



Inheritance of Northern Corn Leaf Blight Resistance in Advanced Generations of Maize (*Zea mays* L.)

Bipasha Datta ^a, Duddukur Rajasekhar ^a,
Thounaojam Bharti ^a and Devyani Sen ^{a*}

^a School of Crop Improvement, College of Post-graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya-793103, India.

Authors' contributions

This work was carried out in collaboration among all authors. Author DS conceptualized the research work. Authors DS and BD designed the experiments, data analysis, interpretation and wrote the manuscript. Authors BD and TB did data collection. Authors BD and DR did advance generations. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/ijpss/2025/v37i25300>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/130650>

Original Research Article

Received: 01/12/2024
Accepted: 03/02/2025
Published: 05/02/2025

ABSTRACT

Developing genetically resistant maize varieties to mitigate yield losses would reduce reliance on chemical control measures. This study underlines the substantial genetic variability and heritability of northern corn leaf blight (NCLB) resistance within a recombinant inbred line (RIL) population, highlighting the genetic basis of the trait. ANOVA revealed highly significant genetic variability among families at the 1% level, confirming the presence of sufficient variability for effective selection. The progression from F₅ to F₆ generations demonstrated the effectiveness of selection, as seen from reduced AUDPC scores in the F₆ generation. A genetic gain of -7.74 and a heritability estimate of 48% further validated the success of selection based on lower AUDPC scores. The

*Corresponding author: E-mail: devyani.sen@gmail.com;

Cite as: Datta, Bipasha, Duddukur Rajasekhar, Thounaojam Bharti, and Devyani Sen. 2025. "Inheritance of Northern Corn Leaf Blight Resistance in Advanced Generations of Maize (*Zea Mays* L.)". *International Journal of Plant & Soil Science* 37 (2):41-47. <https://doi.org/10.9734/ijpss/2025/v37i25300>.

regression analysis supported by the significant positive correlation ($r = 0.65$) revealed a significant association between F_5 selections and the F_6 AUDPC scores, as seen from an R^2 value of 0.42 and a moderate predictive slope of 0.52. These associations suggest that while selection is effective in predicting advanced-generation performance, the residual variability points to the need for incorporating additional genetic or environmental factors to improve predictive accuracy. These findings emphasize the predominance of genetic factors in NCLB resistance and the stability of resistance traits across the two generations, offering insights into the genetic control of the trait. By providing a solid foundation for breeding efforts targeting durable resistance, this study contributes to the development of maize varieties with enhanced NCLB resistance and supports sustainable agricultural practices.

Keywords: AUDPC; heritability; maize; NCLB; selection.

1. INTRODUCTION

Resistance breeding is a critical area of research in crop improvement, particularly for economically significant crops like maize. Maize, the world's most grown staple crop occupies about 193.7 million hectares worldwide, with an average productivity of 5.75 tons per hectare (Shekhar and Singh, 2021). An extremely versatile crop grown across different ecological zones, however, maize is a vulnerable host to various foliar diseases which can severely impair yields and cause economic losses. Northern Corn Leaf Blight (NCLB), caused by *Exserohilum turcicum*, is one such globally prevalent disease of maize (Chen et al., 2016).

In warm and humid conditions that promote the disease, spindle-shaped lesions form on the leaves. These lesions spread rapidly in susceptible hosts, reducing their photosynthetic capacity and ultimately affecting the yield (Hurni et al., 2015; Zhu et al., 2022). These challenges necessitate sustainable management strategies, with resistance breeding emerging as a primary solution since it represents a long-term and sustainable approach.

Breeding disease-resistant genotypes offers several advantages, including reduced reliance on fungicides, increased productivity, and improved environmental sustainability (Galiano-Carneiro and Miedaner, 2017). Moreover, understanding the genetic basis of resistance traits accelerates the development of improved varieties, strengthens food security, and promotes ecosystem stability. Advances in molecular tools, such as marker-assisted selection (MAS), have further enabled researchers to identify genetic markers linked to resistance. By integrating these markers into breeding programs, researchers can develop resilient maize varieties (Yin et al., 2003) that

empower farmers to manage disease pressures effectively and maintain stable crop production.

To complement molecular approaches, robust phenotyping is essential for accurately assessing disease resistance. One of the widely used phenotyping methods is the Area Under the Disease Progress Curve (AUDPC) - a quantitative measure that estimates the intensity of disease spread over time (Welz and Geiger, 2000). This method accounts for the dynamic nature of disease progression allowing researchers to compare different genotypes. AUDPC is especially useful in breeding programs, where it helps in identifying and selecting disease-resistant varieties. It can be used to screen and evaluate large populations for resistance under controlled or field conditions, leading to identification of genotypes that can withstand disease pressures more effectively (Jeger and Viljanen-Rollinson, 2001).

Based on AUDPC scores as a tool, for identifying resistance in maize populations, this study was formulated to investigate the inheritance of NCLB across two selfing generations of maize breeding families developed from a biparental mating, involving a cross between two contrasting lines for NCLB disease. The primary objective was to understand the genetic inheritance and follow disease progression in the F_5 and F_6 generations with the goal of improving the selection of resistant lines from this bi-parental population.

2. MATERIALS AND METHODS

2.1 Experimental Material

A mapping population was developed using two parental lines: RM16 (resistant) and SS1 (susceptible). The F_1 progeny were selfed to advance the population from the F_2 to the F_6 generation. The advanced generations,

specifically the F₅ and F₆, were evaluated for the inheritance of NCLB resistance. Phenotyping was done for 119 F₅ families and 113 selected F₆ individuals over two growing seasons to assess NCLB disease resistance. Field trials were carried out over two consecutive seasons in Ri-Bhoi District, Meghalaya, India, a natural hotspot for NCLB occurrence. Routine intercultural practices were performed throughout the growing seasons to maintain an agronomically healthy standing crop.

2.2 Phenotyping Based on AUDPC Scores

Phenotyping was based on calculation of AUDPC scores. At the beginning of the growing season, the causal organism was isolated and cultured on potato dextrose agar medium. Inoculum was then prepared and applied by spraying on 25-30 days old seedlings. Once disease symptoms appeared, the progression of the disease was recorded at 3 days interval for a period of 15 days. From this disease progression data, area under disease progress curve (AUDPC) was calculated (Madden et al., 2007).

$$AUDPC = \sum_{i=1}^n \left(\frac{y_i + y_{i+1}}{2} \right) (t_{i+1} - t_i)$$

where, n = total number of observations, y_i = disease area at the ith observation and t_i = time at the ith observation. The recorded AUDPC scores were analysed using basic statistics, including the calculation of the mean, variance, mode, and median, in order to understand the nature of the phenotypic data.

2.3 Statistical Analysis

An ANOVA was done to determine if differences for response to NCLB across the families and generations are statistically significant.

Frequency distribution analysis and response to selection which included studies on selection differential and genetic gain to ultimately calculate the realized heritability of disease progression was also done (Singh and Chaudhary, 1981).

Here, selection differential S = iσ_p

Where, i= intensity of selection (10%) and σ_p is the phenotypic standard deviation

Genetic gain (R) was calculated as the difference between mean values of the F₆ generation and the original F₅ generation.

Realized heritability h² was calculated as h² = R/iσ_p

Pearson's correlation and regression analysis to determine the goodness of fit were also performed to understand the nature of association between F₅ families and the selections advanced to the F₆ generation.

3. RESULTS

3.1 Analysis of Variance (ANOVA)

ANOVA (Table 1) indicated highly significant differences among the families at 1 % level of significance, implying the presence of genetic variability within the RIL population for response to NCLB disease incidence. This variability is important for identifying lines with enhanced resistance to the disease. Conversely, the marginally significant difference observed between generations suggests that the disease pressure experienced by both generations was largely comparable. This finding implies that the heritability of disease response is predominantly governed by genetic factors, with minimal influence from environmental variation. All in all, these results reinforce the stability of the trait across generations, highlighting the role of genetic control over NCLB resistance (Ding et al., 2015).

Table 1. ANOVA of AUDPC Scores for disease progression in F₅ and F₆ generations

Source of Variation	SS	df	MS	F	P-value	F critical
Genotype (Families)	7964.55	112	71.11**	4.47	0.00**	1.37
Generation	65.70	1	65.70	4.13	0.05	3.93
Error	1782.74	112	15.92			
Total	9812.99	225				

*p < 0.05; **p < 0.01

3.2 Frequency Distribution and Response to Selection

Based on the frequency distribution studies of the F_5 families, F_5 selections and the F_6 generation, the mean AUDPC score decreased from F_5 (21.03) to F_6 (13.29) as shown in Fig. 1. This reflects effective selection, with reduced disease severity in subsequent generations. The median and mode also decreased across generations, indicating increase in the F_6 population's disease resistance.

The variability was lower in the F_6 generation, likely due to selection pressure narrowing the range of phenotypes. While the F_5 generation recorded a slight positive kurtosis (0.78), the F_6 generation with a kurtosis of 1, recorded a

sharper peak. The right-skewed distribution in the F_6 generation implied that most individuals were concentrated around lower AUDPC scores. The range of AUDPC scores decreased from F_5 (40.94) to F_6 (31.57), further confirming reduced variability. The minimum AUDPC scores decreased from 5.49 in F_5 to 2.75 in F_6 , showing that selection effectively retained the individuals with better resistance.

A selection differential of 16.23 and a genetic gain of -7.74 were achieved for a selection intensity of 10%. The overall phenotypic standard deviation in the F_5 generation was 9.33. Identifying lines with lower AUDPC scores is desirable, as it signifies higher resistance to NCLB occurrence. The heritability was calculated to be 48% (Fig. 2).

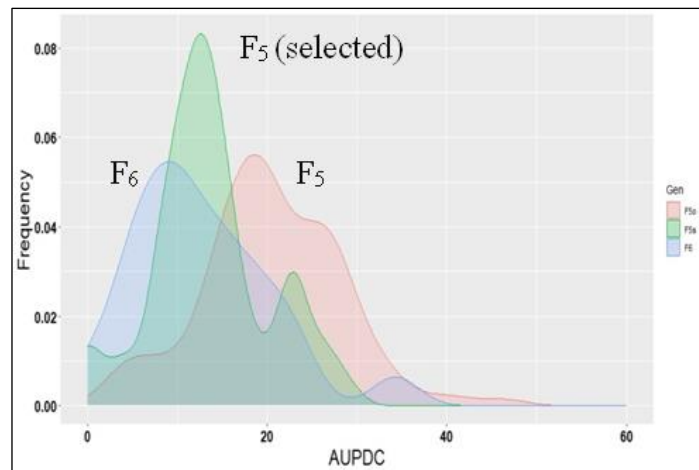


Fig. 1. Frequency distribution graph the F_5 families, selected F_5 RILs and F_6 RILs

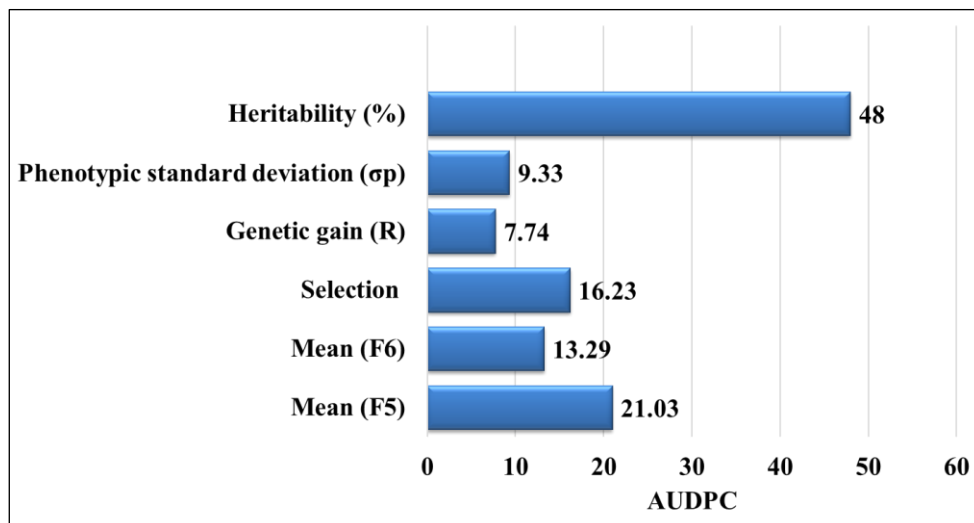
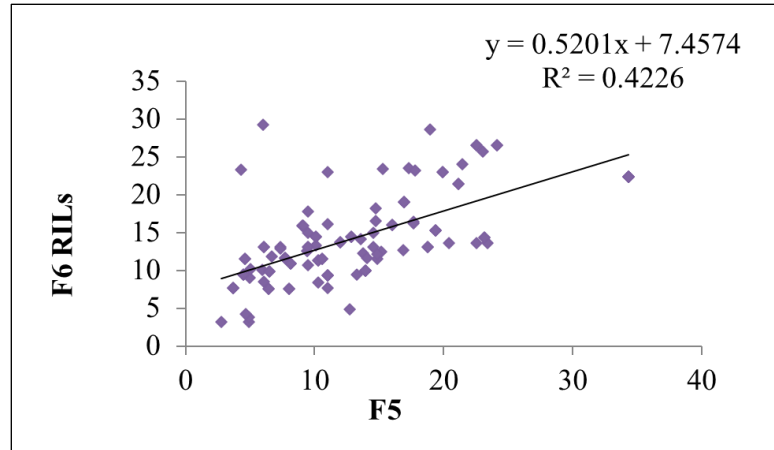


Fig. 2. Response to selection for NCLB disease progress (AUDPC) in the F_5 and F_6 selfing generation

Table 2. Regression ANOVA for F₅ and F₆ generations

Source	df	SS	MS	F	Significance F
Regression	1	2511.22	2511.22	81.23	0.00
Residual	111	3431.67	30.91		
Total	112	5942.89			

**Fig. 3. A regression graph depicting the strong association between F₅ families and F₆ selections**

3.3 Association Studies

Pearson's correlation studies revealed a highly significant 'r' value of 0.65 between F₅ and F₆ generations for AUDPC scores indicating a strong positive relationship between the two generations. For the scatterplot, a positive slope of 0.52, combined with the significant F-statistic and *p*-value (Table 2), confirms that F₅ values have a significant, moderate predictive effect on the F₆ RILs. The R² value and the residual variability indicated that while the model captures a meaningful relationship, additional factors not included in the regression (e.g., environmental influences, epistasis, or other genetic effects) account for a considerable portion of the variation in F₆ as well (De Souza et al., 2020). This analysis highlights the partial predictability of traits in advanced generations (F₆) based on earlier selection in F₅, demonstrating the impact of selection while pointing to areas where model refinement or additional variables could improve predictive accuracy (Fig. 3).

4. DISCUSSION

This study comprehensively evaluated genetic variability, heritability, and response to selection for NCLB resistance in maize, focusing on F₅ and F₆ generations of a biparental population. The results provide significant insights into the

genetic control of resistance, demonstrating the effectiveness of phenotypic selection on the basis of AUDPC scores to improve resistance breeding strategies. The highly significant genetic variability among RILs at the family level, as revealed by ANOVA, highlights the diversity present within the population for resistance to NCLB. This variability is a prerequisite for identifying and advancing superior genotypes with enhanced resistance (Falconer and Mackay, 1996; Ohunakin et al., 2021). Additionally, the comparable performance across generations (marginally significant differences) highlights the role of genetic factors in determining resistance, reinforcing the heritability and stability of the trait across different conditions.

The frequency distribution analysis revealed a clear shift in population characteristics due to selection pressure, as seen in the reduction of AUDPC scores from F₅ to F₆ generations. The narrowing variability and sharper kurtosis in F₆ indicated that selection was effective in concentrating resistance traits while screening out the less favorable phenotypes. The right-skewed distribution in F₆, along with the reduction in range and minimum AUDPC scores, confirmed that selection effectively identified and retained individuals with higher resistance. Notably, the achieved genetic gain combined with a heritability estimate of 48%, highlight the

substantial progress made in improving resistance. These results are particularly significant, given that NCLB resistance is influenced by both vertical (monogenic) and horizontal (polygenic) resistance mechanisms (Galiano-Carneiro and Miedaner, 2017; Welz and Geiger, 2000; Poland et al., 2011). The regression and correlation analyses further emphasized the partial predictability of F_6 generation traits based on F_5 values, as seen from the moderate positive slope, high correlation coefficient ($r = 0.65$), and significant regression statistics. While these results validate the effectiveness of phenotypic selection, the residual variability needs to be addressed in future studies through advanced genomic approaches, such as SNP-based QTL mapping, GWAS (Genome-Wide Association Studies), and genomic selection. These studies would help refine predictive models and enhance the precision of selection efforts (Galiano-Carneiro et al., 2021; Bi et al., 2024). These tools can also help unravel the complex genetic architecture of NCLB resistance, identifying key loci that contribute to disease resistance (Ndlovu et al., 2024).

To further strengthen the breeding program, multi-environment trials across diverse agro-climatic zones are up next. Such trials would ensure the adaptability and stability of resistant lines (Ohunakin et al., 2021), particularly in regions with varying disease pressure, soil conditions, and climatic factors. This is especially critical along the foothills of North east India, which relies heavily on organic farming and where maize is an important crop for economic stability (Singh et al., 2021). Developing NCLB-resistant varieties for this region supports the goals of sustainable agriculture by reducing yield losses, minimizing fungicide dependency, and promoting environmentally friendly farming practices.

7. CONCLUSION

Overall, by focusing on genetic resistance, the findings contribute to the development of resilient maize varieties. These outcomes have broader implications for maize breeding in other regions with similar environmental conditions and disease pressures. The work done reinforces the potential of genetic improvement to transform maize into a more reliable crop for diverse agricultural systems, particularly in regions like the NEHR, where it serves as a vital component of rural livelihoods and poultry feed production

systems. Additionally, integration of advance technologies such as genomic selection can enhance the breeding efficiency and significantly shorten the duration of improvement breeding programs. Furthermore, these studies provide a strong foundation for in-depth evaluation of phenotype-genotype relationships at genomic level, which is valuable for advancing resistant breeding efforts.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

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

ACKNOWLEDGEMENTS

The authors sincerely thank the College of Post-Graduate Studies in Agricultural Sciences and Central Agricultural University (Imphal) for providing the necessary resources and support to conduct this research.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Bi, Y., Jiang, F., Yin, X., Shaw, R. K., Guo, R., Wang, J., & Fan, X. (2024). Identification of candidate gene associated with maize northern leaf blight resistance in a multi-parent population. *Plant Cell Reports*, 43(7), 189.
- Chen, G., Wang, X., Long, S., Jaqueth, J., Li, B., Yan, J., & Ding, J. (2016). Mapping of QTL conferring resistance to northern corn leaf blight using high-density SNPs in maize. *Molecular Breeding*, 36, 1-9.
- De Souza, M. H., Pereira Júnior, J. D., Steckling, S. D. M., Mencialha, J., Dias, F. D. S., Rocha, J., et al. (2020). Adaptability and stability analyses of plants using random regression models. *PLOS ONE*, 15(12), e0233200.
- Ding, J., Ali, F., Chen, G., Li, H., Mahuku, G., Yang, N., et al. (2015). Genome-wide association mapping reveals novel sources of resistance to northern corn leaf blight in maize. *BMC Plant Biology*, 15, 1-11.
- Falconer, D. S., & Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics* (Pearson Education Limited).

- Galiano-Carneiro, A. L., & Miedaner, T. (2017). Genetics of resistance and pathogenicity in the maize *Setosphaeria turcica* pathosystem and implications for breeding. *Frontiers in Plant Science*, 8, 1490.
- Galiano-Carneiro, A. L., Kessel, B., Presterl, T., & Miedaner, T. (2021). Intercontinental trials reveal stable QTL for northern corn leaf blight resistance in Europe and in Brazil. *Theoretical and Applied Genetics*, 134, 63-79.
- Hurni, S., Scheuermann, D., Krattinger, S. G., Kessel, B., Wicker, T., Herren, G., et al. (2015). The maize disease resistance gene *Htn1* against northern corn leaf blight encodes a wall-associated receptor-like kinase. *Proceedings of the National Academy of Sciences*, 112(28), 8780-8785.
- Jeger, M. J., & Viljanen-Rollinson, S. L. H. (2001). The use of the area under the disease-progress curve (AUDPC) to assess quantitative disease resistance in crop cultivars. *Theoretical and Applied Genetics*, 102, 32-40.
- Madden, L. V., Hughes, G., & Bosch, F. V. D. (2007). *The Study of Plant Disease Epidemics*.
- Ndlovu, N., Gowda, M., Beyene, Y., Das, B., Mahabaleswara, S. L., Makumbi, D., et al. (2024). A combination of joint linkage and genome-wide association study reveals putative candidate genes associated with resistance to northern corn leaf blight in tropical maize. *Frontiers in Plant Science*, 15, 1448961.
- Ohunakin, A. O., Odiyi, A. C., & Akinyele, B. O. (2021). Genetic variance components and GGE interaction of tropical maize genotypes under northern leaf blight disease infection. *Cereal Research Communications*, 49, 277-283.
- Poland, J. A., Bradbury, P. J., Buckler, E. S., & Nelson, R. J. (2011). Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *Proceedings of the National Academy of Sciences*, 108(17), 6893-6898.
- Shekhar, M., & Singh, N. (2021). The impact of climate change on changing pattern of maize diseases in Indian subcontinent: A review. *Maize Genetic Resources-Breeding Strategies and Recent Advances*.
- Singh, R. K., & Chaudhary, B. D. (1981). *Biometrical Methods in Quantitative Genetic Analysis*.
- Singh, R., Babu, S., Avasthe, R. K., Das, A., Praharaj, C. S., Layek, J., et al. (2021). Organic farming in North–East India: Status and strategies. *Indian Journal of Agronomy*, 66(5), 163-179.
- Welz, H. G., & Geiger, H. H. (2000). Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breeding*, 119(1), 1-14.
- Yin, X., Wang, Q., Yang, J., Jin, D., Wang, F., Wang, B., & Zhang, J. (2003). Fine mapping of the *Ht2* (*Helminthosporium turcicum* resistance 2) gene in maize. *Chinese Science Bulletin*, 48, 165-169.
- Zhu, M., Ma, J., Liu, X., Guo, Y., Qi, X., Gong, X., et al. (2022). High-resolution mapping reveals a *Ht3*-like locus against northern corn leaf blight. *Frontiers in Plant Science*, 13, 968924.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2025): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:

<https://pr.sdiarticle5.com/review-history/130650>