Rapid Detection and Spatial Risk Assessment of Banana Bract Mosaic Virus (BBrMV) in Abaca (Musa textilis Nee) in the Caraga Region, Philippines

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Rapid Detection and Spatial Risk Assessment of Banana Bract Mosaic Virus (BBrMV) in Abaca (Musa textilis Nee) in the Caraga Region, Philippines

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Abstract: *Abaca (Musa textilis Nee), a vital fiber crop in the Philippines, faces significant threats from Banana Bract Mosaic Virus (BBrMV), which causes considerable yield losses. Traditional detection methods like RT-PCR are costly and impractical for field use. This study evaluates a rapid, field-deployable loop-mediated isothermal amplification (LAMP) assay developed by PhilFIDA for BBrMV detection. A total of 447 abaca samples from Agusan provinces were analyzed, with 80 testing positive. The assay utilized specific primers and SYBR Green for visual detection, demonstrating high sensitivity and rapid results. MaxEnt ecological modeling was used to generate a partial risk map, predicting high BBrMV suitability in Agusan del Norte and Agusan del Sur, moderate risk in Surigao provinces, and low risk in Dinagat Islands. This integrated approach highlights the potential of combining molecular diagnostics and geospatial modeling to inform surveillance and targeted interventions, thereby supporting sustainable abaca production and effective virus management in vulnerable areas.*

Keywords: Banana Bract Mosaic Virus; Abaca; LAMP assay; MaxEnt modeling; Disease risk mapping

1. INTRODUCTION

Abaca (Musa textilis Nee), or Manila hemp, is a vital economic crop in the Philippines, prized for its superior fiber strength, durability, and elasticity. Its unique qualities make it a critical raw material for specialized paper products like currency notes and teabags, as well as high-strength cordage, durable textiles, and advanced composite materials. Abaca cultivation underpins rural economies, supporting millions of farmers. In 2023, the Caraga Region significantly contributed to the national abaca fiber supply, producing about 13.9% of the total yield [1]. However, this productivity is increasingly threatened by various factors, primarily viral pathogens. Among the most significant is the Banana Bract Mosaic Virus (BBrMV). First reported in the Philippines in 2000 [2], BBrMV severely impacts fiber quality and yield by causing stunting and foliar deformation. Transmitted by aphid vectors like Pentalonia nigronervosa, BBrMV poses complex management challenges due to its latent infection period—where plants are asymptomatic but infectious—and variable symptom expression, making early detection and control difficult for farmers. Asymptomatic carriers often serve as undetected reservoirs, leading to widespread virus dissemination. Conventional diagnostic methods, such as Enzyme-Linked Immunosorbent Assay (ELISA) and Reverse Transcription-Polymerase Chain Reaction (RT-PCR), are effective for laboratory identification but have significant limitations in field settings, especially in resource-constrained abaca-growing areas. ELISA often lacks the sensitivity for low viral titers, risking false negatives [3], while RT-PCR requires sophisticated infrastructure, expensive equipment, skilled personnel, and specialized reagents [4]. Its multi-step nature also makes it time-consuming and prone to contamination outside controlled labs. To address these gaps and enhance field-based surveillance, this study utilized the LAMParA (LAMP-based Pathogen Rapid Assay) Kit developed by the Philippine Fiber Industry Development Authority (PhilFIDA). This portable diagnostic tool leverages loop-mediated isothermal amplification (LAMP) technology for rapid, cost-effective, and reliable BBrMV detection in field conditions. LAMP operates at a single, constant temperature, eliminating the need for expensive thermocyclers. Its high amplification efficiency and specific primers enable fast reactions and superior sensitivity compared to conventional PCR. Furthermore, this study incorporated Species Distribution Modeling (SDM) using the Maximum Entropy (MaxEnt) algorithm for region-specific disease risk planning and targeted interventions. MaxEnt is ideal for presence-only data, common in disease records, effectively correlating environmental and biophysical variables with known virus locations to predict potential distribution. This spatial analysis approach helps understand and predict disease spread. Sung et al. [5] demonstrated the effectiveness of area-weighted sampling for SDMs in Korean red pine, noting that optimal sample sizes save significant time and resources in data collection, especially vital in developing countries. Their work shows how efficient sampling and accurate size determination can estimate species distributions under climate change, aiding ecosystem adaptation plans. However, SDMs have inherent uncertainties due to model complexity and varying performance, with factors like species niches influencing results [6]. Most SDMs, excluding MaxEnt, use pseudo-absence data, highlighting the need for careful true absence data examination. The intricate interactions among environmental factors in these models are also not fully understood, necessitating further research. These uncertainties can impact policy and decision-making for conservation and disease management. In the Caraga region, integrating geospatial analysis with molecular findings has proven valuable for disease management. A study on Banana Bunchy Top Virus (BBTV), for instance,

successfully mapped its spatial distribution [7]. Model validation indicated a good fit between observed and expected data. Binary Logistic Regression also pinpointed specific municipalities (Properidad, Las Nieves, Sibagat) with predicted infected abaca, and a hotspot map showed high-risk areas like Butuan City, Las Nieves, Bayugan, Esperanza, and Sibagat [7]. This prior work emphasizes that spatial mapping enables targeted interventions and resource allocation, improving understanding of disease dynamics for effective management. This current study builds on these insights by focusing specifically on Banana Bract Mosaic Virus (BBrMV). It integrates advanced molecular diagnostics with geospatial modeling to strengthen surveillance, support early detection, and inform spatially-targeted disease management for sustained abaca cultivation in Caraga. This study specifically aimed to: (1) validate the field applicability and diagnostic reliability of the LAMParA Kit for BBrMV detection in abaca field samples from the Caraga Region; (2) identify the spatial distribution and prevalence of BBrMV occurrence using field surveys and LAMP diagnostics; and (3) develop a partial BBrMV risk map for the Caraga Region using MaxEnt modeling to inform proactive and spatially-informed disease management strategies.

2. MATERIALS AND METHODS

2.1 Field Sampling and Location

Field surveillance was conducted across selected abaca-producing municipalities in the provinces of Agusan del Norte, Agusan del Sur, Surigao del Norte, and Surigao del Sur in the Caraga Region. Sampling sites were selected based on accessibility, production significance, and historical incidence of viral infections. Geocoordinates of each sampling site were recorded using a GPS device to enable spatial referencing. Leaf samples were collected from symptomatic and asymptomatic abaca plants following PhilFIDA's surveillance protocol.

2.2 Sample Selection, Availability, and Collection

In this study, all 80 abaca samples selected for molecular analysis across the Caraga region tested positive for Banana Bract Mosaic Virus (BBrMV) using the LAMParA kit, reinforcing the widespread presence of the virus in symptomatic plants. Specifically, all 20 tested samples from Agusan del Norte (collected in Kitcharao, Cabadbaran, Las Nieves, Santiago, and Amparo) were positive. Similarly, in Agusan del Sur, 21 samples from Talacogon, San Luis, Esperanza, Prosperidad, and Sibagat tested positive. Surigao del Norte reported 17 positive samples from Gigaquit and Mainit, while Surigao del Sur had 22 positives from Lianga, Marihatag, San Agustin, San Miguel, and Tago.

The LAMParA kit utilizes Loop-Mediated Isothermal Amplification (LAMP) technology, a powerful nucleic acid amplification method that amplifies viral genetic material at a single, constant temperature, typically around 65 C, without the need for expensive and complex thermocyclers required by PCR. The assay targets highly conserved regions of the BBrMV genome using a set of four to six specific primers (two outer, two inner, and sometimes two loop primers), which enable rapid and highly specific amplification. Detection of amplification is based on a visual color change caused by the inclusion of SYBR Green I dye in the reaction mix. In the presence of amplified DNA (indicating BBrMV presence), the SYBR Green I intercalates into the double-stranded DNA, emitting a green fluorescence visible under white light, allowing for quick, on-site diagnosis typically within 30-60 minutes. Conversely, a negative result maintains an orange hue, indicating the absence of the virus. Positive and negative controls were included in each run to ensure the validity and reliability of the results. This method proved highly reliable and efficient for detecting BBrMV in field-collected samples, as previously supported by other studies demonstrating LAMP's effectiveness for plant virus detection [14, 21]. The confirmation of these field positives through LAMP diagnostics, when integrated with geospatial analysis and GIS mapping, further confirms the extensive spread of BBrMV throughout the region, emphasizing the urgent need for effective disease monitoring and management strategies. The combination of rapid field detection using the LAMParA kit and spatial risk mapping provides a valuable framework for timely intervention to control the virus and protect abaca production.

2.3 Detection of BBrMV using the LAMParA Kit

In this study, all 80 abaca samples collected across the Caraga region tested positive for Banana Bract Mosaic Virus (BBrMV) using the LAMParA kit, underscoring the virus's widespread presence. Specifically, all 20 tested samples from Agusan del Norte—collected in municipalities such as Kitcharao, Cabadbaran, Las Nieves, Santiago, and Amparo—were positive. Similarly, in Agusan del Sur, 21 samples from Talacogon, San Luis, Esperanza, Prosperidad, and Sibagat tested positive. Surigao del Norte reported 17 positive samples from Gigaquit and Mainit, while Surigao del Sur had 22 positives from Lianga, Marihatag, San Agustin, San Miguel, and Tago. The distribution of positive samples by province showed Surigao del Norte with the highest share (34%), followed by Agusan del Norte (27%), Agusan del Sur (21%), and Surigao del Sur (18%). The LAMParA kit utilizes Loop-Mediated Isothermal Amplification (LAMP) technology, which amplifies viral genetic material at a single temperature without the need for expensive, complex laboratory equipment. Detection is based on a color change caused by SYBR Green I dye, which emits green fluorescence under white light when the virus is present, allowing for quick, on-site diagnosis. This method proved highly reliable and efficient for detecting BBrMV, as previously supported by other studies [8, 14]. Geospatial analysis with GIS further confirmed the extensive spread of BBrMV throughout the region, emphasizing the urgent need for effective disease monitoring and management strategies. The combination of rapid field detection using the LAMParA kit and spatial risk mapping provides a valuable framework for timely intervention to control the virus and protect abaca production.

2.4 BBrMV Occurrence and Environmental Variables

The geographical coordinates of BBrMV positive samples were meticulously gathered from the metadata compiled during Abaca Project phases 1 and 2. For species distribution modeling, a suite of environmental variables was obtained. Bioclimatic variables (e.g., mean annual temperature, precipitation of wettest month, temperature seasonality) and specific biophysical

variables such as wind speed and solar radiation were sourced from the WorldClim version 2.1 climate data for the period 1970-2000 (https://worldclim.org/data/worldclim21.html), boasting a fine spatial resolution of 30 seconds (approximately 1 km^2). The choice of these variables is critical as they directly or indirectly influence the life cycle, population dynamics, and dispersal of the aphid vector (Pentalonia nigronervosa), as well as the replication and persistence of the BBrMV within the host plant and environment. For instance, temperature and precipitation directly affect aphid reproduction and survival rates, while wind speed can significantly influence long-distance dispersal of winged aphids. Additional biophysical variables, including the Digital Elevation Model (DEM) and soil type data, were acquired from the Philippines' National Mapping and Resource Information Authority (NAMRIA) and the Department of Agriculture - Bureau of Soils and Water Management (DA-BSWM), respectively. These layers were processed to a consistent 1 km spatial resolution. The DEM was subsequently utilized in ArcGIS 10.8 software to derive secondary topographic variables, namely aspect (direction of slope) and slope (steepness), which can influence microclimates, water drainage, and suitability for abaca cultivation and vector habitats. The soil layer, originally in vector format, was converted into a raster format at a uniform 1 km spatial resolution. All these environmental data layers were compiled and processed using ArcGIS 10.8 to ensure consistent spatial resolution, extent, and raster size, thereby creating a coherent dataset for MaxEnt modeling. Each processed layer was then exported into ASCII (*.asc) format, the required input format for MaxEnt software.

2.5 MaxEnt Algorithm Modeling

The MaxEnt software version 3.4.4, downloaded from the American Museum of Natural History's biodiversity informatics website [9], was employed to model the potential distribution and risk levels of Banana Bract Mosaic Virus (BBrMV) in the Caraga Region. MaxEnt was chosen for its proven effectiveness with presence-only data, a common scenario in disease occurrence datasets, and its ability to infer environmental suitability for a species (or in this case, a disease) by finding the probability distribution of maximum entropy subject to constraints imposed by the observed presence locations and environmental layers.

Environmental variables (in ASCII format) and virus occurrence data (as a CSV file containing latitude and longitude for each positive sample) were uploaded into MaxEnt for analysis. The model was configured to run with 15 replicates, utilizing a subsampling method for cross-validation to reduce bias and provide a more robust estimation of the virus's likely geographic distribution. During each replicate, the data was randomly partitioned so that 75% of the occurrence points were used to train the model, while the remaining 25% were reserved for testing its predictive performance. This data partitioning approach, combined with multiple replicates, allowed for rigorous evaluation of the model's accuracy and stability. Default MaxEnt settings for feature types (linear, quadratic, product, threshold, hinge) and regularization parameters were applied, allowing the model to fit the data appropriately without overfitting. The model was allowed up to 5,000 iterations to ensure convergence and improve accuracy. Model performance was primarily assessed using the Area Under the Receiver Operating Characteristic Curve (AUC), which measures the model's ability to discriminate between presence and absence locations (though actual absences were not used, random background points were used for evaluation).

2.6 GIS Mapping

This study used MaxEnt modeling to predict where Banana Bract Mosaic Virus (BBrMV) is most likely to occur in the Caraga region. The risk maps produced by MaxEnt were imported into a Geographic Information System (GIS) program called QGIS. In QGIS, these maps were combined with other important information such as land use and local government boundaries to give a clearer picture of the areas at risk. Different colors were used on the map to show low, medium, and high risk zones of BBrMV. Using GIS tools, the study was able to identify which areas have higher chances of infection and how these relate to environmental factors like farming patterns or landscape features. This combined method of using MaxEnt and GIS makes it easier for farmers and local officials to understand where the virus may spread, helping them focus their efforts on monitoring and controlling the disease more effectively. This approach turns complex data into useful information for managing BBrMV in abaca plantations.

3. RESULTS AND DISCUSSION

3.1 Common Symptoms of BBrMV in Abaca

Abaca samples collected during the Abaca Project phases 1 and 2 exhibited a range of characteristic viral symptoms across the Caraga provinces, reflecting the widespread impact of Banana Bract Mosaic Virus (BBrMV) and potentially other co-infecting viruses. The presence of diverse and often overlapping symptoms underscores the complexity of viral pathologies affecting abaca, where mixed infections, especially with Abaca Bunchy Top Virus (ABTV), are frequently observed [10]. This variability significantly challenges timely and accurate disease identification in the field, thereby highlighting the critical need for reliable molecular diagnostic tools to complement traditional symptom-based surveys and improve disease management strategies.

In Agusan del Norte, common symptoms observed included distinct mosaic leaf patterns, pseudostem discoloration, along with more severe manifestations such as rosetting (reduced internode length leading to a compact, rosette-like appearance), generalized chlorosis (yellowing of leaves), necrosis (tissue death), severe stunted plant growth, and the distinctive bunchy top appearance (Figure 1). Similar complex symptom profiles were observed in Agusan del Sur, where additional signs such as mottling (irregular patches of light and dark green), generalized leaf discoloration, and curling of leaf margins were also recorded. In Surigao del Norte, infected plants primarily showed mosaic symptoms, chlorosis, stunted growth, mottling, and bunchy top, while Surigao del Sur samples predominantly displayed leaf yellowing and curling. These symptom expressions are highly consistent with prior reports by Sta. Cruz et al. [10], which extensively documented the frequent occurrence of mixed viral infections in abaca, including BBrMV and Abaca Bunchy Top Virus (ABTV), further complicating

accurate field diagnosis based solely on visual inspection. Studies by Bateson and Dale [11], and Magnaye and Espino [12] further corroborate these observations, consistently confirming the association of these complex and variable symptoms with BBrMV infection. The severe stunting and foliar deformation directly impact fiber length and yield, while reduced photosynthetic capacity due to chlorosis and mosaic patterns leads to weakened plants and diminished fiber quality, ultimately resulting in significant economic losses for abaca farmers. The difficulty in early identification due to latent periods and symptom variability allows the virus to spread widely before effective intervention can be implemented.

Fig. 1. The common disease symptoms observed from Agusan del Norte during the sample collection. Abaca sucker showing mosaic on leaf, rosette, chlorosis, necrosis, stunted growth, bunchy top (A), mosaic symptoms on the abaca leaf (B), and curling, chlorosis, mosaic on leaves, rosette, stunted growth, and bunchy top (C, D).

3.2 Detection of BBrMV using the LAMParA Kit

In Agusan del Norte, all tested samples (80 in total) were positive for Banana Bract Mosaic Virus (BBrMV), including samples from Kitcharao, Cabadbaran, Las Nieves, Santiago, and Amparo. In Agusan del Sur, 21 samples from Talacogon, San Luis, Esperanza, Prosperidad, and Sibagat also tested positive. Surigao del Norte had 17 positive samples from Gigaquit and Mainit, while Surigao del Sur had 22 positive samples from Lianga, Marihatag, San Agustin, San Miguel, and Tago. The LAMParA kit detected positive results by the presence of green fluorescence in tubes treated with SYBR Green I under white light, with all 80 samples in the Caraga region testing positive for BBrMV.

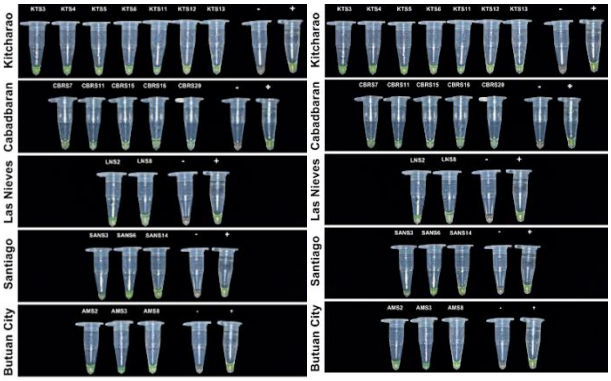

Fig. 2. Detection of Banana Bract Mosaic Virus (BBrMV) using the LAMParA kit in samples collected from various municipalities of Agusan del Sur and Surigao del Norte. Each set includes test samples (left to right), along with the negative control (orange hue) and positive control (green hue) indicating the presence or absence of BBrMV.

The spatial data, visualized through GIS maps, confirmed the widespread presence of the virus across all four provinces from which samples were collected. The province-wise distribution of positive samples revealed Surigao del Norte with the highest share (34%), followed by Agusan del Norte (27%), Agusan del Sur (21%), and Surigao del Sur (18%). This provincial distribution suggests that while BBrMV is pervasive, there might be varying degrees of infection intensity or historical presence in different areas, possibly influenced by factors such as abaca planting density, aphid vector populations, or local agricultural practices. For instance, the higher proportion in Surigao del Norte might indicate a longer history of infection or environmental conditions more favorable to vector activity and virus spread in that province.

3.3 MaxEnt BBrMV Risk Map

(see Fig. 3) The distribution of BBrMV risk levels in terms of area (ha) in the Caraga region is as follows: 79% shows no risk, 15% low risk, 5% moderate risk, and 1% high risk for BBrMV. Table 1 shows the breakdown of risk levels. A total of 1,442,794.06 hectares in no risk areas, 271,609.12 hectares in low risk areas, 64,862.03 hectares in moderate risk areas, and 13,800.00 hectares in high risk areas, with a total examined area of 1,793,064.673 hectares.

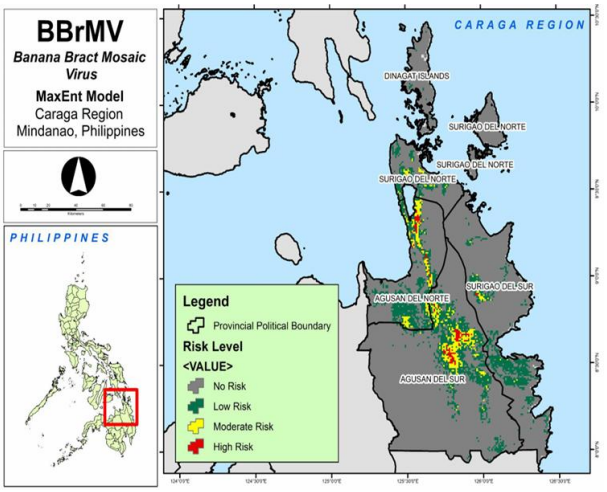

Fig. 2. MaxEnt-generated risk map of Banana Bract Mosaic Virus (BBrMV) distribution in the Caraga

Region, showing spatial patterns of no risk, low, moderate, and high-risk zones.

Table 1. Area-based breakdown of BBrMV risk levels in the Caraga Region.

Risk Level	Area (Hectares)	Percentage (%)
No Risk	1,442,794.06	79
Low Risk	271,609.12	15
Moderate	64,862.03	5
High Risk	13,800.00	1
Total	1793065.21	100

(see Fig.3) This study assessed the spatial distribution and risk levels of Banana Bract Mosaic Virus (BBrMV) across the Caraga region using MaxEnt-based species distribution modeling. Results revealed marked variability in infection risk across provinces. Agusan del Sur had the most extensive high-risk area (~9,300 hectares), followed by Agusan del Norte (~4,500 hectares). In contrast, Surigao del Sur and Surigao del Norte exhibited predominantly moderate-risk areas, covering approximately 64,800 and 3,800 hectares, respectively. The Dinagat Islands showed a comparatively low-risk zone (~1,590 hectares). At the municipal level, high-risk clusters were identified, with Jabonga (1,898 ha), Santiago (764 ha), Butuan City and Cabadbaran (~600 ha each) leading in Agusan del Norte. In Agusan del Sur, Prosperidad (3,929 ha), San Luis (1,978 ha), and Talacogon (886 ha) were the most affected. These spatial risk estimates provide valuable insights for prioritizing disease surveillance, quarantine measures, and targeted intervention. While the data offer a strong foundation for resource allocation, future refinements should consider incorporating temporal dynamics, vector presence, and environmental variability to enhance predictive power and disease forecasting.

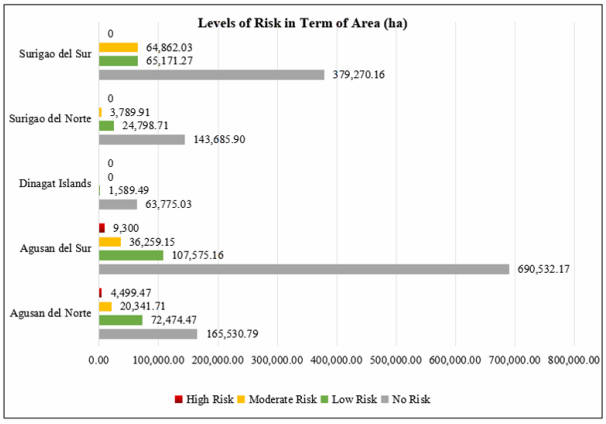

Fig. 4. Area-based breakdown of BBrMV risk levels in the Caraga Region, displaying the total hectares under each risk category (no risk, low, moderate, high) derived from the MaxEnt model.

The successful deployment of the LAMParA Kit demonstrates its practical applicability in field-based diagnostics for BBrMV, especially in geographically isolated and laboratory-limited areas. The kit's high sensitivity and rapid turnaround time address the constraints of RT-PCR and ELISA methods, particularly for in situ surveillance. Furthermore, the use of MaxEnt modeling provides a powerful framework to understand the environmental correlates of BBrMV distribution. The identification of key climatic variables influencing viral presence aligns with the vector ecology of aphids, which thrive in warm, humid environments. The model's predictive capability supports proactive disease management by enabling spatially targeted monitoring and resource allocation. Integration of molecular diagnostics and ecological modeling establishes a robust platform for early warning systems, thereby enhancing the resilience of abaca production systems in Caraga.

4. CONCLUSION AND RECOMMENDATIONS

This study establishes the field applicability and diagnostic reliability of the LAMParA Kit, a loop-mediated isothermal amplification (LAMP)-based detection system developed by the Philippine Fiber Industry Development Authority (PhilFIDA), for the rapid identification of Banana Bract Mosaic Virus (BBrMV) in Musa textilis (abaca). All 80 field-collected samples from representative abaca-growing localities across the Caraga region tested positive for BBrMV, suggesting a widespread prevalence of the virus. The LAMP assay's rapid turnaround and minimal equipment requirement underscore its suitability for decentralized, field-based diagnostics in resource-limited agricultural settings. To complement molecular diagnostics with spatial epidemiological insights, species distribution modeling (SDM) using the MaxEnt algorithm was employed, which revealed clear spatial gradients of infection risk, with Agusan del Norte and Agusan del Sur emerging as high-risk zones. This dual approach—combining point-based molecular detection with predictive geospatial analytics—provides a scalable framework for early warning and precision disease management in abaca plantations. However, while the LAMP assay demonstrated high sensitivity, further validation against conventional PCR or sequencing is warranted to confirm specificity, especially under field conditions. Environmental variables affecting vector populations, virus persistence, and host susceptibility also require integration into future epidemiological models. The insights from this study are particularly relevant for regional disease containment, fiber production planning, and the design of spatially-informed extension services. Based on the results, we recommend the formal integration of the LAMParA Kit into the regional plant health surveillance system, particularly within the diagnostic protocols of PhilFIDA and local government units (LGUs) involved in abaca development. Routine monitoring using this kit should be prioritized in high-risk areas identified by MaxEnt modeling, specifically Agusan del Norte and Agusan del Sur. Furthermore, cross-validation with PCR-based methods should be conducted periodically to ensure diagnostic consistency and to identify potential false positives or negatives in field use.

It is also recommended that future research incorporate climatic variables, aphid vector dynamics (Pentalonia nigronervosa), and seasonality into the MaxEnt framework to build predictive epidemiological models capable of forecasting outbreaks. Finally, capacity-building activities should be initiated for local agricultural technicians and farmer cooperatives, focusing on the application of LAMP diagnostics and the

interpretation of spatial risk maps for responsive disease management. This integrated approach will contribute to the sustainable production of abaca and the resilience of fiber crop systems in the Caraga region.

5. REFERENCES

[1] Philippine Statistics Authority (PSA). (2023). Abaca production in the Philippines. Retrieved from https://psa.gov.ph

[2] Sharman, M., Gambley, C. F., Oloteo, E. O., Abgona, R. V. J., & Thomas, J. E. (2000). First record of natural infection of abaca (Musa textilis) with banana bract mosaic potyvirus in the Philippines. Australasian Plant Pathology, 29(1), 69-69. https://doi.org/10.1071/AP00012

[3] Ward, E., Foster, S. J., Fraaije, B. A., & McCartney, H. A. (2004). Plant pathogen diagnostics: Immunological and nucleic acid-based approaches. Annals of Applied Biology, 145(1), 1-16. https://doi.org/10.1111/j.1744-7348.2004.tb00354.x

[4] Mumford, R. A., Macarthur, R., & Boonham, N. (2006). Advances in molecular diagnostics for plant viruses. European Journal of Plant Pathology, 116, 1-17. https://doi.org/10.1007/s10658-006-9058-3

[5] Sung, S.-Y., Lee, D.-K., Park, C., Kim, H.-G., et al. (2018). Assessing effective sampling method and sample size for species distribution modeling of Korean Red Pine (Pinus densiflora). 九州大学大学院農学研究院紀要 (Journal of the Faculty of Agriculture, Kyushu University), 63(2), 211-221. https://doi.org/10.5109/1955384

[6] Buisson, L., Thuiller, W., Casajus, N., Lek, S., & Grenouillet, F. (2010). Uncertainty in ensemble forecasting of species distribution. Global Change Biology, 16(4), 1145-1157. https://doi.org/10.1111/j.1365-2486.2009.02002.x

[7] Gagula, A. C., Animo, H. A. F., Tajale, M. R., & Parac, E. P. (2024). Determining the correlation between Abaca (Musa textilis) distribution patterns and Bunchy Top Disease Prevalence in the Caraga Region through spatial point pattern and statistical analysis. Proceedings of International Exchange and Innovation Conference on Engineering & Sciences (IEICES), 10, 532-537. https://doi.org/10.5109/7323312

[8] Koh, R.B.L., Barbosa, C.F.C., Aquino, V.M. et al. (2020). Rapid, simple detection of banana bract mosaic virus in abaca using a one-step reverse transcription loop-mediated isothermal amplification (RT-LAMP) assay. Journal of General Plant Pathology, 86, 433–441. https://doi.org/10.1007/s10327-020-00949-9

[9] Phillips, S. J., Dudík, M., & Schapire, R. E. (n.d.). Maxent software for modeling species niches and distributions (Version 3.4.1) [Computer software]. American Museum of Natural History. Retrieved from http://biodiversityinformatics.amnh.org/open_source/maxent/

[10] Sta. Cruz, F., Cruz, B. G., & Alviar, A. (2016). Serological and molecular detection of mixed bunchy top and mosaic virus infections in Abaca (Musa textilis Nee). Philippine Agricultural Scientist, 99, 88–98.

[11] Bateson, M. F., & Dale, J. L. (1995). Banana bract mosaic virus: Characterisation using potyvirus specific degenerate PCR primers. Archives of Virology, 140(3), 515-527. https://doi.org/10.1007/BF01718428

[12] Magnaye, L. V., & Espino, R. R. (1990). Note: Banana bract mosaic a new disease of banana. Philippine Agriculturist, 73, 55-59. https://www.cabidigitallibrary.org/doi/full/10.5555/19922316885

[13] Siljo, A., & Bhat, A. I. (2014). Detection of Cardamom mosaic virus and Banana bract mosaic virus in cardamom using SYBR Green based reverse transcription-quantitative PCR. VirusDisease, 25, 137-141.