

Research Article

Development of a predictive model for northern corn leaf blight (NCLB) resistance in maize through SSR markers association and validation

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Abstract - Northern corn leaf blight (NCLB), caused by fungal pathogen *Exserohilum turcicum*, is a major foliar disease of maize, particularly under cool and humid conditions during the dry season (November-February) as observed at the Chai Nat Field Crops Research Center. Severe infections during the reproductive stage can significantly reduce grain yield. Although chemical fungicides are available, their environmental impact makes host plant resistance a sustainable solution. This study aimed to assess the association and predictive accuracy of simple sequence repeat (SSR) markers for NCLB resistance, to support efficient selection of resistant genotypes in maize breeding programs. Three SSR markers, bnlgl198, umc2038 and umc2210, were evaluated for their association with NCLB resistance in 280 sweet corn genotypes derived from two populations, namely CH66C1 and HX75C1. Chi-square test was initially used to perform single marker analysis in order to assess the association between each SSR marker and resistance to NCLB. Markers that showed significant associations were subsequently used to construct prediction models using regression analysis. Model performance was then evaluated using Adjusted R², F-value and receiver operating characteristic (ROC) curve analysis. Five-fold cross-validation was employed to estimate predictive reliability. All three markers, bnlgl198, umc2038, and

umc2210, were significantly associated with NCLB resistance. The model, including umc2038 and bnlg198, showed a positive correlation coefficient of 0.6, an adjusted R^2 of 0.57 and the highest F-value (36.4), indicating that these markers explained 57% of phenotypic variation. The model's predictive accuracy was classification as moderate to high with an area under the ROC (AUC) curve of 0.78. The best threshold identified was 0.51, yielding a true positive rate (TPR) of 0.88, indicating that the model could correctly classify 88% of resistant lines.

Keywords: Northern corn leaf blight, single marker analysis, SSR marker, maize resistance, marker-assisted selection

1. Introduction

Northern corn leaf blight (NCLB), caused by the fungal pathogen *Exserohilum turcicum*, which exhibits high genetic diversity (Turgay et al., 2020) and has become one of the most prevalent and severe diseases affecting maize worldwide. It is widely distributed across Europe, Asia, North and South America, and Africa (CABI, 2025). Early infection with *E. turcicum* before the silking stage leads to the development of large foliar lesions before kernel formation, ultimately resulting in 50-70% yield reduction (De Rossi et al., 2022). In Thailand, a study by Phruetthitthep et al. (2021) reported varying level resistance among genotypes, with a significant reduction in ear with husk fresh weight observed in susceptible genotypes.

The progression of NCLB symptoms begins with chlorotic lesions—yellowing spots caused by chlorophyll depletion. Under optimal environmental conditions, lesions progress into elliptical, cigar-shaped necrotic areas within 7-12 days after infection. These lesions appear gray to brown due to *E. turcicum* sporulation, facilitating rapid dissemination across extensive leaf surfaces. The aggressive nature of NCLB enables it to spread faster than many other maize foliar diseases, posing a significant threat to crop productivity.

To combat this disease, breeding for genetic resistance has become a key strategy. From a genetic perspective,

several resistance genes located at the *Ht* (*Helminthosporium turcicum*) locus confer race-specific resistance to *E. turcicum* (Leonard et al., 1989). Navarro et al. (2020) reported that maize plants carrying the resistance genes *Ht1*, *Ht2*, *Ht3*, and *Htn1*, responded differently to *E. turcicum* infection compared to susceptible lines. *Ht1* conferred resistance to races 0, but not to race 1, or 23N, which represented both compatible and incompatible were used. The results showed that maize carrying the *Ht1* gene developed chlorotic and necrotic lesions, indicating resistance to race 0 but susceptibility to race 1 and 23N. Maize with *Ht2* exhibited leaf chlorosis and small necrosis lesions, showing a similar race-specific resistance pattern. *Ht3* developed chlorotic spots and was also susceptible to races 1 and 23N. While *Htn1*, which does not confer race-specific resistance, displayed quantitative resistance, with either no visible lesions or wilt-like symptoms, as previously described by Raymundo and Hooker (1981). Delayed lesion development—up to four weeks after infection—provided effective protection during the critical stage of crop growth.

Integrating genetic knowledge and molecular biotechnologies into breeding strategies can accelerate the development of resistant maize. While conventional breeding remains foundational, it is often time-consuming and resource-intensive. Molecular breeding technologies, particularly marker-assisted selection

(MAS), have proven to be a powerful tool for accelerating genetic improvement in crops.

Bentolila et al. (1991) successfully mapped the *Ht1* resistance gene, which confers resistance to NCLB, in multiple populations and commercial maize hybrids using the molecular markers *sgcr506* and *umc150B*. Subsequently, Puttarach et al. (2016) reported that polymorphic SSR markers closely linked to the *Ht1* gene were identified in F_2 populations derived from crosses between two pairs of maize lines: high susceptible and high resistance to NCLB. Two SSR markers, *bnlg1721* and *umc1042*, located on chromosome 2, showed close linkage with the *Ht1* gene and could be effectively used as selection markers for identifying resistant individuals in sweet corn F_2 populations.

Recent studies have applied machine learning and statistical models to improve phenotypic trait prediction using molecular and morphological data. For example, classification of *Arabidopsis* miRNAs achieved AUC values up to 0.998 (Elhariri et al., 2014), while Wu et al. (2007) used leaf features and probabilistic neural networks to classify 32 plant species with over 90% accuracy. Genome-wide approaches, such as elastic net regularization (Guzzetta et al., 2010) and phenotypic prediction from root traits (Zhao et al., 2016), further demonstrate the potential of these models in breeding. These findings highlight the growing relevance of predictive modeling in MAS applications. The objective of this study was to assess the association and predictive accuracy of SSR markers for resistance to NCLB in order to support the effective selection of resistant genotypes in maize breeding.

2. Materials and methods

The CH66C1 and HX75C1 populations were developed as parental inbred lines for generation F_1 hybrids with enhanced resistance to NCLB through heterosis.

Consequently, in the analysis of the association between molecular markers and resistance traits, no population structure was considered, as the hybrids were derived from a single cross and thus shared a common genetic background without subpopulation differentiation.

2.1 Plant materials and DNA extraction

The seeds of two S_6 selfed sweet corn populations, namely CH66C1 and HX75C1, were obtained from the Chai Nat Field Crops Research Center, Field Renewable Energy Crops Research Institute, Department of Agriculture, Thailand. Healthy seeds were selected and germinated for approximately two weeks at the Khon Kaen Field Crops Research Center. The CH66C1 population consisted of 138 lines, including 74 NCLB-resistant lines and 64 susceptible lines, while the HX75C1 population comprised 142 lines, consisting of 53 NCLB-resistant lines and 89 susceptible lines. The entire experiment was conducted from October 2023 to September 2024.

The resistance or susceptibility to NCLB of each genotype was previously evaluated under field conditions at the Chiang Mai Field Crops Research Center during the 2022 growing season. A 1-5 visual rating scale was used to assess disease severity, where a score of 1 indicated no symptoms and 5 indicated more than 75% of the leaf area was affected. Genotypes with scores ranging from 1-3 were classified as resistant, and those with scores of 4-5 were classified as susceptible. These phenotypic classifications were used as the basis for model development in the present study.

Young leaves were excised into small pieces and placed into screw-cap tubes containing DNA extraction buffer from a DNA extraction kit (DNAsecure Plant Kit, TIANGEN, China). The samples were then ground using a Bead Mill Homogenizer (Revvity, USA), followed by centrifugation to pellet debris. DNA extraction was

performed according to the manufacturer's protocol. The extracted DNA was then quantified for concentration and purity using a Nano DOT Microspectrophotometer (Hercuvan, UK). Finally, the DNA samples were diluted to a final concentration of 10 ng/ μ L for further analysis.

2.2 PCR amplification

DNA amplification using PCR was performed with three pairs of SSR primers: bnlgl198 (Forward- GTTTG-GTCTTGCTGAAAAATAAAA, Reverse- GCTGGAGGCCTACATTAT TATCTC; Min et al., 2012), umc2038 (Forward- ACAGAAACCAATGCATGTGATGAG, Reverse- TGCATGGTTGCTTCAGCAGT; Wende et al., 2018) and umc2210 (Forward- AGC GGGTCGATCTTTCTCT-TAGTT, Reverse- GATGCACCATTTT AGTGAGCGAT; Min et al., 2012). The reactions were conducted at the Molecular Agricultural Laboratory of the Khon Kaen Field Research Center, Thailand.

The preparation of the PCR mixture was modified from the protocol of the AllTaq Master Mix and PCR Core Kits (QIAGEN, Germany) with a total reaction volume of 10 μ L per reaction. The reaction mixture consisted of 4x AllTaq master mix, 0.5 μ M of each primer, 125x Master mix trace and 15 ng of genomic DNA. The PCR amplification was carried out under the following conditions: Initial PCR activation at 95°C for 2 min, followed by 35 cycles of PCR, which include denaturation at 95°C for 10 sec, primer-specific annealing at 52°C for bnlgl198, umc2038, and 55°C for umc2210, each for 30 sec and extension at 72°C for 20 sec. A final extension was performed at 72°C for 10 min. The PCR products were then separated by agarose gel electrophoresis using a 3.5% agarose gel containing ViSafe Green Gel Stain (Vivantis, Malaysia) in 0.05 x TBE buffer, under an electric field of 100 volts for 2 hrs.

Data recording was conducted by assigning the symbols A, B and C to represent the alleles of the primers bnlgl198, umc2038 and umc2210, respectively. Numerical values were used to indicate each DNA band or allele position. If an allele was detected at the first position, it was recorded as '1' (e.g., A1, B1, and C1). For subsequent alleles, sequential numbers were assigned, such as '2, 3,' (e.g., A2, A3,). The recorded allele data were used for statistical analysis to determine the association between SSR markers and resistance to NCLB.

2.3 Statistical analysis

2.3.1 Single marker analysis

The data analysis was conducted using Single Marker Analysis (SMA) with the Chi-square test to assess the association between SSR alleles and resistance to NCLB in the hybrid sweet corn S_6 population. The allele frequencies of SSR markers were compared between the resistant and susceptible groups. If the Chi-square value was statistically significant ($P \leq 0.05$), it indicated that the SSR alleles were associated with NCLB resistance.

2.3.2 Regression coefficient (R^2) analysis

The regression coefficient analysis was used to determine the association between SSR markers and the severity of NCLB, based on the regression coefficient and statistical significance. The analysis was conducted using statistical software to calculate the Adjusted R^2 , which is a corrected value accounting for the number of variables in each model. This value represents the phenotypic variance explained (PVE) through the statistical model. The Adjusted R^2 was used to evaluate the effectiveness of each marker within the model, where a higher Adjusted R^2 indicates that the SSR marker explains a greater proportion of the phenotypic variance and has potential for use in marker-assisted selection (MAS).

2.3.3 Model accuracy analysis

2.3.3.1 Receiver operating characteristic (ROC) curve

The ROC curve is generated by plotting the relationship between the true positive rate (TPR), which represents the proportion of samples that are correctly classified as resistant and the false positive rate (FPR), which represents the proportion of samples that are incorrectly classified as resistant while actually being susceptible.

2.3.3.2 The area under the curve (AUC) represents the area under the ROC curve

The area under the curve (AUC) represents the area under the ROC curve and serves as an indicator of how well the model can distinguish between resistant and susceptible plants. AUC values range from 0.5 to 1.0 (Corbacioglu & Aksel, 2023).

AUC = 1.0 indicates that the model achieves perfect classification.

AUC > 0.8 suggests that the model has high accuracy.

AUC = 0.5 implies that the model has no predictive power.

The AUC was computed using the 'pROC' package in R.

2.3.3.3 Determination of the optimal threshold

The optimal threshold can be determined using Youden' index statistic,

which is calculated according to the formula by Schisterman et al. (2005) as:

$$J = \text{TPR} - \text{FPR}$$

The threshold that maximizes J is the best cutoff point, ensuring the model achieves the most effective classification of resistant and susceptible plants.

2.3.3.4 Cross-validation

Model performance was validated using five-fold cross-validation. The dataset was randomly partitioned into five subsets; each subset was used once as a validation set while the remaining subsets served as training data. Average performance metrics were computed across folds to ensure model reliability and generalizability.

3. Results and discussion

3.1 SSR amplification-PCR

This study performed DNA amplification using the PCR technique with SSR markers bnlg198, umc2038, and umc2210. The PCR products of each marker were separated and sized, with each DNA band representing an allele specific to the corresponding primer. The first allele position is designated as A1 (susceptible allele) and the second allele as A2 (resistant allele) (Fig. 1). For markers umc2038 and umc2210, the alleles are designated as B and C, respectively. All markers exhibit a co-dominant inheritance pattern, allowing for the detection of both homozygous and heterozygous genotypes.

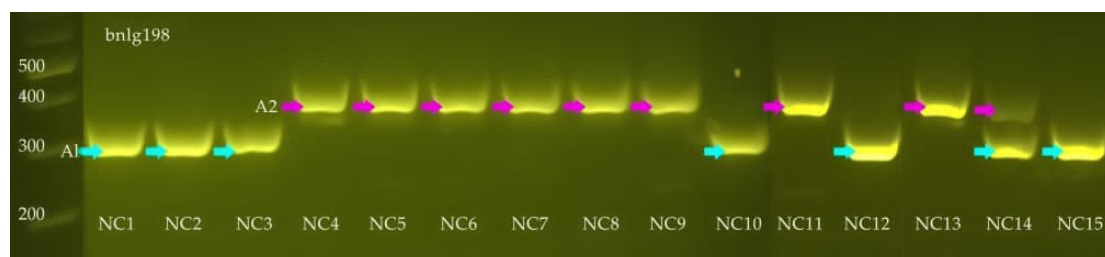


Figure 1. PCR amplification using SSR marker bnlg198 was analyzed on 3.5% agarose gel electrophoresis. DNA bands represent allele position. Allele A1 was indicated by blue arrows, and allele A2 was indicated by pink arrows. Most samples are homozygous, except NC14, which is heterozygous. Allele A1 was observed in susceptible sample, while allele A2 was observed in resistant samples. The first lane shows the DNA size marker in base pairs (bp).

3.2 Association analysis between SSR markers and NCLB resistance using single marker analysis (SMA)

Data analysis was conducted using SMA, a technique used to assess the association between molecular marker genotypes and traits of interest to plant breeders. These include associations with texture quality (Kumar et al., 2019), disease resistance and yield-contributing traits (Narayanan et al., 2024).

In the present study, the association between three SSR markers (bnlg198, umc2038, and umc2210) and resistance to NCLB was analyzed using the chi-square test. Significant associations were observed in both the CH66C1 and HX75C1 sweet corn populations. The chi-square test was used to evaluate whether the distribution of marker genotypes differed significantly between resistant and susceptible groups, thereby identifying potential quantitative trait loci (QTLs) associated with NCLB resistance.

A high chi-square value indicates a significant difference between the resistant and susceptible groups. The significant P-value ($P<0.001$) for bnlg198 and umc2038 suggest a strong genetic linkage with resistance traits, while a lower significance level ($P<0.05$) (Table 1) may exhibit weaker association or be influenced by other genetic or environmental factors.

The bnlg198 and umc2038 markers showed a strong association with resistance to NCLB, making them promising candidate markers for marker-assisted selection (MAS) in future sweet corn breeding programs. In contrast, although umc2210 exhibited a statistically significant association its correlation with NCLB resistance was lower compared to the other two markers. This may be due to the quantitative nature of disease resistance, which is typically controlled by multiple genes and influenced by environmental factors. According to Wang et al. (2012), the genes controlling NCLB resistance are governed by either dominant or quantitative gene action.

Table 1. Chi-square analysis of SSR markers associated with NCLB resistance in S₆ sweet corn populations.

Populations	Markers	Chi-square	P-value
CH66C1	bnlg198	26.4	0.001
	umc2038	18.1	0.001
	umc2210	10.5	0.05
HX75C1	bnlg198	14.5	0.001
	umc2038	19.4	0.001
	umc2210	11.1	0.05

3.3 Regression-based model for predicting NCLB resistance using SSR markers

Regression coefficient analysis is a widely applied method in SMA to evaluate the association between molecular markers and genetic traits. The adjusted R² value, which accounted for the number of variables in the model, represented the percentage of phenotypic variance

explained by the molecular markers (Shafi et al., 2021). A higher adjusted R² value indicated stronger and more accurate marker-trait associations, improving the reliability of genetic effect estimations.

The r value (correlation coefficient) represented the strength of the linear relationship between SSR markers and NCLB resistance. In this study, r value

increased from 0.50 in model 1 to 0.74 in model 3, suggesting that incorporating multiple markers into the regression model strengthens the association with NCLB resistance. The highest *r* value (0.74) in model 3 implied that the

combined effect of umc2038, bnlg198, and umc2210 explains a greater proportion of phenotypic variance. Additionally, the significant *P*-value (*P*<0.001) confirms the robustness of these associations (Table 2).

Table 2. Statistical evaluation of models based on genetic marker association.

Model	Markers			<i>r</i> value	Adjust R ² (%)	F-value	P-value
1	umc2038			0.50	0.25	30.5	0.001
2	umc2038	bnlg198		0.60	0.57	36.4	0.001
3	umc2038	bnlg198	umc2210	0.74	0.60	28.9	0.001

Adjusted R² was used to assess model performance, with higher values indicating better predictive capability. Model 1, which included only umc2038, explained 25% of the phenotypic variance. The inclusion of bnlg198 in model 2 increased adjusted R² to 57%, demonstrating a stronger association. Model 3, incorporating umc2210, showed a slight improvement to 60%, though the F-value declined, suggesting the umc2210 may not substantially enhance the model's predictive power (Table 2).

The umc2038 marker, according to data from the website (www.maizegdb.org), is located on chromosome 4 and associated with C2C2-GATA-*Transcription factor 4* (GATA4). GATA4 proteins have been classified as key regulators of light-responsive gene expression, influencing chlorophyll accumulation at high levels (Manfield et al., 2007; Luo et al., 2010; Behringer et al., 2014). Light plays a pivotal role in triggering plant immune responses via PAMP-triggered immunity (PTI) and enhances the production of reactive oxygen species (ROS), a fundamental mechanism by which plants defend themselves against pathogens (Zhu et al., 2022; Zhang et al., 2023). Although no direct link between GATA4 and NCLB resistance has been previously reported, this study found that model 1 revealed that umc2038

alone explained 25% of the phenotypic variance, indicating its significant role in light-mediated defense responses.

The bnlg198 marker is located on chromosome 2 and is associated with *Ht1*, a major resistance gene in maize that confers qualitative resistance against NCLB (Patterson et al., 1965; Munkvold, 2016). The *Ht1* gene follows a single-gene inheritance pattern and exhibits dominant gene action (Hooker, 1981). This gene specifically provides resistance against *E. turcicum* race 0, 2, 3, N, 2N, 23, and 23N (Geiger & Heun, 1989; Pataky et al., 1998). Recent studies have reported that *Ht1* encodes a nucleotide-binding, leucine-rich repeat (NLR) protein, which functions in the effector-triggered immunity (ETI) pathway. This immune response is activated upon pathogen recognition through pattern recognition receptors (PRRs), serving as molecular sensors within the host plant defense system. Upon activation, NLR proteins initiate a defense response by inducing the production of ROS and accumulating callose, thereby restricting fungal growth and triggering programmed cell death in infected cells (Jones & Dangl, 2006; Tsuda & Katagiri, 2010).

Model 2, comprising umc2038 and bnlg198, explains 57% of the phenotypic variance and shows the highest F-value

(36.4), indicating the strongest association with NCLB resistance. The enhanced performance of model 2 from the complementary function of its markers: *umc2038* (linked to *GATA4*) strengthens light-mediated immunity, while *bnlg198* (associated with *Ht1*) confers effector-triggered immunity (ETI). The combination of *umc2038* and *bnlg198* in model 2 likely provides a dual-layered defense integrating light-enhanced immunity and specific pathogen resistance, making it more effective than model 1 and model 3.

The *umc2210* marker is located on chromosome 8, within the *Htn1* locus. This locus is known to confer quantitative resistance and partial resistance to NCLB (Hurni et al., 2015). Upon genetic transcription, the *Htn1* gene encodes wall-associated receptor-like kinases (RLKs), which function as receptor-like proteins embedded in the plant cell wall. These proteins play a crucial role in detecting pathogen recognition receptors (PRRs) from pathogenic organisms, thereby activating pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) (Boller & Felix, 2009; Monaghan & Zipfel, 2012). This mechanism effectively delays lesion formation following *E. turcicum* infection by approximately four weeks and inhibits fungal sporulation (Raymundo et al., 1981; Welz & Geiger, 2000; Hurni et al., 2015).

Despite its role in quantitative and partial resistance, *umc2210* exhibited a relatively weak effect in the regression model compared to *umc2038* and *bnlg198*. The inclusion of *umc2210* in model 3 resulted in only a slight increase in adjusted R^2 (from 57% - 60%). This suggested that while *umc2210* contributed to NCLB resistance, its effect may be polygenic rather than a major determinant in this population.

3.4 Model accuracy assessment

The model developed in this study achieved an AUC value of 0.78 (Figure 2),

indicating moderate to high predictive accuracy. AUC is a widely used metric for evaluating a model's ability to distinguish between two classes—in this case, resistant and susceptible genotypes. An AUC value ranges from 0 to 1.0, where a value of 0.5 indicates no discrimination, and a value close to 1.0 reflects better model performance.

This finding is consistent with previous studies, which have demonstrated that AUC is a reliable metric for evaluating classification performance. Moreover, AUC has been shown—both theoretically and empirically to be independent of class prevalence, making it particularly useful in imbalanced datasets (Hanley & McNeil, 1982; Zweig & Campbell, 1993; Manel et al., 2001; McPherson et al., 2004).

The Youden index, a commonly used statistical measurement for diagnostic effectiveness, can balance sensitivity (true positive rate; TPR) and specificity to determine an optimal classification threshold (Ierimonti et al., 2021; Fluss et al., 2005). The metric identifies the point on the ROC curve that maximizes the difference between the true positive rate and the false positive rate, thereby achieving the best trade-off between correctly identifying positives and minimizing false alarms. The highest possible value of the Youden index is 1, which is achieved when sensitivity reaches 100% and the false positive rate (FPR = 1 - specificity) is 0% (Kullaa, 2014). In the current study, the ROC curve and Youden index were used to identify the optimal threshold for disease prediction. A similar approach has been reported by Li et al. (2020), who applied the Youden index to estimate the optimal cutoff point based on ROC analysis.

In our analysis, the optimal threshold was identified at 0.51. At this threshold, the model achieved a TPR of 0.88 (88%), indicating strong performance in correctly identifying resistance plants. This result underscored the practical relevance of the

model in supporting resistance-based plant selection and breeding programs, where accurate identification of resistant

individuals was essential for genetic improvement and effective disease management.

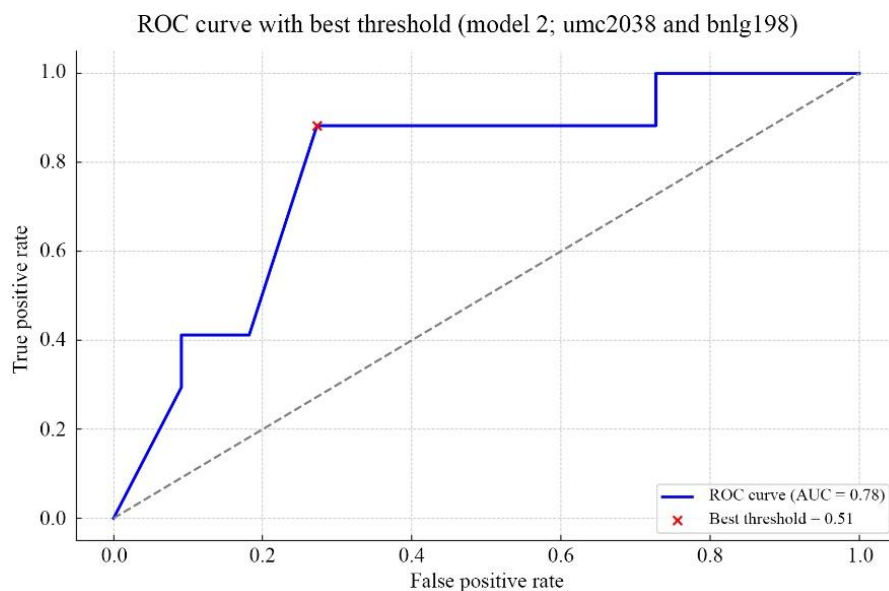


Figure 2. Receiver operating characteristic (ROC) curve for model 2 (umc2038 and bnlgl98). The model achieved an AUC of 0.78, indicating moderate to high accuracy. The optimal threshold (0.51) identified using Youden's index statistic, maximizes classification performance.

4. Conclusions

In conclusion, the combination of markers umc2038 and bnlgl98 demonstrated strong potential for identifying NCLB-resistant genotypes, reflecting underlying mechanisms related to both light-regulated growth and race-specific defense responses. The model supports the use of these loci as candidate markers for early-generation marker-assisted selection (MAS). However, validation across populations and environments is needed before broad application.

The findings underscore the value of multi-locus marker models over single-marker approaches in improving selection efficiency. Future research should focus on validating the model under diverse field conditions and exploring its integration with genomic selection frameworks to enhance breeding precision and resilience.

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