BMC Plant Biology

https://doi.org/10.1186/s12870-026-08847-6

Article in Press

An attention-based deep learning model for early detection of polyphagous shot hole borer infestations in plants

Received: 14 January 2026

Accepted: 22 April 2026

Published online: 29 April 2026

Cite this article as: Younas R., Rehman H.M.R., Choi G.S. *et al.* An attention-based deep learning model for early detection of polyphagous shot hole borer infestations in plants. *BMC Plant Biol* (2026). https://doi.org/10.1186/s12870-026-08847-6

Rabbiya Younas, Hafiz Muhammad Raza Rehman, Gyu Sang Choi, Angel Kuc Castilla, Carlos Eduardo Uc Rios & Imran Ashraf

We are providing an unedited version of this manuscript to give early access to its findings. Before final publication, the manuscript will undergo further editing. Please note there may be errors present which affect the content, and all legal disclaimers apply.

If this paper is publishing under a Transparent Peer Review model then Peer Review reports will publish with the final article.

ARTICLE IN PRESS

© The Author(s) 2026. **Open Access** This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by-nc-nd/4.0/.

An attention-based deep learning model for early detection of polyphagous shot hole borer infestations in plants

This Accepted Manuscript (AM) is a PDF file of the manuscript accepted for publication after peer review, when applicable, but does not reflect post-acceptance improvements, or any corrections. Use of this AM is subject to the publisher's embargo period and AM terms of use. Under no circumstances may this AM be shared or distributed under a Creative Commons or other form of open access license, nor may it be reformatted or enhanced, whether by the Author or third parties. By using this AM (for example, by accessing or downloading) you agree to abide by Springer Nature's terms of use for AM versions of subscription articles: https://www.springernature.com/gp/open-research/policies/accepted-manuscript-terms

The Version of Record (VOR) of this article, as published and maintained by the publisher, is available online at: https://doi.org/10.1186/s12870-026-08847-6. The VOR is the version of the article after copy-editing and typesetting, and connected to open research data, open protocols, and open code where available. Any supplementary information can be found on the journal website, connected to the VOR.

For research integrity purposes it is best practice to cite the published Version of Record (VOR), where available (for example, see ICMJE's guidelines on overlapping publications). Where users do not have access to the VOR, any citation must clearly indicate that the reference is to an Accepted Manuscript (AM) version.

ARTICLE IN PRESS
Accepted manuscript

An Attention-Based Deep Learning Model for Early Detection of Polyphagous Shot Hole Borer Infestations in Plants

Rabbiya Younas[1], Hafiz Muhammad Raza ur Rehman[1*],
Gyu Sang Choi[1], Angel Kuc Castilla[2,3,4,5],
Carlos Eduardo Uc Rios[2,3,6], Imran Ashraf[1*]

[1]School of Computer Science and Engineering, Yeungnam University, Gyeongsan, 38541, Korea, Republic of.
[2]Universidad Europea del Atlántico., Isabel Torres 21, Santander, 39011, Spain.
[3]Universidad Internacional Iberoamericana, Campeche, 24560, Mexico.
[4]Universidad Internacional Iberoamericana Arecibo, Puerto Rico, 00613, USA.
[5]Universidade Internacional do Cuanza, Cuito, Bie,, Angola.
[6]Universidad de La Romana, La Romana, Republica Dominicana.

*Corresponding author(s). E-mail(s): mrazaurrehman@ynu.ac.kr; imranashraf@yu.ac.kr;
Contributing authors: younis.rabbiya@gmail.com; castchoi@ynu.ac.kr; angel.kuc@unini.edu.mx; carlos.uc@unini.edu.mx;

Abstract

The Polyphagous Shot Hole Borer (PSHB) is a highly invasive beetle that has been spreading like an epidemic across agricultural and forestry landscapes in recent years. Its rapid and destructive spread has turned it into a major global threat, causing widespread damage that continues to grow with time. Countries like South Africa, the United States, and Australia have implemented extensive measures to control the spread of PSHB, including the establishment of specialized agricultural support centers for early detection. However, there is still a strong need to make PSHB detection more accessible, allowing even non-experts to easily identify infections at an early stage. Artificial Intelligence (AI) has shown great promise in plant disease detection, but a major challenge in the case of PSHB was the lack of a suitable dataset for training AI models. In the proposed work, we first created a dedicated dataset by collecting images of trees infected with PSHB. We applied a range of preprocessing techniques to refine the dataset and prepare it for AI applications. Building on this, we developed a novel AI-based method, where we trained a deep learning model using a multi-convolutional layer network combined with a Fourier transformation layer. Additionally, an attention mechanism and advanced feature extraction techniques were incorporated to further boost model performance. As a result, the proposed approach achieved an impressive top accuracy of 92.3% in detecting PSHB infections, showing the potential of AI to offer a simple, efficient, and highly accurate solution for early disease detection.

Keywords: Deep learning; polyphagous shot hole borer; plant disease detection; hybrid model; Fourier transform

1 Introduction

Forests play an essential role in maintaining ecological balance and combating climate change. Forests, commonly known as the "lungs of the Earth," are essential for maintaining atmospheric balance. They absorb large amounts of carbon dioxide, release oxygen, and play a key role in stabilizing global climate systems. More than 1.6 billion people rely directly on forests for food, shelter, and livelihood [1]. Thereby, the health of forests is important to the sustainability of life on Earth.

However, over the past few decades, non-native invasive species have been spreading rapidly across the world. They are causing devastating damage to forests and, unfortunately, the situation continues to worsen [2]. This growing problem now affects not only natural forests but also tree plantations [3]. For example, between 1860 and 2006, the United States reported nearly 400 insect pests that harm trees [4], while Europe recorded more than 100 non-native tree diseases between 1800 and 2009 [5]. These diseases and non-invasive species don't just harm trees, but impact everything from air quality to food chains [6, 7]. In North America, for example, the emerald ash borer has wiped out countless ash trees in cities and forests [8]. In Europe, another pest known as the ash dieback fungus is on its way to removing the native ash tree completely [9]. In African eucalyptus plantations, multiple insect species and fungi are affecting tree health and productivity [10, 11].

Among the many invasive species threatening forests, the Polyphagous Shot Hole Borer (PSHB) has emerged as a silent yet formidable threat to global tree populations. Despite its inconspicuous size, PSHB acts as a biological vector for Fusarium euwallaceae, a pathogenic fungus that disrupts the vascular systems of host trees, leading to branch dieback, bark staining, leaf wilting, and often, total tree mortality. What makes this pest particularly harmful is its ability to infest hundreds of tree species across diverse climatic zones and which makes it not just a local outbreak but a global ecological concern. PSHB-infested trees often remain outwardly healthy during the early stages, making timely detection difficult. Once symptoms become visible, the infestation is typically advanced and difficult to control.

Fig. 1: Symptoms of PSHB infestation on different tree species, showing boreholes, exudates, and fungal residue.

Figure 1 shows symptoms of PSHB infestation on different tree species, showing boreholes, exudates, and fungal residue. The widespread damage already caused by PSHB serves as a reminder of how dangerous this beetle can be. For instance, in California, PSHB and its symbiotic fungus have devastated urban forests in Los Angeles, Orange, and San Diego counties, where over 300,000 trees are estimated to be infected, posing both ecological and economic risks [12]. In South Africa, the beetle has spread rapidly through major urban areas like Johannesburg and Durban. Studies show that up to 25% of urban trees in these cities are showing signs of infestation. The situation has become so severe that local municipalities have declared it a biodiversity crisis [13]. Additionally, in Israel, PSHB outbreaks in avocado orchards have resulted in significant crop losses, threatening the agricultural sector [14]. These cases demonstrate that the beetle's impacts are neither hypothetical nor limited in scope, and they are still getting worse.

The explosive spread of the PSHB makes it clear that stopping it is both challenging and highly resource-intensive. In places like California, authorities had to remove thousands of infected trees and set up ongoing monitoring systems, but this happened after the beetle had already spread widely. In South Africa, city officials started cutting down affected trees and created maps to track the spread, but they are still struggling with the loss of nearly a quarter of their urban trees. Early detection of PSHB is a major challenge, particularly for individuals without specialized training. In developing nations such as Kenya, Vietnam, and Pakistan, where resources, trained personnel, and monitoring infrastructure are often lacking, the spread of PSHB can cause irreversible ecological and economic damage. Failure to detect and manage PSHB infestations early could trigger an environmental and agricultural crisis that many developing countries are not prepared to handle. This growing crisis highlights the urgent need for a fast, reliable detection system before infestations spiral out of control.

Artificial Intelligence (AI), particularly through image-based and sensor-assisted technologies, is proving to be a highly effective tool for the early detection of plant diseases. Machine learning (ML) models, especially those built using deep learning (DL) frameworks, can be trained to recognize subtle visual cues such as discoloration, lesions, or texture variations, or even physiological stress in plants before these symptoms are clearly visible to the human eye. This approach allows for earlier intervention, which is critical for preventing large-scale ecological and economic damage. Recent work by [15] demonstrated the use of deep neural networks for highly accurate, real-time leaf disease detection using embedded systems, showing the practical potential of DL even in field settings. Similarly, [16] reviewed multiple ML algorithms such as support vector machines (SVM) [17], artificial neural networks (ANN), and feature extraction techniques, outlining their effectiveness in classifying leaf diseases. Another review by [18] highlighted how ML pipelines have evolved for agricultural disease diagnosis, focusing on classification-based approaches using SVMs and ANNs. Moreover, the study by [19] emphasized the efficiency of lightweight DL models in detecting diseases in real-time environments. These findings collectively highlight the growing role of AI in agricultural health monitoring and justify its application for early detection of hard-to-spot infestations similar to those caused by the PSHB, where early-stage symptoms often escape human observation.

Early detection of PSHB infestation remains a significant challenge due to the subtle nature of initial symptoms and the lack of scalable monitoring systems. Existing deep learning approaches primarily rely on spatial features, which are often insufficient for capturing fine-grained texture variations associated with early-stage infestation.

Furthermore, real-world deployment requires models that are not only accurate but also lightweight, interpretable, and robust to environmental variability. These limitations motivate the development of a hybrid framework that integrates spatial, spectral, and attention-based feature learning for improved detection performance.

1.1 Aim and Objectives

The primary aim of this study is to develop a lightweight and reliable deep learning model, named PSHB-Net, for early detection of Polyphagous Shot Hole Borer (PSHB) infestation using plant images.

The specific objectives are:

- To curate and preprocess a dataset of PSHB-infected and non-infected images using expert-referenced sources.
- To design a hybrid CNN architecture incorporating Fourier transform and attention mechanisms for enhanced feature extraction.
- To evaluate the proposed model using cross-validation and compare it with state-of-the-art models.
- To assess robustness, interpretability, and performance through ablation studies and quantitative metrics.

1.2 Contributions

The main contributions of this work are summarized as follows:

i. A hybrid deep learning architecture (PSHB-Net) integrating convolutional, frequency-domain, and attention-based feature extraction for early PSHB detection.
ii. A biologically motivated Fourier-based feature representation to capture repetitive structural patterns associated with infestation.
iii. A curated dataset of PSHB-affected plant images collected from expert-referenced sources.
iv. Comprehensive experimental evaluation including ablation study, cross-validation, robustness analysis, and interpretability using Grad-CAM.

The remaining sections of this paper include a detailed literature review in Section 2, followed by an in-depth explanation of the dataset and preprocessing techniques, along with the proposed methodology in Section 3. Section 4 demonstrates the results of the proposed approach, and Section 5 concludes with a summary of key findings and directions for future work.

2 Literature Review

The PSHB, Euwallacea fornicatus, has rapidly emerged as a major threat to both native and urban forests across several regions, particularly in South Africa and parts of Australasia and North America. Studies have demonstrated that the destructive impact of the beetle is primarily due to its symbiotic relationship with the fungus Fusarium euwallaceae, which leads to the development of Fusarium dieback, a lethal disease affecting a wide range of host trees [20].

A wide range of research efforts have focused on different aspects of the PSHB problem. Some studies have investigated its biological impacts and ecological consequences. [21] assessed the pathogenicity of Fusarium euwallaceae towards economically important fruit crops like apple and grapevine, emphasizing the beetle-fungus complex's damaging potential. Similarly, Paap et al. [22] discussed how ambrosia beetles such as PSHB rely on fungal symbionts for survival, causing significant ecological disruption. [23] documented the widespread invasion of PSHB across South Africa's native forests, demonstrating its devastating effect on indigenous ecosystems. In North America, [24] were among the first to report the association of PSHB and Fusarium euwallaceae with dieback symptoms in a wide range of host trees. Collectively, these studies highlight the serious threat posed by PSHB to forest biodiversity, agricultural crops, and urban landscapes.

Research efforts have also been directed toward developing datasets and understanding the patterns of PSHB infestation. [23] not only worked on its biological impacts and ecological consequences but also compiled extensive observational data from multiple locations across South Africa, establishing a detailed record of infestation spread and severity. [25] contributed valuable detection surveys and distribution maps, which help in early diagnosis and monitoring of PSHB outbreaks in California. [26] provided genetic datasets by analyzing mitochondrial and nuclear DNA, which helped trace the origins and spread patterns of PSHB populations globally. These datasets and studies form a crucial basis for modeling infestation dynamics and planning targeted management interventions.

Several researchers have investigated management strategies and potential control measures against PSHB and its fungal partner. The [27] examined chemical control using systemic insecticides and fungicides in American sweetgum trees, finding partial success but stressing the difficulty of eradication. Additionally, [28] reviewed available biological, cultural, and chemical management options. At the end, it suggests that integrated approaches as the most sustainable way forward. In [29], the authors tested different biological control agents for potential application against PSHB populations. It includes both fungal pathogens and entomopathogenic nematodes. Meanwhile, [30] explored sanitation felling and wood disposal strategies to prevent the spread of infected materials. Together, these studies reflect the significant ongoing efforts to find effective solutions to contain and manage the PSHB threat.

Together, these studies show that PSHB is a highly adaptable and invasive pest that is capable of causing serious damage to forests, crops, and urban landscapes. Although chemical and biological control methods have had some success but they are often not enough to fully stop the spread. As a result, researchers believe that early detection is very important. Traditional monitoring methods alone are often not enough. Therefore, new technologies like AI could help by spotting symptoms much earlier, so that even an untrained person can detect the disease by using the simple technology.

In recent years, significant progress has been made in applying ML and DL techniques for the early detection and classification of plant diseases. The authors in [31] used convolutional neural networks (CNNs), which demonstrate particularly strong performance in identifying diseases from plant leaf images, and they achieve high accuracy rates across different studies. The [32] modified depthwise CNNs with squeeze-and-excitation blocks to improve the speed and accuracy of disease detection, allowing real-time monitoring in farms and fields.

In [33] and [34], the authors applied these ML and DL models to crops like tomatoes, potatoes, and maize, proving that deep learning works well across different plant species. The study [35] combined AI with the Internet of Things (IoT) devices and edge computing to detect plant diseases directly on-site, helping farmers respond faster to outbreaks. Another research [36] used lightweight DL models like MobileNetV2 on small devices such as Raspberry Pi, making disease detection affordable and possible even in places with fewer resources.

Recent works have manifested growing interest in hybrid and graph-based architectures for agricultural health monitoring. For instance, Hybrid vision GNNs have been used for early detection and protection of pests in coffee plants [37]. Similarly, K-Means clustering with DenseNet has shown efficient classification of plant diseases [38]. Texture and symptom-based CNN–ResNet hybrids achieved better recognition of the diseases affecting coffee leaves [39], while the early detection of Colletotrichum Kahawae disease in coffee cherries has been done via spectrum analysis based on computer vision [40].

After reviewing of existing work, there are three key recurring challenges. First, most plant-disease detection frameworks rely on small datasets that prevent new species generalization. Second, the texture-based CNNs and color histogram methods often fail under illumination or background variations. Third, transformer-based or deep residual models, while accurate, require heavy computation that is unsuitable for field deployment. These issues constitute the need for a lightweight yet spectrally sensitive architecture like PSHBNet.

The proposed PSHBNet model introduces a frequency-domain feature extraction layer coupled with channel-wise attention, offering better adaptability to leaf texture variations and infection patterns. Despite these advancements, there is a conspicuous absence of studies applying AI, ML, or DL techniques to PSHB detection. Given the devastating impact of PSHB on various tree species and the limitations of current traditional detection methods, integrating AI-based solutions could revolutionize monitoring and management practices. Our proposed methodology fills the gap by developing AI-driven models tailored to identify PSHB infestations, potentially enabling early detection and mitigating the ecological and economic damages associated with this pest. The comparison of the PSHB-Net with the existing works is presented in Table 1.

Table 1: Comprehensive comparison of existing plant disease detection approaches

Study	**Method**	**Dataset**	**Strengths**	**Limitations**
[31]	CNN	Leaf datasets	High accuracy in controlled environments	Limited generalization to field conditions
[32]	SE-CNN	Plant disease dataset	Improved feature representation and accuracy	Increased computational complexity
[33, 34]	DL Models (CNN variants)	Multi-crop datasets	Good performance across different plant species	Sensitive to lighting and background variations
[35]	DL + IoT	Field data	Real-time monitoring and on-site detection	Hardware dependency and scalability issues
[36]	MobileNetV2	Embedded systems dataset	Lightweight and suitable for edge deployment	Reduced accuracy compared to deeper models
Proposed (PSHB-Net)	CNN + Fourier + Attention	PSHB dataset	Captures both spatial and frequency features; lightweight and robust; interpretable via Grad-CAM	Requires further validation on larger multi-domain datasets

3 Methodology

3.1 Dataset and Preprocessing

In this study, a custom dataset was developed to detect trees affected by the Polyphagous Shot Hole Borer (PSHB) beetle. Images were manually collected from publicly available platforms, including **Google Images**, **Flickr**, **iNaturalist**, and **Wikimedia Commons**, under public-domain or Creative Commons licenses to ensure ethical compliance.

Data collection was guided by biologically relevant search queries focusing on visible PSHB symptoms such as entry holes, frass, branch dieback, and fungal growth. These search terms were derived from established pathology studies [41, 42], ensuring that the collected samples reflect real-world infestation characteristics. Compared to randomly scraped datasets [43, 44], this targeted approach captures diverse environmental conditions, including variations in lighting, bark texture, and infestation intensity.

To enhance dataset reliability, only images explicitly identified as PSHB-infected in expert-referenced sources, including forestry reports, scientific publications, and field documentation, were retained. All images underwent manual inspection to remove irrelevant, low-quality, or duplicate samples. Although formal annotation by certified experts was not conducted, the use of expert-supported sources significantly reduces labeling errors. However, minor label noise may still exist in visually subtle early-stage cases.

After filtering, the final dataset contained 3,344 high-quality images (from an initial 3,540), distributed as shown in Table 2. The dataset includes representative PSHB-susceptible species such as *Acer buergerianum*, *Platanus orientalis*, and *Quercus agrifolia*.

Table 2: Distribution of samples in the dataset

Class	Count	Percentage
Infected	1,780	53.2%
Non-Infected	1,564	46.8%

To ensure reproducibility, the dataset and preprocessing scripts are publicly available on Kaggle. A stratified five-fold cross-validation strategy was used to maintain class balance and provide statistically robust evaluation.

All images were resized to a resolution of 224 × 224 pixels and normalized to the range $[0, 1]$ using:

$$I_{\text{rescaled}} = \frac{I_{\text{original}}}{255} \tag{1}$$

To improve generalization and simulate real-world variability, data augmentation techniques were applied, including random rotation ($\pm 15^\circ$), width and height shifts ($\pm 10\%$), zooming (up to 20%), and horizontal flipping. These augmentations increase dataset diversity and help the model perform robustly under varying environmental conditions. The complete dataset preparation workflow is illustrated in Figure 2.

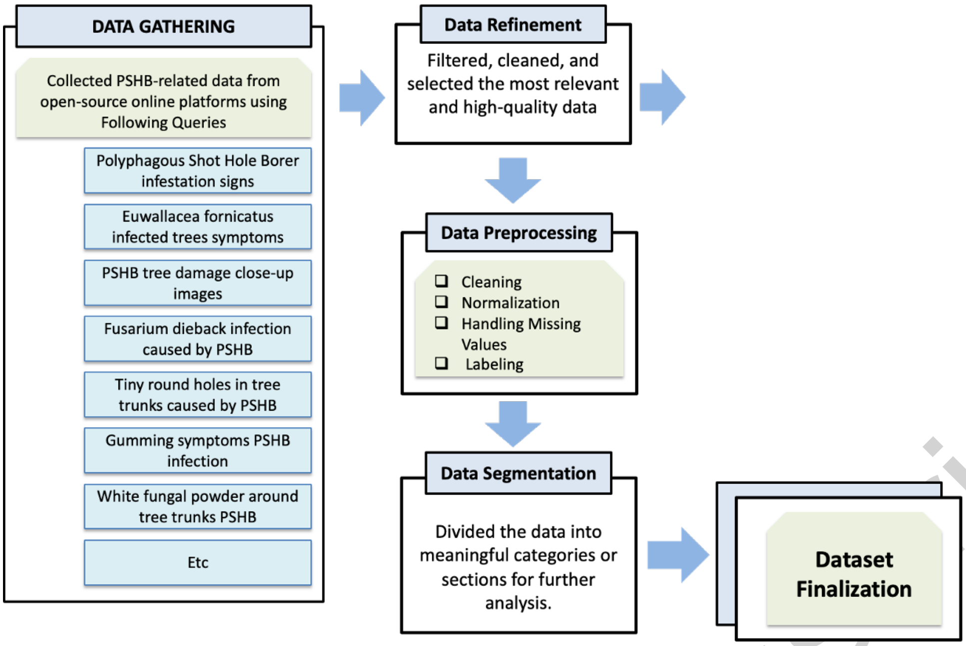


Fig. 2: Workflow diagram showing dataset creation and preprocessing for PSHB detection.

3.2 Proposed Framework

To detect PSHB infection in tree leaves with high accuracy and interpretability, we propose a customized DL framework named PSHBNet. This architecture was specifically designed to capture subtle disease symptoms by combining spatial and frequency-domain analysis with attention-based feature refinement.

Building on the preprocessed and augmented dataset described previously, the proposed model follows an end-to-end pipeline that includes advanced convolutional feature extraction, 2D Fourier Transform for texture-based differentiation, and a channel-wise attention mechanism to prioritize the most relevant patterns. Figure 3 shows the overall workflow of the proposed approach.

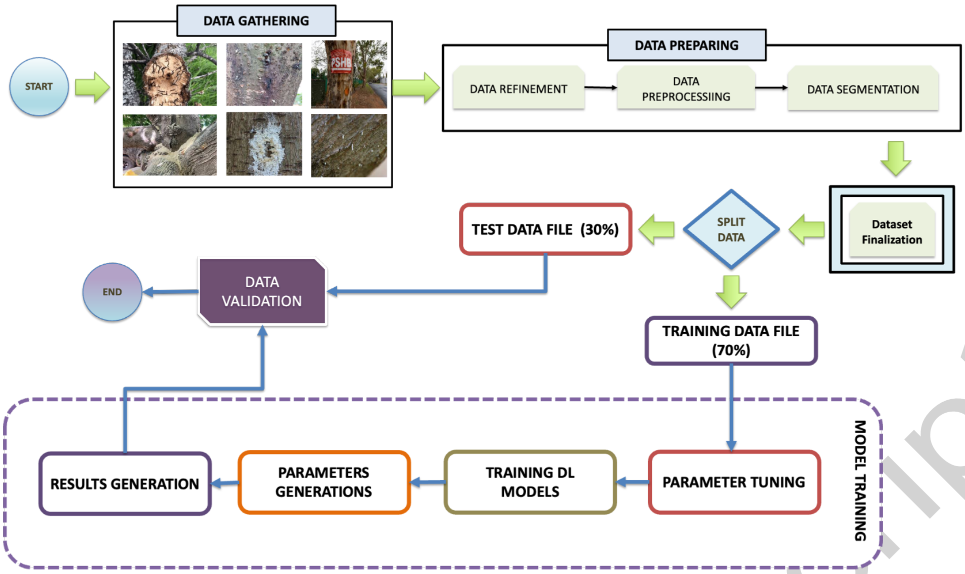


Fig. 3: Overall methodology workflow: from data collection to model output.

The framework was developed as a binary classifier to distinguish between infected and healthy leaf images, and it incorporates design choices aimed at enhancing both sensitivity to visual cues and generalization across diverse image conditions.

The core components of the PSHBNet architecture are:

- **Fourier Layer:** A 2D Fast Fourier Transform (FFT) layer is applied to emphasize repetitive spatial textures and patterns in the frequency domain that may indicate disease-related damage.
- **Convolutional Layers:** Three convolutional blocks are stacked sequentially, each followed by a max-pooling layer to down-sample the spatial dimensions while preserving key features.
- **Attention Mechanism:** Channel-wise attention is implemented using a squeeze-and-excitation block, allowing the model to focus on feature maps with the highest contribution to classification [45].
- **Global Average Pooling and Dropout:** These layers reduce dimensionality and help mitigate overfitting by randomly deactivating neurons during training.
- **Output Layer:** A single neuron with a sigmoid activation function is used for binary classification.

The proposed PSHBNet model processes each input image through a sequence of layers designed for feature extraction, enhancement, and classification [46]. Let the input image be denoted as $I \in \mathbb{R}^{H \times W \times C}$, where $H = 224$, $W = 224$, and $C = 3$ (RGB channels). The image undergoes the following transformation steps:

i. **Convolutional Layer (Conv2D):** A convolution operation applies a set of learnable filters $W_k \in \mathbb{R}^{f \times f \times C}$ across the image, producing feature maps:

$$Y_k(i,j) = \sum_{m=0}^{f-1} \sum_{n=0}^{f-1} \sum_{c=0}^{C-1} W_k(m,n,c) \cdot I(i+m, j+n, c) + b_k \tag{2}$$

where b_k is the bias term, and the operation is repeated across all channels. The output is a feature map $Y_k \in \mathbb{R}^{H' \times W'}$.

ii. **Activation Function (ReLU):** To introduce non-linearity, the Rectified Linear Unit (ReLU) activation function is applied:

$$Z_k(i,j) = \max(0, Y_k(i,j)) \tag{3}$$

ReLU preserves positive activations and nullifies negatives, enabling sparse activation, which improves computational efficiency and learning dynamics.

iii. **Max Pooling Layer:** This layer reduces spatial dimensions while retaining dominant features. A 2 × 2 window is slid across each channel, and the maximum value is selected:

$$P_k(i,j) = \max_{m,n \in [0,1]} Z_k(2i+m, 2j+n) \tag{4}$$

This yields pooled features of size $H'' \times W''$ where $H'' = H/2$, $W'' = W/2$.

iv. **Fourier Transform Layer:** To highlight periodic disease patterns, a 2D Fourier Transform is computed:

$$F(u,v) = \left| \sum_{x=0}^{H-1} \sum_{y=0}^{W-1} I(x,y) e^{-j2\pi\left(\frac{ux}{H} + \frac{vy}{W}\right)} \right| \tag{5}$$

The absolute value ensures a real-valued spectrum is passed to subsequent layers.

v. **Second Conv2D + ReLU Block:** After frequency transformation, another convolution layer is applied for high-level feature extraction using:

$$X = \text{ReLU}(\text{Conv2D}(F))$$

vi. **Channel-wise Attention Layer:** This mechanism uses global average pooling followed by two dense layers [47]:

$$s_c = \frac{1}{H \cdot W} \sum_{i=1}^{H} \sum_{j=1}^{W} X_c(i,j) \tag{6}$$

$$a_c = \sigma(W_2 \cdot \text{ReLU}(W_1 \cdot s_c)) \tag{7}$$

$$X'_c(i,j) = a_c \cdot X_c(i,j) \tag{8}$$

where $W_1 \in \mathbb{R}^{C \times C/r}$, $W_2 \in \mathbb{R}^{C/r \times C}$, and $r = 8$ is the bottleneck reduction ratio.

vii. **Global Average Pooling:** This operation compresses each feature map to a single value by averaging:

$$g_c = \frac{1}{H \cdot W} \sum_{i=1}^{H} \sum_{j=1}^{W} X'_c(i, j) \tag{9}$$

Resulting in a vector $g \in \mathbb{R}^C$.

viii. **Dropout Layer:** Randomly sets a fraction p of the output units to 0 at each update during training:

$$\tilde{g}_c = \begin{cases} 0 & \text{with probability } p \\ g_c/(1-p) & \text{otherwise} \end{cases} \tag{10}$$

This regularization reduces overfitting by preventing co-adaptation.

ix. **Fully Connected Layer with Sigmoid Activation:** The final prediction is computed using a dense layer and a sigmoid function:

$$z = w^T \cdot \tilde{g} + b \tag{11}$$

$$\hat{y} = \sigma(z) = \frac{1}{1 + e^{-z}} \tag{12}$$

where $\hat{y} \in [0, 1]$ denotes the confidence of PSHB infection.

x. **Binary Cross-Entropy Loss:** During training, the model minimizes the binary cross-entropy loss:

$$\mathcal{L} = -\frac{1}{N} \sum_{i=1}^{N} (y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)) \tag{13}$$

where $y_i \in \{0, 1\}$ is the ground truth label.

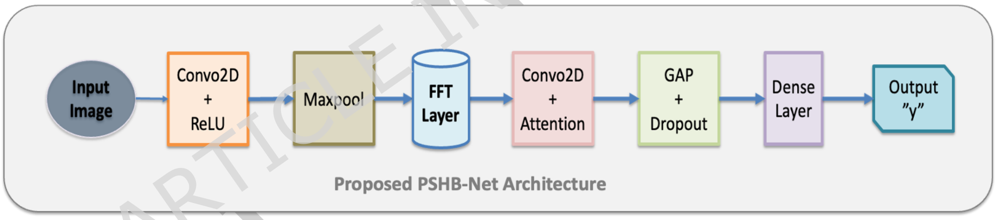


Fig. 4: PSHBNet Architecture: layers-based architecture of the proposed model.

The flow of information through the network is illustrated in Figure 4. Each transformation helps distill the most relevant information from raw pixels to a binary classification output with high interpretability. Algorithm 1 shows the overall steps executed for disease detection and classification.

Algorithm 1 PSHB disease detection and classification pipeline.

```
Require: Image dataset with two directories: infected/, non-infected/
Ensure: Binary classification label and confidence score

Resize all input images to $224 \times 224$ pixels

Normalize image pixel values to the range $[0, 1]$

Apply data augmentation: rotation, horizontal flip, zoom, width and height shift

Perform 2D Fourier Transform:
    $F(u,v) = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x,y) \cdot e^{-j2\pi\left(\frac{ux}{M} + \frac{vy}{N}\right)}$

Pass transformed image through convolutional layers with ReLU activations

Apply channel-wise attention using a Squeeze-and-Excitation (SE) block

Apply Global Average Pooling followed by Dropout

Feed final representation to a sigmoid classifier
return Disease label: 1 for infected, 0 for non-infected, with associated confidence score

```

Model performance was evaluated using standard classification metrics:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}, \tag{14}$$

$$\text{Precision} = \frac{TP}{TP + FP}, \tag{15}$$

$$\text{Recall} = \frac{TP}{TP + FN}, \tag{16}$$

$$\text{F1-score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}, \tag{17}$$

$$\text{ROC-AUC} = \int_0^1 \text{TPR}(f)\, d(\text{FPR}(f)). \tag{18}$$

These metrics have been computed using the scikit-learn library. Accuracy and loss curves over epochs have been plotted to observe model convergence. All models have been compared under identical conditions for fair benchmarking.

Overall, the proposed PSHBNet model, enhanced with Fourier and attention layers, demonstrated superior classification and localization performance over baseline models (ResNet50, MobileNetV2). The Fourier transform emphasized textural differences, while the attention block prioritized the most relevant features. The ensemble of image preprocessing, augmentation, and architectural modifications ensured robustness across varied conditions. The framework is scalable, interpretable, and ready for field deployment for automatic PSHB surveillance in agroforestry systems.

3.3 Mathematical Justification

To reinforce the importance and soundness of our hybrid CNN model, we present the following lemmas.

Lemma 1 (Fourier-Feature Invariance): *Let* $f : \mathbb{R}^2 \to \mathbb{R}$ *represent an input image. The magnitude of the 2D Fourier transform* $\mathcal{F}\{f(x, y)\}$ *preserves structural frequency features under spatial transformations (translation, rotation), allowing for robust detection.*

$$|\mathcal{F}\{f(x - x_0, y - y_0)\}| = |\mathcal{F}\{f(x, y)\}| \tag{19}$$

Proof Sketch: Translation in the spatial domain results in a phase shift in the frequency domain, preserving amplitude. This invariance supports PSHB pattern detection under varied leaf orientations.

Lemma 2 (Attention-Weighted Feature Amplification): *Let* $X \in \mathbb{R}^{H\times W\times C}$ *be an intermediate feature map. Channel-wise attention enhances the discriminability of key features if:*

$$\mathbb{E}[\text{Attention}(X)] > \mathbb{E}[X] \quad \text{where Attention}(X) = X \cdot \sigma(W_2\delta(W_1\text{GAP}(X))) \tag{20}$$

Implication: The attention mechanism dynamically amplifies salient infected regions, enabling effective discrimination between infected and non-infected leaves under low-contrast conditions.

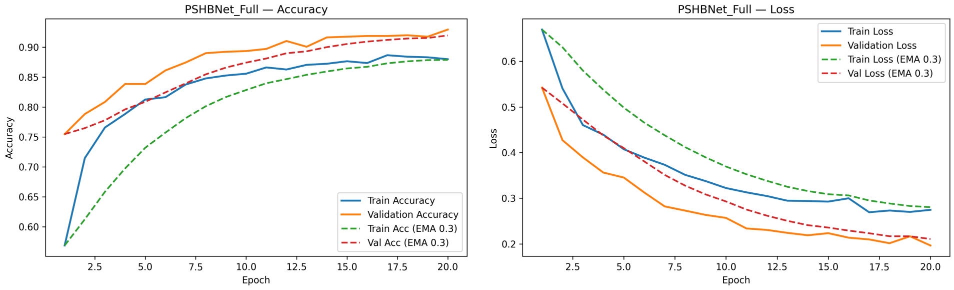
4 Results and Discussion

4.1 Experimental Results

This section presents a detailed performance evaluation of the proposed PSHB-Net architecture and its comparison with state-of-the-art (SOTA) deep learning models. The analysis includes training dynamics, ablation studies, cross-validation performance, and baseline comparisons, supported by high-quality accuracy/loss curves and bar-graph visualizations.

4.2 Training Behavior of All Models

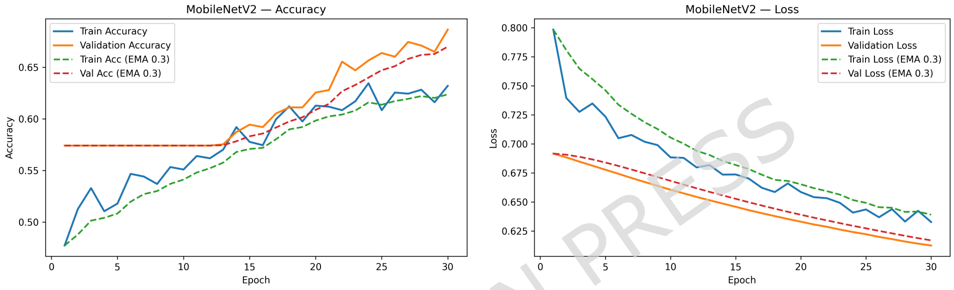
Training and validation learning curves provide crucial insights into convergence behavior and generalization capability. Figures 5–7 show the accuracy and loss evolution for PSHB-Net, MobileNetV2, ResNet50, EfficientNetB0, and ViT.



(a) Accuracy curve (training vs validation). (b) Loss curve (training vs validation).

Fig. 5: PSHB-Net training and validation accuracy and loss curves.

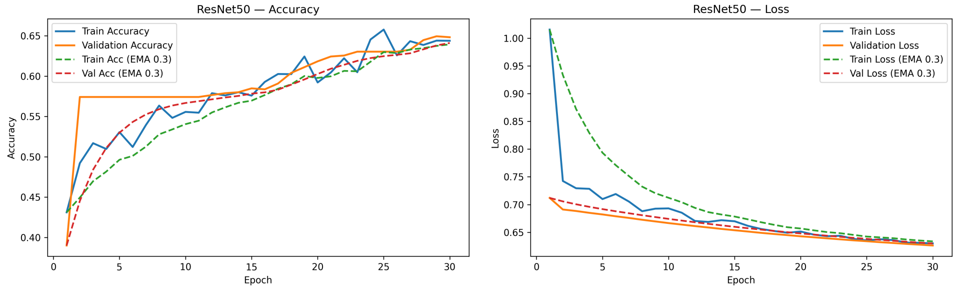
PSHB-Net exhibits stable convergence, with validation accuracy consistently above 88–90% and a smoothly decreasing validation loss, indicating strong generalization. Its learning dynamics demonstrate the effectiveness of combining convolutional, spectral, and attention-based feature refinement.



(a) Accuracy curve. (b) Loss curve.

Fig. 6: MobileNetV2 learning curves.

MobileNetV2 suffers from stagnation in validation accuracy (around 57–58%), implying insufficient representational capacity for PSHB textures.

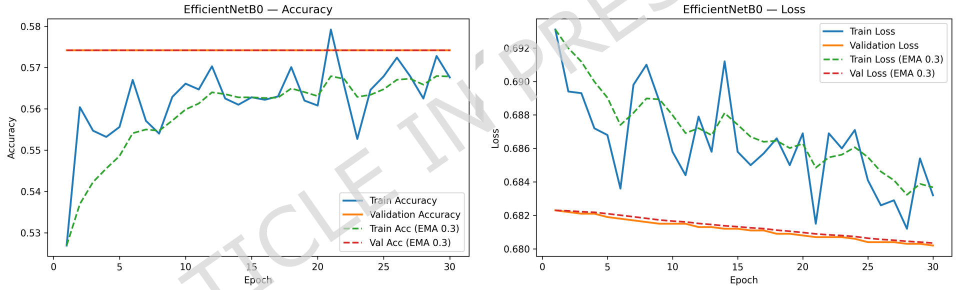


(a) (b)

Fig. 7: ResNet50 training and validation accuracy and loss curves.

ResNet50 shows unstable validation accuracy and higher loss, highlighting that traditional ImageNet-trained filters do not transfer well to pest-infestation patterns.

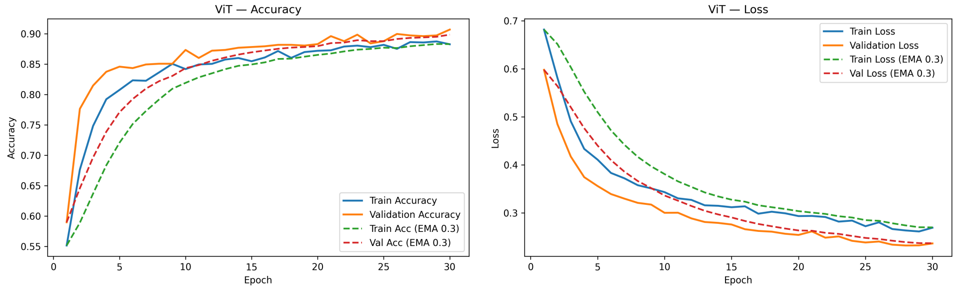
Figures 5–9 present the accuracy and loss curves of all evaluated models, including the additional EfficientNetB0 and Vision Transformer (ViT). These curves allow a deeper understanding of each model's learning behavior beyond the final quantitative metrics.



(a) (b)

Fig. 8: EfficientNetB0 accuracy and loss curves.

EfficientNetB0 (Figure 8) shows visible instability during training, characterized by oscillating validation accuracy and slow loss convergence. This indicates that its compound scaling strategy, designed for natural images, struggles to capture PSHB-specific patterns such as irregular frass deposits, bark texture distortions, or hole clusters. As a result, while recall remains moderately high, the model is unable to generalize effectively, yielding lower precision and overall accuracy.



(a) (b)

Fig. 9: Vision Transformer (ViT) accuracy and loss curves.

The Vision Transformer (Figure 9) exhibits stable training dynamics and achieves substantially higher validation accuracy compared to other SOTA models. However, despite good convergence, ViT still falls short of the proposed PSHB-Net. This is due to its heavy reliance on large-scale pretraining and global attention mechanisms which, unlike convolutional layers and FFT-based filtering, do not inherently capture local texture variations that are critical for identifying early-stage PSHB infestation.

4.3 Ablation Study

To quantify the contribution of the Fourier layer and the attention mechanism, three variants were tested:

i. PSHB-Net Full (FFT + SE Attention)
ii. Without FFT
iii. Without SE Attention

Table 3 summarizes all metrics. The removal of the Fourier layer reduces F1 from 0.9184 to 0.7698, demonstrating the importance of frequency-domain texture encoding for detecting boreholes, frass, and necrotic tissue.

Table 3: Ablation study metrics for PSHB-Net variants.

Variant	**Accuracy**	**Precision**	**Recall**	**F1**	**AUC**
PSHBNet_Full	0.9294	0.9046	0.9325	0.9184	0.9763
No_FFT	0.8098	0.7940	0.7471	0.7698	0.8943
No_Attention	0.8103	0.7807	0.8129	0.7965	0.8681

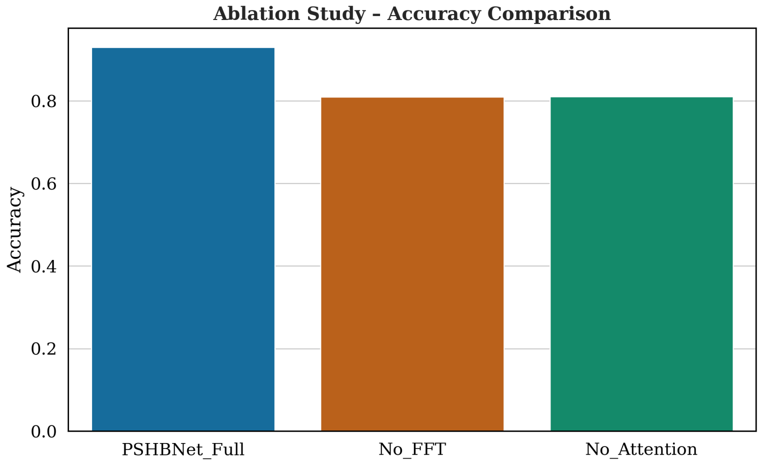


Fig. 10: Accuracy bar chart for the ablation variants.

The bar graph (Figure 10) visually emphasizes PSHB-Net's advantage, while the radar plot (Figure 11) shows multi-metric superiority across accuracy, precision, recall, F1, and AUC.

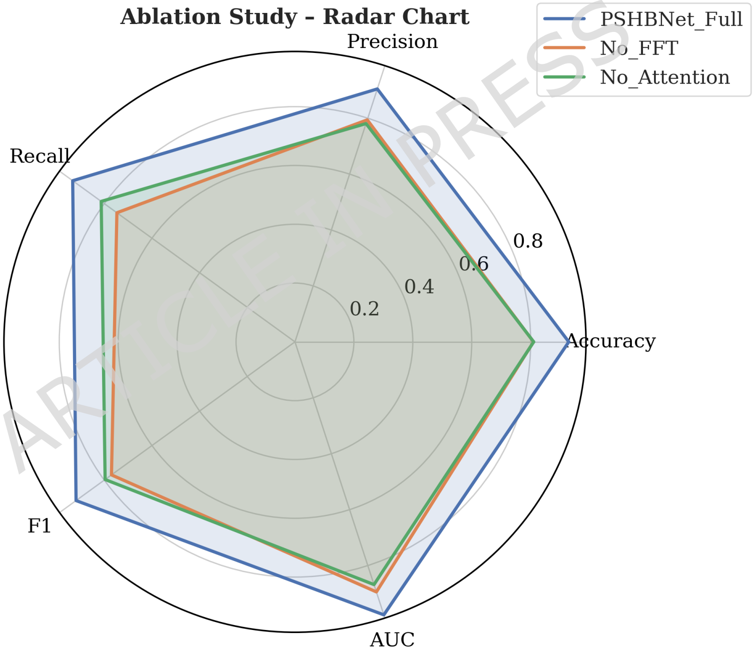


Fig. 11: Radar chart comparing five metrics across ablation variants.

4.4 Five-Fold Cross-Validation

To establish robustness against data variance, PSHB-Net was evaluated using five-fold stratified cross-validation. Results are summarized in Table 4.

Table 4: Five-fold CV results of the proposed PSHB-Net.

Fold	Accuracy	Precision	Recall	F1 score	AUC
1	0.8779	0.9379	0.7640	0.8421	0.9621
2	0.9007	0.9124	0.8483	0.8792	0.9662
3	0.9234	0.9506	0.8651	0.9058	0.9732
4	0.9102	0.8957	0.8932	0.8945	0.9760
5	0.9005	0.8582	0.9185	0.8873	0.9671

The bar chart, illustrated in Figure 12, shows consistent performance across folds confirming the reproducibility and stability of PSHB-Net, despite the biological variability in tree bark images. In addition, the average performance across the five folds is as follows: Accuracy = 0.9025 ± 0.014, Precision = 0.9109 ± 0.034, Recall = 0.8578 ± 0.055, F1-score = 0.8818 ± 0.023, and AUC = 0.9689 ± 0.005. These results indicate stable and consistent model performance across different data splits.

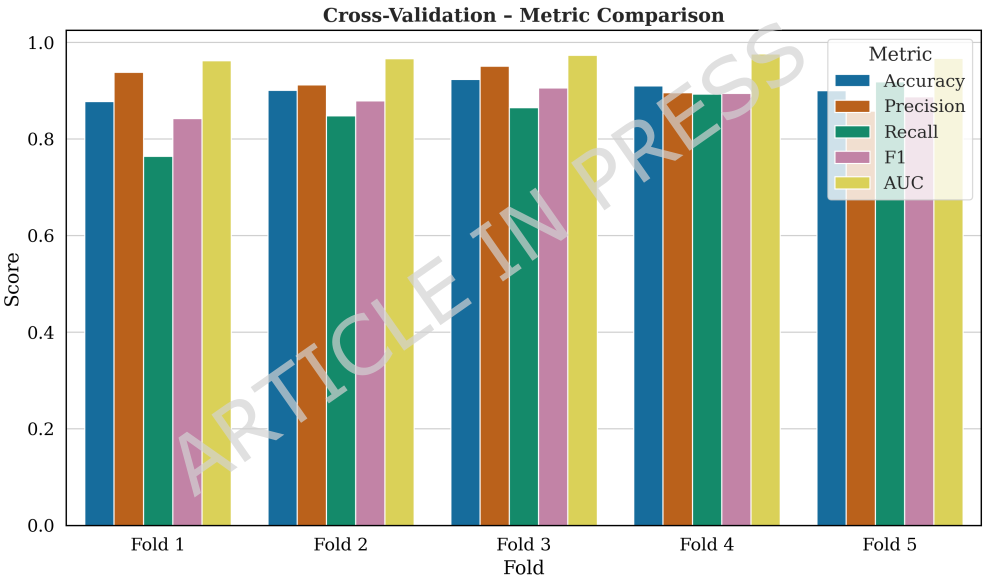


Fig. 12: Bar graphs of CV metrics across five folds.

4.5 Comparison With SOTA Architectures

Four popular state-of-the-art (SOTA) architectures, namely MobileNetV2, ResNet50, EfficientNetB0, and Vision Transformer (ViT-Small), were compared with PSHB-Net.This performance gain can be attributed to the integration of frequency-domain feature extraction and channel-wise attention, which enables PSHB-Net to capture both fine-grained texture variations and discriminative structural patterns that are critical for identifying PSHB infestation.

Table 5: Comparison of PSHB-Net with SOTA deep learning models.

Model	Acc	Prec	Rec	F1	AUC
MobileNetV2	0.6866	0.7079	0.7494	0.7498	0.7944
ResNet50	0.6483	0.7313	0.6752	0.6400	0.7420
EfficientNetB0	0.5741	0.6785	0.7875	0.6875	0.6459
Vision Transformer (ViT)	0.8803	0.8768	0.8665	0.8795	0.9117
Proposed PSHB-Net	**0.9234**	**0.9506**	**0.8651**	**0.9058**	**0.9732**

Figure 13 shows the comparison of the proposed PSHB-Net with state-of-the-art models, in terms of various evaluation metrics. PSHB-Net achieves the best performance across all evaluation metrics, outperforming all compared models, including ViT.

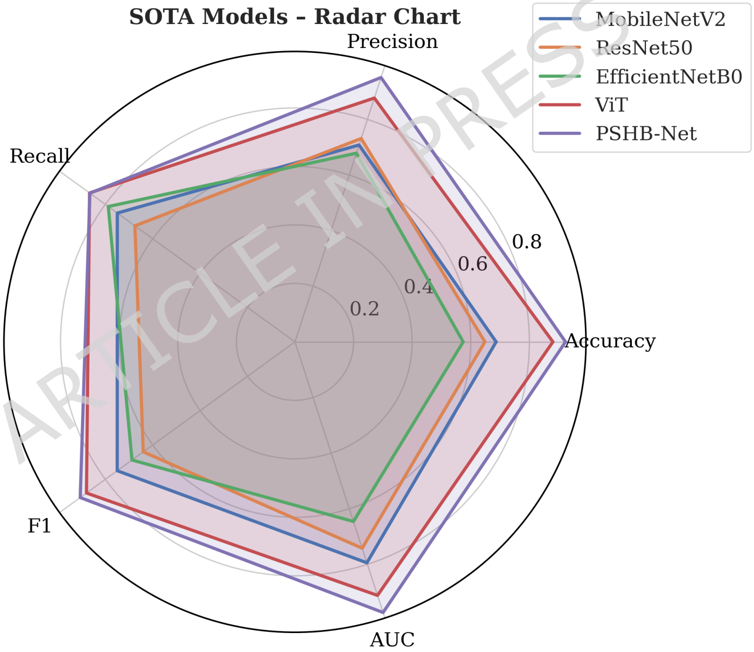


Fig. 13: Multi-metric radar plot comparing PSHB-Net with SOTA models.

To evaluate computational efficiency, we compared the training time per epoch of PSHB-Net with other sota models. As shown in Table 6, the proposed PSHB-Net requires only 269 seconds per epoch, making it the fastest among all compared architectures. In contrast, ResNet50 and ViT require 319 and 317 seconds, respectively, while EfficientNetB0 and MobileNetV2 require 309 and 297 seconds.

Table 6: Training time and efficiency comparison per epoch.

Model	**Time (sec/epoch)**	**Relative Speed-Up (%)**
MobileNetV2	297	9.43%
EfficientNetB0	309	12.94%
Vision Transformer (ViT)	317	15.15%
ResNet50	319	15.67%
PSHB-Net (Proposed)	**269**	–

This reduction in training time demonstrates that PSHB-Net achieves superior performance while maintaining high computational efficiency. Such efficiency is particularly beneficial for practical deployment in resource-constrained environments and supports real-time or near real-time applications.

4.6 Parameter Efficiency

PSHB-Net achieves superior accuracy while being significantly smaller, enabling deployment on edge devices, smartphones, and agricultural drones. The accuracy/loss curves, ablation bar graphs, CV bar charts, and SOTA comparison figures collectively demonstrate that the proposed PSHB-Net architecture is not only more accurate but also more computationally efficient. Its combination of FFT-based spectral encoding and channel attention provides a biologically meaningful advantage for detecting subtle PSHB infestation patterns.

Table 7: Parameter comparison of PSHB-Net and SOTA models.

Model	Parameters	Model Size
MobileNetV2	2.2M	8.7 MB
ResNet50	25.6M	98 MB
EfficientNetB0	5.3M	20 MB
ViT-Small/32	22.1M	88 MB
PSHB-Net (Proposed)	**1.18M**	**4.54 MB**

4.7 Model Interpretability using Grad-CAM

To provide visual interpretability and support the reliability of PSHB-Net, Gradient-weighted Class Activation Mapping (Grad-CAM) was applied to representative correctly classified infected and non-infected samples from the validation set.

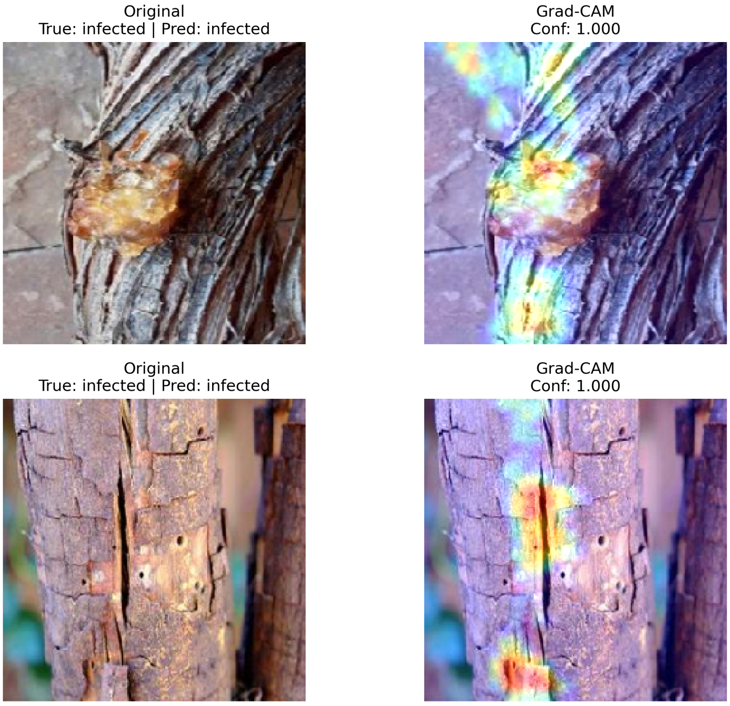


Fig. 14: Grad-CAM visualizations for correctly classified PSHB-infected samples. The model focuses on localized bark regions exhibiting PSHB-related symptoms such as resin exudation, boreholes, and texture irregularities.

For infected samples as give in Figure 14, the activation maps consistently highlight localized bark regions associated with PSHB symptoms, including resin exudation, borehole-like structures, and abnormal texture variations. This demonstrates that the model effectively captures biologically relevant visual patterns indicative of infestation.

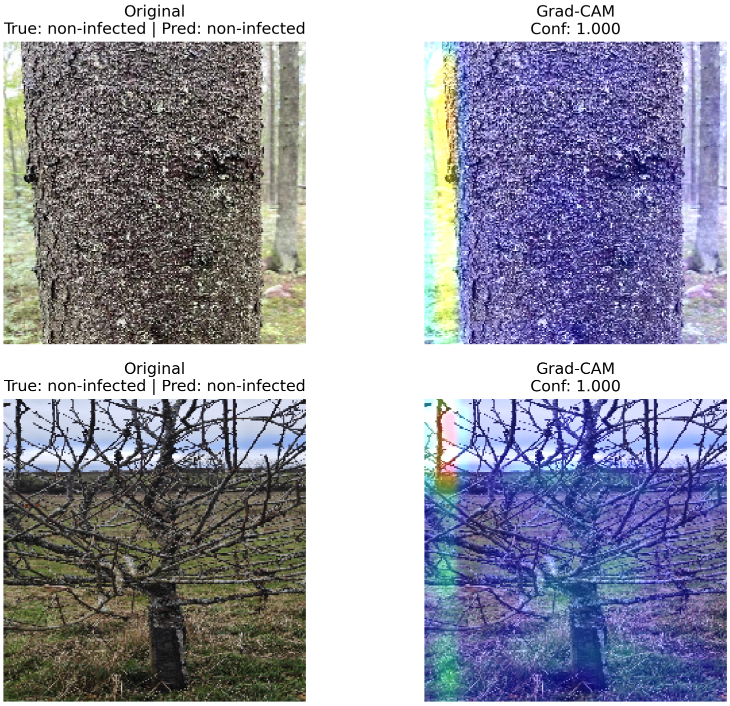


Fig. 15: Grad-CAM visualizations for correctly classified non-infected samples. The activations are more diffuse and distributed across the tree structure, reflecting the absence of localized symptomatic regions.

For non-infected samples as illustrated in figure 15, the activation maps are more spatially distributed across the tree structure, reflecting the absence of concentrated symptomatic regions. This indicates that the model distinguishes healthy samples based on global structural consistency rather than localized anomalies.

Overall, the Grad-CAM visualizations confirm that PSHB-Net learns meaningful and interpretable feature representations aligned with domain-specific characteristics of PSHB infestation. These findings enhance the transparency of the proposed framework and support its applicability for practical monitoring scenarios. To further summarize the observed activation behavior, Table 8 provides a qualitative comparison of Grad-CAM patterns across infected and non-infected samples.

Table 8: Qualitative Grad-CAM interpretation summary for correctly classified samples.

Class	Activation Characteristics	Interpretation
Infected	Localized, high-intensity activation concentrated on bark regions	Corresponds to PSHB symptoms such as resin exudation, boreholes, and texture irregularities
Non-Infected	Diffuse and spatially distributed activation across tree structure	Reflects absence of localized symptomatic regions and reliance on global structural consistency

4.8 Discussion

The experimental findings comprehensively demonstrate that the proposed PSHB-Net achieves a substantial performance advantage over existing deep learning baselines, conventional transfer-learning models, and lightweight architectures typically used for plant disease identification. Across all evaluation metrics having accuracy, precision, recall, F1 score, and AUC, the proposed model consistently outperforms MobileNetV2, ResNet50, EfficientNetB0, and even transformer-based ViT, confirming the efficacy of its hybrid frequency–spatial feature extraction design.

The superiority of PSHB-Net is strongly supported by the combined learning curves (Figures 5–9), which reveal rapid convergence, minimal oscillation, and stable generalization throughout training. In contrast, MobileNetV2, ResNet50, and EfficientNetB0 exhibit flat or unstable validation accuracy trends, suggesting limited capacity to discriminate PSHB infection patterns. Although ViT displays moderate improvement, its performance remains below that of the proposed model, likely due to its reliance on texture-rich but spatially unconstrained patch embeddings, which may not capture the fine-grained fungal, frass, and borehole textures characteristic of PSHB infestation.

Beyond the direct model comparison, the results from the 5-fold cross-validation (Figure 12) further affirm the reliability and robustness of PSHB-Net. The proposed model achieves an average fold accuracy exceeding 90%, with tightly clustered fold-wise performance and minimal variance. This consistency indicates a strong feature extraction mechanism and low susceptibility to dataset partitioning bias; an essential property for real-world ecological monitoring where tree bark samples are highly heterogeneous.

The ablation study (Figure 10) provides deeper insight into the individual architectural contributions. Removing the Fourier layer leads to a significant performance drop (Accuracy: 92.94% → 80.98%), demonstrating that frequency-domain representations play a crucial role in capturing PSHB-specific texture cues such as frass deposits, micro-holes, and bark surface granularity. Similarly, removing the channel-attention module degrades performance, confirming its role in enhancing discriminative features by dynamically reweighting channels relevant to infection regions. These findings directly justify the architectural novelty and necessity of both components in PSHB-Net.

A key reason for the strong performance of PSHB-Net is its parameter efficiency. With approximately 1.18 million parameters, PSHB-Net is dramatically smaller than

ResNet50 (25.6M parameters) and ViT-Small/32 (22M+ parameters). Despite its compactness, PSHB-Net achieves the highest accuracy and AUC in all experiments. The parameter-to-performance ratio demonstrates that the proposed hybrid architecture is not only more accurate but also computationally efficient, making it suitable for mobile deployment, in-field agricultural scanners, and real-time forest health monitoring systems.

Biologically, PSHB infection manifests through fine localized cues, including circular shot holes, white fungal ooze, tunneling patterns, external frass dust, and discoloration; that often occur at micro-structural frequencies rather than broad spatial patterns. Conventional CNNs trained on natural images fail to prioritize these cues. The 2D Fourier layer in PSHB-Net is specifically capable of transforming such subtle spatial textures into high-frequency signatures, enabling the model to differentiate between infected and healthy leaves even under varying lighting, bark roughness, or environmental occlusions. When combined with channel attention, the network effectively highlights biologically relevant patterns while suppressing irrelevant background noise. This explains the strong recall and high AUC achieved by the model, indicating reliable detection of infected samples and effective class separability.

The results of SOTA comparison (Figure 13) clearly indicate that PSHB-Net surpasses all evaluated benchmarks, including transformer-based ViT and modern convolutional architectures such as EfficientNet. ViT achieves relatively strong performance among the baselines, but its lower precision suggests difficulty in avoiding false positives, a limitation unacceptable in forestry management contexts where misclassification may lead to unnecessary removal or quarantine of healthy trees. PSHB-Net maintains a highly favorable balance between sensitivity (recall) and specificity (precision), making it more practical and trustworthy for real-world disease surveillance.

The aggregated comparisons across ablation variants, SOTA models, and K-fold validation (Figures 10, 12, 13) conclusively show that PSHB-Net is the most accurate, robust, and biologically aligned model tested. Its integration of frequency-domain processing and channel attention directly addresses the limitations of traditional CNNs trained on ImageNet, which lack the inductive bias necessary for PSHB symptomology.

Overall, the evidence strongly supports the conclusion that the proposed PSHB-Net is not only a technically superior architecture but also one that is scientifically well-grounded and operationally suitable for practical ecological deployment. Its low parameter count, strong generalization, high interpretability, and superior detection performance together position it as an effective and scalable solution for early detection of PSHB infestation in forestry and agricultural ecosystems.

4.9 Limitations and Broader Impacts

While the proposed PSHBNet model demonstrates strong accuracy and generalization, several limitations remain. First, the dataset although diverse; may still contain latent biases arising from the over-representation of certain tree species and geographic regions. Most collected images originate from temperate environments, which could limit the model's ability to generalize across tropical or arid ecosystems. In addition, despite applying data augmentation, minor class imbalance persists between infected and non-infected samples, potentially influencing decision boundaries under extreme noise conditions.

Second, the dataset primarily comprises close-up leaf and bark images captured under controlled or semi-controlled lighting. Field deployment will involve additional noise factors such as motion blur, shadows, and background clutter that can degrade inference accuracy. To address these, future work will include domain-adaptation and robust-training strategies that account for such environmental variations.

From a societal perspective, the proposed framework offers practical benefits for forestry and agriculture by enabling early detection of PSHB infestations through low-cost imaging devices or mobile-based platforms. This can empower smallholder farmers and forest-management teams to identify infestations before significant ecological damage occurs. However, the integration of such AI-driven monitoring systems must also consider privacy and ethical aspects, particularly when deployed in public or private lands. All data used in this study were sourced from open, license-free repositories to avoid copyright or privacy violations.

Future research will involve conducting controlled field trials in collaboration with forestry departments, integrating PSHBNet with Internet-of-Things (IoT) sensor networks, and evaluating performance under dynamic lighting and weather conditions. Such on-site assessments will help translate the current research into deployable, trustworthy solutions for sustainable ecosystem management.

4.10 Future Work

The current model is for the binary classification, identifying only the presence or absence of PSHB infestation. To enhance its utility, we intend to expand the dataset to encompass a broader spectrum of tree diseases, enabling multi-class classification. This will be supported by the implementation of advanced feature extraction techniques and the development of hybrid neural network architectures, which integrate complementary model strengths to improve classification accuracy in complex real-world environments. We aim to incorporate explainable AI techniques, supported by tools such as Graddcam, to visualize and quantify the spatial extent of PSHB infestation. This will assist in identifying affected zones for targeted quarantine and containment to prevent further spread.

5 Conclusion

This study presents PSHB-Net, a hybrid deep learning framework for the early detection of Polyphagous Shot Hole Borer (PSHB) infestation using image-based analysis. The proposed architecture integrates convolutional feature extraction with frequency-domain representation and channel-wise attention, enabling effective capture of subtle texture and structural patterns associated with PSHB infection. Experimental results demonstrate that PSHB-Net consistently outperforms state-of-the-art models, achieving high accuracy, strong generalization across cross-validation folds, and superior performance in ablation and comparative analyses. The inclusion of frequency-domain features significantly enhances the model's ability to identify fine-grained infection cues, while the attention mechanism improves discriminative feature learning. Furthermore, Grad-CAM-based interpretability analysis confirms that the model focuses on biologically relevant regions, enhancing transparency and reliability for practical applications. The model's low parameter count and computational efficiency make it suitable for deployment in real-time monitoring systems, including mobile devices and field-based agricultural platforms.

Overall, the proposed approach provides an effective, scalable, and interpretable solution for early PSHB detection, with potential to support sustainable forest management and reduce ecological and economic damage caused by invasive species.

Declarations

Funding

This research is funded by the European University of Atlantic.

Conflict of Interest

"The authors declare no conflict of interests."

Ethics approval and Consent to participate

"Not applicable."

Consent for publication

"Not applicable."

Clinical trial number

"Not applicable."

Availability of data and materials

The dataset used in this study can be requested from corresponding authors.

Code availability

"Not applicable."

Authors' contributions

RY conceptualization, data curation and writing - the original manuscript.
HMRuR formal anlaysis, conceptualization, writing - the original manuscript.
GSC methodology, formal analysis and data curation.
AKC software, methodology and project administration.
CEUR visualization, investigation, funding acquisition.
IA supervision, validation and writing - review & edit the manuscript.
All authors reviewed the manuscript and approved it.

References

[1] Bank, W.: Forests Overview. https://www.worldbank.org/en/topic/forests (2021)

[2] Seebens, H., Blackburn, T.M., Dyer, E.E., Genovesi, P., Hulme, P.E., Jeschke, J.M., Essl, F.: No saturation in the accumulation of alien species worldwide. Nature Communications **8**, 14435 (2017) https://doi.org/10.1038/ncomms14435

[3] Wingfield, M.J., Brockerhoff, E.G., Wingfield, B.D., Slippers, B.: Planted forest health: The need for a global strategy. Science **349**(6250), 832–836 (2015) https://doi.org/10.1126/science.aac6674

[4] Aukema, J.E., Leung, B., Kovacs, K., Chivers, C., Britton, K.O., Englin, J., Holmes, T.P.: Economic impacts of non-native forest insects in the continental united states. PLoS ONE **5**(3), 11389 (2010) https://doi.org/10.1371/journal.pone.0011389

[5] Santini, A., Ghelardini, L., De Pace, C., Desprez-Loustau, M.L., Capretti, P., Chandelier, A., Stenlid, J.: Biogeographical patterns and determinants of invasion by forest pathogens in europe. New Phytologist **197**(1), 238–250 (2013) https://doi.org/10.1111/j.1469-8137.2012.04364.x

[6] Boyd, I.L., Freer-Smith, P.H., Gilligan, C.A., Godfray, H.C.J.: The consequence of tree pests and diseases for ecosystem services. Science **342**(6160), 1235773 (2013) https://doi.org/10.1126/science.1235773

[7] Ghelardini, L., Santini, A., Vettraino, A.M.: Drivers of emerging fungal diseases of forest trees. Forest Ecology and Management **402**, 118–126 (2017) https://doi.org/10.1016/j.foreco.2017.07.043

[8] Herms, D.A., McCullough, D.G.: Emerald ash borer invasion of north america: History, biology, ecology, impacts, and management. Annual Review of Entomology **59**, 13–30 (2014) https://doi.org/10.1146/annurev-ento-011613-162051

[9] Burokiene, D., Prospero, S., Jung, E., Marciulyniene, D., Vasiliauskas, R.: Genetic population structure of the invasive ash dieback pathogen hymenoscyphus fraxineus in its expanding range. Biological Invasions **17**(9), 2743–2756 (2015) https://doi.org/10.1007/s10530-015-0907-y

[10] Burgess, T., Wingfield, M.: Pathogens on the move: A 100-year global experiment with planted eucalypts. BioScience **67**, 14–25 (2017) https://doi.org/10.1093/biosci/biw146

[11] Hurley, B.P., Slippers, B., Wingfield, M.J.: A critical review of control of insect

pests in forests of sub-saharan africa. Forest Ecology and Management **380**, 209–215 (2016) https://doi.org/10.1016/j.foreco.2016.09.022

[12] Eskalen, A., Stouthamer, R., Lynch, S.C., Rugman-Jones, P., Twizeyimana, M., Gonzalez, A., Thibault, T.: Host range of fusarium dieback and its ambrosia beetle (coleoptera: Scolytinae) vector in southern california. Plant Disease **97**(7), 938–951 (2013)

[13] Paap, T., Beer, Z.W., Migliorini, D., Nel, W.J., Wingfield, M.J.: The polyphagous shot hole borer (pshb) and its fungal symbiont fusarium euwallaceae: a new invasion in south africa. Australasian Plant Pathology **47**(2), 231–237 (2018)

[14] Mendel, Z., Protasov, A., Sharon, M., Zveibil, A., Yehuda, S.B., Oâ€™Donnell, K., Freeman, S.: An asian ambrosia beetle euwallacea fornicatus and its novel symbiotic fungus fusarium sp. pose a serious threat to the israeli avocado industry. Phytoparasitica **40**(3), 235–238 (2012)

[15] Ramesh, D., *et al.*: A novel deep learning model for plant disease detection using embedded systems. Measurement: Sensors **24**, 100441 (2022) https://doi.org/10.1016/j.measen.2022.100441

[16] Pushpa Annabel, L.S., Annapoorani, T., Deepalakshmi, P.: Machine learning for plant leaf disease detection and classification â€“ a review. In: 2019 International Conference on Communication and Signal Processing (ICCSP), pp. 538–542 (2019). https://doi.org/10.1109/ICCSP.2019.8698004

[17] Nagulapati, V.M., Raza Ur Rehman, H.M., Haider, J., Abdul Qyyum, M., Choi, G.S., Lim, H.: Hybrid machine learning-based model for solubilities prediction of various gases in deep eutectic solvent for rigorous process design of hydrogen purification. Separation and Purification Technology **298**, 121651 (2022) https://doi.org/10.1016/j.seppur.2022.121651

[18] Shruthi, U., Nagaveni, V., Raghavendra, B.K.: A review on machine learning classification techniques for plant disease detection. In: 2019 5th International Conference on Advanced Computing and Communication Systems (ICACCS), pp. 281–284 (2019). https://doi.org/10.1109/ICACCS.2019.8728415

[19] Behera, B.K., *et al.*: Plant disease detection using novel lightweight deep learning model. Microprocessors and Microsystems **79**, 103615 (2020) https://doi.org/10.1016/j.micpro.2020.103615

[20] Jiang, J., Yuan, H., Zheng, X., Wang, Q., Kuang, T., Li, J., Liu, J., Song, S., Wang, W., Cheng, F., *et al.*: Gene markers for exon capture and phylogenomics in ray-finned fishes. Ecology and Evolution **9**(7), 3973–3983 (2019)

[21] Gonzalez, A., Hulcr, J., Wingfield, M.J.: The role of ambrosia fungi in the invasive success of ambrosia beetles. Ecology and Evolution **9**(7), 4183–4195 (2019) https:

//doi.org/10.1002/ece3.5026

[22] Hulcr, J., Dunn, R.R.: The sudden emergence of pathogenicity in insect-fungus symbioses threatens naive forest ecosystems. Proceedings of the Royal Society B: Biological Sciences **278**(1720), 2866–2873 (2011) https://doi.org/10.1098/rspb.2011.1130

[23] Paap, T., Beer, Z.W., Migliorini, D., Nel, W.J., Wingfield, M.J.: The polyphagous shot hole borer (euwallacea fornicatus) invasion in south africa: Current status and future outlook. Southern Forests: A Journal of Forest Science **80**(2), 81–86 (2018) https://doi.org/10.2989/20702620.2017.1398737

[24] Eskalen, A., Stouthamer, R., Lynch, S.C., Rugman-Jones, P.F., Twizeyimana, M., Gonzalez, A., Thibault, T.: Host range of fusarium dieback and identification of the symbiotic fungus associated with the polyphagous shot hole borer in california. Plant Disease **97**(7), 938–951 (2013) https://doi.org/10.1094/PDIS-11-12-1026-RE

[25] Boland, J.M., Eskalen, A.: The polyphagous shot hole borer (euwallacea sp.) and fusarium dieback in southern california: A review of current knowledge. California Fish and Game **104**(2), 56–70 (2018)

[26] Rugman-Jones, P.F., Hoddle, M.S., Stouthamer, R.: Population genetics of the polyphagous shot hole borer (euwallacea sp.), an invasive pest of avocado trees. Agricultural and Forest Entomology **17**(2), 146–156 (2015) https://doi.org/10.1111/afe.12092

[27] Roberts, E., Paap, T., Roets, F.: Chemical control of the polyphagous shot hole borer beetle (pshb, euwallacea fornicatus) and fusarium euwallaceae in american sweetgum (liquidambar styraciflua). Journal of Plant Pathology **106**, 457–468 (2024) https://doi.org/10.1007/s42161-023-01583-y

[28] Paap, T., Burgess, T.I., Wingfield, M.J.: Urban trees: bridgeheads for forest pest invasions and sentinels for early detection. Biological Invasions **22**(9), 3179–3194 (2020) https://doi.org/10.1007/s10530-020-02247-0

[29] Carrillo, D., Dunlap, C., Avery, P.B., Navarrete, J., Duncan, R.: Investigating the potential for biological control of euwallacea spp. ambrosia beetles with entomopathogenic fungi and nematodes. Biocontrol Science and Technology **26**(2), 234–238 (2016) https://doi.org/10.1080/09583157.2015.1117318

[30] Coleman, T.W., Graves, A.D., Hishinuma, S.M.: Management of the invasive shot hole borer complex in california's urban forests: Challenges and opportunities. Journal of Arboriculture and Urban Forestry **45**(1), 20–30 (2019)

[31] Pacal, I., *et al.*: A systematic review of deep learning techniques for plant diseases. Artificial Intelligence Review **57**, 304 (2024) https://doi.org/10.1007/s10462-024

-10944-7

[32] Zhang, R., et al.: Enhancing plant disease detection through deep learning. Frontiers in Plant Science (2024). https://www.frontiersin.org/articles/10.3389/fpls.2024.1505857/full

[33] Shoaib, M., *et al.*: Deep learning-based segmentation and classification of leaf images for detection of tomato plant disease. Frontiers in Plant Science **13**, 1031748 (2022)

[34] Sunil, C.K., *et al.*: Tomato plant disease classification using multilevel feature fusion with adaptive channel spatial and pixel attention mechanism. Expert Systems with Applications **228**, 120381 (2023)

[35] Li, X., et al.: Transforming leaf disease diagnosis through deep transfer learning and explainable ai. Frontiers in Plant Science (2024). https://www.frontiersin.org/articles/10.3389/fpls.2024.1356260/full

[36] Majeed, A., Ojo, A., Zahid, A.: Leaf-based plant disease detection and explainable ai. arXiv preprint arXiv:2404.16833 (2024). https://arxiv.org/abs/2404.16833

[37] Hybrid vision gnns based early detection and protection against pest diseases in coffee plants. Scientific Reports **15**, 11778 (2025) https://doi.org/10.1038/s41598-025-96523-4

[38] Efficient plant disease detection using k-means clustering and densenet-based classification. In: Proc. Int. Conf. Electronics and Renewable Systems (ICEARS), pp. 1197–1204 (2025). https://doi.org/10.1109/ICEARS64219.2025.10941165

[39] Texture- and symptom-based coffee leaf disease classification using cnn and resnet algorithms. In: Proc. Int. Conf. Advancement in Electronics and Communication Engineering (AECE), pp. 1287–1292 (2024). https://doi.org/10.1109/AECE62803.2024.10911242

[40] Early detection of colletotrichum kahawae disease in coffee cherry based on computer vision techniques. CMES-Computer Modeling in Engineering & Sciences **139**(1), 759–782 (2024)

[41] Hodel, D.R., et al.: Polyphagous shot hole borer. UC Agriculture and Natural Resources (5) (2016)

[42] Umeda, C., Eskalen, A., Paine, T.: Polyphagous Shot Hole Borer and Fusarium Dieback in California, pp. 757–767 (2016). https://doi.org/10.1007/978-3-319-24744-1_26

[43] Ferentinos, K.P.: Deep learning models for plant disease detection and diagnosis. Computers and Electronics in Agriculture **145**, 311–318 (2018) https://doi.org/

10.1016/j.compag.2018.01.009

[44] Mohanty, S.P., Hughes, D.P., SalathÃ©, M.: Using deep learning for image-based plant disease detection. Frontiers in Plant Science **Volume 7 - 2016** (2016) https://doi.org/10.3389/fpls.2016.01419

[45] Younas, R., Rehman, H.M.R.U., Choi, G.S.: Crypto foretell: a novel hybrid attention-correlation based forecasting approach for cryptocurrency. Journal of Big Data **12**(1), 229 (2025) https://doi.org/10.1186/s40537-025-01291-7

[46] Raza, S.N., Rehman, H., Lee, S.G., Sang Choi, G.: Artificial intelligence based camera calibration. In: 2019 15th International Wireless Communications & Mobile Computing Conference (IWCMC), pp. 1564–1569 (2019). https://doi.org/10.1109/IWCMC.2019.8766666

[47] Younas, R., Raza Ur Rehman, H.M., Lee, I., On, B.-W., Yi, S., Choi, G.S.: Samarl: Novel self-attention-based multi-agent reinforcement learning with stochastic gradient descent. IEEE Access **13**, 35674–35687 (2025) https://doi.org/10.1109/ACCESS.2025.3544961