

RESEARCH ARTICLE

Identification of Downy Mildew Disease Stages in Salad Cucumber Using Machine Learning

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Abstract: Salad Cucumber (SC) is a commercially important crop grown in Sri Lanka, which spans a life cycle about 120 days. Downy mildew (DM) is a critical disease affecting different stages of SC life cycle, which significantly reduces the yield and shortens the growing season. Early detection and management of DM is essential for maintaining crop health and reducing economic losses. DM has different stages in its progression, and the early detection of those stages is important to adopt measures to treat and control. Often, early signs of DM go unnoticed, leading to detection only after severe damage to SC cultivation. Although extensive research exists on identifying DM in SC, studies focusing on stage-wise disease identification remain limited. During the study, a stage wise image dataset for DM was collected from selected tunnel environments in Monaragala and Matara districts. After pre-processing, the dataset was then compared under different experimental data setups using MobileNetV2, EfficientNetB0, ResNet50, VGG16, DenseNet121 and a customized Convolutional Neural Network (CNN). The customized CNN outperformed other models, achieving the highest classification accuracy of 93%, demonstrating its effectiveness in recognizing different stages of DM in SC. When integrated with relevant agronomic information, customized CNN can support early detection, prevention, and timely application of remedies for DM in SC where it shows strong potential as a practical solution for cultivators. This highlights how machine learning (ML) can assist disease detection and monitoring, thereby supporting precision agriculture applications and improving decision-making in crop production.

Keywords: Disease Stage Classification, Downy Mildew, Machine Learning, Precision Agriculture, Salad Cucumber.

Introduction

Salad Cucumber (SC) (*Cucumis sativus* L.), from the Cucurbitaceae family, is a commercially important crop in Sri Lanka grown for its tender, crisp fruits used in salads and cooking. SC is grown in open fields and protected structures, with increasing use of controlled environments for high-value markets. Cultivation is concentrated in agro-ecological zones such as the Low Country Wet Zone and Up-Country Intermediate Zone (Department of Agriculture Sri Lanka, 2020, 2025). The life cycle of SC in Sri Lanka spans about 120 days, starting with germination (0–7 days), followed by seedling/transplanting (7–14 days), vegetative growth

(15–30 days), flowering (30–50 days), and fruit development (50–70 days). Harvesting begins around day 50 and can continue until day 120, depending on the variety and conditions (Department of Agriculture Sri Lanka, 2025).

Downy mildew (DM), caused by *Pseudoperonospora cubensis*, is a critical disease affecting cucumber production worldwide, including Sri Lanka (Chaban *et al.*, 2000, Weizheng *et al.*, 2008, Call *et al.*, 2012). It can significantly reduce yields and shorten the growing season (Chaban *et al.*, 2000). This pathogen is an obligatory parasite and fungus-like organism that does not rely on biological vectors for transmission;

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instead, it spreads rapidly via environmental means. Wind disperses the sporangia (asexual spores) over long distances, while rain splashes and water droplets facilitate local spread. The stages of DM disease in SC include the initial stage (spore deposition), incubation stage, development stage, advanced infection, and terminal stage. Initial symptoms manifest as small pale green lesions on the upper surfaces of lower leaves, which soon develop into yellow, angular spots bounded by leaf veins. As the disease progresses, grayish or purplish mold forms on the undersides of leaves from the seedling stage to maturity. In later stages, infected leaves turn brown, dry out, and die, severely reducing the plant's photosynthetic capacity. The rapid leaf necrosis leads to stunted plant growth and poor fruit development. If not controlled in time, DM can cause devastating yield losses ranging from 30% to total crop failure, posing a major threat to commercial cucurbit production. Effective disease forecasting, resistant cultivars, and integrated pest management strategies are critical for mitigating its impact (Permanent Crop Clinic Sri Lanka, 2013, Priyantha, 2014, Schuh and Grabowski, 2022). Hence early detection and management of DM is critical for maintaining crop health and reducing economic losses.

In the existing research, there are plenty of research which performed in detecting the diseases of the SC, notably the DM disease. Mia *et al.*, (2021) conducted a comparative study between traditional machine learning approaches and CNN-based transfer learning for the detection of various cucumber diseases, including DM, powdery mildew, mosaic virus, belly rot, scab, and cottony leak. Their findings indicated that the MobileNetV2 model beaten traditional methods, achieving an overall classification accuracy of 93.23%, thus demonstrating its effectiveness in automated cucumber disease diagnosis. Another study by Nancy and Kiran, (2025) investigated the identification of cucumber and grape diseases, specifically powdery mildew, DM, and target leaf spot, employing a multi-SVM algorithm with a custom kernel. Their approach achieved a mean average precision (mAP) of 90.62%, excelled in the performances over YOLOv5m model, which attained a mAP of 84.6%, thereby demonstrating the efficacy of their customized SVM method for disease detection in these crops. Zhang *et al.*, (2019), introduced GPDCNN, a streamlined convolutional architecture that combines dilated convolution and global pooling. The method they have presented achieved accuracy of 94.65% in identifying cucumber leaf diseases, including DM disease. Similarly, Shivaraj and Haladappa, (2025) conducted a comparative study on seven convolutional neural network (CNN) models for the classification of diseases of cucumber leaves. They

have trained and evaluated DenseNet121, InceptionV3, ResNet50V2, VGG16, Xception, MobileNetV2, and NASNet. The results indicated that the ResNet50V2 outperformed the rest of six models with accuracy of 99.37%. However, these research studies only focused on the disease identification and did not consider the disease stage-wise classification.

Severity impact detection in plant diseases is vital for precision agriculture, as it supports timely, stage-specific interventions that minimize yield loss and promote sustainability. Unlike generic binary models, severity assessment quantifies infection levels, enabling more informed decisions on pesticide use, resource distribution, and yield prediction (Faye *et al.*, 2023). However, despite the critical importance of severity-based detection, relatively few studies have focused on disease stage-wise or severity-level classification. Palma *et al.*, (2022), introduced a novel method of detection of plant disease severity using leaf images. This method uses a positive non-linear dynamical system that processes leaf images to isolate symptomatic disease patterns, effectively distinguishing diseased regions without the need for prior training or disease-specific models. The study conducted by Abdulridha *et al.*, (2022), explored the integration of remote sensing and machine learning (ML) for detecting DM severity stages in watermelon using hyperspectral imaging and spectral vegetation indices (VIs). Multilayer Perceptron (MLP) and Decision Tree (DT) methods utilized in distinguishing healthy plants from those at varying disease severity (DS) stages. The results indicated that the Multilayer Perceptron (MLP) model achieved superior classification accuracy overall, however, its performance was limited at low disease severity levels, recording only 62.3% accuracy. Classification accuracy improved notably with increasing severity, reaching 86–90% in laboratory conditions and 69–91% in field settings. The study by Weizheng *et al.*, (2008), presents an automated method for assessing the severity of leaf spot diseases through image analysis. They developed a system that segments the leaf region using Otsu's thresholding, detects disease spots based on hue values in the HSI color space.

However, existing studies on disease stage-wise or severity-based classification have several significant limitations. Most remarkably, they lack scientifically defined baselines for determining severity thresholds, and the stage-specific classification labels used in these studies are often inconsistent or empirically derived. A stage-wise detection of the DM disease of SC is yet to be explored.

In conclusion, although assessing disease severity provides substantial benefits for pest and disease management by enabling precise, data-driven interventions tailored to infection intensity, there remains a significant gap in stage-wise severity impact detection. Therefore, this research was designed to address this gap by proposing a scientifically grounded AI-based approach for the stage-wise detection of DM disease of SC. This study offers a novel contribution to the field and paves the way for future advancements in disease stage wise severity classification within precision agriculture.

Materials and Methods

Dataset

The proposed Machine Learning (ML) model by the researchers focuses on stage-wise classification of DM disease in SC. An image dataset consisting of both infected and healthy leaves was collected from two primary sources: four privately owned SC growing tunnels in Athiliwewa, Wellawaya, and two SC growing tunnels managed by the Department of Crop Science at the University of Ruhuna. The collected dataset was then labelled with the assistance of domain experts from the Department of Agriculture (DoA) and

the Department of Crop Science, based on the visually identifiable features corresponding to each stage of DM disease on SC leaves. The set of visual features used to differentiate the stages of DM disease in SC leaves, is presented in Table 1.

Since the initial stage is asymptomatic with no visible symptoms, no images were annotated for this stage. Furthermore, due to the limited number of samples representing the incubation stage, image data from this stage were excluded from model training to minimize potential bias and ensure model robustness. Images corresponding to the terminal stage were also omitted from training, as identification at this stage holds limited agronomic relevance given that severe and irreversible crop damage has already taken place. The model training was conducted using data labelled for the development stage, advanced infection stage, and healthy leaves.

The image dataset was annotated based on the visual features presented in Table 1, reflecting the disease stages of DM in SC. Representative samples are presented in Figure 1.

Table 1. Visual features used for stage-wise classification of DM disease in SC leaves

Classification label	Visual Features
Healthy	• Leaf appearance: Uniform bright or dark green with no visible lesions or discoloration. • Surface condition: Smooth surface, no water-soaked or oily spots. • Other signs: - Veins are clearly visible without distortion or yellowing. - No fungal growth or sporulation; turgid, uncurled leaves.
Initial stage (Spore deposition)	• The pathogen's sporangia are deposited on the plant's surface, usually on the lower side of leaves. • No visible symptoms are seen initially.
Incubation stage	• Initial symptoms: Small, irregular yellow spots (chlorotic lesions) appear on the upper leaf surface, often near leaf margins. • Distribution: Lesions are sparse and localized, usually limited to 5–10% of the leaf area. • Leaf texture: Slight discoloration, slight deformation.
Development stage	• Lesion spread: Yellow lesions expand and combine to cover a more significant portion of the leaf. • Tissue condition: Interveinal chlorosis increases; tissue between veins may start to collapse or necrotize. • Coverage: Affects 30–50% of the leaf surface.
Advanced infection	• Lesion dominance: Extensive and merged lesions covering >60% of the leaf. • Leaf necrosis: Large areas of the leaf become necrotic (brown/black), dry, and fragile. • Defoliation risk: Leaves may begin to die off and detach prematurely. • Fungal growth: Visible fungal colonies may cover lesion areas.
Terminal stage	• Defoliation leads to plant death. • Fruits, if present, may be undersized or malformed.

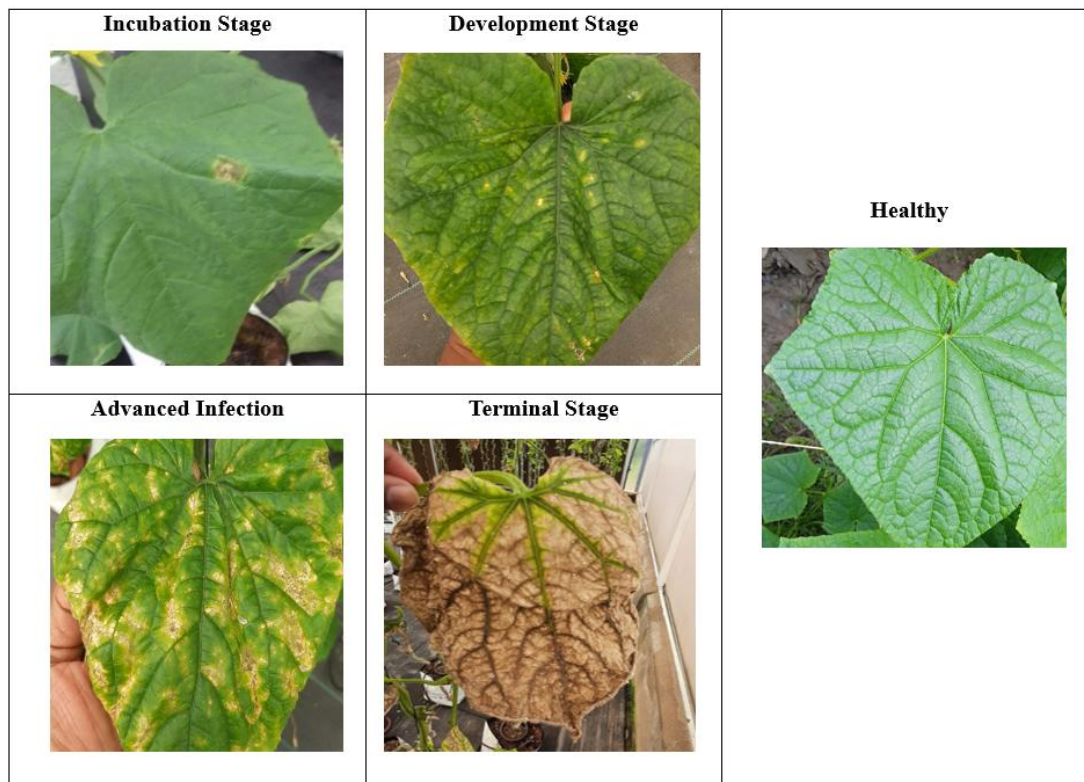


Figure 1. Sample images for each downy mildew disease stage in cucumber

Preprocessing techniques

The labelled image dataset was pre-processed through annotation, cropping, and augmentation using tools such as LabelMe and Python within the Google Colab environment. A summary of the procedures performed at each step is provided below:

Image annotation: Bounding box annotations were applied to categorize the images into three classes: healthy, development stage, and advanced infection.

Image cropping: Using a Python script, regions of interest (ROIs) were cropped from the original images

based on metadata extracted from the LabelMe annotation files.

Image augmentation: The dataset was augmented with the Albumentations library employing techniques including rotation, random scaling, horizontal and vertical flipping, random brightness and contrast adjustment, shift-scale-rotate, hue-saturation-value (HSV) transformations, and resizing.

The following table summarizes the dataset after pre-processing.

Table 2. Summary of the original, cropped and augmented dataset

Data label	Original image count	Cropped image count	After augmentation
Healthy	299	351	1000
Development Stage	160	174	1000
Advanced Infection	263	325	1000
Total	722	850	3000

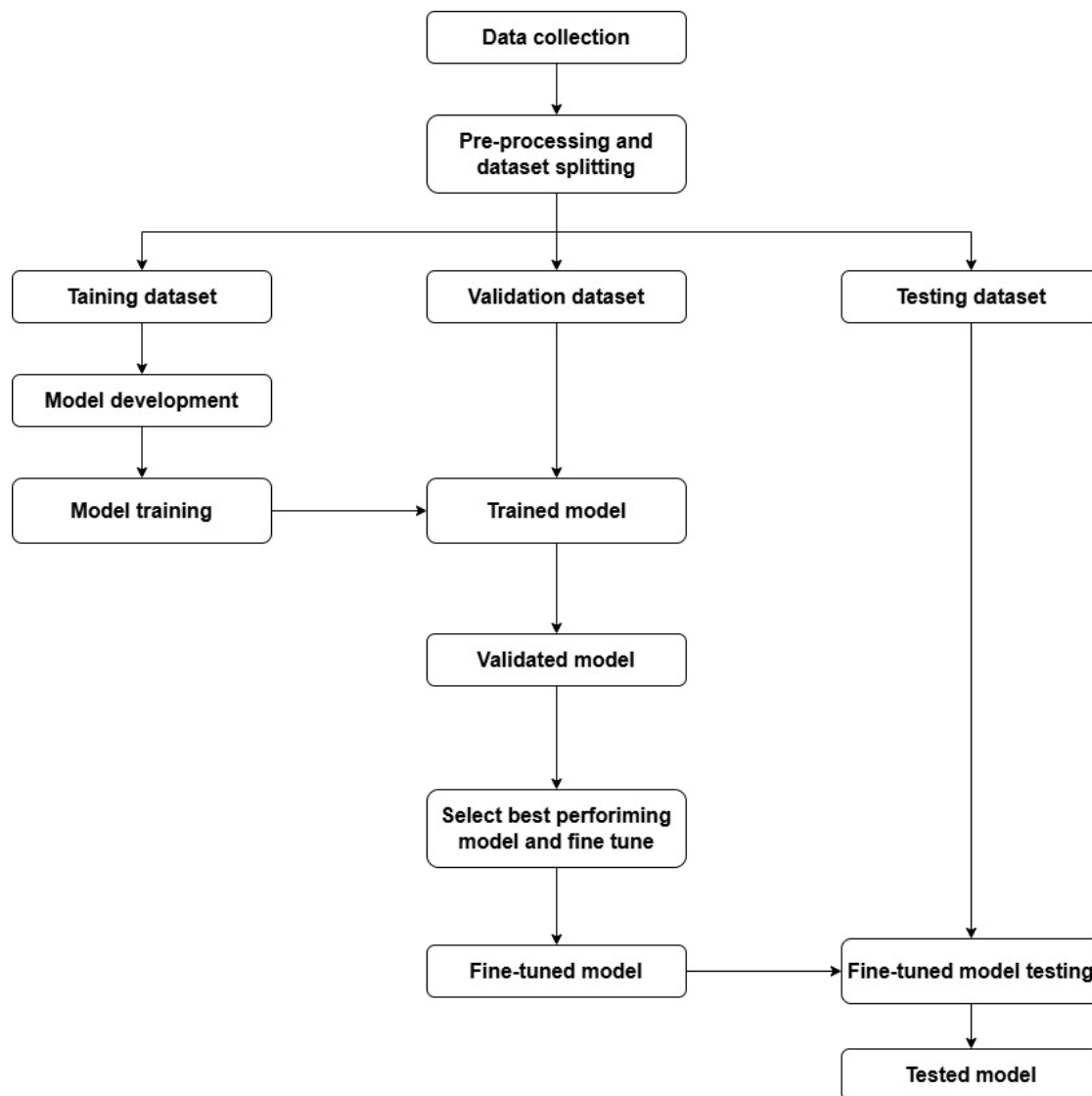


Figure 2. Overview of the methodology used for model development, training, validation and testing

Following pre-processing, the dataset was divided into three distinct subsets: 70% for training, 15% for validation, and 15% for testing. This split was employed to facilitate the development, validation, and performance assessment of the machine learning model.

The overall methodology followed in this study is summarized in the following diagram shown in Figure 2.

Experimental setup of Model development

The ML model was developed by using three experimental setups under two dataset configurations:

Mode 01- using the cropped image dataset, and Mode 02 - using the augmented image dataset.

Experiment 01 - Evaluation of pre-trained deep learning models using transfer learning: “Ex_01”

In this experimental setup, five pre-trained deep learning models MobileNetV2, EfficientNetB0, ResNet50, VGG16, and DenseNet121 used within a transfer learning framework. The main reasons for selecting these models were to achieve an optimal balance between accuracy and computational efficiency, supporting transfer learning and lightweight model. The original classification layers from each model were removed and retained only the

convolutional base to extract high-level spatial features from the input images. On top of these frozen base layers, then constructed a custom classification head comprising a GlobalAveragePooling2D layer, one or more Dropout layers to reduce overfitting, and a final Softmax layer to perform multi-class classification. This pipeline enables robust transfer learning for the task of stage-wise classification of DM disease in SC leaves. By leveraging features learned from the ImageNet dataset, integrating domain-specific dataset, and integrating a customized classification head, it was optimized the models for accurate and generalized performance in this research context.

Experiment 02 - Evaluation of fine tune models:
“Ex_02”: Based on the initial performance evaluations, it was selected two models, MobileNetV2 and VGG16 for a second experimental phase which implemented a two-stage fine-tuning process to optimize classification performance for the DM disease stages in SC. In the first stage (initial training), the original fully connected classification layers were removed from both models and replaced them with a custom classification head, consisting of GlobalAveragePooling2D, Dropout, and Softmax layers customized for multi-class disease stage prediction. The models were compiled using the Adam optimizer and categorical cross-entropy loss function, with accuracy as the performance metric, and trained for 10 epochs while keeping the convolutional base frozen so that only the new classifier layers were trainable. Following this, in the second stage (fine tuning), we unfroze the entire base model and then selectively re-froze the first 15 layers to retain low-level, generalizable feature representations learned during pre-training. The remaining deeper layers were fine-tuned over 30 epochs to adapt the models more effectively to the domain-specific features of the DM disease in SC dataset.

Experiment 03 - Evaluation of customized CNN:
“Ex_03”: In this experiment it was designed and developed a customized Sequential Convolutional Neural Network (CNN)-based model, named PnD_Seq, comprising 69,827 trainable parameters. This model was implemented using the Keras Sequential API and follows a structured architecture tailored for the DM disease stage classification task. The architecture begins with convolutional and pooling layers for hierarchical feature extraction. The initial convolutional block employs 16 filters with a 3×3 kernel to capture low-level visual patterns such as edges and textures, followed by a ReLU activation to introduce non-linearity and a MaxPooling2D layer to reduce spatial dimensions and computational

complexity. The second convolutional block increases the filter count to 32, enhancing the model's ability to learn more abstract and discriminative features. Subsequent blocks maintain the 32-filter configuration, enabling progressive refinement of spatial hierarchies essential for effective classification. Each convolutional layer is consistently followed by a MaxPooling operation to preserve semantic information while controlling overfitting and computational overhead. The classifier head includes a Flatten layer to convert the final 3D feature maps into a 1D vector, followed by a dense layer with 32 neurons to capture high-level representations. The final output layer comprises N_CLASSES neurons, each corresponding to a class label, with a Softmax activation function to generate a probability distribution across all disease stages. Table 3 presents the compiled model architecture, highlighting the number of trainable parameters and structural components of the PnD_Seq model.

Table 3. PnD_Seq model components and parameters

Layer	Output Shape	No. of Parameters
02 Sequential layers	256,256,3	0
Conv2D	254,254,16	448
Max pooling	127,127,16	0
Conv2D	125,125,32	4,640
Max pooling	62,62,32	0
Conv2D	60,60,32	9,248
Max pooling	30,30,32	0
Conv2D	28,28,32	9,248
Max pooling	14,14,32	0
Conv2D	12,12,32	9,248
Max pooling	6,6,32	0
Flatten	1152	0
Dense	32	36,896
Dense	3	99
Total parameters	69,827	
Trainable parameters	69,827	
Non-Trainable parameters	0	

Model training and validation

The model training process was conducted under two distinct dataset modes across above-said model development experiments, all utilizing the designated training dataset. These configurations were structured

to evaluate the models' ability to generalize under varying data preparation strategies. In Mode 01, models were trained exclusively on the cropped dataset without the application of any data augmentation techniques. This mode served as a baseline to assess model performance using the raw, unaltered visual features inherent in the dataset. It replicated practical scenarios where pre-processing capabilities are constrained due to limitations in time, computational resources, or data availability. In contrast, Mode 02 involved training exclusively on the augmented dataset. This mode aimed to enhance the models' generalization and robustness by mitigating over-fitting and better approximating real-world variability, particularly valuable when labelled data are scarce. All three model development experiments (Ex_01, Ex_02, and Ex_03) were evaluated under both modes, yielding a total of 18 trained models. This experimental design enables a systematic comparative analysis of model performance under distinct training strategies, providing insights into the impact of data augmentation on model effectiveness.

For model evaluation, the research employed several validation metrics, including accuracy, precision, recall, Area Under the ROC Curve (AUC), and Top-2 Categorical Accuracy, to assess the system's performance.

Results and Discussion

Experiment 01

The experiment 01 under mode 01, the following results were captured as illustrated in Table 4. Then in mode 2, above-said models were trained on the augmented dataset and evaluated using validation metrics across training and validation phases. Following Table 5 summarizes the results.

In Ex_01, five pre-trained CNN architectures MobileNetV2, EfficientNetB0, ResNet50, VGG16, and DenseNet121 were evaluated using both cropped and augmented datasets. DenseNet121 delivered the highest classification performance across metrics such as accuracy, AUC, and loss reduction, particularly when trained on augmented data. However, its computational complexity made it unsuitable for mobile deployment. MobileNetV2, by contrast, offered a favourable balance between generalization capability, competitive accuracy, and lightweight architecture, positioning it as the most practical model for real-time, resource-constrained applications. VGG16 demonstrated moderate but consistent performance and was retained for further fine-tuning due to its compatibility with mobile deployment pipelines. EfficientNetB0 and ResNet50 were excluded from subsequent phases owing to their consistently inferior performance across all evaluation metrics.

Table 4. Experiment 01 – Model 01 – Training, validation and testing results summary

Stage	Metric	MobileNetV2	EfficientNetB0	ResNet50	VGG16	Dense Net121
Training	Accuracy	0.7380	0.4215	0.4012	0.5818	0.6699
	AUC	0.8798	0.6214	Not gathered	0.7442	0.8574
	Loss	0.6659	1.0544	1.1175	0.9435	0.7212
	Precision	0.7555	0.4486	0.4359	0.6521	0.7181
	Recall	0.6236	0.0400	0.2205	0.4365	0.5901
	Top_2_accuracy	0.9275	0.7992	Not gathered	0.8177	0.8828
Validation	Accuracy	0.8047	0.4141	0.4297	0.7031	0.7891
	AUC	0.9225	0.6055	Not gathered	0.8219	0.9485
	Loss	0.5725	1.0565	1.0525	0.8385	0.4921
	Precision	0.8235	0.0000e+00	0.0000e+00	0.7952	0.9062
	Recall	0.6562	0.0000e+00	0.0000e+00	0.5156	0.6797
	Top_2_accuracy	0.9531	0.7969	Not gathered	0.8281	0.9531
Testing	Accuracy(%)	73.28	41.22	42.75	64.12	72.52
	Loss	0.6260	1.0586	1.0514	0.8808	0.5529

Table 5: Experiment 01 – Mode 02 - Training, validation and testing results summary

Stage	Metric	MobileNetV2	EfficientNetB0	ResNet50	VGG16	Dense Net121
Training	<i>Accuracy</i>	0.7576	0.3240	0.3425	0.5856	0.7155
	<i>AUC</i>	0.9120	0.4814	Not gathered	0.7766	0.8875
	<i>Loss</i>	0.5664	1.1130	1.1188	0.8813	0.6322
	<i>Precision</i>	0.7855	0.3284	0.4212	0.6695	0.7467
	<i>Recall</i>	0.7203	1.8516e-04	0.0357	0.4198	0.6571
	<i>Top_2_accuracy</i>	0.9530	0.6440	Not gathered	0.8746	0.9346
Validation	<i>Accuracy</i>	0.8244	0.3333	0.4289	0.6467	0.8200
	<i>AUC</i>	0.9401	0.4998	Not gathered	0.8261	0.9438
	<i>Loss</i>	0.4786	1.0988	1.0910	0.8166	0.4812
	<i>Precision</i>	0.8474	0.0000e+00	0.0000e+00	0.7308	0.8599
	<i>Recall</i>	0.8022	0.0000e+00	0.0000e+00	0.4222	0.7911
	<i>Top_2_accuracy</i>	0.9689	0.6667	Not gathered	0.9333	0.9756
Testing	<i>Accuracy (%)</i>	79.11	33.33	44.22	59.56	79.56
	<i>Loss</i>	0.5112	1.0987	1.0919	0.8770	0.5058

Experiment 02

For mode 01, the experiment 02 yielded following results as presented in the Table 6.

Table 6: Experiment 02 - Mode 01 - Training, validation and testing metrics results summary

Stage	Metric	Mobile NetV2	VGG16
Training	<i>Accuracy</i>	0.7887	0.8561
	<i>AUC</i>	0.9405	0.9651
	<i>Loss</i>	0.4674	0.3584
	<i>Precision</i>	0.8208	0.8758
	<i>Recall</i>	0.7692	0.8467
	<i>Top_2_accuracy</i>	0.9526	0.9852
Validation	<i>Accuracy</i>	0.8594	0.8203
	<i>AUC</i>	0.9641	0.9505
	<i>Loss</i>	0.3472	0.4385
	<i>Precision</i>	0.8560	0.8306
	<i>Recall</i>	0.8359	0.8047
	<i>Top_2_accuracy</i>	0.9922	0.9844
Testing	<i>Accuracy (%)</i>	82.44	80.92
	<i>Loss</i>	0.4735	0.4561

MobileNetV2 and VGG16 were assessed across training, validation, and testing stages using a range of performance metrics for augmented dataset as shown in Table 7. Building upon the initial benchmarking, Ex_02 focused on fine-tuning MobileNetV2 and VGG16 under two dataset conditions. In Mode 01 (cropped dataset), VGG16 exhibited superior training performance but displayed overfitting, whereas MobileNetV2 achieved better generalization during

Table 7: Experiment 02 - Mode 02 - Training, validation and testing metrics results summary

Stage	Metric	Mobile NetV2	VGG16
Training	<i>Accuracy</i>	0.7907	0.9180
	<i>AUC</i>	0.9311	0.9863
	<i>Loss</i>	0.4991	0.2201
	<i>Precision</i>	0.8082	0.9206
	<i>Recall</i>	0.7740	0.9143
	<i>Top_2_accuracy</i>	0.9710	0.9981
Validation	<i>Accuracy</i>	0.8311	0.9111
	<i>AUC</i>	0.9604	0.9819
	<i>Loss</i>	0.3968	0.2365
	<i>Precision</i>	0.8341	0.9172
	<i>Recall</i>	0.8267	0.9111
	<i>Top_2_accuracy</i>	0.9756	0.9911
Testing	<i>Accuracy (%)</i>	82.44	91.33
	<i>Loss</i>	0.3977	0.2574

validation and testing, reaffirming its suitability for mobile inference scenarios. In Mode 02 (augmented dataset), VGG16 significantly outperformed MobileNetV2 across all evaluation metrics, demonstrating robust generalization and achieving the highest overall accuracy. These findings indicate that VGG16, when coupled with comprehensive data augmentation, is better suited for applications emphasizing classification accuracy. In contrast, MobileNetV2 remains the optimal choice for real-time deployment in resource-constrained environments due to its efficiency and consistent generalization.

Experiment 03

In mode 01, the model trained on the cropped dataset demonstrated strong performance across all phases. During training, it achieved a high accuracy of 91.99% with a low loss of 0.1872, indicating effective learning and convergence. In the validation phase, the model maintained solid generalization with an accuracy of 87.50% and a loss of 0.3026, suggesting minimal overfitting and stable performance on unseen data. During testing, the accuracy declined slightly to 79.39% with a corresponding loss of 0.4890, yet remained within an acceptable range for practical deployment. Overall, the results confirm that the model, despite its simplicity, is capable of capturing complex features and generalizing effectively in real-world scenarios.

On the mode 02, the customized sequential CNN model (PnD_Seq), trained on an augmented dataset, demonstrated strong performance across all phases. During training, it achieved a high accuracy of 94.80% with a low loss of 0.1582, indicating effective learning and robust feature extraction. In the validation phase, the model sustained solid generalization with an accuracy of 90.44% and a loss of 0.2455, reflecting stability and minimal overfitting despite increased input variability. Testing results confirmed excellent generalization, with a high accuracy of 92.89% and a low loss of 0.2201. These improvements over the prior cropped dataset mode highlight the efficacy of data augmentation in enhancing both robustness and predictive performance, establishing PnD_Seq as a reliable and efficient model for real-world pest and disease detection.

These findings underscore the critical role of dataset diversity and augmentation in improving model robustness and classification effectiveness in domain-specific agricultural applications.

The Table 8 which contains results of fine-tuned MobileNetV2, fine-tuned VGG16 and custom made PnD_Seq model under augmented dataset mode further supports the said argument.

Figure 3 illustrates the training and validation accuracy and loss of VGG16, MobileNetV2, and the proposed PnD_seq customized CNN model.

VGG16 shows steady convergence with minimal overfitting, while MobileNetV2 displays fluctuating performance, indicating limited stability. The PnD_seq customized CNN achieves the most consistent and higher accuracy with stable loss reduction, demonstrating superior generalization and learning efficiency.

The comparative analysis across Ex_02 and Ex_03 highlights the superior performance of the custom-designed PnD_Seq model trained on the augmented dataset. While VGG16, fine-tuned under Mode 02, demonstrated excellent classification accuracy and generalization across standard evaluation metrics outperforming MobileNetV2 in Ex_02 the task-specific architecture of PnD_Seq achieved even greater performance consistency custom-made to the domain. Under Mode 02, PnD_Seq attained approximately 93% classification accuracy. Unlike generic pre-trained models, PnD_Seq was optimized for the specific morphological characteristics of disease symptoms in cucumber leaves. These results highlight that while transfer learning models like VGG16 are effective with augmented data, domain-specific lightweight CNN architectures can surpass them in both accuracy and computational efficiency when carefully designed and trained on diverse datasets. Consequently, PnD_Seq emerges as the most suitable and scalable model for real-world agricultural deployment, particularly in precision disease stage classification tasks where targeted diagnosis and decision support are critical.

Table 8. Fine-tuned MobileNetV2, fine-tuned VGG16 and custom made PnD_Seq model results under mode 02

Stage	Metric	MobileNetV2	VGG16	PnD_seq
Training	Accuracy	0.7907	0.9180	0.9480
	Loss	0.4991	0.2201	0.1582
Validation	Accuracy	0.8311	0.9111	0.9044
	Loss	0.3968	0.2365	0.2455
Testing	Accuracy (%)	82.44	91.33	92.89
	Loss	0.3977	0.2574	0.2201

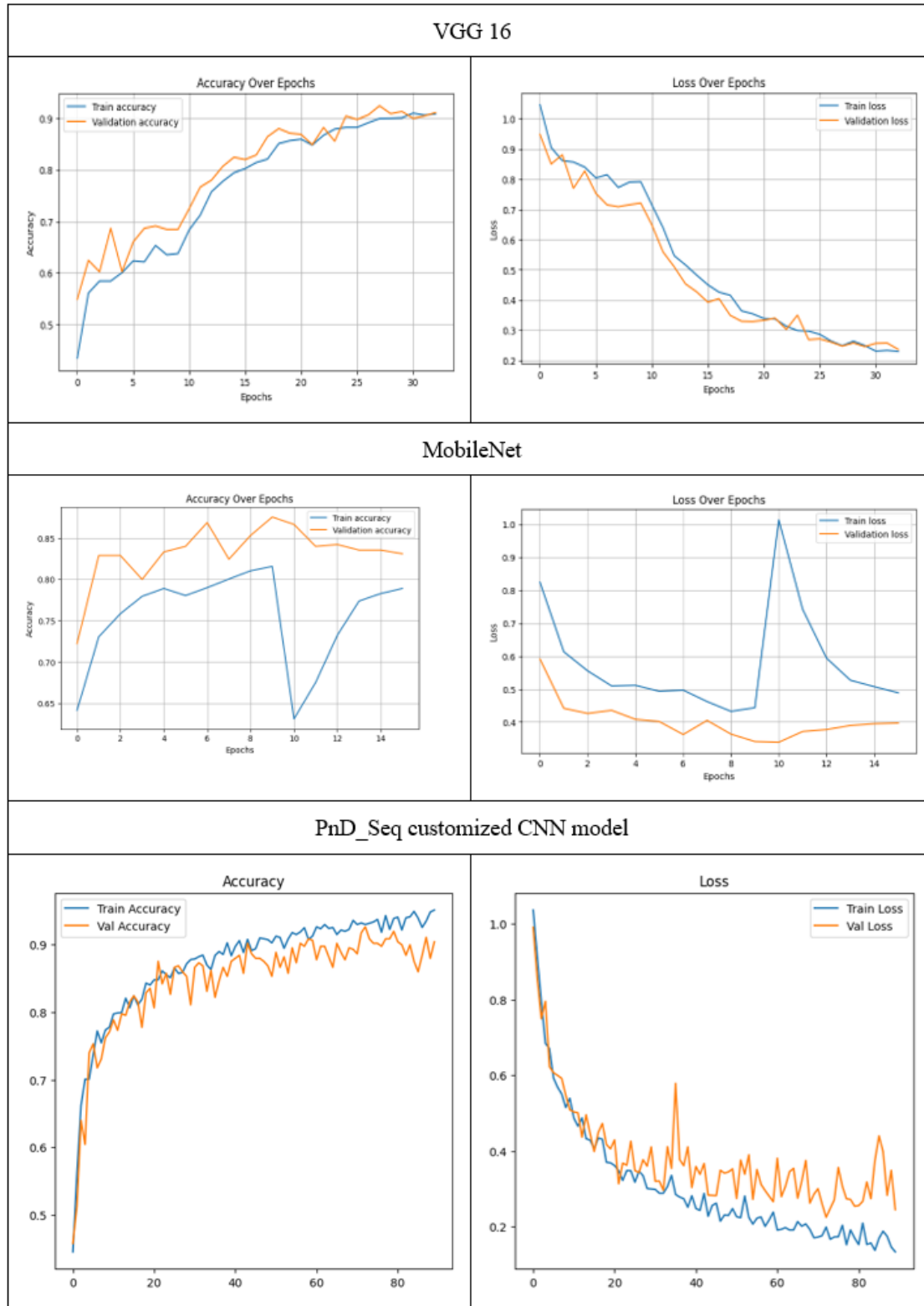


Figure 3: Comparative training and validation accuracy and loss curves for VGG16, MobileNetV2, and the proposed PnD_seq customized CNN model

Selected ML model PnD_Seq tested with unseen data. Figure 4 shows the confusion matrix for the model's performance on the test set for the selected PnD_Seq model. The matrix presents the number of true positives, false positives, true negatives, and false negatives for each class: DM_Development, DM_Advanced_Infection, and Healthy. The selected PnD_Seq model demonstrated a strong ability to classify the development stages of DM disease in SC leaves, achieving a class-wise accuracy of 92% for general stage classification, 91% for advanced infection detection, and 96% for healthy leaf identification.

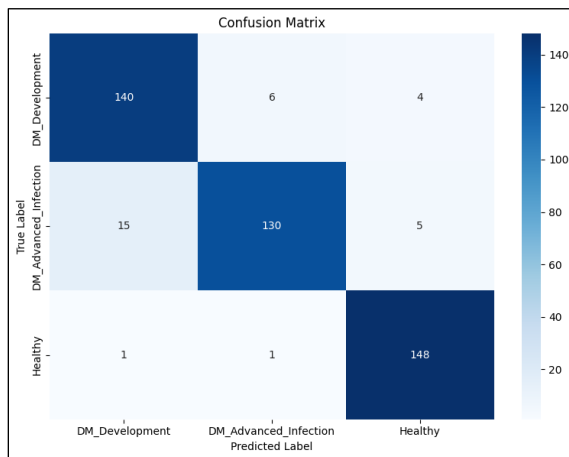


Figure 4: PnD_Seq confusion matrix

The overall classification accuracy of the model was 93% as shown in Table 9, indicating robust generalization across the selected disease stages.

Table 9: PnD_Seq confusion report

	Precision	Recall	F1-score	Support
DM_Development	0.90	0.93	0.92	150
DM_Advanced_Infection	0.95	0.87	0.91	150
Healthy	0.94	0.99	0.96	150
Accuracy			0.93	450
Macro average	0.93	0.93	0.93	450
Weighted average	0.93	0.93	0.93	450

Recent studies on DM disease detection in SC reveal the growing effectiveness of deep learning over traditional machine learning approaches. Mia *et al.*, (2021) demonstrated that MobileNetV2 outperformed conventional methods with 93.23% accuracy, while

Zhang *et al.*, (2019) achieved 94.65% using GPDCNN, which enhanced feature extraction through dilated convolution. Nancy and Kiran, (2025) obtained 90.62% mean average precision with a multi-SVM approach, though their method was less capable of capturing complex visual patterns compared to CNNs. Shivaraj and Haladappa, (2025) reported that 99.37% accuracy using ResNet50V2, highlighting the strength of residual learning, albeit at higher computational costs. Abdelhak *et al.*, (2022) explored DM severity in watermelon using hyperspectral imaging, achieving 62.3% accuracy. Despite modest results, their study underscored the challenge of quantifying disease severity. In comparison, the present research focuses on stage-wise classification of DM in SC, achieving 93% accuracy through a customized CNN and transfer learning approach. Unlike prior binary classification studies, this work introduces fine-grained stage discrimination, offering greater insight into disease progression.

Conclusion

This research study presents a novel and custom machine learning model, PnD_Seq, for the stage-wise identification of DM disease in SC. With contrast to existing works, the proposed model effectively classifies the DM disease progression stages by analysing visual symptoms in SC leaves, so automating the traditionally manual and expert-dependent process of binary disease diagnosis. The high classification accuracy and strong generalization observed particularly when trained with augmented data demonstrate the model's robustness and applicability in real-world agricultural settings.

However, several limitations and deployment challenges must be considered to enhance the practical relevance of this work. Firstly, stage-wise data collection for diseases like DM remains limited and scarce, posing challenges for training robust models across all disease progression stages. Expanding the dataset with more diverse and representative samples is essential to improve model generalization. Furthermore, while this study focuses on DM in SC, the framework could potentially be adapted for stage-wise classification of other diseases, provided sufficient annotated data is available. From a deployment perspective, delivering the model effectively to end-users, particularly farmers, presents challenges such as developing lightweight models that can operate efficiently on mobile devices with limited computational resources. Additionally, creating intuitive mobile applications that facilitate easy use and integration into daily farming practices is critical for adoption. Addressing these issues will be critical to

translate AI-driven disease detection from research into scalable, farmer-friendly tools in precision agriculture.

In conclusion, the work highlights the potential of AI-driven solutions to enhance disease detection towards the stage-wise disease classification which can shape the precision agriculture.

Acknowledgement

This research was supported by the Accelerating Higher Education Expansion and Development (AHEAD) Operation of the Ministry of Higher Education funded by the World Bank. The authors also acknowledge the support of the agriculture instructors and officials of Department of Agriculture (DoA), the Department of Crop Science at the University of Ruhuna, and the farmers for their valuable assistance and cooperation throughout this study.

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