

Rice Leaf Diseases Detection Using Dilated Convolutional Support Vector Machine Method with Test-Time Data Augmentation

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ABSTRACT

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In 2023, Indonesia's rice production declined by approximately 0.23% compared to 2022. A primary cause of reduced crop productivity among Indonesian farmers is the delayed detection of rice leaf diseases. In the era of artificial intelligence, early detection of rice leaf diseases is crucial for improving harvest quality and controlling disease spread. Early detection can be achieved through image data analysis. While the Convolutional Neural Network (CNN) is a popular method for image processing, it can require significant computational resources. This study aims to enhance rice leaf disease detection performance by employing the Dilated CNN method with Support Vector Machine (SVM) and incorporating Test-Time Augmentation (TTA). The dataset used in this study was obtained from Kaggle and consists of 3,364 images distributed across four classes, namely Brown Spot with 532 images, Hispa with 565 images, Leaf Blast with 779 images, and Healthy with 1,488 images. The proposed detection model employs Dilated CNN for feature extraction, SVM for classification, and TTA to improve model robustness to image variations during inference. The evaluation results show that the Dilated CNN-SVM model with randomized TTA achieved an average accuracy of $83.55\% \pm 0.24\%$ across five independent runs. These results demonstrate the effectiveness of the proposed approach in detecting rice leaf diseases from image data. Furthermore, the findings indicate that incorporating TTA improves the performance of the proposed detection system.



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A. INTRODUCTION

In Indonesia, agriculture is the most important sector for supporting the second Sustainable Development Goal (Zero Hunger) (Hiywotu, 2025). In this regard, Indonesia is a major producer of agricultural products, one of which is rice. However, in 2023, Indonesia's rice production decline by approximately 0.23% compared to 2022. One of the primary causes of the drop in crop productivity among Indonesian farmers is rice leaf diseases that are detected too late (Rijal et al., 2024). Rice leaf diseases are highly diverse, among of them are leaf diseases that are difficult to distinguish due to their strikingly similar characteristics. Furthermore, the presence of rice leaf diseases can cause significant losses of up to 37% during the harvest season (Pradana & Pamekas, 2025).

Amid rapid technological advancement, the Indonesian's government is facing not only a decline in rice productivity, but also a shrinking number of young farmers (Wardani, 2024). Addressing these challenges requires agricultural technology innovation that integrates

technology with the younger generation, aiming to achieve sustainable food security and leverage innovative technology in the era of artificial intelligence (Gamage et al., 2024). In the era of artificial intelligence, the early detection of rice leaf diseases is crucial for improving harvest quality and controlling the spread of disease (Aggarwal et al., 2022). Without in-depth analysis, farmers struggle to identify the diseases affecting their rice crops and determine the necessary remedial actions (Rizkyansyah & Susilawati, 2024). These issues indicate that the analysis of disease detection in rice plants requires a method that is more adaptive and sophisticated, and capable of deeply understanding the characteristics of rice leaf diseases based on image data (Ahad et al., 2023; Kulkarni & Shastri, 2024).

One method that can be used to understand the characteristics of rice leaf disease images is deep learning. Deep learning involves model learning that utilizes a multi-layered structure (Krishna et al., 2018). A prominent deep learning technique is the Convolutional Neural Network (CNN). This method has gained popularity due to its ability to learn in a manner similar to the human brain (Indolia et al., 2018). It has been widely applied to analyze various types of images, including mammograms images (Ragab et al., 2019), diabetic retinopathy images (Pratt et al., 2016), dermoscopic images (Fu'adah et al., 2020), some of plant leaf diseases (Fitriani et al., 2026). Because of its good capabilities, CNNs are good for complex problems and big data. As a result, the training process on CNN methods will need a long time.

In addition, standard CNNs have several limitations, one of which is their relatively high computational requirements, which can result in longer processing times (Han et al., 2021). Previous research has shown that integrating CNN for feature extraction with SVM for classification can improve computational efficiency while maintaining high classification performance (Gnanamalar et al., 2023). Research by (Putra et al., 2020) also demonstrated that a modified Convolutional Support Vector Machine method achieved higher accuracy and faster performance in image data classification than the standard CNN method. The study further showed that applying feature reduction or selection methods, such as Principal Component Analysis (PCA) and Relief, before classification can improve classification performance. These findings support the use of SVM as an alternative classifier and PCA to reduce the dimensionality of extracted features before classification. Furthermore, (Khasanah et al., 2023) found that the Dilated Convolutional Neural Network achieved higher accuracy than the standard CNN, suggesting that dilated convolution can enhance the performance of CNN-based image classification. Therefore, integrating Dilated CNN for feature extraction, PCA for feature dimensionality reduction, and SVM for classification provides a potential approach to address the limitations of standard CNN-based classification.

Based on these findings, this study proposes a modified Dilated Convolutional Support Vector Machine method for detecting rice leaf diseases. The proposed approach employs a Convolutional Neural Network with a modified dilation factor for feature extraction, followed by a Support Vector Machine as the classifier. Additionally, Test-Time Data Augmentation is incorporated to further improve the robustness of the proposed method. These measures aim to improve detection performance and advance the application of mathematical computing technologies in the food sector.

B. METHODS

This study aims to develop a modified Convolutional Neural Network (CNN) approach for rice leaf disease detection by integrating Dilated CNN, Principal Component Analysis (PCA), Support Vector Machine (SVM), and Test-Time Augmentation (TTA). Dilated CNN is employed for feature extraction to expand the receptive field of the convolutional layers, while PCA is used to reduce the dimensionality of the extracted features before classification. SVM is then employed as the classifier, and TTA is applied during the testing phase to improve the robustness of the model to variations in input images. The overall workflow of the proposed method is illustrated in Figure 1.

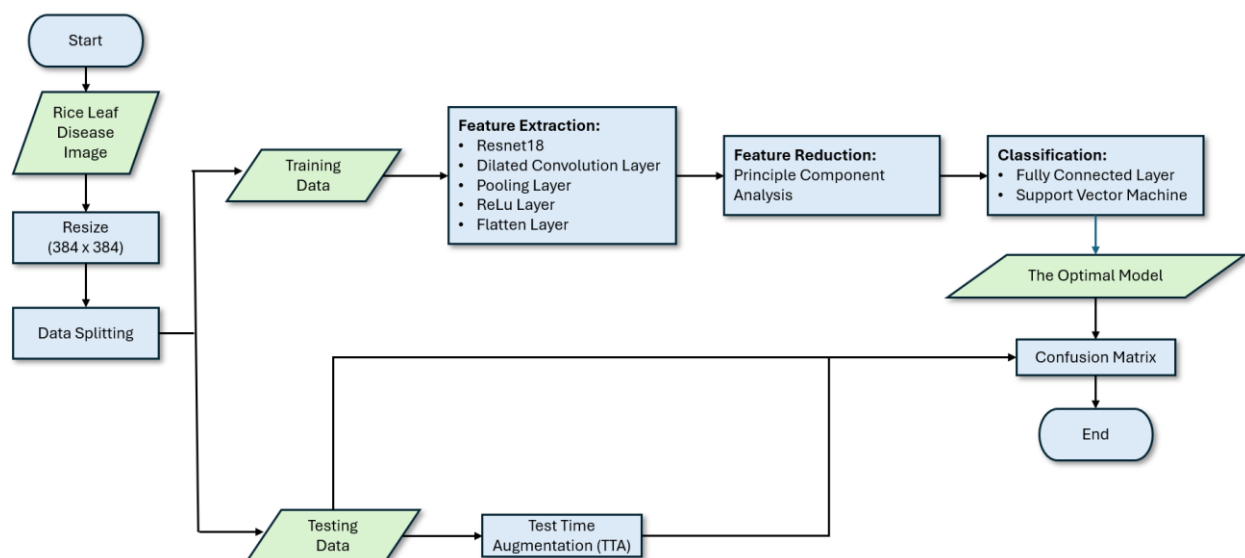


Figure 1. Flowchart The Purposed Method

1. Preprocessing

The dataset used in this study was obtained from an open-source dataset available on Kaggle, with image dimensions varying across the dataset. Since the model uses ResNet18 with an input size of 384×384 pixels, all images were resized to 384×384 pixels to ensure a consistent input size for the model. After the resizing process, the dataset was divided into training and testing sets using an 80:20 ratio. The training set was used to develop and train the models, while the testing set was used to evaluate the performance of the trained models. The resulting training and testing data were then used as inputs for the subsequent stages of the proposed method.

2. Feature Extraction

a. ResNet 18

Residual Network (ResNet) is one of the CNN architectures designed to address the performance degradation problem in very deep networks. The primary advantage of ResNet-18 is the use of residual connections, also known as skip connections, which allow information and gradients to flow directly across multiple layers, thereby helping to stabilize the training process and mitigate the vanishing gradient problem (Venkata

Sai Abhishek et al., 2022). The framework of the residual learning block is illustrated in Figure 2(a), while the ResNet-18 architecture is shown in Figure 2(b).

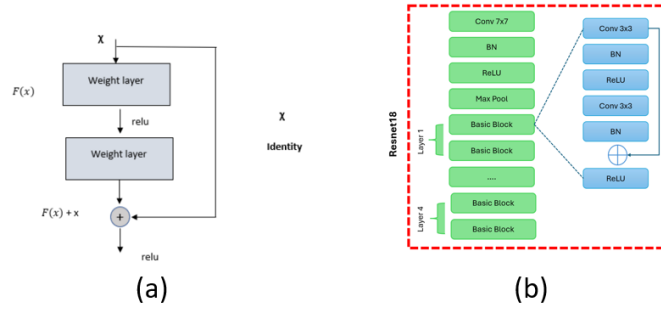


Figure 2. (a) Framework of the Residual Learning Block (He et al., 2016)
(b) Resnet18 Block

b. Convolution Layer

A convolution layer is a mathematical operation that combines two-dimensional image arrays to extract spatial features (Wang et al., 2018). The convolution operation can be controlled by a dilation factor, which determines the spacing between the elements of the convolution kernel. When the dilation factor is set to 1, the operation corresponds to a standard convolution. When the dilation factor is greater than 1, the operation becomes a dilated convolution, which expands the receptive field of the convolution operation. The general equation for the two-dimensional convolution operation is given in Equation (1) and the difference between standard convolution and dilated convolution is illustrated in Figure 3.

$$F_{(i)} = \sum_{a=0}^{L-1} \sum_{b=0}^{L-1} W_{(a,b)} \times G_{(i+da, j+db)} \quad (1)$$

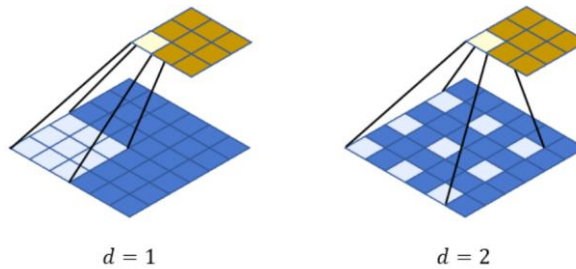


Figure 3. Convolution Layer; Dilated Convolution Layer (Lei et al., 2019)

In this study, the standard ResNet-18 architecture is modified by adding dilated convolution layers after the ResNet-18 architecture. When the dilation factor is greater than 1, the convolution operation becomes a dilated convolution, allowing the convolution kernel to cover a wider spatial region of the input feature map. The dilated convolution approach was adopted from (Khasanah et al., 2023). In this study, a dilation factor of 2 is used for Dilated Conv 1, followed by a dilation factor of 4 for Dilated Conv

2. The dilated convolution operation is calculated using Equation (1) by incorporating the corresponding dilation factor.

c. Pooling Layer

Pooling layer are categorized into two types, Average Pooling and Max Pooling. The illustration of Pooling layer is shown in Figure 4 (Khasanah et al., 2023; Putra et al., 2020).



Figure 4. Pooling Layer

d. Rectified Linear Unit (ReLU) Layer

The ReLU layer is the most commonly used activation function in Convolutional Neural Networks. The Rectified Linear Unit (ReLU) activation function can be defined by Equation (2) (Khasanah et al., 2023).

$$y = \begin{cases} x, & \text{jika } x \geq 0 \\ 0, & \text{jika } x < 0 \end{cases} \quad (2)$$

e. Batch Normalization

Batch Normalization is a deep learning technique that used to normalizing the output layer. This technique aims to achieving a more stable distribution during the training process. This technique was introduced to accelerate training and facilitate model convergence (Ioffe & Szegedy, 2015).

f. Flatten Layer

Flatten Layer is a technique used to convert the output of the preceding process into a vector, as the classification process requires vector input. An illustration of the flattening process is shown in Figure 5.

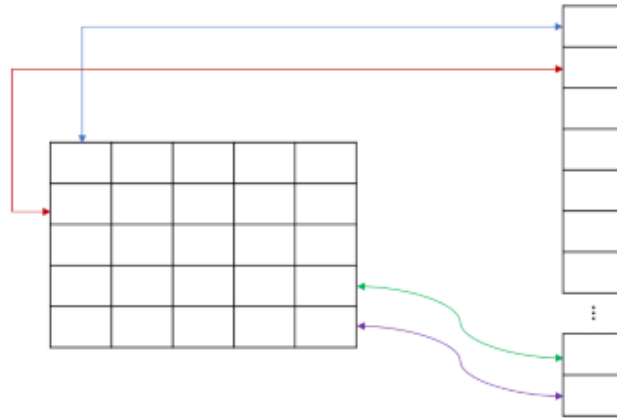


Figure 5. Flatten Layer Illustration

3. Feature Extraction

In this step, feature reduction is performed using Principal Component Analysis (PCA). PCA works by identifying directions, or principal components, with the greatest variance in the data. The first principal component captures the largest amount of variance, while subsequent components capture the remaining variance. The goal is to reduce the number of features while retaining as much information as possible (Perry et al., 2025).

4. Test-Time Augmentation (TTA)

Test-Time Data Augmentation (TTA) is a method that leverages data augmentation during the testing phase to produce an averaged output. The method is based on augmenting test data using random rotation, followed by counter-rotating the predicted output signal (Uvdal & Mirkhalaf, 2024). During the testing process, the data is not merely predicted once; instead, it is enlarged multiple times at varying angles.

5. Classification

a. Neural Network (Fully Connected Layer)

A fully connected layer consists of multiple layers composed of neurons that are fully connected to the preceding layer. The input values for the fully connected layer are derived from the output of the feature extraction layer. The output values of the fully connected layer can be calculated using Equation (3).

$$z_{(i)} = b_{(i)} + \sum_{j=1}^c x_{(j)} w_{(i,j)} \quad (3)$$

b. Support Vector Machine for Multi Class

Multi-class classification can be performed using a technique known as pairwise classification, also referred to as "one-against-one." This technique is used to assist in classifying more than two classes. Given a classification problem with a training dataset, namely:

$$D = \{(\bar{x}_1, y_1), (\bar{x}_2, y_2), \dots, (\bar{x}_l, y_l)\} \subset \mathbb{R}^n$$

In this technique, a decision surface must be constructed for every possible pair of classes. Let $g^{p,q}: \mathbb{R}^n \rightarrow \{p, q\}$ be denoted as the decision surface that separates the class pairs p and q with $p \neq q$ and $\{p, q\} \subset \{1, 2, \dots, M\}$. Then, train each decision surface with

$$g^{p,q}(\bar{x}) = \sum_{i=1}^{|D^{p,q}|} y_i \alpha_i^{p,q} k(\bar{x}_i, \bar{x}) - b^{p,q}$$

On the dataset $D^{p,q} = D^p \cup D^q$, where $D^p = \{(\bar{x}, y) | (\bar{x}, y) \in D \wedge y = p\}$ and $D^q = \{(\bar{x}, y) | (\bar{x}, y) \in D \wedge y = q\}$. The illustration of the Support Vector Machine for multi-class classification can be seen in Figure 6.

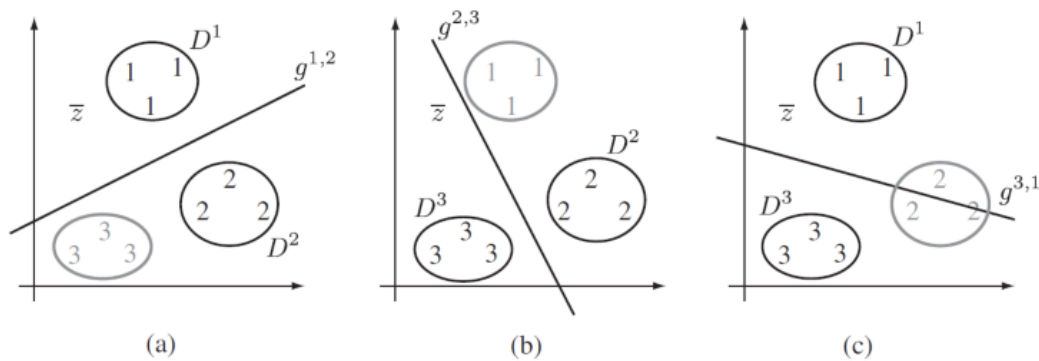


Figure 6. Support Vector Machine for Multi-Class Classification (Hamel, 2009)

Based on Figure 6, the classification result for point (a) is class 1, the classification result for point (b) is class 3 and the classification result for point (c) is class 1.

6. Confusion Matrix

Confusion Matrix is an evaluation table used to measure the performance of a classification model by comparing the model's predictions against the actual labels (ground truth). Based on the confusion matrix, the number of correct and incorrect predictions for each class can be determined (Khasanah et al., 2023; Li et al., 2021).

Table 1. Confusion Matrix

		Actual Values	
		Positive	Negative
Predictive Values	Positive	True Positive (TP)	False Positive (FP)
	Negative	False Negative (FN)	True Negative (TN)

True Positive (TP) refers to cases in which both the actual value and the predicted value are positive. True Negative (TN) refers to cases in which both the actual value and the predicted value are negative. False Positive (FP) refers to cases in which the predicted value is positive

while the actual value is negative. False Negative (FN) refers to cases in which the predicted value is negative while the actual value is positive.

Accuracy

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100\% \quad (4)$$

Precision

$$Precision = \frac{TP}{TP + FP} \times 100\% \quad (5)$$

Recall

$$Recall = \frac{TP}{TP + FN} \quad (6)$$

F1-Score

$$f1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (7)$$

Based on the evaluation result by using confusion matrix, the value of accuracy, precision, recall, and F-1Score will be produced. Those can determine the good or bad performance of the built classification system (Khasanah et al., 2023). The performance criteria table can be seen on Table 2.

Table 2. Performance Criteria (Zheng et al., 2025)

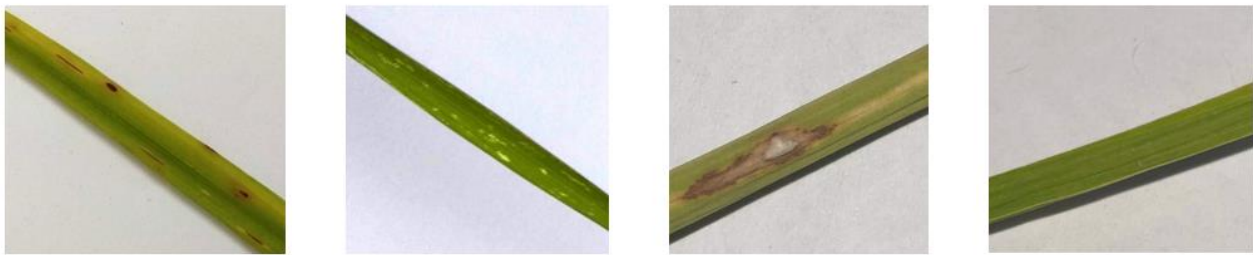
Percentage	Criteria
> 90%	Excellent
70% – 90%	Good
60% – 70%	Fairly Good
< 60%	Poor

C. RESULT AND DISCUSSION

This research proposes a new methodology that combines a dilated CNN architecture as a feature extraction method, PCA as a feature reduction method, SVM and a fully connected layer as classification models, and Test-Time Augmentation (TTA). Four experiments for rice leaf disease detection are presented in this study. These experiments use the Dilated CNN method, Dilated CNN with Test-Time Augmentation, Dilated Convolutional Support Vector Machine, and Dilated Convolutional Support Vector Machine with Test-Time Augmentation (TTA). The data used in this study were obtained from the Kaggle dataset (<https://www.kaggle.com/datasets/shayanriyaz/riceleafs?resource=download>). The dataset consists of four categories of rice leaf diseases, as shown in Table 3, while sample images are shown in Figure 6.

Table 3. Dataset Kaggle of Rice Leaf Disease

No	Diagnose	Origin Dataset
1	Brown Spot	532
2	Hispa	565
3	LeafBlast	779
4	Healthy	1488
Total		3364

**Figure 6.** BrownSpot; Hispa; Leaf Blast; Healthy

The proposed method consists of several stages, starting with Dilated CNN for feature extraction, followed by PCA for feature dimensionality reduction and SVM for classification. For the models using TTA, Test-Time Augmentation is applied during the testing phase, where multiple augmented versions of the test images are generated and their predictions are aggregated to obtain the final prediction. In this study, four model configurations were evaluated to investigate the contribution of the SVM classifier and TTA. The first configuration uses Dilated CNN with a fully connected layer as the classifier. The second configuration combines Dilated CNN with TTA while retaining the fully connected layer as the classifier. The third configuration uses Dilated CNN for feature extraction, followed by PCA and SVM for classification. The fourth configuration combines Dilated CNN, PCA, and SVM with TTA during the testing phase. The architecture of the proposed method and the experimental configurations are illustrated in Figure 1.

Several parameters were considered in the implementation of the proposed method, including the input image size, batch size, number of training epochs, learning rate, optimizer, and model architecture. The ResNet-18 architecture generally uses an input image size of 224×224 pixels. However, in this study, the input image size was set to 384×384 pixels because preliminary experiments using 224×224 pixels resulted in lower classification performance. The larger input size was selected to preserve more spatial information from the rice leaf images, particularly the visual characteristics of disease symptoms. The model was trained using a batch size of 8 for 30 epochs with the Adam optimizer and a learning rate of 0.0002. Weighted cross-entropy loss and weighted random sampling were also implemented to address the imbalance among the rice leaf disease classes.

The Dilated CNN model without TTA achieved an accuracy of 77.20%. When TTA was applied, the model was evaluated across multiple independent runs to account for the randomness introduced by the augmentation process. The average accuracy obtained from these runs indicates the effect of TTA on the classification performance of the Dilated CNN model. The detailed accuracy results and standard deviation for different numbers of TTA runs

are presented in Table 4. These results show the consistency of the model performance under randomized TTA and provide an indication of the stability of the obtained accuracy.

Table 4. Accuracy and Standard Deviation of Dilated CNN with TTA

Number of Runs	Accuracy	Standard Deviation
5	80.45%	0.82%
10	80.51%	0.89%
15	80.47%	0.73%
20	80.43%	0.68%

The Dilated CNN with SVM model achieved an accuracy of 81.37% without TTA. This result is higher than that of the Dilated CNN model without TTA, which achieved an accuracy of 77.20%. When TTA was combined with the Dilated CNN with SVM model, the classification performance increased further, with an average accuracy of $83.81\% \pm 0.64\%$ based on 20 independent runs. The accuracy and standard deviation obtained from different numbers of TTA runs are presented in Table 5. The comparison across different numbers of runs is used to evaluate the stability of the accuracy under randomized TTA.

Table 5. Accuracy and Standard Deviation of Dilated CNN + SVM with TTA

Number of Runs	Accuracy	Standard Deviation
5	83.55%	0.27%
10	83.55%	0.47%
15	83.66%	0.48%
20	83.81%	0.64%

Confusion matrix of the best seed in 20 runs is presented in Figure 7. The model correctly classified 575 out of 671 test images, resulting in an accuracy 85.54%. The results indicate good overall classification performance, although several misclassifications between classes were still observed. The Brown Spot class achieved a recall of 0.89, with 93 out of 104 images correctly classified. Six Brown Spot images were misclassified as Healthy, while one was predicted as Hispa and four were predicted as Leaf Blast. The Healthy class achieved a precision of 0.90 and a recall of 0.88, with 263 out of 298 images correctly classified. However, 28 Healthy images were misclassified as Hispa, representing the most prominent misclassification in the confusion matrix. This misclassification may be related to similarities between the visual characteristics of healthy leaves and early-stage Hispa symptoms, as well as variations in image appearance and lighting conditions. For the Hispa class, 88 out of 113 images were correctly classified, while 19 images were misclassified as Healthy. Consequently, Hispa achieved the lowest precision, recall, and F1-score among the four classes, with values of 0.69, 0.78, and 0.73, respectively. Meanwhile, the LeafBlast class achieved the highest precision of 0.92, with 130 out of 156 images correctly classified and a recall of 0.83.

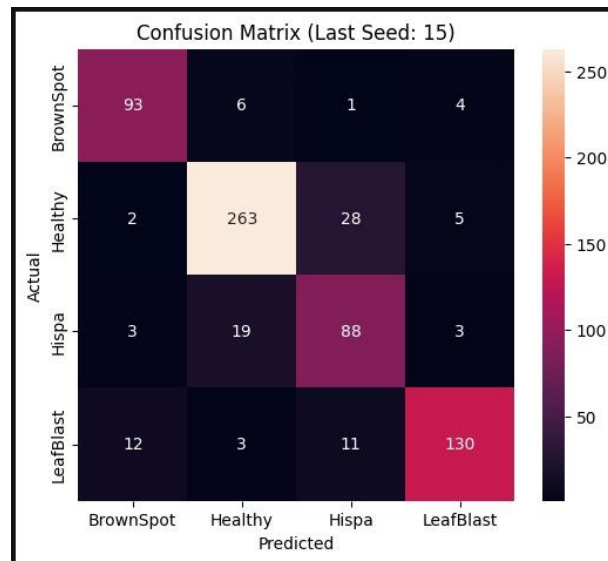


Figure 7. Confusion Matrix of The Best Result

Several previous studies have investigated the application of deep learning and machine learning methods for rice leaf disease detection. These studies have explored different approaches to improve classification performance, such as the use of CNN architectures, feature extraction methods, feature reduction techniques, and alternative classification models. A summary of relevant previous studies, including the methods, datasets, and classification results, is presented in Table 6.

Table 6. Comparison with Previous Study

Source	Dataset	Class	Total Data	Accuracy
This Study	Rice Leafs	4 Class (BrownSpot, LeafBlast, Hispa, Healthy)	3355	83.81% $\pm$ 0.64%
(Paula & Pribadi, 2026)				75.84%
(Rana et al., 2025)	Rice Diseases Image Dataset		2092	84%
(Bhujel & Shakya, 2022)	Rice Disease			89.13%

Based on the comparison presented in Table 6, the proposed method does not achieve the highest average accuracy among the compared studies. However, it demonstrates a substantial improvement over Paula & Pribadi (2026), which used the same Rice Leafs dataset and reported an accuracy of 75.84%. The proposed method achieved an average accuracy of 83.81% $\pm$ 0.64%, representing an improvement of 7.97 percentage points under the same dataset conditions. Furthermore, among the 20 independent TTA runs, the proposed method achieved a maximum accuracy of 85.54%, which exceeds the 84% accuracy reported by (Rana et al., 2025). Although this maximum accuracy remains lower than the 89.13% reported by Bhujel and Shakya (2022), the comparison with studies using different datasets should be interpreted with caution. Overall, the results indicate that the proposed combination of Dilated CNN, PCA, SVM, and TTA can substantially improve classification performance on the Rice Leafs dataset and can achieve competitive performance compared with previous studies.

D. CONCLUSION AND SUGGESTIONS

Based on the experimental results, the use of SVM improved the classification accuracy of the Dilated CNN model. The accuracy increased from 77.20% with Dilated CNN to 81.37% with Dilated CNN-SVM, representing an improvement of 4.17 percentage points. The application of TTA further improved the performance of the Dilated CNN-SVM model, increasing the average accuracy from 81.37% to $83.81\% \pm 0.64\%$ across 20 independent runs. The highest accuracy obtained among the 20 runs was 85.54%, which demonstrates that TTA can further improve classification performance, although the accuracy varies across randomized runs. These results indicate that both SVM and TTA contributed to improving the classification performance of the proposed approach.

Despite the improvement in classification performance, some misclassifications remained, particularly between the Healthy and Hispa classes, due to similarities in their visual characteristics. Future research can evaluate the proposed method using different rice leaf disease datasets to assess its generalization and robustness across different data distributions. Testing the method on datasets collected from different sources, environments, and image conditions may provide a more comprehensive evaluation of its applicability to rice leaf disease detection.

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