23	1.33	88.06	18.13	35.61	51.05	47.01	23.93
22	UG-264	2.57	82.41	10.77	28.07	38.60	44.17	22.02
23	UG-265	2.73	90.17	8.73	24.16	36.48	42.36	21.02
24	UG-266	1.50	85.06	11.04	28.66	38.69	44.33	22.12
25	UG-267	2.60	89.17	7.99	22.34	35.86	41.86	20.50
26	UG-268	2.30	87.39	9.83	22.15	44.55	43.46	21.68
27	UG-269	2.50	89.01	7.91	29.18	27.13	41.64	20.24
28	TG37A	2.93	89.70	13.09	30.07	43.60	46.42	23.51
29	JL501	1.73	89.89	16.19	35.03	46.41	42.89	22.73
30	GG7	2.57	90.75	15.09	33.28	45.57	45.42	23.93
	GM	2.28	88.91	11.82	28.30	41.32	43.97	22.08
	SE	0.13	0.48	0.78	1.29	3.30	0.31	0.30
	CD5	0.36	1.36	2.19	3.65	9.34	0.88	0.86
	CD1	0.48	1.81	2.92	4.85	12.43	1.17	1.15
	CV	9.69	0.94	11.36	7.88	13.83	1.22	2.39

Plagiarism Report

(By DrillBit Software)

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File name (pdf)	:	DB_report_[ANUSHKA KUNTAL]_ [GPB_RCA_22-01-02-09-41].pdf
Title of the thesis	:	**Variability and Path Analysis in Spanish Bunch Groundnut (*Arachis hypogaea* L.)**
Total pages in the thesis	:	61
Assigned ID by DrillBit Software	:	2091744
Plagiarism Level (%)	:	8%
Date	:	08.07.2024

(Dr. Pratap Bhan Singh)

(Name and Signature of Major Advisor) (Dean /Head /Assistant Librarian/ In-charge)