

Recent Advances in AI-Based Rice Disease Detection: Performance, Efficiency, and Generalization

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Abstract

The effects of rice diseases on plant health, yield and grain quality are detrimental and therefore, accurate and efficient disease identification is necessary. With the recent development of artificial intelligence (AI), machine learning (ML), and deep learning (DL), disease images of rice have been analyzed automatically with different results depending on the data sets, disease categories, imaging conditions, analysis tasks, and analysis protocols. This study features a systematic review of recent studies on AI applications for rice disease detection, focusing on those published between 2023 and 2026. All 25 studies were chosen and subject to thematic analysis by disease, data characteristics, computational method, analytical tasks, reported performance, computational needs, limitations and future scope. The review includes CNN-based classification, transfer learning, attention mechanisms, light-weight MobileNet architectures, knowledge distillation, object detection, semantic segmentation, hyperspectral and temporal imaging, and domain adaptation. Overall, the synthesis suggests a trend towards more efficient models, localization of disease at a spatial scale rather than an image scale, region level analysis, and multimodal disease assessment. Lightweight architectures showed promise in reducing computational load and advanced imaging and domain-adaptation methods tackled early detection and cross-domain variability. Lack of diversity in dataset, multi-region validation, standardizing computational evaluation, testing in real fields, and generalization across environmental conditions were found to be key research gaps. The results underscore the importance of considering recognition accuracy along with computational efficiency, dataset diversity, and generalisation ability, when creating robust and efficient rice disease detection systems.

Keywords: Rice disease detection, Deep learning, Artificial intelligence, Computer vision, Lightweight models, Object detection, Hyperspectral imaging, Domain adaptation

1. Introduction

Rice (*Oryza sativa*) is one of the major food crops and rice diseases can cause a negative impact on the health of the plant, rice yields and rice grain quality. Correct disease identification is an important element for proper disease management and minimizing possible losses. Traditional disease diagnosis has relied primarily on visual assessment and experience for the most part, which may prove difficult when symptoms look alike, when they occur at early disease stages, or when symptoms differ with varying environmental conditions.

Manual diagnosis suffers from certain drawbacks and this has led to the development of image-based computational methods for automatic rice disease diagnosis. Deep learning methods have shown that they are able to learn discriminative visual features directly from disease images, which diminishes the reliance on handcrafted features. CNN-based models have been studied for rice disease classification, and comparative studies have analyzed the different CNN architectures and transfer-learning approaches to classify various categories of rice diseases [1]. CNN architectures have also been enhanced by adding residual learning and attention mechanisms to boost visual representation of the disease, including small and irregular symptoms [2]. Dense connectivity with attention mechanisms has additionally aided in feature propagation and disease-feature representation within the identification of rice diseases [3].

Recent studies have also shown the CNN-based disease recognition to be extended to customised architectures and to wider plant disease diagnosis. CNN-based systems have been studied for rapid disease diagnosis under changes of image quality and illumination, environment and background characteristics [4]. CNN based architectures have shown good classification accuracy for rice leaf diseases; and the variability of the datasets and the need for field testing should also be taken into account [5]. The difference between manually designed feature extraction and automatic feature learning in paddy disease prediction has also been emphasized by comparing the traditional machine learning with the deep learning techniques [6]. This progress highlights the growing importance of deep learning in automatic rice disease detection and points out the necessity to consider the performance of the models under different experimental conditions.

Another important consideration in the rice disease detection is the computational efficiency. Larger and deeper networks can deliver powerful feature representation but use more computational power, limiting it to use on devices with limited computational resources. There has been therefore a growing interest on lightweight architectures, in particular, MobileNet based architectures. To reduce the number of parameters and the amount of computation operations of the model, LiSA-MobileNetV2 proved to be lightweight by using structural simplification, Swish activation, and attention mechanisms compared to the original MobileNetV2 [7]. In addition, a lightweight attention mechanism with two branches was explored, combined with MobileNetV2, during the real-time rice leaf disease detection on edge devices, focusing on the relationship between recognition capability and deployment efficiency [8]. Other approaches have been investigated for transferring useful representations from larger teacher networks to compact student models, such as knowledge distillation and multi-scale feature extraction to facilitate the creation of a computationally efficient disease detection system [9].

Rice disease detection has also been extended from image-level classification to the localization, segmentation and analysis of rice diseases in various imaging conditions. Object detection methods can detect disease symptoms as well as their spatial positions, and segmentation methods can provide more detailed information about disease affected regions. Hyperspectral observations, and advanced imaging approaches such as temporal observations, can provide additional information for research of early disease symptoms and disease progression. The differences in the domain of training and target environments also underscore the need for cross-environment generalization within and across varieties, geographical regions, environmental conditions, and imaging settings.

Rice disease detection models do not only have to be judged by their accuracy. There are significant variations in disease categories, size and composition of datasets, imaging conditions, pre-processing methods, analysis methods, evaluation standards, and computational requirements between studies. The high accuracy on a controlled dataset does not guarantee the same accuracy for example in other rice varieties, geographical regions, environmental conditions, or images taken in the field. Other analysis goals, such as classification, object detection, and segmentation, have their own distinct evaluation measures, as well as distinct analysis goals themselves. Thus, across the wide variety of experiments, direct numerical comparisons of models can be misleading as to the relative performance.

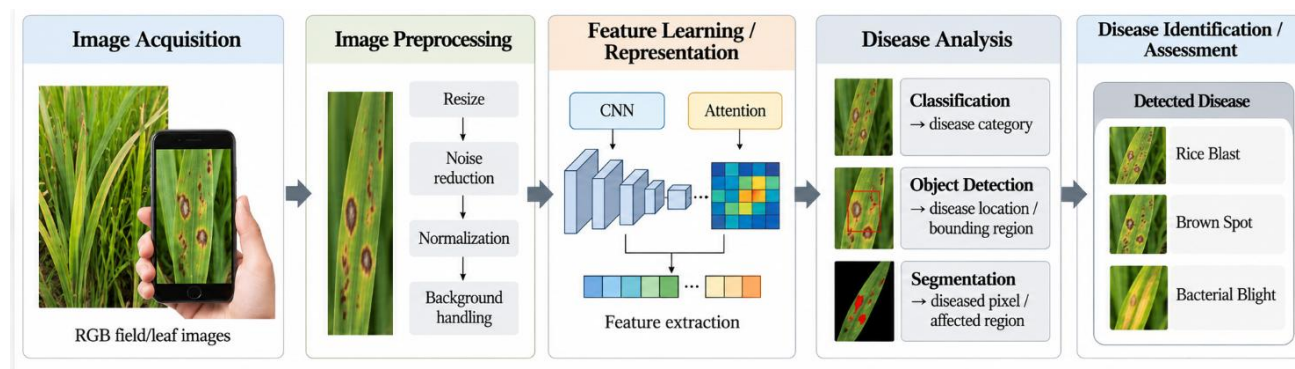


Fig. 1. General workflow of AI-based rice disease detection from image acquisition to automated disease identification and assessment.

This study aimed to examine the latest methods in rice disease detection using AI technology and specifically focus on published studies from 2023 to 2026. The reviewed literature was analysed based on the disease type, characteristics of the datasets, computational approach, analytical task, reported performance, computational requirements, limitations and future scope. The relationships between recognition performance and computational efficiency; the effect of dataset properties and evaluation conditions on reported results; and the necessity of validation across a wider range of environmental and field conditions were given special consideration. The aim of the review was to summarize recent methodological advances and research directions on rice disease detection systems geared towards practical field application for effective recognition, computational efficiency and better generalization.

2. Literature Review

Recent works on rice disease detection revealed that the conventional image classification was gradually shifted to lightweight networks, object detection, segmentation, advanced imaging, and domain-adaptive approaches. The reviewed studies showed a growing emphasis on increasing the recognition accuracy while simultaneously minimizing computational efforts and addressing variability of field conditions, disease occurrence, and image acquisition.

2.1 Lightweight Deep Learning Approaches

For practical applications such as mobile devices and edge computing, computational efficiency became an important consideration for practical rice disease detection. Lightweight architectures reduced computational cost of deep networks without sacrificing meaningful disease-related feature representations. Li et al. [10] proposed a rice leaf disease recognition model based on MobileNetV3 to enhance channel feature attention and feature fusion. The architecture enhanced the representation of channels-wise features and fused features from various levels to achieve better disease detection. The study provided evidence of the feasibility of attention and feature-fusion methods for advancing lightweight rice disease classification, and further testing of the methods in different disease categories and seasons was required. Object detection approaches were further extended to rice disease analysis from image-level classification to the localization of diseased regions. In the research of rice disease detection, Zhang et al. [11] proposed an improved model based on RT-DETR for rice disease detection and solved the problem of multi-source complex image environment disease location. The method helped identify disease areas and minimized reliance on traditional classification-based analysis. Reliable detection continued to be a challenge with respect to small symptoms, complex backgrounds and disease appearance variations. Gu and Han [12] came up with the idea of CDM-YOLO, a new method of rice disease detection in natural environments. The model added improvements for multi-scale disease detection and addressed the challenges of field-acquired images. The study showed that YOLO-based models might be useful for disease localization in more realistic environments.

The small, overlapping symptoms still caused problems due to their small size and similarity to other leaf structures. Cao et al. [13] proposed Pyramid-YOLOv8 model to detect rice blast. The pyramid-based design enhanced the representation of the features of rice blast at different scales and facilitated the better recognition of rice blast symptoms. Rice-leaf blast was mainly studied and it was difficult to extrapolate the findings to other rice diseases. Transformer-based methods also paved the way for a broader study of rice diseases which went beyond the traditional methods of classification and detection. Dai et al. [14] explored Transformer-based segmentation for rice disease analysis and offered region-based disease leaf area analysis. Segmentation provided detailed information about disease distribution, which was more detailed than that provided by image-level classification. Disease features, imaging conditions and the quality and diversity of training data remained influential, as before, for performance. To address this, Pan et al. [15] explored an SSD-YOLO based lightweight detection method with the help of squeeze and excitation mechanism. The method used involved object localization, attention-based feature enhancement, and a relatively light computational structure. The study results showed the feasibility of lightweight detection models for practical rice disease localization while the need for expanding the coverage of diseases and conducting validation in the field remained significant.

2.2 Dataset Diversity and Evaluation

Reported performance was unreliable and variable, depending on procedures for evaluation and on the composition of the datasets. Elakya et al. [16] conducted a study on stratified cross validation for classification of rice diseases and have highlighted the importance of maintaining balance among the disease classes in the evaluation of the model. Stratified evaluation mitigated the potential for class imbalance to impact performance estimates. Larger and more heterogeneous data sets were needed to make more confident evaluations of the robustness of the models in various disease groups and under field conditions. Amon et al. [17] compared machine learning and deep learning techniques to detect brown spot and narrow brown spot diseases. The study drew parallels between computational methods for diseases that have similar symptoms in the visual domain, and emphasised the importance of feature learning for disease recognition. Disease coverage was limited and could not make direct comparisons on performance for the entire spectrum of rice diseases.

CNN based rice disease detection in India was studied by Kumar et al. [18]. The study proved the feasibility of deep learning in the recognition of rice diseases in the agricultural scenario in India. Despite this, geographic variation was still considered to be as important as disease appearance and imaging conditions might differ among regions, rice varieties and cultivation environments. Greater geographic testing of validity was then needed for increased generalizability.

2.3 Advanced Imaging and Disease Progression Analysis

Conventional RGB images were complemented with more information provided by advanced imaging techniques. Wang et al. [19] used time-series hyperspectral imaging and deep learning techniques to analyze the progression of rice blast. The temporal hyperspectral observations were used to analyze the development of the disease at various stages, and to give spectral information which was not available from conventional RGB imaging. This method needed specialized imaging equipment and was less available for use in the field. Chen et al. [20] used hyperspectral imaging and deep learning to monitor bakanae disease at an early stage. The potential of hyperspectral approaches to disease surveillance was seen during early stages with the help of the spectral information that supported the disease related characteristics. But the specialized imaging needs and computational complexity were still obstacles to agricultural implementation.

Another significant challenge was generalization of the image domains. In order to enhance the performance of rice disease recognition, Chen et al. [21] proposed an attention mechanism-based domain-adaptive approach. The method focused on differences from the source to the target image domains and strived to enhance recognition when the training and application domains are different. Domain adaptation was found to be a useful tool to mitigate the impact of imaging condition change, but adequate information from target domains was also required for good domain adaptation.

2.4 The current reviews and research directions.

The review studies of the recent years were more general in scope and oriented towards the development of computer vision and deep learning technologies for plant and rice disease detection. Anwar et al. [22] discussed the computer vision techniques used in plant disease detection and explained how it has advanced from image-based detection to automated detection. The review pointed out the advances of deep learning, image processing, and computer vision in disease control and management of agriculture. Seelwal et al. [23] did a systematic review of deep learning applications in the diagnosis of rice diseases and discussed the trends and future directions in the research area. The review highlighted the rising trend of CNN-based models, transfer learning, attention mechanisms, and automatic image analysis for rice disease recognition. Limitations of the data sets and the need for improved validation under real agricultural conditions were also identified. Ismail et al. [24] gave a detailed survey of deep learning methods for rice disease detection with a focus on datasets, methods and directions for future research. The review showed that there were differences in how the datasets were compiled, the classification of diseases, the preprocessing steps, the architecture of the models and the evaluation metrics, which affected the comparison of the reported results. The need for standardized evaluation and more representative datasets remained as critical needs for reliable model comparisons. Ali et al. [25] did a systematic literature review to cover emerging technologies, methodologies, datasets, challenges, etc., and future trends on rice disease detection. Machine learning, deep learning, advanced imaging, and automated detection technologies continued to be a focus of the review. The results also showed that in the future, attention needs to be paid to address the diversity of datasets, efficiency of computation, environmental variation and deployment-related constraints.

Table 1 Summary of Recent AI-Based Rice Disease Detection Studies (2023–2026)

Author	Year	Method	Key Findings	Limitations
Ahad et al. [1]	2023	CNN + TL + Ensemble	Classified nine rice diseases.	Higher computational cost.
Yang et al. [2]	2023	GoogLeNet + Residual + Attention	Improved feature representation for small symptoms.	Small regions and complex backgrounds.
Jiang et al. [3]	2023	Attention-DenseNet	Enhanced feature propagation.	Higher computational requirements.
Devarajan et al. [4]	2026	CNN	Automated rapid disease diagnosis.	Image and environmental variation.
Basha et al. [5]	2026	Custom CNN	97.03% classification accuracy.	Broader dataset and field validation needed.
Kumar et al. [6]	2026	ML + DL	Compared manual and automatic feature learning.	Dataset diversity and wider validation needed.
Xu et al. [7]	2025	LiSA-MobileNetV2	95.68% accuracy with reduced parameters and FLOPs.	Broader field validation needed.
Tasci [8]	2026	DBLA-MobileNetV2	Lightweight attention-based detection.	Limited agricultural validation.
Wang et al. [9]	2026	Multi-scale + KD	Balanced recognition and model compactness.	Fine-grained features may be affected.
Li et al. [10]	2026	MobileNetV3 + ECA	Enhanced lightweight feature representation.	Broader disease and environmental validation.
Zhang et al. [11]	2026	Improved RT-DETR	Detected disease regions under complex conditions.	Small regions and complex backgrounds.
Gu and Han [12]	2026	CDM-YOLO	Multi-scale detection in natural environments.	Small and overlapping symptoms.
Cao et al. [13]	2024	Pyramid-YOLOv8	Improved rice blast detection.	Focused on rice leaf blast.
Dai et al. [14]	2024	Transformer Segmentation	Provided region-level disease segmentation.	Disease and imaging variation affected performance.
Pan et al. [15]	2025	SSD-YOLO + SE	Lightweight disease localization.	Broader disease and field diversity needed.

Elakya et al. [16]	2026	Stratified CV	Improved class representation during evaluation.	Larger, diverse datasets needed.
Amon et al. [17]	2026	ML + DL	Evaluated brown spot and narrow brown spot.	Limited disease coverage.
Kumar et al. [18]	2025	CNN	Evaluated rice disease detection in India.	Wider geographic validation needed.
Wang et al. [19]	2026	Time-Series HSI + DL	Analyzed rice blast progression.	Specialized equipment required.
Chen et al. [20]	2024	HSI + DL	Supported early bakanae disease surveillance.	Specialized imaging required.
Chen et al. [21]	2023	Domain Adaptation + Attention	Addressed image-domain differences.	Limited target-domain information.

2.5 Synthesis of the Literature

From the reviewed literature, it could be seen that the methods of rice disease detection systems evolved from traditional image classification to more specific and deployment focused systems. To tackle computational problems, lightweight networks were used, and to enhance the representation of disease-related features, attention mechanisms and multi-feature fusion methods were used. The extended analysis for object detection and segmentation brought the analysis of the image to the level of spatial identification of diseased areas. There was still significant variation in dataset and evaluation methodology, and these factors had a significant impact on the report. The studies conducted with controlled or limited datasets were useful for evidence of the ability of the model, while the field conditions were additional variations in the illumination, background, disease severity, rice variety and image quality. Advanced imaging techniques were able to give supplemental information in both the spectral and temporal domains, but were not readily available because of the need for specialized equipment. The reviewed studies also revealed that the model's accuracy was not enough to address the applicability of a rice disease model. Model size, inference needs, disease coverage, data diversity, geographical variation, and field validation also affected the practical suitability. Future development, therefore, entailed a balance between recognition ability, computational efficiency, and generalization over a variety of farming conditions.

3. Methodology

3.1 Review Design

The method used in this study was structured literature review to analyze the latest advances in rice disease detection and classification methods based on artificial intelligence (AI), machine learning (ML), and deep learning (DL). The review included mostly studies from 2023-26. The main topics covered were convolutional neural networks (CNNs), light-weight architectures, MobileNet-based models, attention mechanisms, object detection, semantic segmentation, hyperspectral imaging, domain adaptation and knowledge distillation. Focused on recognition performance, computational efficiency, dataset characteristics, evaluation procedures and generalization under different imaging conditions, the review highlighted. We focused our attention on lightweight architectures where recognition ability and computational expenses were carefully studied. The adopted studies were synthesized based on disease category, database characteristics, the computational method, the analytical task, the reported performance, the computational aspects, the limits and scope of the studies.

3.2 Literature Search Strategy

Main scientific databases and digital research platforms were searched, such as ScienceDirect, SpringerLink, IEEE Xplore, MDPI, Frontiers, PLOS ONE and Google scholar, in order to identify relevant literature. The keywords used for rice diseases, artificial intelligence, deep learning, and computer vision were combined to derive search terms. Representative search combinations were rice disease detection, rice leaf disease classification, deep learning for rice disease, CNN rice disease detection, MobileNet rice disease, lightweight rice disease detection, YOLO rice disease detection, hyperspectral rice disease detection and domain adaptation rice disease. The search strategy included traditional image-based disease diagnosis, lightweight networks, object detection and segmentation, hyperspectral image and domain adaptations. Using the database searches, publications were then screened to identify those that met the predefined selection criteria.

3.3 Study Selection and Screening

The identified records were screened in successive stages. Title and abstract were firstly filtered to exclude studies not related to rice disease analysis and not using AI/ML/DL or computer-vision techniques. Full-text review of studies was

then performed on potentially relevant studies. Studies were selected if they provided adequate information on the disease or application focus, computational approach, data set or imaging source, analytical task, principal findings and methodological limitations. Records with multiple copies, unrelated agricultural applications, publications not in the scope of the book and studies where methodological information was lacking were excluded. Four main steps were implemented for the screening process: record identification, title and abstract screening, eligibility assessment by full text and final study inclusion. Figure 3 show that the numbers of records included/excluded at each stage of the PRISMA flow diagram are recorded.

3.4 Inclusion and Exclusion Criteria

Consistency across the literature was maintained when the selection process was decided before the final synthesis.

Inclusion criteria

- Studies related to the detection, classification, segmentation, or monitoring rice diseases.
- Research on: Artificial Intelligence (AI), Machine Learning (ML), Deep Learning (DL), Computer Vision or related computational methods.
- Studies mainly from 2023-2026.
- Researchers who have provided enough methodological information and findings to lead the reader to the results.
- Studies on image-based disease analysis or hyperspectral analysis or other computer vision based disease analysis.
- Selected recent preprints, where appropriate, methodological information was provided, peer-reviewed journal and conference publications.

Exclusion Criteria

- Other types of studies not involving rice disease analysis.
- Conventional (non-AI) disease diagnostics research.
- Repeated publications of the same study.
- Studies that do not provide enough information to be compared with other studies methodologically.
- Articles about crop-disease other than rice.
- References of studies beyond the specified publication period, if necessary for the context of the work.

3.5 Data Extraction and Analysis

The identified studies were sorted by different topics of information, such as author, year, disease and application focus, dataset characteristics, computational approach, model architecture, analytical task, reported performance, computational aspects and limitations, and future scope.

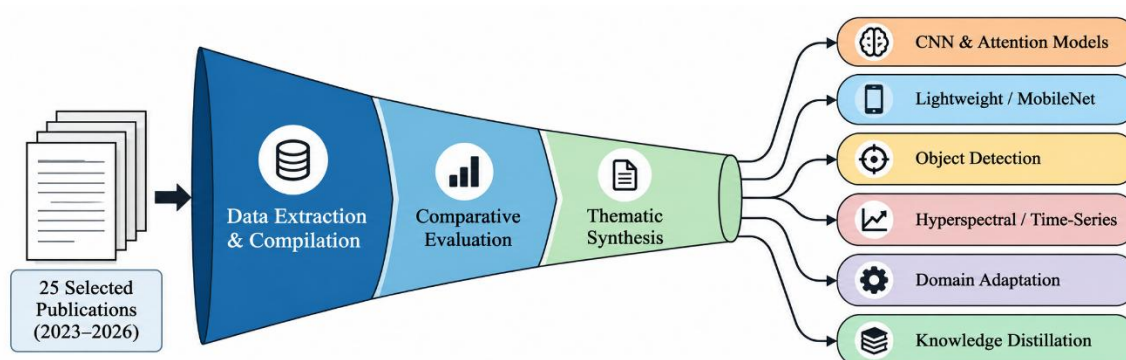


Fig. 2. Framework for data extraction, comparative analysis, and thematic synthesis of the selected rice disease detection studies.

The results of information extraction were compared in order to find commonalities in methodologies and the distinctions between approaches examined. The five key analytical aspects were stressed: recognition performance, computational efficiency, dataset diversity (wide variety of data sets), generalization capability, and methodological limitations. The recognition performance was compared to the metrics provided by each individual study such as accuracy, precision, recall, F1 score and mean Average Precision (mAP) when available. For the parameters that could be used, computational

efficiency was analyzed based on the number of parameters, floating-point operations (FLOPs), inference time, and frames per second (FPS). Detailed characteristics of the datasets were investigated with regard to the number of images available, the image quality, the coverage of the disease classes and the presence of field-based images. The analysis of classification, object detection and segmentation methods was separated from one another since different purposes and assessments were made in each discipline. Lightweight architectures such as MobileNet models were analyzed and discussed in terms of model compactness and recognition results. Due to the fact that hyperspectral and temporal imaging studies included spectral or temporal information different from the traditional RGB, these studies were treated separately. The differences between source and target image domains were considered to evaluate domain-adaptation approaches.

3.5.1 Evaluation Metrics

For classification-based approaches, the principal evaluation metrics were accuracy, precision, recall, and F1-score. These measures were defined using the confusion-matrix components: true positive (TP), true negative (TN), false positive (FP), and false negative (FN).

Accuracy represented the proportion of correctly classified samples:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

Precision represented the proportion of correctly identified positive samples among all samples predicted as positive:

$$\text{Precision} = \frac{TP}{TP+FP} \quad (2)$$

Recall represented the ability of a model to correctly identify positive samples:

$$\text{Recall} = \frac{TP}{TP+FN} \quad (3)$$

F1-score provided a combined measure of precision and recall:

$$F1 = 2 \frac{\text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \quad (4)$$

For object detection studies, mean Average Precision (mAP) was considered where reported. For C evaluated classes, mAP was represented as:

$$mAP = \frac{1}{C} \sum_{c=1}^C AP_c \quad (5)$$

where AP_c represented the Average Precision for class c , and C represented the number of evaluated classes.

The reviewed studies reported a variety of computational indicators and none of these was used as a single indicator of computational efficiency. The number of parameters, the number of FLOPs, inference time, and frames per second were, therefore, kept as individual metrics. This way no common index was created from the mishmash of computational measures.

3.5.2 Comparative and Thematic Analysis

The extracted evidence was not directly ranked by the accuracy of the model. It was qualitatively compared the performance values reported were evaluated in view of the composition of the datasets, the disease coverage, the type of analytical task, the method of evaluation, and imaging conditions. Where great differences were found in experimental settings, direct numerical comparison was not done. The trade-off between recognition ability and computational efficiency was focused on in particular. For the purpose of parameter and computation reduction, lightweight architectures were explored, and for the purpose of other architectural changes that influence disease-feature representation, attention mechanisms, feature fusion, knowledge distillation were explored etc

3.6 PRISMA-Based Screening Framework

The selection process for the studies used the framework Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA). The framework was used to record the identification, screening, eligibility and final inclusion of

literature. The PRISMA flow diagram documented the number of records identified and the number of duplicate records removed, records screened, records excluded in title and abstract screening, full-text articles assessed for eligibility, full-text articles excluded with reasons and studies included in the final review.

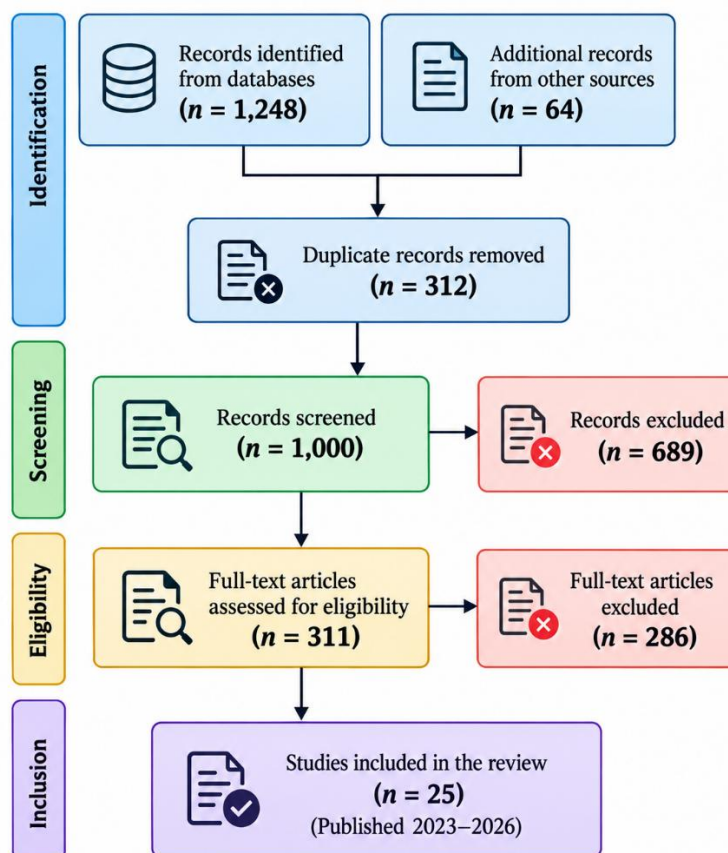


Fig. 3. Literature identification, screening, eligibility screening, and study selection for the review using PRISMA.

3.7 Synthesis of Evidence

Because of the significant differences between datasets, disease categories, imaging conditions, model architectures, analysis tasks, evaluation metrics, and experimental setup, the selected studies were not analyzed statistically (meta-analysis), but instead they were synthesized thematically. The synthesis explored the evolution of CNN-classification based systems to architectures with attention, lightweight networks, object detection, segmentation, Transformer-based architectures, hyperspectral analysis techniques, and domain-adaptation techniques. There were persistent methodological weaknesses in both dataset diversity and environmental variation, computational needs, evaluation procedures, and external validation. Another aspect of the synthesis is the tradeoff between recognition performance and efficiency of computation. To evaluate the extent and relevance of reported parameter reductions and computation requirements, lightweight models were examined, and to examine the broad architectural approaches, they were related to the analytical task and to the type of disease information represented. The observed patterns served as the foundation for discussing the gaps in methodology and future research in the field of rice disease detection.

4. Results and Discussion

4.1 Overview of Reviewed Studies

The review included 25 studies, which were published in the period from 2023 to 2026. Literature selection included CNN classification, lightweight and MobileNet for vision architectures, object detection, semantic segmentation, attention mechanisms, hyperspectral imaging, domain adaptation, and knowledge distillation. The studies were analysed on the basis of recognition performance, computational efficiency, type of dataset, analytical task, generalization capability, limitations,

and scope. The number of selected studies has risen throughout the review period and this trend continued with 4 studies published in 2023, 4 in 2024, 5 in 2025 and 12 in 2026. The increased number of the recent studies highlighted the ongoing advancement of rice disease analysis using AI-based methods. The recent research focused more and more on computational efficiency, feature representation, disease localization, different imaging modalities, and generalization across different image domains.

From the literature reviewed, a trend from traditional CNN-based image classification to more specialized techniques was observed. The CNN has also been employed for disease classification and transfer learning methods have also been helpful in the disease classification problem. Attention mechanisms and feature fusion approaches have been utilized to enhance the disease-feature representation. MobileNet-based lightweight architectures that consider computational constraints. The methods which were applied for object detection and segmentation solved the disease localization and affected region analysis. However, spectral and temporal imaging added another dimension of information in the form of hyperspectral and temporal images, respectively, and domain-adaptation techniques dealt with the domain gap between the source and target images.

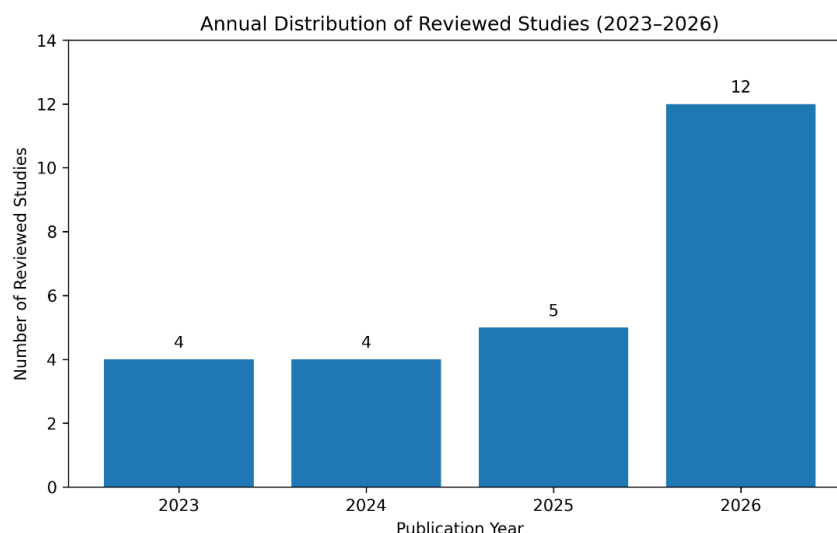


Fig. 4. Annual distribution of the 25 studies included in the review from 2023 to 2026.

4.2 Recognizing performance and methodological trends.

The reviewed studies reported good recognition performance on CNN-based, attention-enhanced and light architectures. CNN-based techniques automatically extracted features from the image characteristics associated with the diseases and several approaches for classification of rice diseases were developed [1-6].

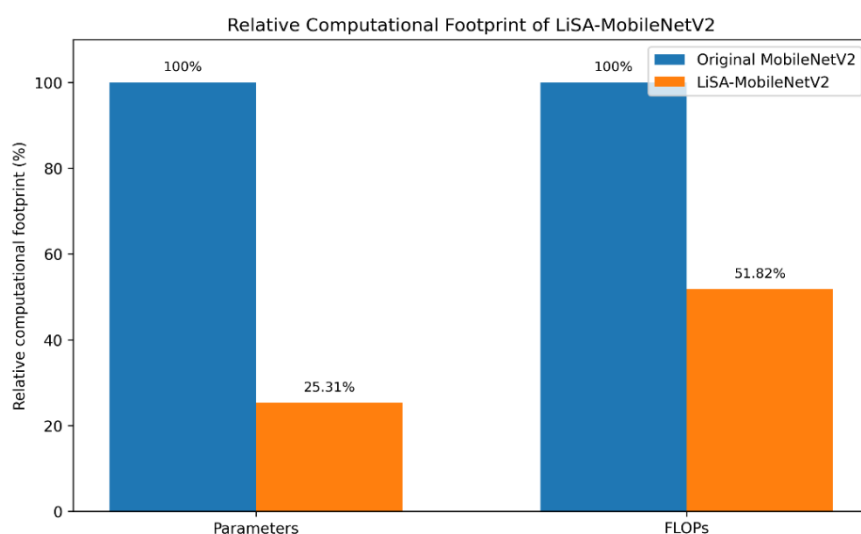


Fig. 5. Relative computational footprint of LiSA-MobileNetV2 compared with the original MobileNetV2 [7].

To capture the disease-related features, especially for small and irregular symptoms, attention mechanisms were added to the architectures like GoogLeNet and DenseNet [2] and [3]. Customized CNN architectures are also found to be performing well in classification, where an accuracy of 97.03% is reported in the classification of rice leaf diseases by Basha et al. [5]. Competitive recognition performance was also reported with lightweight architectures. LiSA-MobileNetV2 tested with the accuracy of 95.68%, and reduced the model parameters and FLOPs by 74.69% and 48.18% respectively compared to the original MobileNetV2 [7]. The results reported here suggested that significant reduction in the number of computations would be possible without compromising disease recognition performance.

However, direct numerical comparison between the studies analyzed was limited due to differences between studies in disease categories, dataset composition, image acquisition conditions, data partitioning, augmentation strategies and evaluation procedures. A uniform relation between the accuracy reported and the properties of the training set and experimental conditions could not be found. The examined evidence showed that besides accuracy-based classification, there was a gradual shift towards model efficiency and robustness. To better represent the diseases and minimize computational cost, attention mechanisms, multi-scale feature extraction, feature fusion, and knowledge distillation were implemented in the architectural aspects of the model [7-10].

4.3 Computational Efficiency and Lightweight Models

Efficient computation was also a key aspect in the latest studies for rice disease detection. CNNs with conventional architectures showed excellent feature-learning performances which might need more computational power. The approach of lightweight architectures dealt with this issue by minimizing the number of model parameters and/or the number of operations in the model, while trying to retain a modest disease-recognition ability. An important avenue of lightweight rice disease analysis was the direction of mobileNet-based approaches. LiSA-MobileNetV2 outperformed the original MobileNetV2 [7] with 95.68% test accuracy, which was also obtained with a reduction in the number of parameters by 74.69% and FLOPs by 48.18%. The results showed that there was a noticeable gain in computational complexity and a maintenance of classification performance.

DBLA-MobileNetV2 added the lightweight attention mechanism in two branches into MobileNetV2 to achieve better results on the extraction of disease features while keeping the network lightweight [8]. MobileNetV3 is the research used and it was used in combination with efficient channel attention and multi-feature fusion to improve the representation of features in a lightweight network [10]. Another way to computational optimization was knowledge distillation. In [9], Wang et al. fused a light-weighted multi-scale network with the knowledge distillation technique to distill useful feature information from a large model to a small model. These compression techniques lowered the computational load of the resulting architecture, but still had to be able to preserve fine-grained disease information.

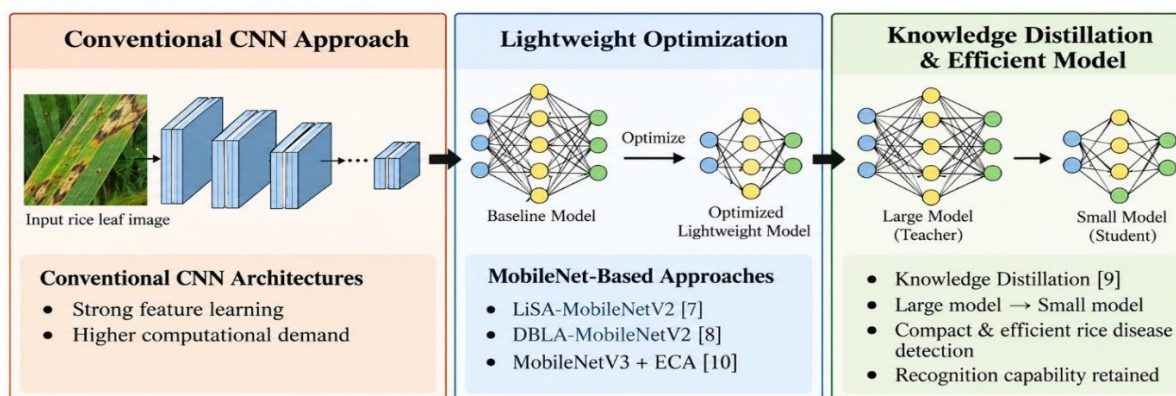


Fig. 6. Conceptual comparison of the performance of the conventional approach and the lightweight approach for rice disease recognition, computational efficiency.

The reviewed studies showed that development of a lightweight model comes at the expense of recognition performance, model compactness, feature representation and computational needs. When reported, FPS and inference time were observed to be good measures of the efficiency of execution depending on the model size and complexity, indicated by parameter count and FLOPS. However, due to the fact that there were no consistent real-device measurements available, it was not possible to compare the practical execution efficiency between all lightweight models.

4.4 Dataset Diversity and Generalization

The characteristics of datasets played an important role in understanding the reported model performance. There were variations in the data subset, disease-class coverage, image background, illumination, leaf orientation, disease severity, rice

variety, and image acquisition conditions that affected the conditions of the models' development and evaluation [16]–[18]. Elakya et al. investigated the stratified cross-validation as an evaluation approach for paddy disease detection problem; they demonstrate the significance of class representation and evaluation design [16]. Studies that were done under Indian conditions too suggested the necessity of wider validation across geographical regions, environmental conditions and rice varieties [18]. Another approach to the differences between training and target image domains was domain adaptation. To solve the differences in image domains, Chen et al. studied an attention-based domain-adaptive rice disease recognition method [21]. These would pertain to the issue of generalization as a trained model in one imaging distribution might experience different backgrounds, light conditions, disease appearances, or acquisition conditions within another distribution. The evidence reviewed showed that, along with recognition performance, there is a need to take into account the dataset diversity and the evaluation design. A high level of performance in one experimental context does not necessarily mean it is the same level in other contexts, either in environment or geographical location. There was a continued need for additional field data, cross-region testing and evaluation in diverse imaging situations.

4.5 Detection, Segmentation, and Advanced Imaging Approaches

The studies reviewed identified a progression towards image level disease classification to methods that also locate disease and/or affected areas. Most of the classification approaches classified the disease type for the input images, while object detection approaches not only classified the disease type but also localization of the disease in space [11]–[13], [15].

Two methods—RT-DETR and YOLO—were explored for disease detection in more complex visual scenarios. The improved RT-DETR was used for the detection of rice diseases, and the CDM-YOLO was used for natural environment detection [11], [12]. Incorporating multi-scale information into the rice leaf blast detection algorithm, Pyramid-YOLOv8 was introduced [13]. Another lightweight detection method, feature-enhancement mechanisms, was given by SSD-YOLO [15]. Even in a detection-oriented approach, small disease areas, and overlapping symptoms and complicated backgrounds were difficult conditions. To resolve a more detailed analysis, the task of semantic segmentation was taken up which aimed at identifying the disease affected regions at the pixel level. AISOA-SSformer utilized a Transformer-based model to generate a regional-level supplement to the image-level classification, for rice leaf disease segmentation [14]. The segmentation methods could also give more detailed disease region information, but the computational and data requirements were different to the conventional classification methods.

Beyond the traditional RGB images, hyperspectral and temporal imaging allowed rice disease analysis. For the early surveillance of bakanae disease in rice, Chen et al. integrated hyperspectral imaging and deep learning [20]. Wang et al. monitored the progression of rice blast using time-series hyperspectral imaging with deep learning [19]. These methods used additional spectral or temporal data that were not provided by conventional RGB images, but required special imaging equipment and more complicated data processing. The comparison revealed a high level of influence of analytical task on model requirements. Disease-level recognition, detection added a spatial localization, segmentation added detailed information on affected region, and hyperspectral or temporal approaches added other spectral or temporal information. Performance measures for these tasks were not assumed to be readily and consistently interchangeable since the goals and criteria were different.

4.6 Critical Synthesis and Research Gaps

The literature surveyed indicated that significant advances have been made towards rice disease detection using artificial intelligence, with some common drawbacks.

The key challenges were the diversity of the datasets and the environmental variation. Many studies tested models under particular dataset and imaging conditions, and there was no direct evidence for the generalization of the models across geographic regions, rice varieties, backgrounds, illumination conditions, and disease stages [16]–[18], [21].

Various lightweight architectures, MobileNet models, knowledge distillation, attention mechanisms, and feature optimization were the focus of increasing computational efficiency [7]–[10]. Progress was reported for model compactness, both in terms of reduction of parameters and reduction of FLOPs; however, the computational measurements were not consistently reported using the same criteria. The data on real-device inference time, frames per second (FPS), memory usage, and hardware-specific performance were less uniform across the studies that were reviewed.

The direct comparison was also affected by task and metric heterogeneity. Each classification, object detection, and segmentation focused on a different analytical goal, and employed a different evaluation measure. The results of the classification studies could not be directly compared to the results obtained from detection and segmentation studies without taking the underlying task and evaluation protocol into account.

Another limitation was disease and data coverage. Several studies were directed specifically towards a certain disease category or a specific imaging condition [13], [17], [19], [20]. The wider the coverage of the disease and more diverse the data, the more evidence of generalization there will be.

The identification of disease early in the season was a new area of research. The additional information obtained from hyperspectral imaging and temporal analysis were for early surveillance and analysis of disease progression [19], [20]. These methods also involved more complex equipment and processing needs, establishing an additional equilibrium

between the richness of the information provided and its computational/operational complexity. Validation was still needed in real world to extrapolate from laboratory or controlled-dataset performance to real-world applications to agriculture. Future evaluations should be biased towards using a wider range of field images and geographically distributed testing, computational measurements, and realistic imaging conditions to validate. The synthesis showed that the advancement of rice disease detection methods cannot be measured by the success of disease recognition. The reported results were influenced by the model architecture, computational efficiency, characteristics of the datasets, analytical task, modality of the imaging, and the generalizability of the results. Lightweight architectures clearly showed a research path to the development of efficient models for computations, and detection, segmentation, hyperspectral imaging, and domain adaptation opened the door to new information on diseases that could be obtained.

The reviewed studies yielded a major research trend towards achieving a balance between the recognition performance, computational efficiency, dataset diversity and generalization capability. These factors would need to be investigated simultaneously and not optimized for a single performance measure in a limited experimental environment.

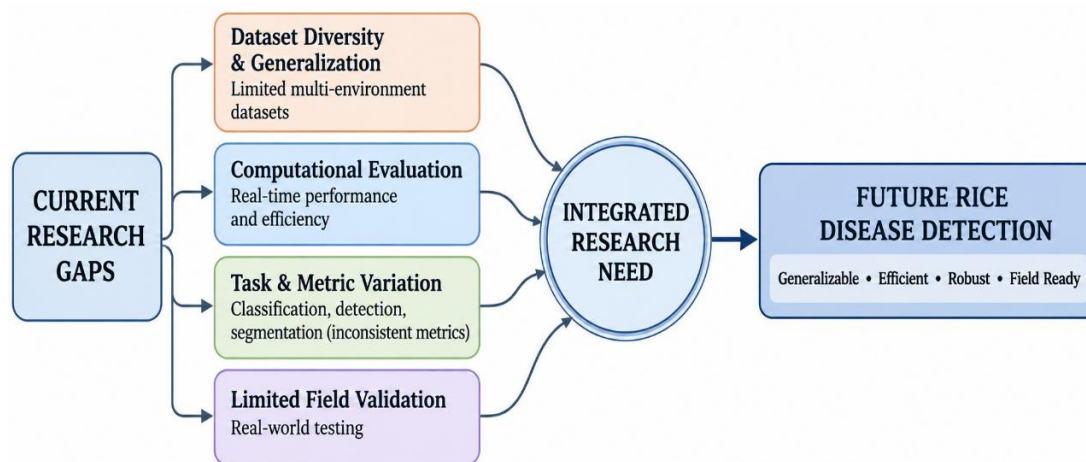


Fig. 7. Future research directions for rice disease detection based on identified research gaps.

5. CONCLUSION AND FUTURE SCOPE

5.1 Conclusion

A total of 25 studies covering the period of 2023 to 2026, addressing the use of AI, machine learning, and deep learning techniques for rice disease detection were reviewed. The literature that was reviewed included CNN-based classification, lightweight architectures, MobileNet architectures, attention mechanisms, object detection, semantic segmentation, hyperspectral imaging, temporal imaging, domain adaptation, and knowledge distillation. CNN-based methods were still popular for the classification of rice diseases due to their capability of learning the image features related to a disease automatically. Research into attention mechanisms, residual connections, dense feature propagation, and feature-fusion strategies, to better represent diseases and features, was carried out [1]–[6]. In recent years, there has been growing emphasis on computational efficiency, especially with the use of lightweight models such as those based on the MobileNet architecture. LiSA-MobileNetV2 achieved the test accuracy of 95.68% and reduced the number of parameters by 74.69% and the number of FLOPs by 48.18% compared to the original MobileNetV2 [7]. The results demonstrated the potential of lightweight architectures in reducing the computational burden without sacrificing useful recognition capability.

This was also observed in the reviewed studies where there was a progression from classifications of images to disease localization and region-level analysis. Object detection techniques were employed using YOLO and RT-DETR methods, whereas segmentation, which gave detailed information about the regions of disease, used the Transformer technique [11]–[15]. Additional spectral and temporal data were added with hyperspectral and time-series imaging for disease surveillance analysis and disease progression [19], [20]. Image domain adaptation methods were used to highlight differences between image domains and the need for generalization from the original domain [21]. It was also observed that the comparison revealed that reported recognition performance was not independent of the dataset characteristic, disease coverage, image condition, analytical task, and evaluation method. Not all studies were able to be directly compared numerically due to various experimental conditions. A recurring issue in the literature reviewed was the diversity of the datasets, the environmental variability, the computation needs, and the general validation.

The review therefore led to a research pathway focused on a potential balance between recognition performance, computational costs, the diversity of datasets, and the generalization performance. Efficient development was not enough,

as good model evaluation also had to be carried out under a variety of conditions to provide convincing evidence of practical applicability.

5.2 Future Scope

Future research should place greater emphasis on diverse and representative rice disease datasets covering different geographical regions, rice varieties, environmental conditions, disease stages, and imaging conditions. Broader datasets can provide stronger evidence of model generalization than evaluation using restricted or highly controlled image collections. Further development of lightweight architectures can support computationally efficient rice disease analysis. MobileNet-based networks, knowledge distillation, efficient attention mechanisms, feature optimization, and related model-compression techniques can be investigated to reduce parameters and computational requirements while preserving disease-related information [7-10].

Future studies should also improve standardized computational evaluation. Parameter count and FLOPs can be reported together with inference time, FPS, memory requirements, and hardware specifications where possible. Consistent reporting would make computational comparisons among lightweight models more meaningful.

Cross-region and cross-domain validation represents another important direction. Models should be evaluated using image distributions that differ from the training data to examine robustness under changes in illumination, background, disease appearance, imaging devices, and agricultural environments. Domain-adaptation approaches can also be further investigated for reducing performance differences between source and target domains [21]. Greater attention can also be given to early disease identification and disease progression monitoring. Hyperspectral and time-series imaging have demonstrated the potential of spectral and temporal information for disease surveillance [19-20]. Future research can investigate ways to obtain such information with lower equipment and processing requirements.

Further work should distinguish clearly among classification, detection, and segmentation objectives and adopt task-appropriate evaluation metrics. Multi-task approaches combining disease classification with localization or affected-region analysis can also be investigated where sufficient annotated datasets are available. Finally, future studies should place greater emphasis on external and field-based validation. Evaluation using diverse field images and realistic acquisition conditions can provide stronger evidence of model robustness than performance obtained under a single controlled experimental setting. Such validation, combined with computationally efficient architectures and standardized evaluation, can support the development of reliable and resource-efficient rice disease detection systems.

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