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INHERITANCE PATTERN OF LATE LEAF SPOT RESISTANCE IN F_1, F_2 AND BACKCROSS GENERATIONS OF GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

Late leaf spot (LLS), caused by *Phaeoisariopsis personata* is one of the major foliar diseases limiting groundnut productivity. Host-plant resistance is considered an important component of sustainable management of the disease. The present investigation was conducted at the Research Farm, Department of Genetics and Plant Breeding, RVSKVV, Gwalior, M.P. during *kharif*, 2025 to study the inheritance pattern of late leaf spot resistance using modified 1-9 disease-rating scale in different generations of groundnut. Four crosses, *viz.*, TG-86 × DH-245, TG-86 × DH-257, Nitya Harita × DH-245 and Nitya Harita × DH-257, were evaluated along with their parental genotypes in F_1, F_2, BC_1 and BC_2 generations. The male parents, DH-245 and DH-257 exhibited resistance to late leaf spot. The female parent Nitya Harita and TG-86 were found to be susceptible to LLS. Among the progenies, the F_2 and BC_2 generations of Nitya Harita × DH-257 recorded the lowest disease score of 1. Nitya Harita × DH-245 also showed a comparatively stable resistant reaction, with scores of 3 in F_1, F_2 and BC_2. The TG-86-based crosses exhibited greater variation among generations and generally had higher disease scores.

***Key words*:** Groundnut, late leaf spot, inheritance, segregating generations, backcross and disease resistance.

Introduction

Groundnut (*Arachis hypogaea* L.), also known as peanut, is an important self-pollinated leguminous oilseed crop belonging to the family fabaceae. It is an annual herbaceous plant characterized by geocarpic fruiting, in which the developing pods mature below the soil surface. Groundnut is believed to have originated in South America and is cultivated extensively in tropical and subtropical regions because of its adaptability to diverse agro-climatic conditions. The cultivated groundnut is an allotetraploid species (2n = *4x* = 40, AABB), which is believed to have originated through hybridization between the diploid progenitors *Arachis duranensis* (A-genome) and *Arachis ipaensis* (B-genome), followed by chromosome doubling (Janila *et al.*, 2013a). Groundnut is an economically important crop valued primarily for its high-quality edible oil and protein-rich kernels. The seeds generally contain substantial amounts of oil and protein and are consumed directly as food or processed into oil, peanut butter, confectionery products and other food products. Groundnut also contributes to soil fertility through biological nitrogen fixation and provides valuable haulms that are used as livestock feed. Its importance is particularly high in developing countries, where it contributes to household nutrition, farm income and the edible-oil industry (Zhuang *et al.*, 2019) Despite its economic and nutritional importance, groundnut productivity is constrained by several biotic and abiotic stresses, with fungal diseases such as late leaf spot and rust being among the major constraints to stable

production. Severe infection can reduce the effective leaf area of plants and consequently interfere with the accumulation of assimilates required for pod development and seed filling.

Late leaf spot is caused by the fungal pathogen *Phaeoisariopsis personata* (Berk. & Curt.) generally becomes more pronounced as the crop advances towards maturity. Leaf spot diseases are among the most important foliar diseases affecting groundnut production worldwide. Under intensive production systems in the USA, where fungicide application is routinely practiced, yield losses due to leaf spots have generally been estimated at around 10%. In contrast, under the semi-arid tropics, where disease management is often limited, leaf-spot infections can cause yield reductions exceeding 50%. When leaf spots occur in combination with rust, yield losses may reach as high as 70% under severe disease epidemics (Subrahmanyam *et al*., 1984; McDonald *et al*., 1985). In India, late leaf spot is widely distributed across groundnut-growing regions and is considered one of the major constraints to productivity, particularly during the rainy season. Under favourable conditions and in the absence of effective disease management, LLS alone can result in yield losses of more than 50%, with reported losses generally ranging from approximately 15-59% depending on genotype, location, disease severity and season (Gujar *et al*., 2025). The disease is also of considerable importance in Madhya Pradesh. Groundnut leaf-spot epidemics have been documented in the Gwalior region, where severe early and late leaf-spot infection has been observed under field conditions. Several studies in central India demonstrated that groundnut leaf-spot severity is strongly associated with warm and humid weather conditions, confirming the potential for serious disease development in the region during the rainy season (Gangwar *et al*., 2014; Pooniya *et al*., 2020 and Sonaniya *et al*., 2025).

Field evaluation using a standardized visual disease-rating scale has consequently been widely used to identify resistant germplasm and breeding materials (Subrahmanyam *et al*., 1995). The inheritance of resistance to late leaf spot has been studied through conventional genetic analysis, quantitative trait locus (QTL) mapping and marker-assisted approaches. Earlier genetic studies have shown that resistance may involve both nuclear and maternal effects, with additive genetic effects contributing substantially to resistance expression (Janila *et al*., 2013b). Molecular studies have further demonstrated that resistance is associated with several genomic regions rather than being controlled by a single universal locus. Khedikar *et al*., (2010) identified multiple QTLs associated with late leaf spot resistance, while subsequent studies confirmed major and minor genomic regions contributing to the trait (Clevenger *et al*., 2018; Han *et al*., 2018; Chu *et al*., 2019). The expression of foliar disease resistance can also vary with environment and disease pressure. Management of LLS mainly relies on repeated applications of fungicides. Although fungicides can effectively reduce disease development, their continuous use increases production costs and may contribute to environmental contamination and the development of fungicide resistance. Therefore, the development and utilization of resistant cultivars is considered a more economical, environmentally sustainable and practical approach for managing LLS. Incorporation of resistance into high-yielding and agronomically desirable groundnut backgrounds is consequently an important objective of groundnut improvement programmes. Resistance to LLS in groundnut is generally considered a quantitative trait, with its expression influenced by genetic background and environmental conditions (Chaudhari *et al*., 2019). The inheritance of resistance may therefore involve several genes with varying effects rather than a single gene controlling the trait. Understanding the genetic control of LLS resistance is essential for selecting suitable parents, designing effective breeding populations, and improving the efficiency of selection in segregating generations. Studies on the inheritance of LLS resistance have reported differences in the relative contribution of additive and non-additive genetic effects, indicating that the genetic architecture of the trait can vary among parental combinations. Thus, the evaluation of segregating generations remains useful for identifying combinations in which resistance is expressed sufficiently well to support selection.

In view of the substantial yield losses associated with LLS and the limitations of chemical control, understanding the inheritance of LLS resistance is of considerable importance for developing resistant groundnut cultivars (Benagi, 1995). The development of disease-resistant cultivars is considered one of the most practical and economical approaches for reducing losses associated with the disease. The present investigation was therefore undertaken to study the inheritance of LLS resistance in selected groundnut crosses and to determine the nature and magnitude of genetic effects governing the expression of the trait. The information gained from this study will help in identifying effective selection strategies for incorporating LLS resistance into improved groundnut breeding material.

Table 1: Modified 9-point scale for Late Leaf Spot used for screening of groundnut.

Disease Score	Phenotype Description	Disease Severity (%)
1	No disease	0
2	Lesions present largely on lower leaves; no defoliation	1–5
3	Lesions present largely on lower leaves, few on middle leaves; defoliation of some leaflets evident on lower leaves	6–10
4	Lesions present on lower and middle leaves but severe on lower leaves; defoliation of some leaflets evident on lower leaves	11–20
5	Lesions present on lower and middle leaves; over 50% defoliation of lower leaves	21–30
6	Severe lesions on lower and middle leaves; lesions present but less severe on top leaves; extensive defoliation of lower leaves; some defoliation on middle leaves	31–40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and middle leaves	41–60
8	Defoliation of all lower and middle leaves; severe lesions on top leaves evident	61–80
9	Almost all leaves defoliated, leaving bare stem; some leaflets may remain but show severe leaf spot	81–100

Materials and Methods

Experimental Material

The investigation was carried out during *kharif*, 2025 using four parental lines and their derived segregating generations. TG-86 and Nitya Harita were used as female parents, while DH-245 and DH-257 were used as male parents.

Four crosses were considered in study:

1. TG-86 × DH-245
2. TG-86 × DH-257
3. Nitya Harita × DH-245
4. Nitya Harita × DH-257

For each cross, observations were recorded on their F_1, F_2, BC_1 and BC_2 generations. The BC_1 generation represented the backcross to the respective female parent, whereas BC_2 represents the backcross developed using the respective male parent.

Disease assessment

Late leaf spot reaction was assessed using the 1-9 visual disease-rating scale developed by Subrahmanyam *et al*., (1995) (Table 1). The scale provides a numerical estimate of disease severity, with lower values representing greater resistance.

Results and Discussion

Reaction of parental lines

Marked differences were observed among the four parental lines used in the study. DH-245 recorded the lowest disease score of 1 and was classified as highly resistant. DH-257 recorded a score of 2 and was classified as resistant. In contrast, TG-86 recorded a score of 7 and Nitya Harita recorded a score of 6, both were classified as susceptible (Table 2).

Table 2: Reaction of parental lines to late leaf spot.

Parent	Disease score	Reaction
TG-86 (female)	7	Susceptible
Nitya Harita(female)	6	Susceptible
DH-245 (male)	1	Highly resistant
DH-257(male)	2	Resistant

The contrasting disease reactions of the parents provided useful variation for examining the expression of resistance in the derived generations. DH-245 and DH-257 were the two clear sources of resistance in the material studied. Their low disease scores make them particularly relevant as donor parents for incorporating resistance into susceptible breeding backgrounds. The identification of resistant sources through field screening is consistent with the established approach for improving foliar disease resistance in groundnut. Previous studies have also demonstrated that resistance can be accumulated through breeding and that several genomic regions contribute to late leaf spot resistance (Khedikar *et al*., 2010; Clevenger *et al*., 2018).

Performance of TG-86 × DH-245

The TG-86 × DH-245 cross showed considerable variation among generations. The F_1 recorded a disease score of 5, while the F_2 recorded 6. The BC_1 generation, obtained by backcrossing to TG-86, recorded the highest score of 7. In contrast, the BC_2 generation, which was

Table 3: Disease reaction of generations derived from TG-86 × DH-245.

Generation	Disease score	Reaction
F_1- TG-86 × DH-245	5	Moderately resistant
F_2- by selfing F_1	6	Susceptible
BC_1- (TG-86 × DH-245) × TG-86	7	Susceptible
BC_2- (TG-86 × DH-245) × DH-245	3	Resistant

Table 4: Disease reaction of generations derived from TG-86 × DH-257.

Generation	Disease score	Reaction
F_1- TG-86 × DH-257	7	Susceptible
F_2- by selfing F_1	5	Moderately resistant
BC□ - (TG-86 × DH-257) × TG-86	7	Resistant
BC, - (TG-86 × DH-257) × DH-257	2	Susceptible

backcrossed to DH-245, recorded a considerably lower score of 3 (Table 3).

Performance of TG-86 × DH-257

The contrasting scores among the generations are noteworthy. Although DH-257 was resistant the TG-86 × DH-257 combination displayed the greatest average disease score among the four crosses. The F_1 and BC_1 generations reflected high disease score of 7. Conversely, the F_2 had a disease score of 5 and BC_2 showed a score of 2 (Table 4).

Performance of Nitya Harita × DH-245

The Nitya Harita × DH-245 cross performed considerably better than either of the crosses involving TG-86. The F_1, F_2 and BC_2 generations each recorded a disease score of 3, while BC_1 recorded 5 (Table 5).

Performance of Nitya Harita × DH-257

Among all four crosses, Nitya Harita × DH-257 showed the lowest mean disease score. The F_1 recorded a score of 3, the F_2 and BC_2 reflected high resistance with score of 1 and BC_1 has the disease score of 7 (Table 6).

Comparison among cross combinations

The mean disease score of each cross was calculated from its F_1, F_2, BC_1 and BC_2 generations (Table 7).

The two Nitya Harita-derived crosses therefore showed better overall disease reactions than the TG-86-derived crosses. Among them, Nitya Harita × DH-257 was particularly favourable because the F_2 and BC_2 generations both exhibited highly resistant reactions.

Table 5: Disease reaction of generations derived from Nitya Harita × DH-245.

Generation	Disease score	Reaction
F_1- Nitya Harita × DH-245	3	Resistant
F_2- by selfing F_1□	3	Resistant
BC_1- (Nitya Harita × DH-245) × Nitya Harita	5	Moderately resistant
BC_2- (Nitya Harita × DH-245) × DH-245	3	Resistant

Table 6: Disease reaction of generations derived from Nitya Harita × DH-257.

Generation	Disease score	Reaction
F_1- Nitya Harita × DH-257	3	Resistant
F_2- by selfing F_1	1	Highly resistant
BC_1- (Nitya Harita × DH-257) × Nitya Harita	7	Susceptible
BC_2- (Nitya Harita × DH-257) × DH-257	1	Highly resistant

Discussion

The present observations indicate that late leaf spot resistance varied substantially among generations within individual crosses. The resistant parents DH-245 and DH-257 did not produce uniformly resistant reactions in all their derived generations. Similarly, the susceptible parents did not necessarily result in uniformly susceptible progeny. This pattern is congruent with the quantitative nature of late leaf spot resistance reported in previous genetic and molecular studies. Some studies have reflected the involvement of both nuclear and maternal effects, with additive effects playing an important role in resistance towards LLS (Khedikar *et al*., 2010; Janila *et al*., 2013b; Clevenger *et al*., 2018; Han *et al*., 2018; Chu *et al*., 2019).

In the cross TG-86 × DH-245 and TG-86 × DH-257 the relatively low score in BC_2 compared with BC_1 suggests that recovery of the male genetic background was associated with improved disease reaction. This is genetically reasonable because the male parent itself showed a resistant reaction to LLS. The relatively poor mean performance of these cross may be associated with genetic background effects and segregation. Since late leaf spot resistance is known to have a quantitative component, differences among generations can occur depending on the combination and proportion of resistance-associated alleles inherited by the progeny.

In the combinations Nitya Harita × DH-245 and Nitya Harita × DH-257 relatively consistent scores across the F_1, F_2 and BC_2 generations indicate a favourable expression of resistance in this cross. The BC_1 score was somewhat higher, which may reflect the greater

Table 7: Comparative performance of the four cross combinations.

Cross	Female Parent	Male Parent	F_1	F_2	BC_1	BC_2
TG-86 × DH-245	7	1	5	6	7	3
TG-86 × DH-257	7	2	7	5	7	2
Nitya Harita × DH-245	6	1	3	3	5	3
Nitya Harita × DH-257	6	2	3	1	7	1

contribution of the susceptible Nitya Harita background. The consistency observed in three of the four generations makes this combination useful for further evaluation. In particular, the F_2 generation with low scores provides a suitable starting point for selection within a segregating population.

Such differences indicate that genetic background and segregation can substantially affect the observed phenotype. The influence of environmental conditions should also be considered. Field expression of late leaf spot resistance can vary with disease pressure and environmental conditions and significant genotype × environment effects have been reported in groundnut populations (Chaudhari *et al*., 2019). Consequently, confirmation of the resistance observed here would require evaluation over multiple seasons or environments.

The present findings are broadly in agreement with earlier work showing that resistance to late leaf spot is genetically complex. QTL mapping studies have repeatedly identified several genomic regions associated with resistance. Khedikar *et al*., (2010) detected multiple QTLs for late leaf spot resistance in a recombinant inbred population. Chu *et al*., (2019) further identified major QTLs associated with late leaf spot resistance on several chromosomes, demonstrating that relatively large-effect loci can occur within an overall quantitative genetic background. Ahmad *et al*., (2020) also identified major QTLs for late leaf spot resistance in an F_2 population derived from GJG17 × GPBD4. Sonaniya *et al*., (2025) also find several resistant generations in the studied crosses. The presence of resistance in some segregating generations but not others does not necessarily indicate instability of the resistance genes; rather, it may reflect segregation and differences in the genetic background in which resistance alleles are expressed.

Conclusion

The use of resistant donor genotypes in crosses with susceptible or agronomically superior cultivars provides an opportunity to study the inheritance of LLS resistance and identify promising segregants. Segregation studies and evaluation of disease severity or lesion development can provide valuable information on the genetic mechanisms governing resistance. Such information is particularly useful for determining the appropriate breeding strategy and generation at which effective selection should be practiced.

The study revealed substantial variation in late leaf spot reaction among the parental and segregating generations of groundnut. DH-245 and DH-257 were identified as the strongest resistant parental sources, with disease scores of 1 and 2, respectively. Among the four cross combinations, Nitya Harita × DH-257 recorded the lowest across generations, followed by Nitya Harita × DH-245. The TG-86-derived combinations were less favourable overall. Nevertheless, the BC_1 generation of TG-86 × DH-245 recorded a score of 3, while the BC_1 generation of TG-86 × DH-257 recorded a score of 2. The F_2 and BC_2 generations of Nitya Harita × DH-257 were particularly promising, both recording a disease score of 1. Nitya Harita × DH-245 also showed a favourable response, with scores of 3 in the F_1, F_2 and BC_2 generations. These combinations can therefore be considered useful material for further breeding and selection for late leaf spot resistance.

The generation-wise variation indicated differential parental contributions and segregation for LLS resistance. The study supports the usefulness of DH-245 and DH-257 as resistance sources and identified Nitya Harita × DH-257 and Nitya Harita × DH-245 as promising combinations for further breeding. The variation observed among generations indicates that resistance expression is influenced by segregation and genetic background. From a breeding standpoint, selection should therefore focus on individual plants within promising segregating populations rather than relying solely on generation means.

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