*Original Research Article*

Genetic Variability and Correlation Analysis in the F2 Population of the cross, TMV 2 × ICGV 16690 for improving the oleic acid content in Groundnut

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ABSTRACT

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| **Aims:** The improvement in crop yield depends upon the magnitude of genetic variability available in breeding material. An investigation was carried out in groundnut F2 population to study variability present and correlation for growth and yield attributes viz, days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of mature pods per plant, pod yield per plant, kernel yield per plant and shelling percentage.**Study design:** Segregating population (F2)**Place and Duration of Study:** Zonal agricultural and horticultural research station, Babbur farm, Hiriyur, Chitradurga **Methodology:** In this study, the widely cultivated groundnut variety TMV 2, known for its adaptability but low oleic acid content (36–40%), was crossed with ICGV 16690, a high-oleate (75–78%) and high-yielding line. A total of 165 F₂ plants derived from this cross were assessed during the *kharif* 2024 season for various growth and yield traits. **Results:** Significant variability was found for pod yield, kernel yield, shelling percentage, total pods, and mature pods per plant. These traits showed high broad-sense heritability, GCV, PCV, and GAM. All traits except shelling percentage had positive skewness and leptokurtic distribution. Pod yield per plant was strongly correlated with kernel yield (r = 0.95), total pods (r = 0.83), mature pods (r = 0.82), plant height (r = 0.61), primary branches (r = 0.50), and shelling percentage (r = 0.33), with similar trends for kernel yield.**Conclusion:** Further evaluation of these segregating materials may facilitate the development of a high oleate and high-yielding variety in the genetic background of the well-adapted TMV 2 variety, contributing to groundnut improvement in Karnataka. |

*Keywords: groundnut, GCV, PCV, Heritability, Genetic advance as per cent of mean*

1. INTRODUCTION

 Groundnut (Arachis hypogaea L.), commonly known as peanut, is a major oilseed crop grown across tropical and warm temperate regions worldwide. Originating in South America, it is now widely cultivated in Asia, Africa, Oceania, and the Americas [1]. Groundnut, a major oilseed in India, accounts for 34% of the country’s total oil production, with 80% of the crop used for edible oil extraction. Groundnut oil is both stable and nutritious due to its balanced saturated and unsaturated fatty acid content. A self-pollinated annual legume of the Fabaceae family, it may undergo some cross-pollination in areas with high bee activity [2]. Known for its high oil, protein, and fiber content [3], peanuts are used for oil extraction, peanut butter, confectionery, roasted snacks, meat extenders, soups, and desserts [4].

 Peanuts contain 21–36.4% protein, 18% carbohydrates, and 36–54% fat, with 30–35% of their fat being polyunsaturated and 40–45% oleic acid, a monounsaturated fatty acid [5]. “They provide at least 10% of the recommended daily intake of vitamin E, folate, niacin, magnesium, copper, phosphorus, and potassium. Additionally, they contain about 100–120 g of fiber per kg” [6].

 “Several studies have looked at the health benefits of regular consumption of peanuts” [7]. “Recent research studies suggest that boiling enhances antioxidant concentration in the peanuts. It has been found that boiled peanuts have two- and four-fold increase in isoflavone antioxidants biochanin A and genistein content, respectively” [8]. “Specifically, nut consumption has been reported to be significantly associated with reduced risk of cancer, cardiovascular, respiratory, infectious, renal and liver disease mortality but not with diabetes or Alzheimer’s disease mortality” [9].

 In groundnut, natural genetic variability is minimal due to limited natural crossing. To overcome this limitation, hybridization has been extensively employed to create new genetic variability for crop improvement. The knowledge on the estimates of the genetic variability parameters with respect to yield and its component traits including the morpho-physiological traits is essential for formulating the selection strategies. Evaluation of heritable and non-heritable components of variability across different traits is essential in choosing appropriate breeding strategies. The entire variability in the population was divided into heritable and non-heritable components, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advancements for various morpho-physiological, yield, and attributing characteristics.

 Typically, breeders focus on improving one or two attributes at a time, so understanding the interrelationships among different traits is crucial for effective simultaneous selection. Yield and quality parameters are complex traits that are highly influenced by environmental factors, making direct selection for these traits less efficient. Correlation studies provide valuable insights into which traits contribute to yield, helping breeders identify superior genotypes within genetically diverse populations. With this background, the present study assessed the F2 population of the TMV 2 × ICGV 16690 cross to analyze genetic variability and the association patterns for growth and yield traits.

2. material and methods

 The groundnut genotypes used in this experiment included TMV 2 as the female parent and ICGV 16690 as the male donor parent. These genotypes were cultivated in the Breeding Cage Facility of the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, during the *Kharif* 2023 season for hybridization. TMV 2 is a well-adapted and widely grown variety with a low oleic acid content (36–40%) and is suitable for both rainy and summer seasons. Male donor ICGV 16690 is a high oleate (78-80%) and high yielding line. The seed material for this study was obtained from the germplasm collection maintained at the Zonal Agricultural and Horticultural Research Station, Hiriyur. Emasculation and artificial pollination were carried out daily for 45 days, beginning from the first day of flowering in the female parent, to produce F1 seeds from the TMV 2 × ICGV 16690 cross. Unshelled pods were obtained from each true F1 hybrid and only sound mature seeds were used for oleic acid analysis using Near-infrared Reflectance spectroscopy (NIRS). The average oleic acid content in F1 hybrids was 67.36 per cent. During the *Rabi/Summer* 2023–24 season, the F1 hybrids were evaluated, followed by the assessment of F2 plants during *kharif* 2024 season at the Zonal Agricultural and Horticultural Research Station, Hiriyur, with a plant spacing of 30 × 10 cm.

 The recorded growth and yield traits for each F2 plant included days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of mature pods per plant, pod yield per plant (g), kernel yield per plant (g), and shelling percentage. The data obtained from F2 population were subjected to the biometrical analysis that included heritability and genetic advance in percent mean. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h²bs), genetic advance over a mean (GAM), kurtosis and skewness were estimated by the formula suggested by Burton and De Vane [10], Johnson et al. [11] and Hanson et al. [12]. Phenotypic coefficients of correlation between all pairs of characters were determined by using variance and covariance components as suggested by Al-Jibouri [13]. The analysis was done by using the R software version 4.1 (‘metan’ package).

3. results and discussion

The F2 population of the TMV 2 × ICGV 16690 cross exhibited an average of 30 days to 50% flowering, with a range of 25 to 36 days (Table 1). The average number of days to maturity was 113, varying between 108 and 118 days. Plant height in this population averaged 26.09 cm, ranging from 13.23 cm to 46.64 cm. The average number of branches per plant was 5, with a range of 1 to 10. For reproductive traits, the F2 population had an average of 16 pods per plant, with a range of 2 to 47, while the number of mature pods per plant averaged 10, varying from 1 to 38. The pod yield per plant averaged 9.16 g, ranging from 0.40 to 38.08 g, whereas the kernel yield per plant had a mean of 4.89 g, with values ranging from 0.16 to 19.42 g. The average shelling percentage was 53.17%, with a range of 15.38% to 76.67%.

**3.1 Variability studies**

The variability estimations for the F2 population of TMV 2 × ICGV 16690 showed differences across traits in terms of genetic variability, heritability, and data distribution patterns (Table 1). Traits with high variability included pod yield per plant, which had high heritability (broad sense heritability), genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance as a percentage of mean (GAM). Similarly, kernel yield per plant and shelling percentage exhibited high values for all these parameters. These findings indicate that this trait is minimally influenced by environmental changes, making it more amenable to improvement through selection due to its additive gene effects. The total number of pods per plant also showed high GCV, PCV and GAM, along with a moderate heritability. The number of mature pods per plant displayed high GCV and PCV, although heritability was moderate. Traits with moderate variability included plant height, which had moderate GCV and heritability but high PCV and GAM. The combination of moderate to high PCV and GCV, along with high heritability and GAM estimates, suggests substantial genetic variability in the trait, with a strong additive genetic influence, making selection highly effective for improvement. The number of primary branches per plant exhibited a high degree of PCV but low GCV, heritability, and GAM. Because there is less variability for this characteristic in the population under study, the results showed that selection for this trait is unsuccessful. Traits with low variability included days to 50% flowering, which had low GCV and GAM, while PCV and heritability were moderate. Days to maturity also showed low GCV and PCV, along with a medium level of heritability. Selection based on these low to moderate estimations of GCV, PCV, heritability and GAM is likely to be unsuitable for crop improvement programs.

**Table 1: Descriptive statistics for growth and yield traits in F2 generation of the cross, TMV 2 × ICGV 16690**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** | **Mean** | **Range** | **S.Em±** | **SD** | **Variance** | **Skewness** | **Kurtosis** | **GCV (%)** | **PCV (%)** | **h2bs (%)** | **GAM (%)** |
| **Minimum** | **Maximum** |
| DFF | 30 | 25 | 36 | 0.26 | 3.33 | 11.07 | 0.15 | -1.13 | 7.06 | 11.03 | 40.97 | 9.31 |
| DM | 113 | 108 | 118 | 0.24 | 3.04 | 9.26 | 0.19 | -1.06 | 1.66 | 2.70 | 37.59 | 2.09 |
| PH | 26.09 | 13.23 | 46.64 | 0.51 | 6.53 | 42.62 | 0.29 | 0.06 | 17.19 | 25.02 | 47.21 | 24.33 |
| NPB | 5 | 1 | 10 | 0.15 | 1.90 | 3.61 | 0.25 | 0.07 | 4.61 | 37.41 | 1.52 | 1.17 |
| TNP | 16 | 2 | 47 | 0.71 | 9.14 | 83.59 | 0.85 | 0.79 | 43.77 | 63.12 | 48.09 | 62.53 |
| NMP | 10 | 1 | 38 | 0.33 | 4.22 | 17.84 | 1.10 | 1.16 | 41.37 | 71.05 | 33.91 | 49.63 |
| PY | 9.16 | 0.40 | 38.08 | 0.60 | 7.41 | 54.95 | 1.28 | 1.61 | 61.12 | 87.21 | 89.12 | 88.23 |
| KY | 4.89 | 0.16 | 19.42 | 0.32 | 4.12 | 22.54 | 1.27 | 1.63 | 86.33 | 89.69 | 87.24 | 91.61 |
| SP | 53.17 | 15.38 | 76.67 | 1.75 | 17.05 | 508.12 | -0.96 | -0.13 | 45.94 | 48.53 | 81.61 | 89.84 |

DFF-Days to fifty percent flowering, DM-Days to maturity, PH-Plant height (cm), NPB- Number of primary branches, TNP-Total number of pods, NMP-Number of mature pods, PY-Pod yield/plant (g), KY- Kernel yield/plant (g) and SP-Shelling percentage.

Narasimhulu et al. [14], Zongo et al. [15], and Vinithashri et al. [16] reported similar levels of GCV, PCV, heritability, and GAM for pod and kernel yield per plant. Zongo et al. [15] and Habite and Ahadu [17] observed high PCV, GCV, heritability, and GAM for shelling percentage in groundnut. Vinithashri et al. [16] and Habite and Ahadu [17] noted comparable variability parameters for the total and mature number of pods per plant, with both studies reporting high PCV and GCV, while Habite and Ahadu [17] additionally observed medium heritability. Padmashree et al. [18] reported medium PCV, GCV, and GAM for the number of primary branches per plant. Zongo et al. [15] recorded low PCV and GCV with medium GAM, whereas Habite and Ahadu [17] reported similarly low variability parameters for days to 50% flowering and days to maturity.

Regarding data distribution, most traits exhibited positive skewness, including days to 50% flowering, days to maturity, plant height, number of primary branches per plant, total number of pods per plant, number of mature pods per plant, pod yield per plant, and kernel yield per plant (Table 1). However, shelling percentage was negatively skewed. Kurtosis varied among traits, with days to 50% flowering, days to maturity and shelling percentage being platykurtic, while traits like pod yield per plant, kernel yield per plant, number of primary branches per plant, total number of pods per plant and number of mature pods per plant showed leptokurtic distributions. Jerish et al. [19] reported a similar frequency distribution for days to 50% flowering. Mohapatra and Khan [20] observed a comparable pattern of platykurtosis and positive skewness for days to maturity and plant height, as well as leptokurtosis and positive skewness for the number of mature pods per plant in groundnut crosses. Rajarathinam et al. [21] and Kamdar et al. [22] reported a similar distribution pattern of positive skewness and leptokurtosis for the number of primary branches per plant and pod yield in groundnut crosses. Rajarathinam et al. [19] and Divyadharsini et al. [23] reported a positively skewed and leptokurtic distribution for total pod number per plant. Divyadharsini et al. [23] further noted a negatively skewed and leptokurtic distribution for kernel yield and shelling percentage, while also observing a positively skewed and leptokurtic distribution for total pod number and pod yield.

**3.2 Correlation studies**

 Phenotypic correlation analyses were conducted to assess the relationships among growth and yield traits. Figure 1 provide a comprehensive overview of these associations. Pod yield per plant showed significant positive associations with kernel yield per plant (r = 0.95), total number of pods per plant (r = 0.83), number of mature pods per plant (r = 0.82), plant height (r = 0.61), number of primary branches per plant (r = 0.50) and shelling percentage (r = 0.33). It also showed non-significant positive and negative associations with days to maturity (r = 0.12) and days to fifty *per cent* flowering (r = -0.039), respectively. Kernel yield per plant showed significant positive associations with number of mature pods per plant (r = 0.80), total number of pods per plant (r = 0.79), plant height (r = 0.55), shelling percentage (r = 0.47) and number of primary branches per plant (r = 0.42). Plant height exhibited a positive significant association with most of the traits under study, including total number of pods per plant (r = 0.55), number of mature pods per plant (r = 0.53), number of primary branches (r = 0.48) and shelling percentage (r = 0.16). Shelling percentage showed significant positive associations with number of mature pods per plant (r = 0.36), total number of pods per plant (r = 0.34), and plant height (r = 0.13). Days to fifty *per cent* flowering and days to maturity did not show any significant associations with any of the traits examined. The majority of the characteristics under investigation, including the total number of pods per plant (r = 0.53) and number of mature pods per plant (r = 0.43) were positively and significantly correlated with the number of primary branches.

 Vasanthi et al. [24] and Hampannavar et al. [25] reported “a negative association between days to 50% flowering and both pod yield per plant and the number of mature pods per plant”. Adlak et al. [26] also documented “a negative association with the total number of pods per plant, pod yield per plant, and kernel yield per plant”. Hampannavar et al. [25] observed “a positive association between shelling percentage and kernel yield per plant, along with a negative association between plant height and days to maturity and a positive association with pod yield per plant and the number of primary branches”. Prabhu et al. [27] and Kamdar et al. [21] reported “a significant positive association between plant height and pod yield per plant, total number of pods per plant, and the number of primary branches per plant”. Similarly, Vasanthi et al. [24] and Hampannavar et al. [25] observed strong positive correlations between plant height and pod yield per plant, while Kamdar et al. [22] also noted significant positive correlations with plant height, number of primary branches per plant, and pod yield per plant. Mubai et al. [28] found a positive non-significant association with shelling percentage and a significant positive correlation with plant height. Vasanthi et al. [24] also reported a significant correlation between the number of mature pods per plant and plant height, number of primary branches per plant, and pod yield per plant. Narasimhulu et al. [14] and Prabhu et al. [27] established “significant positive correlations between shelling percentage, pod yield per plant, and kernel yield per plant. Similarly, Abady et al. [29] observed strong positive correlations with shelling percentage and pod yield per plant, while also noting a non-significant negative correlation with days to 50% flowering”.



**Figure 1: Pearson’s coefficient of correlation for growth and yield traits in F2 population of cross, TMV 2 × ICGV 16690**

The upper diagonal displays the correlation coefficients, while the lower diagonal plots show the distribution of population in each trait.

DFF-Days to fifty percent flowering, DM-Days to maturity, PH-Plant height (cm), NPB- Number of primary branches, TNP-Total number of pods, NMP-Number of mature pods, PY-Pod yield/plant (g), KY- Kernel yield/plant (g) and SP-Shelling percentage. \* Significant at P = 0.05, \*\* Significant at P = 0.01 and \*\*\* Significant at P = 0.001

4. Conclusion

 Significant variability was observed in pod yield per plant, kernel yield per plant, shelling percentage, total number of pods per plant, and the number of mature pods per plant. These traits exhibited high broad-sense heritability, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance as a percentage of mean (GAM). Moreover, all traits except shelling percentage displayed positive skewness and leptokurtic distribution. Pod yield per plant showed strong positive correlations with kernel yield per plant, total number of pods per plant, number of mature pods per plant, plant height, number of primary branches per plant, and shelling percentage. A similar trend was observed for kernel yield per plant. Therefore, characters like total number of pods per plant, number of mature pods per plant, kernel yield per plant and pod yield per plant can be prioritised for further groundnut improvement. These F2 plants should be advanced to the subsequent generations (F4/F5/F6), followed by a phenotypic evaluation to confirm the high-oleate trait along with oil content, yield and other essential traits. The high oleate lines in the genetic background of TMV 2, which is known for its desirable kernel characteristics, should be identified, as this genotype is widely cultivated by farmers and also preferred by processing industries in Karnataka.

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Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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Details of the AI usage are given below:

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2.

3.

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