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Association analysis of yield and yield contributing traits in groundnut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop valued for its high oil and protein content, nutritional quality and economic importance. Improving pod yield through the identification of key yield-contributing traits is a major objective of groundnut breeding programmes. Therefore, a field experiment comprising 70 groundnut genotypes was conducted in a randomized complete block design with three replications at the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh, during Summer 2026 to study trait associations and determine the direct and indirect effects of yield related characters on pod yield. Genotypic correlation coefficients were generally higher than the corresponding phenotypic coefficients, indicating that the observed associations were predominantly governed by genetic factors with comparatively less environmental influence. Pod yield per plant exhibited significant and positive correlations with kernel yield per plant, number of mature pods per plant, harvest index, sound mature kernel, oil content and shelling percentage at both genotypic and phenotypic levels, suggesting their usefulness as selection criteria for yield improvement. Path coefficient analysis identified kernel yield per plant as the trait with the highest positive direct effect on pod yield at both genotypic and phenotypic levels. Number of mature pods per plant, number of primary branches per plant, 100-kernel weight and sound mature kernel also contributed positively at the genotypic level, whereas number of mature pods per plant, 100-pod weight, harvest index and biological yield per plant showed important direct effects at the phenotypic level. The very low residual effects at the genotypic (0.0014) and phenotypic (0.0038) levels confirmed that the studied traits explained nearly all the variation in pod yield, demonstrating the reliability of the path coefficient analysis and their value in groundnut improvement programmes.

Keywords: Groundnut, genotypic correlation, phenotypic correlation, path coefficient analysis, pod yield

1. Introduction

Arachis hypogaea L. represents a significant economic oilseed crop on the international stage, positioning itself as the 13th most important food crop globally. The crop functions as humanity's fourth primary oil resource and third major supplier of plant based proteins. From a botanical perspective, this species constitutes an annual herb within the Fabaceae (Leguminosae) family. The scientific nomenclature originates from Greek terminology, where *Arachis* signifies a pulse crop and *hypogaea* translates to "subterranean," highlighting the distinctive trait wherein pod maturation takes place underground. Chromosomally, groundnut exhibits an allotetraploid configuration ($2n = 4x = 40$) with a fundamental chromosome value of $x = 10$ (Stalker, 1991) [20]. The plant demonstrates cleistogamous pollination mechanisms, which results in predominantly self-fertilizing characteristics (Knauff and Wynne, 1995) [12].

Diverse geographical regions assign different terminologies to this legume. North American regions favor the "peanut," though numerous alternative appellations exist including African nut, Chinese nut, Manila nut, Kipper nut, Hawk's nut, Jar nut, Earth chestnut, Monkey nut, Goober pea, Ground pea and Ground bean (Johnson, 1964) [9]. Within India, the crop receives the traditional name mungphali. Its substantial commercial importance has earned it the prestige title "King of Oilseeds."

This legume thrives across tropical, subtropical and warm temperate zones between approximately 40° N and 40° S latitude bands.

Historical evidence from phylogenetic and geographic analyses indicates the species originated in southern Bolivia along with northern Argentina (Kochert *et al.* 1996) [13]. The genus *Arachis* demonstrates its highest genetic variation across South America, particularly throughout western Brazil, Bolivia, Paraguay and northern Argentina, where wild relatives and ancestral variants are naturally distributed.

The country's low groundnut production is mostly attributable to a lack of adoption of better varieties and uneven performance in a variety of locations, notably rainfed situations. Therefore, the creation of high-yielding cultivars with wide adaptability, fertilizer responsiveness and resistance to biotic and abiotic challenges, together with short seed dormancy, is crucial to increase output. It also has many health benefits including weight gain control (Petersen *et al.*, 2022) [17], prevention of cardiovascular diseases (Feldman, 2002) [5], protection against Alzheimer's disease (Vaishnavi *et al.*, 2023) [21] and cancer inhibition (Wang *et al.*, 2021) [24]. Groundnuts contain 21 - 36.4% protein, 18% carbohydrates, 36-54% fat and 100-120 grams of fibre per kg of kernels (Bonku and Yu, 2020) [2].

Pod yield constituents demonstrate interconnectivity with seed productivity and reciprocal associations among themselves. Understanding connections among yield-determining variables within germplasm assemblages is essential for their effective integration and simultaneous improvement in breeding programs (Dewey and Lu, 1959) [4]. Multiple component characteristics influence seed productivity through both direct mechanistic pathways and indirect mediated influences via interactions with correlated characteristics. This multifaceted nature complicates the selection process for plant breeders attempting to identify appropriate trait combinations for enhancement. Path coefficient statistical methodology facilitates augmented comprehension of these interactive mechanisms by partitioning correlation values into constituent direct influences and mediated indirect contributions. The synergistic deployment of conventional correlation analysis combined with path coefficient methodology furnishes nuanced perspectives regarding productivity-contributing characteristics and their relative significance, substantially enhancing plant breeder decision-making capacity in developing superior high-productivity germplasm within systematic breeding programs.

2. Materials and Methods

The research utilized 70 peanut accessions sourced from the Main Oilseed Research Station at Junagadh Agricultural University, Junagadh procured during the Summer-2026. A Randomized Block Design framework incorporating three replications formed the basis of this experimental setup. Individual genotypes were sown in solitary rows measuring 2.0 m in length with 30 cm intervals between rows and 10 cm spacing between individual plants. Standard agronomic protocols and protective measures against pests and diseases were implemented throughout the cultivation period. Data collection focused on pod yield per plant alongside various associated parameters including days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of mature pods per plant, 100-pod weight (g), kernel yield per plant (g), 100-kernel weight (g), shelling percentage (%), sound mature kernel (%), biological yield per plant (g), harvest index (%), oil content (%) and subsequent correlation analysis along with path coefficient investigation. Oil content was determined using Nuclear Magnetic Resonance

methodology. Five plants from each genotype per replication were assessed for trait evaluation, with the exception of days to 50% flowering and days to maturity which were measured at the plot level rather than individual plant basis.

$$\text{Shelling percentage (\%)} = \frac{\text{Weight of kernels (g)}}{\text{Weight of pod samples (g)}} \times 100$$

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

$$\text{Harvest index (\%)} = \frac{\text{Pod yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

Variance analysis following the randomized block design framework was performed for each trait utilizing the statistical approach detailed by Panse and Sukhatme (1995) [16]. Correlation values at both genotypic (r_g) and phenotypic (r_p) levels were derived through methodology outlined by Al-Jibouri *et al.* (1958) [1]. Genotypic and phenotypic path analysis was executed according to procedures established by Dewey and Lu (1959) [4] utilizing R-Studio software.

3. Results and Discussion

3.1 Analysis of variance

During the Summer-2026 season, a comprehensive evaluation of seventy groundnut genotypes including eight control varieties was executed using a Randomized Complete Block Design (RCBD). Analysis of variance (ANOVA) was performed across all fourteen quantitative and qualitative traits to assess the significance of variation among the genotypes, as detailed in Table 1. Excluding days to maturity, the mean sum of squares attributed to genotypes was highly significant for all evaluated parameters, indicating the presence of extensive genetic diversity within the experimental material across the studied traits. This substantial variability offers significant scope for developing superior, high yielding breeding lines through targeted selection for key agronomic and economic attributes.

3.2 Correlation coefficient analysis

In the present experiment genotypic (r_g) and phenotypic (r_p) correlation coefficients are computed and presented in Table 2. The results of the study are discussed below.

3.2.1 Days to 50% flowering

Days to 50% flowering exhibited significant favourable genetic correlations with days to maturity ($r_g = 0.7753$, $r_p = 0.1936$), number of primary branches per plant ($r_g = 0.7533$, $r_p = 0.4400$), biological yield per plant ($r_g = 0.6974$, $r_p = 0.3524$) and plant height ($r_g = 0.3266$). However, significant unfavourable genetic correlations were observed with harvest index ($r_g = -0.7197$, $r_p = -0.6032$), sound mature kernel ($r_g = -0.7071$, $r_p = -0.6064$), 100-kernel weight ($r_g = -0.6823$, $r_p = -0.5936$), kernel yield per plant ($r_g = -0.5005$, $r_p = -0.4240$), 100-pod weight ($r_g = -0.4871$, $r_p = -0.4007$), pod yield per plant ($r_g = -0.4564$, $r_p = -0.3820$) and shelling percentage ($r_g = -0.3903$, $r_p = -0.2973$). Oil content showed non-significant unfavourable associations ($r_g = -0.1378$, $r_p = -0.1707$), while number of mature pods per plant demonstrated non-significant unfavourable associations ($r_g = -0.0169$, $r_p = -0.1036$).

3.2.2 Days to maturity

Days to maturity exhibited significant positive genetic correlations with days to 50% flowering ($r_g = 0.7753$, $r_p = 0.1936$), biological yield per plant ($r_g = 0.7671$, $r_p = 0.2163$),

plant height ($r_g = 0.7060$, $r_p = 0.1550$) and number of primary branches per plant ($r_g = 0.6618$, $r_p = 0.1696$), with number of mature pods per plant showing positive correlations ($r_g = 0.3124$, $r_p = 0.0711$). Significant negative genetic correlations were observed with 100-pod weight ($r_g = -0.6353$, $r_p = -0.1684$), harvest index ($r_g = -0.6030$, $r_p = -0.2100$), 100-kernel weight ($r_g = -0.5947$, $r_p = -0.1601$), sound mature kernel ($r_g = -0.5221$, $r_p = -0.1702$) and shelling percentage ($r_g = -0.4237$, $r_p = -0.1941$). With kernel yield per plant showed negative correlations ($r_g = -0.2547$, $r_p = -0.0897$), while oil content ($r_g = -0.1762$) and pod yield per plant ($r_g = -0.1464$, $r_p = -0.0329$) demonstrated non-significant negative associations.

3.2.3 Plant Height (cm)

Plant height showed significant positive genetic and phenotypic correlations with days to maturity ($r_g = 0.7060$, $r_p = 0.1550$), number of primary branches per plant ($r_g = 0.5739$, $r_p = 0.3551$), biological yield per plant ($r_g = 0.5349$, $r_p = 0.4162$) and days to 50% flowering ($r_g = 0.3266$), with number of mature pods per plant demonstrating positive correlations ($r_g = 0.1026$, $r_p = 0.1669$). Pod yield per plant and kernel yield per plant showed non-significant positive phenotypic associations ($r_p = 0.1120$ and $r_p = 0.0663$, respectively). Conversely, plant height demonstrated significant negative genetic correlations with harvest index ($r_g = -0.4676$), 100-kernel weight ($r_g = -0.3795$, $r_p = -0.2111$) and 100-pod weight ($r_g = -0.3074$, $r_p = -0.1386$). Non-significant negative associations were recorded with sound mature kernel ($r_g = -0.1797$, $r_p = -0.1198$), kernel yield per plant ($r_g = -0.1358$), pod yield per plant ($r_g = -0.1323$), shelling percentage ($r_g = -0.1008$, $r_g = -0.1222$) and oil content ($r_g = -0.0805$, $r_p = 0.0570$).

3.2.4 Number of primary branches per plant

Number of primary branches per plant exhibited significant favourable genetic correlations with biological yield per plant ($r_g = 0.8268$, $r_p = 0.5809$) and days to 50% flowering ($r_g = 0.7533$, $r_p = 0.4400$) and days to maturity ($r_g = 0.6618$, $r_p = 0.1696$) and plant height ($r_g = 0.5739$, $r_p = 0.3551$), with number of mature pods per plant showing positive correlations ($r_g = 0.0454$, $r_p = 0.1559$). Non-significant positive associations were documented with oil content ($r_g = 0.1407$, $r_p = 0.0386$) and pod yield per plant ($r_p = 0.0488$). However, significant unfavourable genetic correlations were manifested with harvest index ($r_g = -0.6739$, $r_p = -0.4819$) and 100-kernel weight ($r_g = -0.5290$, $r_p = -0.3498$) and sound mature kernel ($r_g = -0.4488$, $r_p = -0.2794$) and shelling percentage ($r_g = -0.3453$, $r_p = -0.2082$) and 100-pod weight ($r_g = -0.2907$, $r_p = -0.2030$). Kernel yield per plant demonstrated negative correlations ($r_g = -0.2655$, $r_p = -0.0169$), remaining statistically non-significant at the genotypic and phenotypic level.

3.2.5 Number of mature pods per plant

Number of mature pods per plant manifested significant favourable genetic correlations with pod yield per plant ($r_g = 0.7108$, $r_p = 0.7842$), kernel yield per plant ($r_g = 0.6502$, $r_p = 0.7474$), harvest index ($r_g = 0.4010$, $r_p = 0.3210$), oil content ($r_g = 0.3891$, $r_p = 0.2469$). Non-significant positive associations were noted with shelling percentage ($r_g = 0.1495$), plant height ($r_g = 0.1026$), number of primary branches per plant ($r_g = 0.0454$) and sound mature kernel ($r_p = 0.0213$). By contrast, significant unfavourable correlations were observed with 100-pod weight ($r_g = -0.6191$, $r_p = -0.4486$) and 100-kernel weight ($r_g = -0.3861$, $r_p = -0.2629$). Non-significant negative associations were documented

with biological yield per plant ($r_g = -0.0728$) and days to 50% flowering ($r_g = -0.0169$, $r_p = -0.1036$) and sound mature kernel ($r_g = -0.0124$).

3.2.6 100-Pod Weight (g)

100-pod weight exhibited significant favourable genetic correlations with 100-kernel weight ($r_g = 0.8396$, $r_p = 0.8226$) and sound mature kernel ($r_g = 0.4642$, $r_p = 0.4350$). Non-significant positive associations were documented with shelling percentage ($r_g = 0.2095$, $r_p = 0.1041$) and harvest index ($r_g = 0.1701$) and kernel yield per plant ($r_g = 0.1394$) and pod yield per plant ($r_g = 0.0968$). However, significant unfavourable correlations were manifested with days to maturity ($r_g = -0.6353$, $r_p = -0.1684$) and number of mature pods per plant ($r_g = -0.6191$, $r_p = -0.4486$) and days to 50% flowering ($r_g = -0.4871$, $r_p = -0.4007$) and plant height ($r_g = -0.3074$, $r_p = -0.1386$) and number of primary branches per plant ($r_g = -0.2907$, $r_p = -0.2030$). Non-significant negative associations were additionally recorded with biological yield per plant ($r_g = -0.2010$, $r_p = -0.0825$) and oil content ($r_g = -0.0166$, $r_p = -0.0030$).

3.2.7 100-Kernel Weight (g)

100-kernel weight manifested significant favourable genetic correlations with 100-pod weight ($r_g = 0.8396$, $r_p = 0.8226$), sound mature kernel ($r_g = 0.5992$, $r_p = 0.5610$), shelling percentage ($r_g = 0.4254$, $r_p = 0.3157$), harvest index ($r_g = 0.4197$, $r_p = 0.4044$) and kernel yield per plant ($r_g = 0.3268$, $r_p = 0.3142$). Non-significant positive associations were noted with pod yield per plant ($r_g = 0.2318$) and oil content ($r_g = 0.1793$). In contrast, significant unfavourable correlations were exhibited with days to 50% flowering ($r_g = -0.6823$, $r_p = -0.5936$) and days to maturity ($r_g = -0.5947$, $r_p = -0.1601$) and number of primary branches per plant ($r_g = -0.5290$, $r_p = -0.3498$) and biological yield per plant ($r_g = -0.4733$, $r_p = -0.2818$) and number of mature pods per plant ($r_g = -0.3861$, $r_p = -0.2629$) and plant height ($r_g = -0.3795$, $r_p = -0.2111$).

3.2.8 Shelling Percentage (%)

Shelling percentage exhibited significant favourable genetic correlations with kernel yield per plant ($r_g = 0.6231$, $r_p = 0.4783$), 100-kernel weight ($r_g = 0.4254$, $r_p = 0.3157$), harvest index ($r_g = 0.3812$, $r_p = 0.2972$), sound mature kernel ($r_g = 0.3375$, $r_p = 0.2409$), pod yield per plant ($r_g = 0.3321$, $r_p = 0.1873$) and oil content ($r_g = 0.2669$, $r_p = 0.2150$). Non-significant positive associations were documented with 100-pod weight ($r_g = 0.2095$, $r_p = 0.1041$) and number of mature pods per plant ($r_g = 0.1495$). However, significant unfavourable correlations were manifested with days to maturity ($r_g = -0.4237$, $r_p = -0.1941$) and biological yield per plant ($r_g = -0.4044$, $r_p = -0.2440$) and days to 50% flowering ($r_g = -0.3903$, $r_p = -0.2973$) and number of primary branches per plant ($r_g = -0.3453$, $r_p = -0.2082$), whereas its association with plant height ($r_g = -0.1008$, $r_p = -0.1222$) remained unfavourable yet non-significant.

3.2.9 Sound mature kernel (%)

Sound mature kernel manifested significant favourable genetic correlations with 100-kernel weight ($r_g = 0.5992$, $r_p = 0.561$), harvest index ($r_g = 0.5365$, $r_p = 0.4891$), 100-pod weight ($r_g = 0.4642$, $r_p = 0.4350$), kernel yield per plant ($r_g = 0.4457$, $r_p = 0.3511$), pod yield per plant ($r_g = 0.4047$, $r_p = 0.3131$), oil content ($r_g = 0.3907$, $r_p = 0.3162$) and shelling percentage ($r_g = 0.3375$, $r_p = 0.2409$). A non-significant positive association was documented with number of mature

Pods per plant at phenotypic level ($r_p = 0.0214$). By contrast, significant unfavourable associations were exhibited with days to 50% flowering ($r_g = -0.5221$, $r_p = -0.6064$), days to maturity ($r_g = -0.5221$, $r_p = -0.1702$), biological yield per plant ($r_g = -0.5004$, $r_p = -0.3111$) and number of primary branches per plant ($r_g = -0.4488$, $r_p = -0.2794$). Additionally, unfavourable relationships were observed with plant height ($r_g = -0.1797$, $r_p = -0.1198$), although statistical significance was not attained.

3.2.10 Pod yield per plant (g)

Pod yield per plant had positive and significant genetic associations with kernel yield per plant ($r_g = 0.9436$, $r_p = 0.9500$), number of mature pods per plant ($r_g = 0.7108$, $r_p = 0.7842$), harvest index ($r_g = 0.6876$, $r_p = 0.4822$), oil content ($r_g = 0.4667$, $r_p = 0.2420$), sound mature kernel ($r_g = 0.4047$, $r_p = 0.3131$) and shelling percentage ($r_g = 0.3321$, $r_p = 0.1873$). Positive yet statistically non-significant correlations were observed with 100-kernel weight at genotypic level ($r_g = 0.2318$) and 100-pod weight ($r_g = 0.0968$) and plant height at phenotypic level ($r_p = 0.1120$) and number of primary branches per plant at phenotypic level ($r_p = 0.0488$). In contrast, significant negative correlations were exhibited with days to 50% flowering ($r_g = -0.4564$, $r_p = -0.3820$) and biological yield per plant ($r_g = -0.2829$). Negative but non-significant correlations were observed with number of primary branches per plant ($r_g = -0.1813$) and days to maturity ($r_g = -0.1464$, $r_p = -0.0329$) and plant height ($r_g = -0.1323$).

3.2.11 Kernel yield per plant (g)

Kernel yield per plant had positive and significant genetic associations with pod yield per plant ($r_g = 0.9436$, $r_p = 0.9500$), harvest index ($r_g = 0.6964$, $r_p = 0.5184$), number of mature pods per plant ($r_g = 0.6502$, $r_p = 0.7474$), shelling percentage ($r_g = 0.6231$, $r_p = 0.4783$), oil content ($r_g = 0.4827$, $r_p = 0.2876$), sound mature kernel ($r_g = 0.4457$, $r_p = 0.3511$) and 100-kernel weight ($r_g = 0.3268$, $r_p = 0.3142$). Positive but non-significant correlations were observed with 100-pod weight ($r_g = 0.1394$) and plant height ($r_p = 0.0663$). The trait exhibited significant negative correlations with days to 50% flowering ($r_g = -0.5005$, $r_p = -0.4240$), biological yield per plant ($r_g = -0.3665$) and number of primary branches per plant ($r_g = -0.2655$) and days to maturity ($r_g = -0.2547$). Negative and non-significant correlation was recorded with plant height at genotypic level ($r_g = -0.1358$).

3.2.12 Biological yield per plant (g)

Biological yield per plant manifested positive and significant genetic correlations with number of primary branches per plant ($r_g = 0.8268$, $r_p = 0.5809$), days to maturity ($r_g = 0.7671$, $r_p = 0.2163$), days to 50% flowering ($r_g = 0.6974$, $r_p = 0.3524$) and plant height ($r_g = 0.5349$, $r_p = 0.4162$). Positive correlations were additionally noted with number of mature pods per plant at phenotypic level ($r_p = 0.2833$), pod yield per plant ($r_p = 0.2648$), kernel yield per plant ($r_p = 0.1627$) and oil content ($r_p = 0.0054$), although some showed non-significant or contradictory associations at the genetic level. By contrast, significant unfavourable associations were demonstrated with harvest index ($r_g = -0.8656$, $r_p = -0.6791$) and sound mature kernel ($r_g = -0.5004$, $r_p = -0.3111$) and 100-kernel weight ($r_g = -0.4733$, $r_p = -0.2818$) and shelling percentage ($r_g = -0.4044$, $r_p = -0.2440$). Non-significant negative correlations were additionally documented with 100-pod weight ($r_g = -0.2010$, $r_p = -0.0825$) and number of mature pods per plant ($r_g = -0.0728$).

3.2.13 Harvest index (%)

Harvest index demonstrated positive and significant genetic correlations with kernel yield per plant ($r_g = 0.6964$, $r_p = 0.5184$) and pod yield per plant ($r_g = 0.6876$, $r_p = 0.4822$) and sound mature kernel ($r_g = 0.5365$, $r_p = 0.4891$) and 100-kernel weight ($r_g = 0.4197$, $r_p = 0.4044$) and number of mature pods per plant ($r_g = 0.4010$, $r_p = 0.3210$) and shelling percentage ($r_g = 0.3812$, $r_p = 0.2972$). Favourable yet statistically non-significant associations were noted with 100-pod weight ($r_g = 0.1701$) and oil content ($r_g = 0.1675$, $r_p = 0.1229$). In contrast, significant unfavourable correlations were demonstrated with biological yield per plant ($r_g = -0.8656$, $r_p = -0.6791$) and days to 50% flowering ($r_g = -0.7197$, $r_p = -0.6032$) and number of primary branches per plant ($r_g = -0.6739$, $r_p = -0.4819$) and days to maturity ($r_g = -0.6030$, $r_p = -0.2100$) and plant height ($r_g = -0.4676$, $r_p = -0.2986$).

3.2.14 Oil content (%)

Oil content manifested significant favourable genetic correlations with kernel yield per plant ($r_g = 0.4827$, $r_p = 0.2876$), pod yield per plant ($r_g = 0.4667$, $r_p = 0.2420$), sound mature kernel ($r_g = 0.3907$, $r_p = 0.3162$), number of mature pods per plant ($r_g = 0.3891$, $r_p = 0.2469$) and shelling percentage ($r_g = 0.2669$, $r_p = 0.2150$). Non-significant positive associations were documented with 100-kernel weight ($r_g = 0.1793$) and harvest index ($r_g = 0.1675$, $r_p = 0.1229$) and number of primary branches per plant ($r_g = 0.1407$, $r_p = 0.0386$) and plant height ($r_p = 0.0570$) and days to maturity ($r_p = 0.0188$) and biological yield per plant ($r_p = 0.0054$). Conversely, unfavourable yet statistically inconsequential associations were demonstrated with days to 50% flowering ($r_g = -0.1378$), days to maturity ($r_g = -0.1762$), plant height ($r_g = -0.0805$), 100-pod weight ($r_g = -0.0166$, $r_p = -0.0030$) and biological yield per plant ($r_g = -0.0096$).

Findings from this investigation align with preceding research in the field. Multiple investigators including Vasanthi *et al.* (2016) [22], Hampannavar *et al.* (2018) [7], Kadam *et al.* (2018) [10] and Wadikar *et al.* (2018) [23] documented considerable positive genotypic correlations linking number of mature pods per plant to pod yield per plant productivity. John and Reddy (2019) [8] identified favourable genotypic associations connecting pod yield per plant to sound mature kernel. Similarly, research by Kumari and Sasidharan (2020) [14] demonstrated positive relationships between pod yield and parameters including number of mature pods per plant, 100-pod weight, kernel yield per plant and 100-kernel weight. Devarakonda *et al.* (2024) [3] established positive genotypic relationships involving pod yield alongside harvest index and shelling percentage, whereas Sravanti *et al.* (2024) [19] detected substantial positive correlations among pod yield and 100-pod weight, 100-kernel weight, kernel yield per plant and sound mature kernel. Such convergent evidence underscores the utility of these particular traits as reliable indicators for selective breeding aimed at enhancing pod yield performance in groundnut cultivation.

3.3 Path coefficient analysis

Path coefficient analysis, first proposed by Wright (1921) [25], is an effective statistical approach used to partition correlation coefficients into direct and indirect effects, thereby providing a clearer understanding of the causal relationships among traits. This technique was subsequently applied by Dewey and Lu (1959) [4] in selection studies on crested wheatgrass and has since become an important tool

in plant breeding research. Path coefficient analysis was performed at both the genotypic (Table 3 and Figure 1) and phenotypic levels (Table 4 and Figure 2) by considering pod yield per plant as the dependent variable.

Residual effects of 0.14% (genotypic) and 0.38% (phenotypic) indicate that the studied traits explained ~99.86% and ~99.62% of pod yield variation respectively, validating the path analysis reliability. At the genotypic level, kernel yield per plant (1.1624) showed the strongest positive direct influence on pod yield per plant, followed by number of mature pods per plant (0.0793), number of primary branches per plant (0.0644), 100-kernel weight (0.0383) and sound mature kernel (0.0049). These observations suggest that employing direct selection tactics focused on these specific attributes would prove beneficial in groundnut improvement initiatives. Phenotypically,

kernel yield per plant (0.9065) again demonstrated the greatest direct influence, followed by number of mature pods per plant (0.1530), 100-pod weight (0.1111), harvest index (0.0672) and biological yield per plant (0.0576). Kernel yield per plant, biological yield per plant, number of mature pods per plant and harvest index demonstrated both positive direct effects and strong correlations with pod yield per plant, suggesting reliable selection criteria.

Previous studies by Solanki *et al.* (2019) [18], John and Reddy (2019) [8], Hampannavar *et al.* (2018) [7], Kiranmai *et al.* (2016), Jain *et al.* (2016) and Mudgalkar *et al.* (2025) [16] consistently support these findings, identifying kernel yield per plant, number of mature pods per plant, biological yield per plant, harvest index and 100-kernel weight as dependable benchmarks for pod yield improvement in groundnut breeding programmes.

Table 1: Analysis of variance (mean sum of square) for fourteen characters under study in groundnut

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of mature pods per plant	100-pod weight (g)	100-kernel weight (g)
Replications	2	27.46**	137.84*	20.86**	11.13**	45.50**	1240.42**	45.93**
Genotypes	69	20.88**	43.37	11.04**	1.80**	36.84**	489.32**	95.88**
Error	138	2.67	31.41	3.16	0.48	6.69	37.79	4.91
Source of variation	d.f.	Shelling percentage (%)	Sound mature kernel (SMK%)	Pod yield per plant (g)	Kernel yield per plant (g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)
Replications	2	36.40**	13.92	97.04**	33.06**	424.05**	23.88	5.74**
Genotypes	69	45.07**	96.02**	20.71**	11.37**	160.86**	555.32**	6.01**
Error	138	7.91	6.24	6.44	2.86	29.08	10.50	0.82

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

Table 2: Estimates of genotypic (r_g) and phenotypic (r_p) correlations coefficients among 14 traits in groundnut

		DFP	DM	PH	PBPP	MPPP	100PW	100KW	SP	SMK	KYPP	BYPP	HI	OC	PYPP
DFP	r_g	1.0000	0.7753**	0.3266**	0.7533**	-0.0169	-0.4871**	-0.6823**	-0.3903**	-0.7071**	-0.5005**	0.6974**	-0.7197**	-0.1378	-0.4564**
	r_p	1.0000	0.1936**	0.1079	0.4400**	-0.1036	-0.4007**	-0.5936**	-0.2973**	-0.6064**	-0.4240**	0.3524**	-0.6032**	-0.1707*	-0.3820**
DM	r_g		1.0000	0.7060**	0.6618**	0.3124**	-0.6353**	-0.5947**	-0.4237**	-0.5221**	-0.2547*	0.7671**	-0.6030**	-0.1762	-0.1464
	r_p		1.0000	0.1550*	0.1696*	0.0711	-0.1684*	-0.1601*	-0.1941**	-0.1702*	-0.0897	0.2163**	-0.2100**	0.0188	-0.0329
PH	r_g			1.0000	0.5739**	0.1026	-0.3074**	-0.3795**	-0.1008	-0.1797	-0.1358	0.5349**	-0.4676**	-0.0805	-0.1323
	r_p			1.0000	0.3551**	0.1669*	-0.1386*	-0.2111**	-0.1222	-0.1198	0.0663	0.4162**	-0.2986**	0.0570	0.1120
PBPP	r_g				1.0000	0.0454	-0.2907*	-0.5290**	-0.3453**	-0.4488**	-0.2655*	0.8268**	-0.6739**	0.1407	-0.1813
	r_p				1.0000	0.1559*	-0.2030**	-0.3498**	-0.2082**	-0.2794**	-0.0169	0.5809**	-0.4819**	0.0386	0.0488
MPPP	r_g					1.0000	-0.6191**	-0.3861**	0.1495	-0.0124	0.6502**	-0.0728	0.4010**	0.3891**	0.7108**
	r_p					1.0000	-0.4486**	-0.2629**	0.1379*	0.0213	0.7474**	0.2833**	0.3210**	0.2469**	0.7842**
100PW	r_g						1.0000	0.8396**	0.2095	0.4642**	0.1394	-0.2010	0.1701	-0.0166	0.0968
	r_p						1.0000	0.8226**	0.1041	0.4350**	0.1843**	-0.0825	0.1812**	-0.0030	0.1800**
100KW	r_g							1.0000	0.4254**	0.5992**	0.3268**	-0.4733**	0.4197**	0.1793	0.2318
	r_p							1.0000	0.3157**	0.5610**	0.3142**	-0.2818**	0.4044**	0.1635*	0.2491**
SP	r_g								1.0000	0.3375**	0.6231**	-0.4044**	0.3812**	0.2669*	0.3321**
	r_p								1.0000	0.2409**	0.4783**	-0.2440**	0.2972**	0.2150**	0.1873**
SMK	r_g									1.0000	0.4457**	-0.5004**	0.5365**	0.3907**	0.4047**
	r_p									1.0000	0.3511**	-0.3111**	0.4891**	0.3162**	0.3131**
KYPP	r_g										1.0000	-0.3665**	0.6964**	0.4827**	0.9436**
	r_p										1.0000	0.1627*	0.5184**	0.2876**	0.9500**
BYPP	r_g											1.0000	-0.8656**	-0.0096	-0.2829*
	r_p											1.0000	-0.6791**	0.0054	0.2648**
HI	r_g												1.0000	0.1675	0.6876**
	r_p												1.0000	0.1229	0.4822**
OC	r_g													1.0000	0.4667**
	r_p													1.0000	0.2420**
PYPP	r_g														1.0000
	r_p														1.0000

*, ** significant at 5% and 1% level, respectively

[r_g = Genotypic correlation coefficients; r_p = Phenotypic correlation coefficients; DFP: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-pod weight (g); 100KW: 100-kernel weight (g); KYPP: Kernel yield per plant (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%); PYPP: Pod yield per plant (g)]

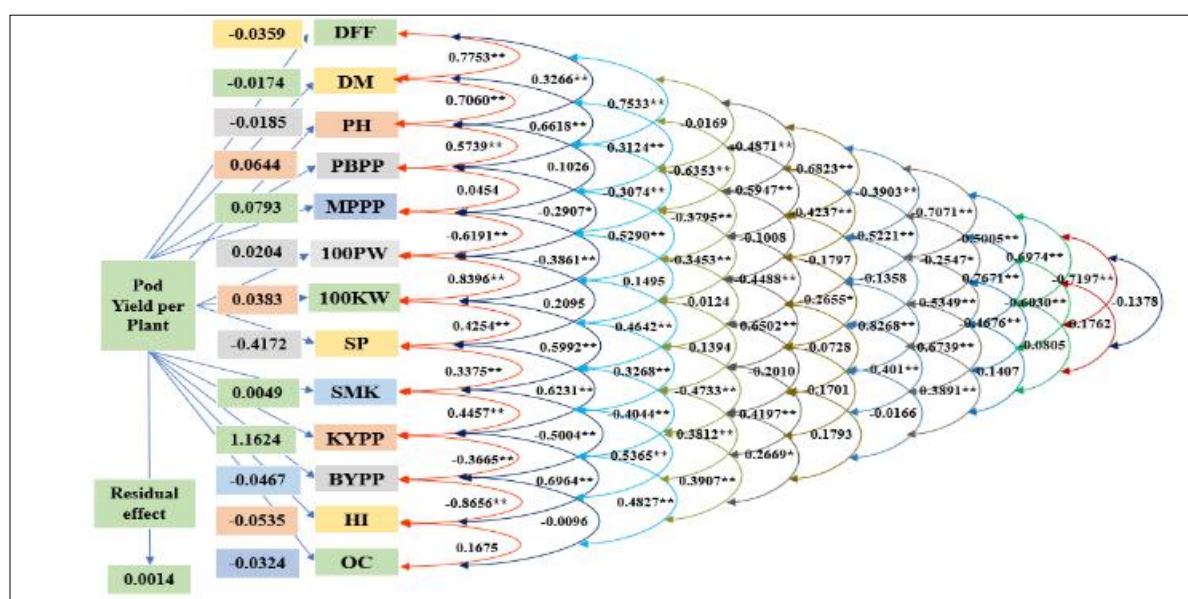
Table 3: Direct and indirect effects (Genotypic path matrix) of thirteen characters on pod yield per plant in groundnut

	DFE	DM	PH	PBPP	MPPP	100PW	100KW	SP	SMK	KYPP	BYPP	HI	OC	PYPP
DFE	-0.0359	-0.0135	-0.0060	0.0485	-0.0013	-0.0099	-0.0261	0.1628	-0.0035	-0.5817	-0.0325	0.03854	0.0044	-0.4564**
DM	-0.0278	-0.0174	-0.0130	0.0426	0.0248	-0.0130	-0.0227	0.1768	-0.0025	-0.2960	-0.0358	0.0322	0.0057	-0.1464
PH	-0.0117	-0.0123	-0.0185	0.0369	0.0081	-0.0063	-0.0145	0.0420	-0.0008	-0.1578	-0.0249	0.0250	0.0026	-0.1323
PBPP	-0.0270	-0.0115	-0.0106	0.0644	0.0036	-0.0059	-0.0202	0.1440	-0.0022	-0.3086	-0.0386	0.0360	-0.0045	-0.1813
MPPP	0.0006	-0.0054	-0.0019	0.0029	0.0793	-0.0126	-0.0148	-0.0623	-0.00006	0.7558	0.0034	-0.0214	-0.0126	0.7108
100PW	0.0174	0.0110	0.0056	-0.0187	-0.0491	0.0204	0.0321	-0.0874	0.0023	0.1620	0.0093	-0.0091	0.0005	0.0968
100KW	0.0245	0.0103	0.0070	-0.0341	-0.0306	0.0172	0.0383	-0.1775	0.0029	0.3798	0.0221	-0.0224	-0.0058	0.2318
SP	0.0140	0.0073	0.0018	-0.0222	0.0118	0.0042	0.0163	-0.4172	0.0016	0.7243	0.0188	-0.0204	-0.0086	0.3321**
SMK	0.0253	0.0091	0.0033	-0.0289	-0.0009	0.0095	0.0229	-0.1408	0.0049	0.5181	0.0233	-0.0287	-0.0126	0.4047**
KYPP	0.0179	0.0044	0.0025	-0.0171	0.0516	0.0028	0.0125	-0.2600	0.0022	1.1624	0.0171	-0.0373	-0.0156	0.9436**
BYPP	-0.0250	-0.0133	-0.0099	0.0532	-0.0057	-0.0041	-0.0181	0.1687	-0.0024	-0.4259	-0.0467	0.0463	0.0003	-0.2829*
HI	0.0258	0.0105	0.0086	-0.0434	0.0318	0.0034	0.0160	-0.1590	0.0026	0.8095	0.0404	-0.0535	-0.0054	0.6876**
OC	0.0049	0.0030	0.0014	0.0090	0.0308	-0.0003	0.0068	-0.1113	0.0019	0.5611	0.0004	-0.0089	-0.0324	0.4667**

Residual effect = 0.0014

*, ** significant at 5% and 1% levels of significance, respectively

[DFE: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-pod weight (g); 100KW: 100-kernel weight (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); KYPP: Kernel yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%); PYPY: Pod yield per plant(g)]



[DFE: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-pod weight (g); 100KW: 100-kernel weight (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); KYPP: Kernel yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%)]

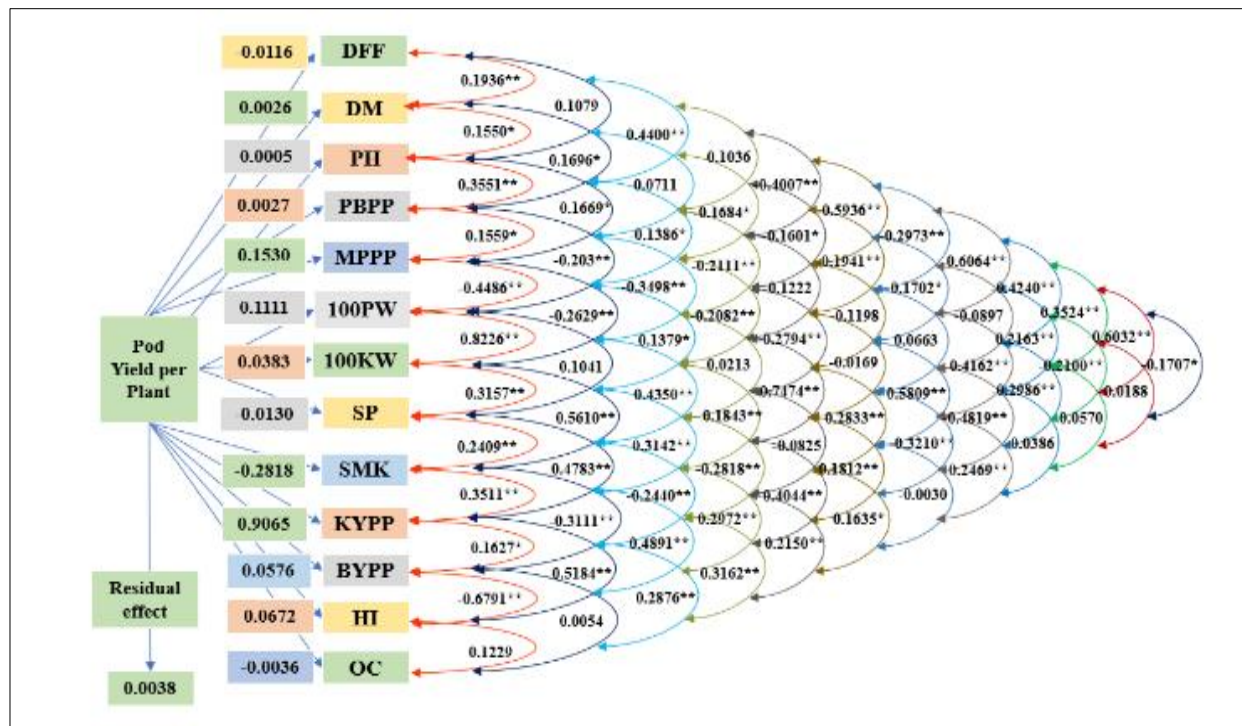
Fig 1: Path diagram depicting genotypic correlation and direct effects of yield attributes on pod yield per plant**Table 4:** Direct and indirect effects (phenotypic path matrix) of thirteen characters on pod yield per plant in groundnut

	DFE	DM	PH	PBPP	MPPP	100PW	100KW	SP	SMK	KYPP	BYPP	HI	OC	PYPP
DFE	-0.0116	0.0005	0.00006	0.0012	-0.0158	-0.0445	0.0077	0.0837	0.0006	-0.3843	0.0203	-0.0405	0.0006	-0.3820**
DM	-0.0022	0.0026	0.00009	0.0004	0.0108	-0.0187	0.0020	0.0546	0.0001	-0.0813	0.0124	-0.0141	-0.00007	-0.0329
PH	-0.0012	0.0004	0.0005	0.0009	0.0255	-0.0154	0.0027	0.0344	0.0001	0.0601	0.0239	-0.0200	-0.0002	0.1120
PBPP	-0.0051	0.0004	0.0002	0.0027	0.0238	-0.0225	0.0045	0.0586	0.0003	-0.0154	0.0334	-0.0323	-0.0001	0.0487
MPPP	0.0012	0.0001	0.0001	0.0004	0.1530	-0.0498	0.0034	-0.0388	-0.00002	0.6775	0.0163	0.0215	-0.0009	0.7842**
100PW	0.0046	-0.0004	-0.00008	-0.0005	-0.0686	0.1111	-0.0107	-0.0293	-0.0004	0.1670	-0.0047	0.0121	0.00001	0.1800**
100KW	0.0069	-0.0004	-0.0001	-0.0009	-0.0402	0.0914	-0.0130	-0.0889	-0.0006	0.2848	-0.0162	0.0271	-0.0006	0.2491**
SP	0.0034	-0.0005	-0.00007	-0.0005	0.0211	0.0115	-0.0041	-0.2818	-0.0002	0.4335	-0.0140	0.0199	-0.0007	0.1874**
SMK	0.0070	-0.0004	-0.00007	-0.0007	0.0032	0.0483	-0.0073	-0.0678	-0.0011	0.3182	-0.0179	0.0328	-0.0011	0.3131**
KYPP	0.0049	-0.0002	0.00004	-0.00005	0.1143	0.0204	-0.0041	-0.1347	-0.0004	0.9065	0.0093	0.0348	-0.0010	0.9500**
BYPP	-0.0041	0.0005	0.0002	0.0016	0.0433	-0.0091	0.0036	0.0687	0.0003	0.1474	0.0576	-0.0456	-0.00002	0.2648**
HI	0.0070	-0.0005	-0.0001	-0.0013	0.0491	0.0201	-0.0052	-0.0837	-0.0005	0.4699	-0.0391	0.0672	-0.0004	0.4822**
OC	0.0019	0.00005	0.00003	0.0001	0.0377	-0.0003	-0.0021	-0.0605	-0.0003	0.2606	0.0003	0.0082	-0.0036	0.2421**

Residual effect = 0.0038

*, ** significant at 5% and 1% levels of significance, respectively

[DFE: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-pod weight (g); 100KW: 100-kernel weight (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); KYPP: Kernel yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%); PYPY: Pod yield per plant(g)]



[DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-pod weight (g); 100KW: 100-kernel weight (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); KYPP: Kernel yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%)]

Fig 2: Path diagram depicting phenotypic correlation and direct effects of yield attributes on pod yield per plant

Conclusion

Genotypic correlation values consistently surpassed phenotypic equivalents, indicating genetic influences dominated over environmental factors. Pod yield per plant exhibited substantial positive correlations with kernel yield per plant, number of mature pods per plant, harvest index, sound mature kernel, oil content and shelling percentage across measurement scales, underscoring their significance for yield improvement. Path coefficient investigation identified kernel yield per plant as the paramount determinant, exhibiting maximal positive direct influence on pod yield per plant at both genotypic and phenotypic levels. Genotypic assessment revealed number of mature pods per plant, number of primary branches per plant, 100-kernel weight and sound mature kernel as secondary contributors, while phenotypic evaluation highlighted number of mature pods per plant, 100-pod weight, harvest index and biological yield per plant demonstrating notable direct effects. Days to maturity showed minimal selection value despite positive direct influence due to unfavourable overall association with pod yield per plant. Negligible residual effects at genotypic (0.0014) and phenotypic (0.0038) levels confirmed evaluated characteristics encompassed nearly complete pod yield variation, validating the path coefficient analysis reliability.

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Conflict of interest: None

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