International Journal of Computer Information Systems and Industrial Management Applications
ISSN 2150-7988 Volume 18(3s) 2026 pp. 1261-1271
https://doi.org/10.70917/ijcisim-2026-4459
Article

# Deep Learning Based Efficient Lightweight Model with Channel and Spatial Attention Mechanism for Rice Disease Detection

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**Abstract:** The accurate identification of rice leaf disease is necessary to protect the crop in time, and numerous deep learning models have high computational demands and are hard to implement in agricultural settings with limited resources. The proposed systems are introduce two small convolutional neural networks to classify rice disease. First one, Modified Lightweight Convolutional Neural Network (MLWCNN), employs depth wise separable convolution and pointwise convolution to minimize the computational cost. The second, Modified Lightweight Model with Channel Attention Convolutional Neural Network (MLWCACNN), is based on the lightweight backbone, but it incorporates channel and spatial attention to enhance the acquisition of disease-related features. The imbalance between classes was dealt with by controlled augmentation, resulting in balanced datasets of 6310 and 2650 images. The 5-fold cross- validation was performed on 224 × 224-sized images, Adam optimization, and conventional classification metrics. MLWCNN obtained average accuracy of 78% on the four-class rice dataset but MLWCACNN obtained accuracy of 98% on the six-class dataset. The models proposed needed 0.047M and 0.059M parameters, respectively, indicating a viable accuracy complexity trade-off to smart agricultural diagnosis.

**Keywords:** Channel attention; Convolutional neural network; Lightweight model; Rice disease identification; Smart agriculture

## 1. Introduction

Rice is a major staple crop, and leaf disease can reduce productivity when symptoms are not detected early. Automated visual diagnosis offers a practical route for supporting farmers, agronomists, and smart agriculture systems by enabling rapid identification of disease symptoms from leaf images. Recent lightweight crop disease recognition studies show that compact convolutional neural networks can support automated detection while reducing the dependence on manual inspection [1]. In this context, computer vision and deep learning can support scalable crop monitoring when model design is aligned with practical deployment constraints.

Convolutional neural networks (CNNs) have achieved strong performance in plant disease recognition, but many high-performing architectures are computationally expensive. Multiscale and VGG-inspired lightweight CNNs have improved recognition accuracy in rice and crop disease tasks, yet their size and computational load can still limit deployment on mobile, embedded, or field-level platforms [2], [3]. Models with large parameter counts and high floating-point operations (FLOPs) are less suitable for low-resource agricultural environments, where memory, power, and processing resources are constrained.

The second difficulty is associated with the conditions of the dataset that is generally met in studies on rice leaf disease. Public datasets have a small amount of images, skewed classes, or not all the field variability is covered. The work on paddy disease datasets and lightweight rice disease recognition benchmarking also suggests that the quality of datasets, the size of the model, and the costs of computation should be viewed as a unit instead of a collection [4], [5]. This imbalance may skew the learning process to favor the majority classes and decrease the recognition accuracy of visually similar or minority disease groups.

This study addresses these challenges through balanced dataset preparation and compact CNN architectures. The first contribution is the preparation of balanced rice disease datasets using controlled augmentation to reduce class imbalance and improve training stability. The second contribution is a Modified Lightweight Convolutional Neural Network (MLWCNN) based on depthwise separable and 1 × 1 pointwise convolution. The third contribution is a Modified Lightweight Model with Channel Attention Convolutional Neural Network (MLWCACNN), which integrates channel and spatial attention to strengthen the representation of discriminative disease patterns. The fourth contribution is a 5-fold cross-validation evaluation using accuracy, precision, recall, F1-score, confusion matrices, parameter count, and GFLOPs. The final contribution is a comparative analysis showing that competitive classification can be obtained with substantially lower computational complexity than several state-of-the-art lightweight CNN models.

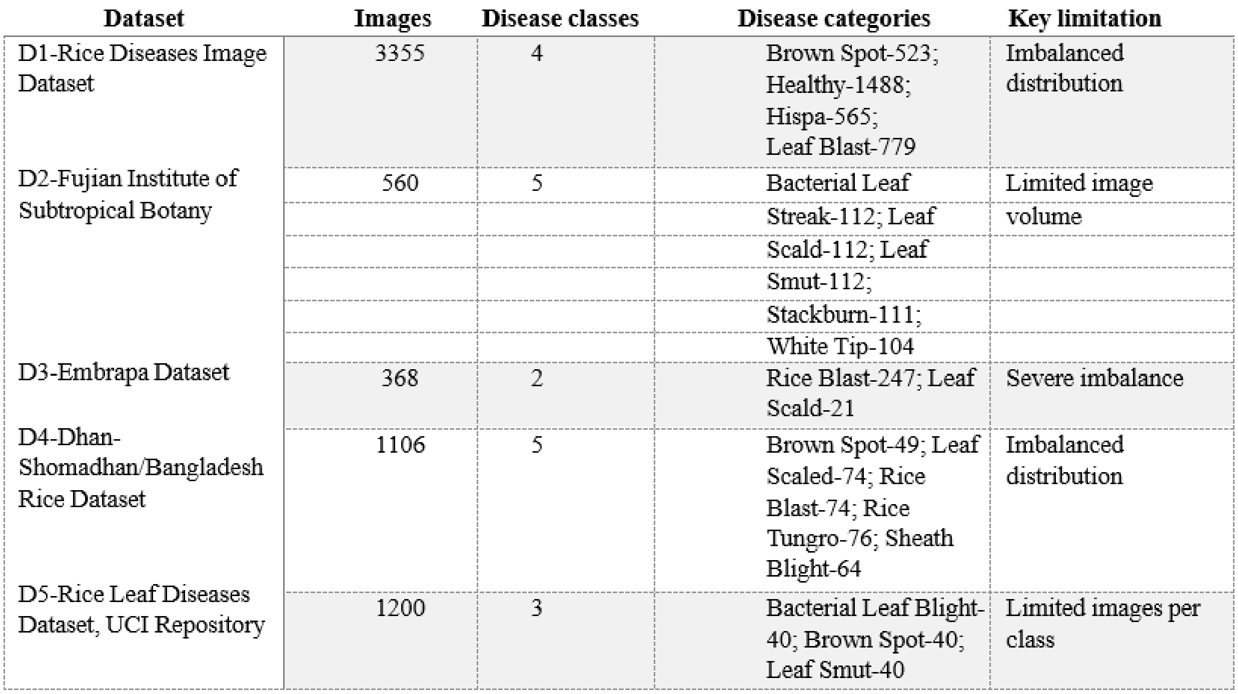
The remainder of the paper is organized as follows. Related datasets and lightweight rice disease models are reviewed first. The materials, augmentation procedure, proposed architectures, experimental setup, and evaluation protocol are then described. The results are reported through cross-validation, class-wise performance, confusion matrices, and computational comparisons, followed by discussion and conclusion.

## 2. Related Work

*Rice Leaf Disease Datasets*

There is a great variance in the scale of rice disease image datasets, class composition, and balance. The D1 rice disease image dataset contains 3355 images across Brown Spot, Healthy, Hispa, and Leaf Blast classes, with the Healthy class representing the largest portion. Other data are smaller or more restricted in disease coverage, including the Fujian Institute of Subtropical Botany dataset, the Embrapa dataset, the Dhan- Shomadhan/Bangladesh rice dataset, and the UCI rice leaf disease dataset. These dataset characteristics, as summarized in Table 1, explain why balancing and augmentation are significant in the development of reliable models.

Table 1. Rice leaf disease datasets and limitations



| Dataset | Images | Disease classes | Disease categories | Key limitation |
|---|---|---|---|---|
| D1-Rice Diseases Image Dataset | 3355 | 4 | Brown Spot-523;<br>Healthy-1488;<br>Hispa-565;<br>Leaf Blast-779 | Imbalanced distribution |
| D2-Fujian Institute of Subtropical Botany | 560 | 5 | Bacterial Leaf Streak-112; Leaf Scald-112; Leaf Smut-112;<br>Stackburn-111;<br>White Tip-104 | Limited image volume |
| D3-Embrapa Dataset | 368 | 2 | Rice Blast-247; Leaf Scald-21 | Severe imbalance |
| D4-Dhan-Shomadhan/Bangladesh Rice Dataset | 1106 | 5 | Brown Spot-49; Leaf Scaled-74; Rice Blast-74; Rice Tungro-76; Sheath Blight-64 | Imbalanced distribution |
| D5-Rice Leaf Diseases Dataset, UCI Repository | 1200 | 3 | Bacterial Leaf Blight-40; Brown Spot-40; Leaf Smut-40 | Limited images per class |

*Lightweight and Attention-Based Deep Learning Models*

Lightweight CNNs have been explored to decrease model size and calculate cost without a significant loss in classification accuracy. Attention modules, compact convolutional blocks, and new CNN structures have been applied in rice blast segmentation and plant disease classification research to enhance the representation of features and manage the complexity of models [6], [7]. Image classification with deep learning has also been extended to more general tasks of diagnosing plant diseases, and lightweight attention networks have been shown to prove useful in disease-relevant image region focus in rice disease recognition [8], [9]. The relevance of strong feature extraction under variability of the data sets is further validated by automated CNN -based paddy leaf disease detection and optimized classification models [10], [11]. Transfer learning and deep CNN-based recognition of rice blasts have enhanced the recognition of disease; however, their application remains reliant on the trade-off between accuracy, generalization, and computational cost [12], [13]. Table 2 compares representative models based on accuracy, parameters, GFLOPs and model size. The accuracy of a number of methods is high; however, the complexity of these methods varies significantly. This encourages a paradigm that focuses on the accuracy- complexity trade-off, instead of focusing on accuracy itself.

The gap that has been identified is that of a small architecture that can be used on the dataset of balanced rice disease and still have very few trainable parameters. Similar vision-based crop analysis has demonstrated that

deep CNNs can aid in assessing the health of plants beyond rice, such as nutrient deficiency and disease- related visual symptoms [14]. The more comprehensive research on existing limitations of deep learning-based plant disease detection highlights that the robustness of the model, the diversity of datasets, and their ability to be applied to the field is still an unsolved issue [15]. Classifiers based on adaptive neuro-fuzzy and transfer learning have also been applied towards plant leaf disease recognition, although their practical application depends on the complexity and inference needs of the resulting model [16], [17]. A recurring theme in research that has been identified in systematic reviews and surveys of plant disease detection is that dataset imbalance, generalization, model complexity, and real-world validation continue to be research issues [18], [19]. Surveys of machine learning classifiers also support the necessity of small, dependable, and implementable plant disease detection systems [20]. The proposed MLWCNN fills this gap with depthwise separable convolution, and the MLWCACNN adds channel and spatial attention to the proposed feature selection without the burden of computation.

Table 2. Lightweight and attention-based rice disease models

| **Ref.** | **Model** | **Accuracy (%)** | **Parameters** | **GFLOPs** | **Size (MB)** | **Key observation** |
|---|---|---|---|---|---|---|
| [1] | Single lightweight CNN | 73 | 0.38M | Not reported | Not reported | Compact baseline with modest accuracy |
| [2] | Multiscale CNN based on VGG | 97 | Not reported | Not reported | 26.1 | High accuracy with larger model size |
| [3] | VGG-ICNN | 96 | 6M | 45.7 | 23.2 | High complexity compared with compact CNNs |
| [5] | MobInc-Net | 99.21 | 2.01M | 0.7 | 8.04 | Very high accuracy with moderate parameters |
| [6] | DFFANet-based segmentation model | 96.15 | 1.4M | Not reported | Not reported | Attention-based rice blast segmentation |
| [9] | Mobile-Atten | 98 | 5.4M | 0.22 | 21.6 | Attention model with high parameter count |

## 3. Materials and Methods

The methodology follows the limitations identified in related work by combining dataset balancing, compact feature extraction, attention-based feature recalibration, and cross-validation. The complete workflow is shown in Figure 1. The process begins with rice leaf image collection and class distribution analysis, followed by augmentation, model training, 5-fold validation, classification assessment, and computational complexity comparison.

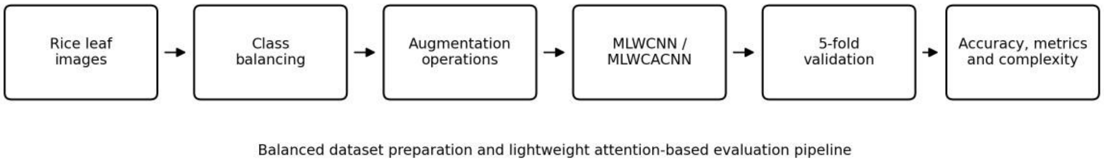


Figure 1. Overall research workflow.

*Dataset Preparation and Augmentation*

Two rice leaf datasets were prepared for experimental analysis. Dataset D1 originally contained 3355 images from four classes: Brown Spot, Healthy, Hispa, and Leaf Blast. The distribution was imbalanced, with the Healthy class contributing 44.35% of the images. Left-right flipping, up-down flipping, and contrast adjustment were applied to balance the distribution, producing 6310 images. The balanced D1 dataset contained 1569 Brown Spot images,1488 Healthy images, 1695 Hispa images, and 1558 Leaf Blast images.

Dataset D2 represented a smaller rice leaf disease collection. The original class-wise counts were Bacterial Leaf Streak-112, Leaf Scald-112, Leaf Smut-112, Stackburn-111, and White Tip-104, with a reported dataset total of 560 images. The labeled class-wise counts sum to 551 images; therefore, the reported total and the listed class counts should be verified during final dataset documentation. After augmentation using left-right flipping, up-down flipping, contrast adjustment, and brightness adjustment, D2 contained 2650 images across six classes, including a Healthy class. Table 3 presents the original and augmented class distributions used for the experiments.

Table 3. Dataset composition before and after augmentation

| ***Dataset*** | ***Class*** | ***Original images*** | ***Original (%)*** | ***Augmented images*** | ***Augmented (%)*** |
|---|---|---|---|---|---|
| *D1* | Brown Spot | 5 | 15.58 | 1569 | 24 |
| *D1* | Healthy | 1 | 44.35 | 1488 | 23 |
| *D1* | Hispa | 5 | 16.85 | 1695 | 26 |
| *D1* | Leaf Blast | 7 | 23.21 | 1558 | 24 |
| *D1* | Total | 3 | 100.00 | 6310 | 100.00 |
| *D2* | Bacterial Leaf | 1 | not reported | 450 | 16 |
| | Streak | | | | |
| *D2* | Leaf Scald | 1 | not reported | 450 | 16 |
| *D2* | Leaf Smut | 1 | not reported | 450 | 16 |
| *D2* | Stackburn | 1 | not reported | 445 | 16 |
| *D2* | White Tip | 1 | not reported | 414 | 15 |
| *D2* | Healthy | not | not applicable | 441 | 16 |
| *D2* | Total | 560 | not reported | 2650 | 100.00 |
| | | 551 listed | | | |

*Proposed MLWCNN Architecture*

The proposed Modified Lightweight Convolutional Neural Network (MLWCNN) was designed to reduce model complexity while retaining disease-discriminative features. As illustrated in Figure 2, the architecture processes 224 × 224 input images through an initial convolution layer, batch normalization, depthwise separable convolution, batch normalization, a 1 × 1 pointwise convolution layer with 64 filters, and a second depthwise separable convolution block. A 1 × 1 pointwise convolution layer with 128 filters is followed by global average pooling, a dense layer with 256 units, dropout with a rate of 0.5, and a final dense layer for classification.

Depthwise separable convolution reduces the number of parameters by decomposing standard convolution into spatial filtering and channel mixing. The 1 × 1 convolution layers further combine channel information with low computational overhead. As a result, MLWCNN requires only 47,620 trainable parameters, corresponding to approximately 0.047M parameters and 0.000095 GFLOPs.

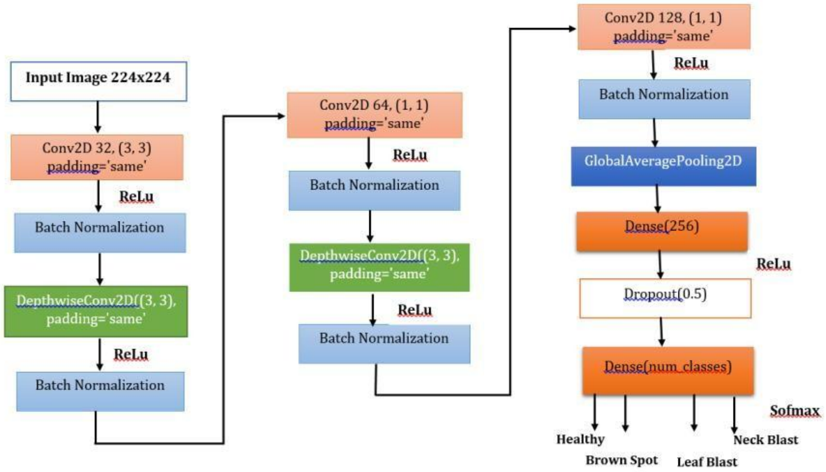


Figure 2. Detailed MLWCNN layer configuration.

*Proposed MLWCACNN Architecture*

The Modified Lightweight Model With Channel Attention Convolutional Neural Network (MLWCACNN) extends the lightweight backbone by integrating channel and spatial attention. Channel attention recalibrates feature maps by assigning higher weights to informative channels and lower weights to less relevant responses. Spatial attention complements this process by emphasizing disease-relevant regions in the leaf image.

Figure 3 and Figure 4 present the proposed attention- based model and its layer-level workflow.

The attention-enhanced variant was developed to improve feature discrimination while keeping the model compact. The final MLWCACNN contains approximately 0.059M parameters and 0.00012 GFLOPs, which is substantially smaller than many previously reported lightweight and attention-based alternatives.

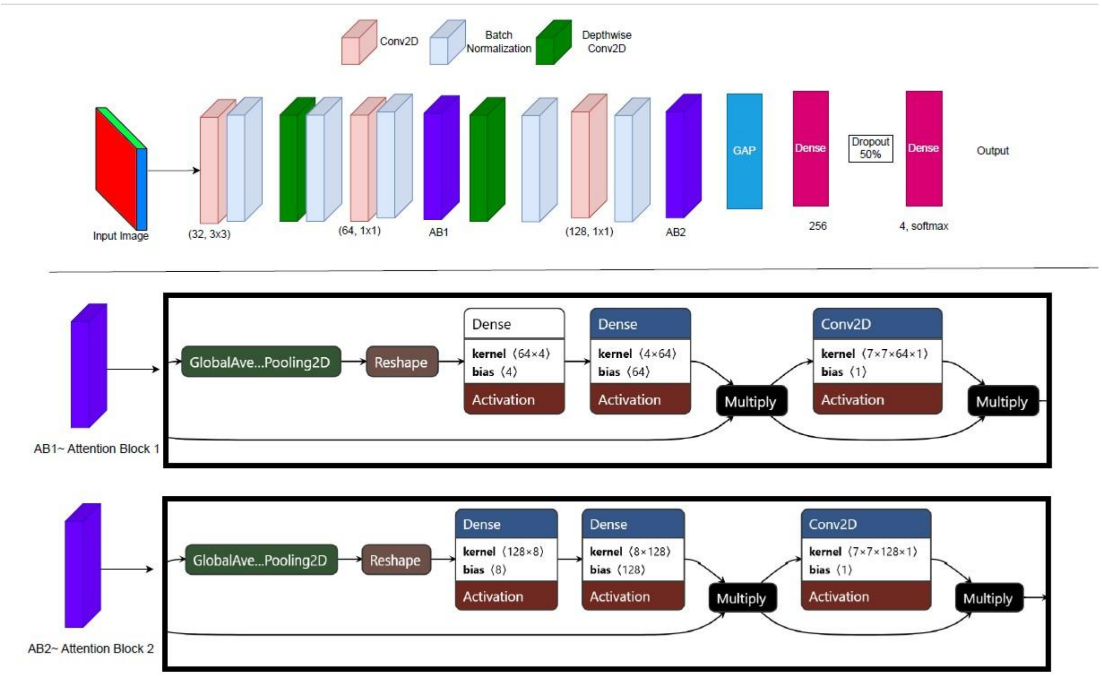


Figure 3. Proposed MLWCACNN architecture.

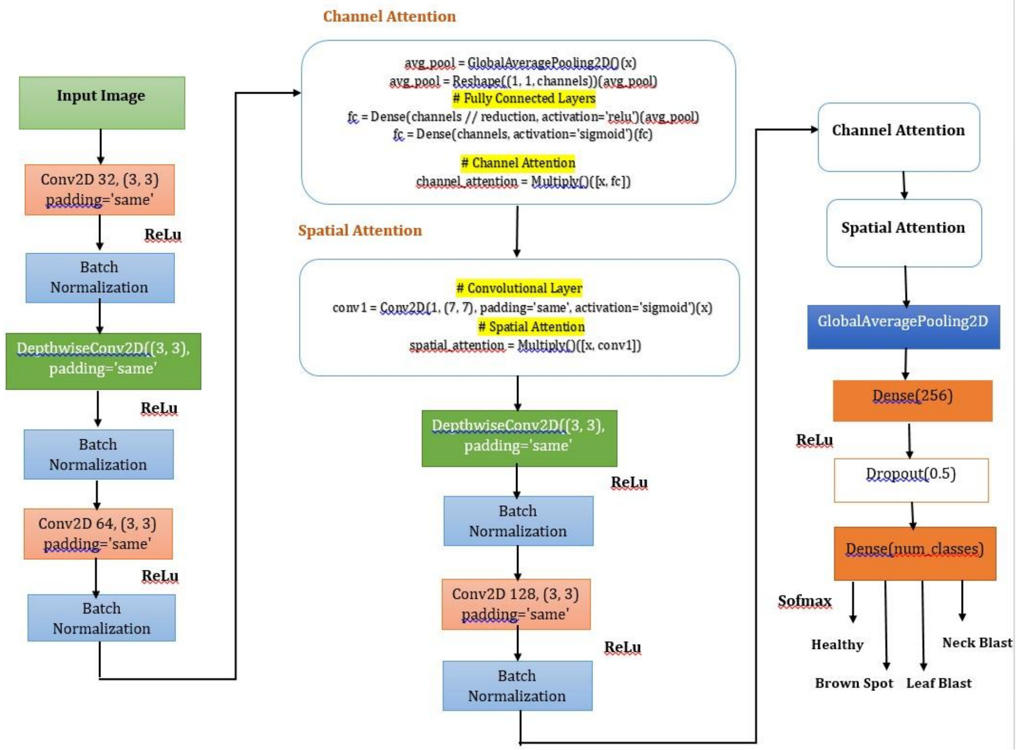


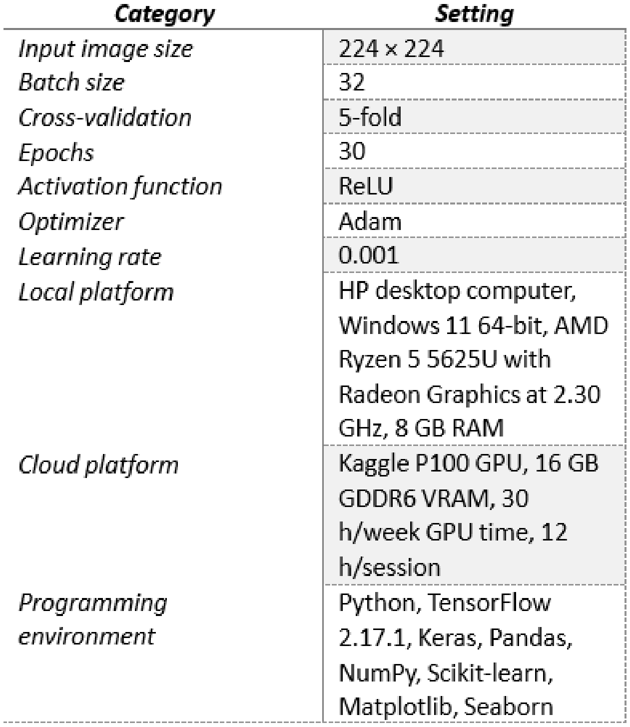
Figure 4. MLWCACNN channel and spatial attention workflow.

*Training Configuration and Evaluation Protocol*

All experiments used 224 × 224 input images, a batch size of 32, 30 training epochs, the rectified linear unit (ReLU) activation function, the Adam optimizer, and a learning rate of 0.001. Model validation was performed using 5-fold cross-validation to reduce the dependence on a single train-test split. The experimental configuration is summarized in Table 4.

The models were evaluated using accuracy, precision, recall, F1-score, confusion matrices, parameter count, and GFLOPs. Accuracy measured the overall proportion of correct predictions, whereas precision, recall, and F1-score provided class-wise insight into false positives and false negatives. Parameter count and GFLOPs were used to assess the suitability of the proposed models for low- resource deployment.

Table 4. Experimental configuration and hyperparameters



| *Category* | *Setting* |
|---|---|
| *Input image size* | 224 × 224 |
| *Batch size* | 32 |
| *Cross-validation* | 5-fold |
| *Epochs* | 30 |
| *Activation function* | ReLU |
| *Optimizer* | Adam |
| *Learning rate* | 0.001 |
| *Local platform* | HP desktop computer, Windows 11 64-bit, AMD Ryzen 5 5625U with Radeon Graphics at 2.30 GHz, 8 GB RAM |
| *Cloud platform* | Kaggle P100 GPU, 16 GB GDDR6 VRAM, 30 h/week GPU time, 12 h/session |
| *Programming environment* | Python, TensorFlow 2.17.1, Keras, Pandas, NumPy, Scikit-learn, Matplotlib, Seaborn |

## 4. Results and Discussion

*Cross-Validation Performance*

Cross-validation was used to evaluate the stability of both proposed models. For D1, MLWCNN achieved fold accuracies of 77%, 78%, 79%, 80%, and 76%, resulting in an average accuracy of 78%. The D1 fold partitioning and confusion matrix are shown in Figure 5 and Figure 6. For D2, MLWCACNN achieved fold accuracies of 97%, 98%, 99%, 98%, and 97%, resulting in an average accuracy of98% in Figure 7. The D2 fold partitioning and confusion matrix are shown in Figure 8 and Figure 9. Table 5 summarizes the fold-level accuracies.

The class-wise performance in Table 6 indicates that MLWCNN recognized Healthy leaves most effectively on D1, with precision, recall, and F1-score values of 0.94, 0.95, and 0.95, respectively. Leaf Blast was the most challenging D1 class, with an F1-score of 0.66, suggesting symptom similarity and misclassification overlap with other disease categories. On D2, MLWCACNN produced consistently high class-wise performance, with most classes reaching F1-scores between 0.95 and 1.00.

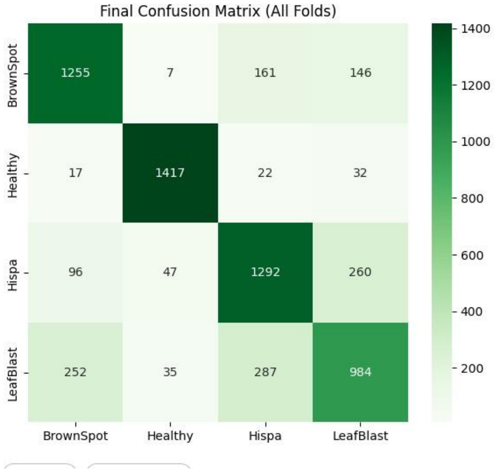
Table 5. Five-fold cross-validation accuracy of proposed models

| *Model* | *Dataset* | *Fold 1 (%)* | *Fold 2 (%)* | *Fold 3 (%)* | *Fold 4 (%)* | *Fold 5 (%)* | *Average (%)* |
|---|---|---|---|---|---|---|---|
| *MLWCNN* | D1 | 77 | 78 | 79 | 80 | 76 | 78 |
| *MLWCACNN* | D2 | 97 | 98 | 99 | 98 | 97 | 98 |

Table 6. Classification performance of proposed models

| ***Model*** | ***Dataset*** | ***Class*** | ***Precision*** | ***Recall*** | ***F1-score*** | ***Support*** |
|---|---|---|---|---|---|---|
| *MLWCNN* | D1 | Brown Spot | 0.77 | 0.80 | 0.79 | 1569 |
| *MLWCNN* | D1 | Healthy | 0.94 | 0.95 | 0.95 | 1488 |
| *MLWCNN* | D1 | Hispa | 0.73 | 0.76 | 0.75 | 1695 |
| *MLWCNN* | D1 | Leaf Blast | 0.69 | 0.63 | 0.66 | 1558 |
| *MLWCNN* | D1 | Accuracy / avg. | 0.78 | 0.78 | 0.78 | 6310 |
| *MLWCACNN* | D2 | Bacterial Leaf Streak | 0.95 | 0.96 | 0.95 | 450 |
| *MLWCACNN* | D2 | Healthy | 0.98 | 1.00 | 0.99 | 441 |
| *MLWCACNN* | D2 | Leaf Scald | 0.98 | 0.94 | 0.96 | 450 |
| *MLWCACNN* | D2 | Leaf Smut | 1.00 | 1.00 | 1.00 | 450 |
| *MLWCACNN* | D2 | Stackburn | 1.00 | 1.00 | 1.00 | 445 |
| *MLWCACNN* | D2 | White Tip | 1.00 | 1.00 | 1.00 | 414 |
| *MLWCACNN* | D2 | Accuracy / avg. | 0.98 | 0.98 | 0.98 | 2650 |

Figure 5. Five-fold validation design for D1.


Final Confusion Matrix (All Folds)

| | BrownSpot | Healthy | Hispa | LeafBlast |
|---|---|---|---|---|
| BrownSpot | 1255 | 7 | 161 | 146 |
| Healthy | 17 | 1417 | 22 | 32 |
| Hispa | 96 | 47 | 1292 | 260 |
| LeafBlast | 252 | 35 | 287 | 984 |

Figure 6. D1 confusion matrix for MLWCNN.

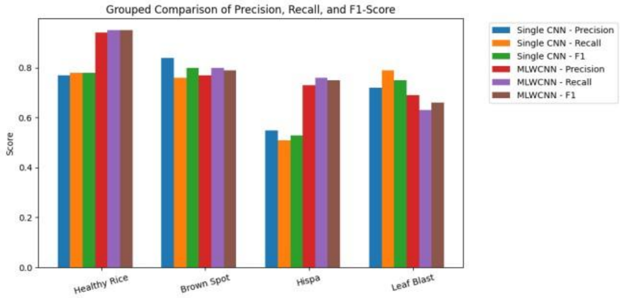


Figure 7. MLWCNN class-wise metric comparison.

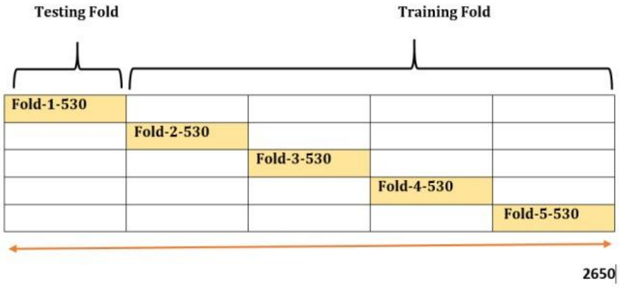


Figure 8. Five-fold validation design for D2.

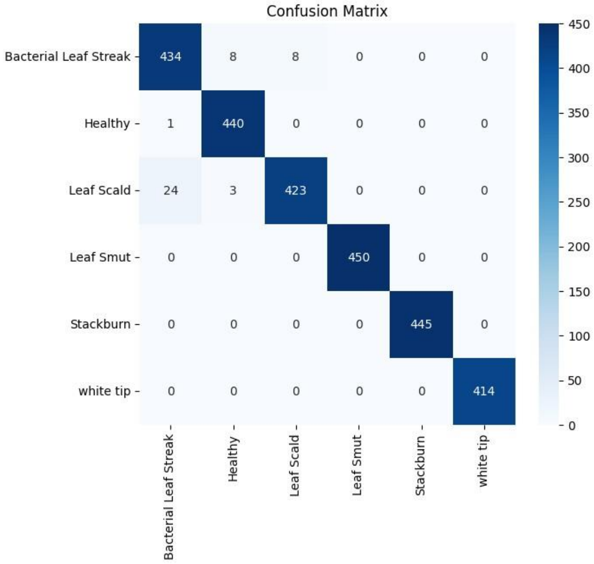


Figure 9. D2 confusion matrix for MLWCACNN.

*Comparison with State-of-the-Art Models*

The proposed models were compared to the representative lightweight and attention-based CNN models reported in crop and rice disease recognition. Table 7 shows that there are two distinct dimensions of performance: classification accuracy and computational complexity. MLWCNN enhanced the D1 baseline accuracy of 73.02 per cent of the single lightweight CNN model [1] to 78 per cent with 0.047M parameters. MLWCACNN obtained the same 98% accuracy as Mobile-Atten [9] and very close to MobInc-Net [5], with much less required parameters.

The model called MobInc-Net showed the greatest accuracy, although the model consumed 2.01M parameters and 0.7 GFLOPs [5]. MLWCACNN on the other hand had 0.059M parameters as well as 0.00012 GFLOPs. This implies that the proposed model offers a good trade- off in accuracy and complexity instead of merely maximizing the accuracy. This tradeoff is visualized in Figure 10 in terms of accuracy, number of parameters and computational cost.

The results can be applied to the automation of agriculture since field operation frequently demands small-sized models which can be run on small hardware. The findings indicate that attention-based feature recalibration is able to enhance discriminative representation without hefty model. However, the analysis is dataset specific. Augmented images enhance the balance of the classes but cannot completely substitute the variability of the real field images taken under varying illumination, background, camera and growth-stage conditions. This weakness is in line with more general findings in the literature on plant disease detection surveys, which focus on external validation, and real-world image diversity [18], [19]. It should then be validated with larger field datasets in the future, deployed in real-time on a mobile device, and explainable attention visualization.

Table 7. State-of-the-art comparison of accuracy and complexity

| ***Model*** | ***Accuracy (%)*** | ***Parameters (M)*** | ***GFLOPs*** | ***Size (MB)*** | ***Main interpretation*** |
|---|---|---|---|---|---|
| *Single lightweight CNN model* | 73.02 | 0.38 | 0.0007 | Not reported | Baseline lightweight model |
| *VGG-ICNN* | 96 | 6.00 | 45.7 | 23.2 | High accuracy with high computational cost |
| *MobInc-Net* | 99.21 | 2.01 | 0.7 | 8.04 | Highest reported accuracy among compared models |
| *Mobile-Atten* | 98 | 5.40 | 0.22 | 21.6 | Attention model with larger parameter count |
| *MLWCNN* | 78 | 0.047 | 0.000095 | Not reported | Compact four-class baseline model |
| *MLWCACNN* | 98 | 0.059 | 0.00012 | Not reported | Competitive accuracy with very low complexity |

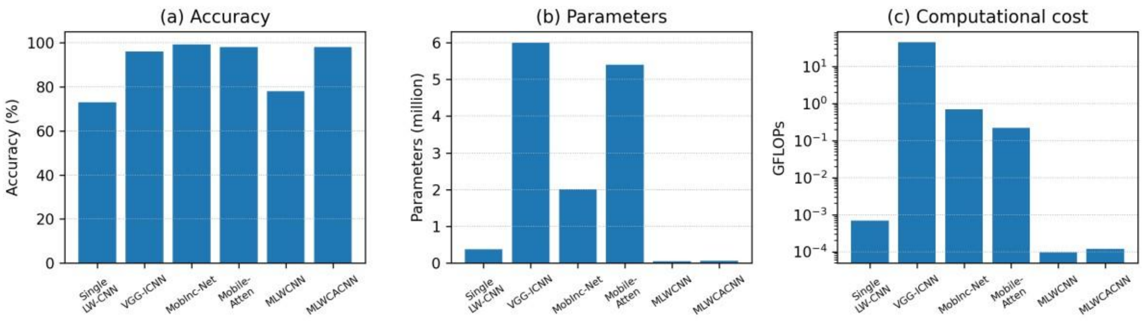


Figure 10. Accuracy and computational complexity comparison.

## 5. Conclusion

This paper introduced two light CNN-based models to identify rice leaf disease. The dataset preparation was done with balanced datasets to minimize the class imbalance and the depth wise separable convolution and pointwise convolution were employed in the proposed MLWCNN to keep the model structure small. The MLWCACNN with attention provided more attention, which is channel and spatial attention to enhance learning of disease-relevant features.

MLWCNN had an average 5-fold accuracy of 78 per cent on the four-class D1 rice disease dataset, compared to 98 per cent for the six-class D2 dataset of MLWCACNN.

The suggested models only needed 0.047M and 0.059M parameters respectively, and their GFLOPs were very low.

The results show that competitive rice disease classification can be obtained with a substantially reduced computational footprint, supporting potential use in smart agricultural and low-resource diagnosis systems. Future work will focus on larger field datasets, external validation, mobile and edge deployment, real-time inference, and explainable visualization of attention responses.

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