Evaluating Custom and Pre-trained CNN Architectures for Scalable Tomato Leaf Disease Classification

Aradhy Tiwari
Research Scholar
Department of CSIT
Guru Ghasidas Vishwavidyalaya
Bilaspur, India

Amit Kumar Saxena
Professor
Department of CSIT
Guru Ghasidas Vishwavidyalaya
Bilaspur, India

Damodar Patel
Research Scholar
Department of CSIT
Guru Ghasidas Vishwavidyalaya
Bilaspur, India

Chandrashekhar
Research Scholar
Department of CSIT
Guru Ghasidas Vishwavidyalaya Bilaspur, India

ABSTRACT

This research proposes a robust deep learning framework for the accurate classification of tomato leaf diseases by leveraging both original and augmented image datasets. The study utilizes a curated set of 1,200 original images spanning six distinct classes, five representing common tomato diseases (Early Blight, Bacterial Spot, Leaf Mold, Yellow Leaf Curl Virus, and Spider Mites) and one healthy class. Through systematic data augmentation, the dataset was expanded to 5,980 samples, enhancing model generalization. A comparative analysis of several convolutional neural network architectures was conducted, including a baseline CNN, a lightweight custom CNN, MobileNetV2, DenseNet121, InceptionV3, and the proposed VGG16-based transfer learning model. The VGG16 model, optimized via fine-tuning, label smoothing, and regularization, achieved the highest accuracy of 99.83%. It demonstrated superior robustness in distinguishing between visually similar disease symptoms. This work reinforces the importance of tailored model architecture and data strategy in agricultural image analysis and contributes to the advancement of intelligent, field-deployable crop health monitoring systems.

Keywords

Tomato Leaf Disease Classification, Deep Learning in Agriculture, Image-Based Classification, Transfer Learning (VGG16), Custom CNN Architecture, Agricultural Image Analysis.

1. INTRODUCTION

Tomato (Solanum lycopersicum) is a globally important horticultural crop cultivated across diverse agroclimatic zones. It is not only a rich source of essential vitamins, minerals, and dietary antioxidants but also holds high economic value for both small-scale farmers and large-scale agricultural enterprises. Despite its significance, tomato production is highly vulnerable to a range of biotic stresses, particularly foliar diseases caused by fungi, bacteria, viruses, and mites [1-3].

These diseases, if not detected and managed in time, can lead to severe yield losses and adversely affect the quality of the produce [4-8]. In this study's, focus on the classification of five major tomato leaf diseases, along with healthy leaves, using deep learning-based image analysis. The selected diseases include Early blight, Bacterial spot, Yellow Leaf Curl Virus (TYLCV), Two-Spotted Spider Mite infestation, and Leaf mold.

Early blight, caused by Alternaria solani, appears as concentric brown to black lesions on older leaves, resulting in tissue necrosis and early leaf drop. Bacterial spot manifests as small, water-soaked dark spots with yellow halos that can merge and form large necrotic areas. TYLCV, a viral disease transmitted by whiteflies, causes upward curling and yellowing of leaves, stunted plant growth, and reduced fruit setting. Spider mite infestation, particularly from Tetranychus urticae, leads to stippling, bronzing, and webbing on the leaf surface due to chlorophyll extraction. Leaf mold, caused by Fulvia fulva, presents as pale yellow patches on the upper surface and a velvety olive mold on the underside of leaves, commonly under humid conditions [8-12].

In contrast, a healthy tomato leaf is uniformly green, free from curling, discoloration, lesions, or pest activity making it a reliable visual reference for automated detection systems. Traditionally, tomato leaf diseases have been identified through manual inspection by trained experts. While this method may be effective in small-scale settings, it is time-consuming, subjective, and unsuitable for large-scale monitoring [13-14].

Furthermore, visual similarities between disease symptoms often lead to misdiagnosis. In response to these limitations, researchers have explored automated disease recognition using computer vision and machine learning techniques. Earlier approaches relied on handcrafted features like color, texture, and shape, combined with classifiers such as Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Random Forest [1-2,15].

However, their performance was constrained by manual feature extraction, sensitivity to background noise, and limited adaptability to real-world conditions [16]. The emergence of deep learning, particularly Convolutional Neural Networks (CNNs), has brought a transformative shift in image-based classification tasks. CNNs are capable of learning complex spatial patterns directly from raw image data without requiring manual intervention [8, 14, 17-18].

In the field of plant disease recognition, deep CNN models such as MobileNetV2, DenseNet121, VGG16, ResNet50, and InceptionV3 have shown promising results, outperforming classical models in terms of accuracy and robustness [19-23] These architectures allow deeper feature extraction and better generalization, especially when combined with techniques like transfer learning and data augmentation [12, 24-25].

To address the ongoing challenge of timely and accurate classification of tomato leaf diseases, this research explores and compares the performance of several deep learning models, including MobileNetV2, Lightweight CNN, VGG16, DenseNet121, and InceptionV3. The study utilizes a curated image dataset comprising five disease categories and one healthy leaf category, creating a six-class classification problem [21, 26].

Data augmentation strategies are employed to introduce variation and reduce the risk of overfitting, while transfer learning is used to leverage pretrained weights for better model convergence and performance [26-27]. The primary goal of this research is to identify the most accurate and computationally efficient model for tomato leaf disease classification, with the potential for deployment in real-time agricultural systems.

Each model is evaluated based on classification accuracy, confusion matrix, and class-wise performance metrics. The findings of this work aim to assist farmers, agricultural technicians, and policymakers by providing intelligent, AI-powered diagnostic tools for early disease detection, thus reducing crop losses and improving agricultural productivity [12,28].

This study presents a deep learning-based approach for classifying tomato leaf diseases using both custom and pre-trained CNN architectures. A curated dataset with six classes was augmented to improve generalization. Models such as VGG16, MobileNetV2, and InceptionV3 were evaluated, with VGG16 achieving the highest accuracy. The research aims to enable scalable, efficient, and real-time disease detection to support intelligent decision-making in modern agriculture.

The following is the structure of the paper. A brief summary of the several studies is given in Section 2. The 3. The Proposed Method is presented in Section 3, while Section 4 presents the Results and discussion. The Conclusion and Future Work are included in the last section.

2. LITERATURE REVIEW

The detection and classification of tomato leaf diseases have seen significant advancements over the past decade, evolving from traditional machine learning techniques to deep learning and transformer-based models optimized for real-world applications.

Early Research and Traditional Machine Learning Approaches (2011–2015): Initial studies in tomato leaf disease detection relied on conventional machine learning algorithms such as K-means clustering, Support Vector Machines (SVM), and Artificial Neural Networks (ANN). [1-2, 29-31] reported classification accuracies ranging between 83% and 95%, but these models depended on manual feature extraction based on color, texture, or shape. [16, 32-35] also explored ANN-based classifiers, highlighting their classification potential, although these models lacked scalability and failed to generalize well under varying environmental conditions due to their reliance on preprocessed or filtered datasets.

Rise of CNN-Based Deep Learning Models (2016–2019): The introduction of Convolutional Neural Networks (CNNs) transformed plant disease detection by enabling automatic feature extraction and improving performance significantly. [36] and [8] leveraged pre-trained models such as AlexNet, VGG16, and GoogleNet, achieving over 99% accuracy on the PlantVillage dataset. [14] also demonstrated that deep CNNs reduced the complexity of preprocessing. [37-39] reinforced the generalization capability of CNNs across various plant disease datasets. However, these studies predominantly relied on the PlantVillage dataset composed of high-quality, lab-captured images which limited real-world applicability.

Emergence of Lightweight, Hybrid, and Real-Field CNN Models (2020–2023): To address the computational burden posed by large pre-trained networks, researchers began exploring lightweight and custom CNN architectures. [40-41] proposed a compact CNN comprising only three convolutional and pooling layers, achieving 91.2% accuracy, surpassing traditional architectures like VGG16 and MobileNet in efficiency and making it suitable for mobile deployment. However, these lightweight models struggled with robustness when tested on noisy or real-field datasets due to their dependence on curated inputs. In parallel, efforts were made to capture more complex spatial-temporal features through hybrid architectures. [23, 42-43] implemented object detection frameworks such as Faster R-CNN and Mask R-CNN, enabling both classification and precise localization of diseased regions. [19] utilized InceptionV3 with transfer learning to achieve a validation accuracy of 88.32%, while) [44] and [14] compared CNN, R-CNN, and Fuzzy-SVM models, identifying ResNet50-based R-CNN as the most effective with a 96.73% accuracy. Recognizing the limitations of laboratory-controlled datasets, subsequent studies emphasized real-field data integration and ensemble learning strategies. [26] trained YOLOv5 on a combination of public and real-field images, achieving 93% accuracy and 95% mean Average Precision (mAP), outperforming Faster R-CNN and EfficientDet. Similarly, [21,34] developed a custom CNN that delivered 95.53% accuracy on a large dataset of over 14,000 tomato leaf images. [22] introduced an ensemble model combining MobileNet and DenseNet, which significantly enhanced performance, achieving 98.12% accuracy and outperforming standalone deep learning models in terms of precision, recall, and F1-score.

State-of-the-Art Deep Learning and Transformer Models (2024): The latest phase in tomato disease detection has seen the integration of deep learning with transformer architectures and IoT-based systems. [12] achieved 99% accuracy using VGG16, while [24] enhanced model adaptability using data augmentation and deep feature fusion. [27] merged cloud-based data acquisition with transfer learning using AlexNet, ResNet, and VGG16, achieving up to 93.7% accuracy. [28] improved YOLOv6 by adding CBAM and BiRepGFPN modules, enhancing the model's performance on small lesion detection.

Research Gap and Future Scope

Existing models focus on general plant disease classification and lack specialization for tomato leaf diseases. This work narrows this gap by targeting tomato-specific diseases with higher precision and relevance.
Most reviewed models are trained on curated datasets and lack real-world validation. This work aims to integrate diverse, field-like tomato leaf images for better practical applicability and robustness.

Prior studies show high accuracy but fail in real-time deployment due to heavy architectures. This work focus is on lightweight models suitable for mobile and edge devices for instant disease detection.

3. PROPOSED METHOD (VGG16-BASED LEAF DISEASE CLASSIFICATION)

In this research, the VGG16 model was selected as the primary architecture for tomato leaf disease classification due to its proven effectiveness in recent image classification studies. Compared to earlier research methods and classical machine learning approaches, VGG16 demonstrated superior accuracy and robustness on custom dataset. It is particularly well-suited for visual tasks involving fine-grained image differences, such as disease spot patterns on leaves.

3.1 Dataset Description

For this study, a custom image dataset was developed to classify six categories of tomato leaf conditions, including five disease-infected classes—Early Blight, Bacterial Spot, Yellow Leaf Curl Virus, Two-Spotted Spider Mite, and Leaf Mold—alongside one Healthy Leaf class.

Fig 1: Class wise sample image of the dataset.

A total of 1,200 original images were collected, ensuring class-wise representation of diverse visual symptoms. These images were further augmented using various techniques such as rotation, zoom, flipping, and brightness adjustments, resulting in an expanded dataset of 5,985 images. All images were resized to 128 × 128 pixels for model compatibility and computational efficiency. The final dataset was split into 80% for training, 10% for validation, and 10% for testing, ensuring balanced distribution across all six classes. Sample images from each category have been included to visually demonstrate the range of disease symptoms and healthy leaf characteristics, providing valuable context for the classification task.

3.2 Model Architecture

The Visual Geometry Group at Oxford developed the deep convolutional neural network VGG16. It consists of 13 convolutional layers and 3 fully connected layers, organized into five convolutional blocks. Each block includes two or three convolutional layers with 3x3 filters followed by a max pooling layer to reduce spatial dimensions. The ReLU activation function is applied after every convolution to introduce non-linearity. After the convolutional blocks, the feature maps are flattened and passed through three dense (fully connected) layers. Dropout and regularization techniques are used to prevent overfitting. Finally, a softmax activation function is used at the output layer to classify images into one of the six target classes.

The architecture of the proposed VGG16-based transfer learning model Table 1 is summarized below,

Table 1: Custom VGG16 Model.

Layer (Type)	Output Shape	Parameters
InputLayer	(None, 150, 150, 3)	0
block1_conv1 (Conv2D)	(None, 150, 150, 64)	1,792
block1_conv2 (Conv2D)	(None, 150, 150, 64)	36,928
block1_pool (MaxPooling2D)	(None, 75, 75, 64)	0
block2_conv1 (Conv2D)	(None, 75, 75, 128)	73,856
block2_conv2 (Conv2D)	(None, 75, 75, 128)	1,47,584
block2_pool (MaxPooling2D)	(None, 37, 37, 128)	0
block3_conv1 (Conv2D)	(None, 37, 37, 256)	2,95,168
block3_conv2 (Conv2D)	(None, 37, 37, 256)	5,90,080
block3_conv3 (Conv2D)	(None, 37, 37, 256)	5,90,080
block3_pool (MaxPooling2D)	(None, 18, 18, 256)	0
block4_conv1 (Conv2D)	(None, 18, 18, 512)	11,80,160
block4_conv2 (Conv2D)	(None, 18, 18, 512)	23,59,808
block4_conv3 (Conv2D)	(None, 18, 18, 512)	23,59,808
block4_pool (MaxPooling2D)	(None, 9, 9, 512)	0
block5_conv1 (Conv2D)	(None, 9, 9, 512)	23,59,808
block5_conv2 (Conv2D)	(None, 9, 9, 512)	23,59,808
block5_conv3 (Conv2D)	(None, 9, 9, 512)	23,59,808
block5_pool (MaxPooling2D)	(None, 4, 4, 512)	0
GlobalAveragePooling2D	(None, 512)	0
Dropout_1	(None, 512)	0
Dense_512	(None, 512)	2,62,656
Dropout_2	(None, 512)	0
Dense_256	(None, 256)	1,31,328
Dropout_3	(None, 256)	0
Output_Softmax (Dense)	(None, 5)	1,285

Total Parameters:

Total params: 15,109,957 (~57.64 MB)

Trainable params: 395,269 (~1.51 MB)

Non-trainable params: 14,714,688 (~56.13 MB)

3.3 Visual Overview of the Proposed Approach

The following flowchart illustrates the complete research methodology adopted in this study. It outlines each key stage involved in the tomato leaf disease classification process, including data preparation, preprocessing, model design, training, evaluation, and comparison. This structured visual representation provides a clear understanding of the proposed approach. The detailed workflow is depicted below in Figure 2.

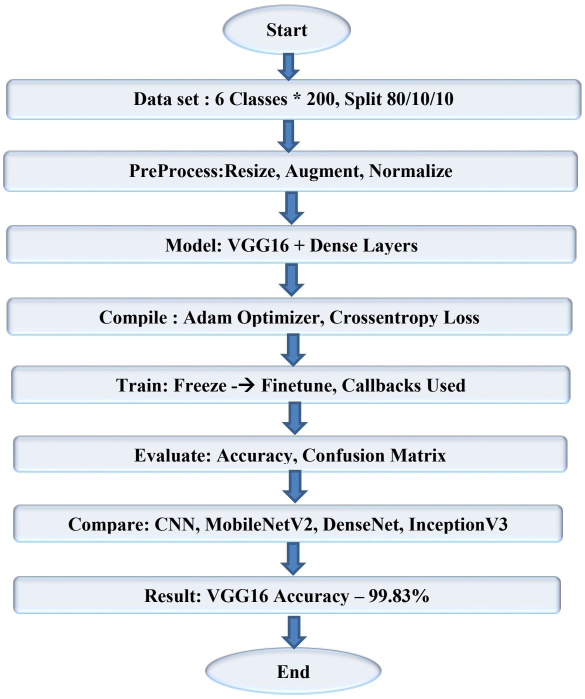

Fig 2: Research flowchart illustrating the stepwise methodology.

3.4 Training Strategy

The model was trained using transfer learning by freezing the initial VGG16 layers. The Adam optimizer and categorical cross-entropy loss were used, with early stopping and dropout techniques applied to prevent overfitting and improve generalization.

3.5 Evaluation Metrics

Model performance was evaluated using accuracy, precision, recall, F1-score, and confusion matrix to analyze class-wise predictions. Additionally, performance was monitored using validation loss trends, training accuracy curves, and classification reports to assess robustness, misclassification patterns, and overall generalization across all six tomato leaf disease categories.

4. RESULT AND DISCUSSIONS

In this research, a transfer learning-based VGG16 model was employed to classify tomato leaf diseases across six categories, including five major infections—Early Blight, Bacterial Spot, Leaf Mold, Spider Mites, and Tomato Yellow Leaf Curl Virus—along with a Healthy class. The model was customized by freezing the convolutional base and adding a Global Average Pooling layer(512 and 256 units respectively), followed by two fully connected dense layers with with ReLU activation and dropout rates of 0.5 and 0.3, respectively, to mitigate overfitting. The final softmax layer outputs class probabilities for multiclass classification. The model was compiled using the Adam optimizer with an initial learning rate of 0.0001 and a categorical cross-entropy loss function with label smoothing. A total of 15,110,214 parameters were used during training, all of which were trainable. The final model size was 57.64 MB, making it lightweight enough for scalable applications. The model was trained for 50 epochs with a batch size of 16 and took approximately 3377 seconds to complete training.

Performance evaluation revealed outstanding results, with an overall classification accuracy of 99.83% on the test dataset. Precision, recall, and F1-score for each class exceeded 99%, demonstrating the model's robustness in identifying even visually similar diseases. For instance, the F1-score for the Spider Mites and Tomato Yellow Leaf Curl Virus classes were 99.50% and 99.49%, respectively. Such high performance confirms the model's reliability and suitability for practical deployment. This model was selected after a thorough literature survey and demonstrates superior accuracy compared to previously reported architectures.

Table 2 presents the classification report of the VGG16-based model, summarizing precision, recall, and F1-score for each tomato leaf disease class.

Table 2: Classification Report of VGG16-Based Model.

Class	Precision	Recall	F1-Score	Support
Early Blight	1	1	1	100
Healthy Leaf	1	1	1	100
Leaf Mold	1	1	1	99
Two-Spotted Spider Mite	0.99	1	0.995	100
Yellow Leaf Curl Virus	1	0.99	0.995	100
Bacterial Spot	1	1	1	100
Accuracy	0.998			
Macro Avg	0.998	0.998	0.998	599
Weighted Avg	0.998	0.998	0.998	599

The training and validation performance of the proposed model is depicted in Figure 3, where it achieved 100% training accuracy and 99.83% validation accuracy with minimal loss.

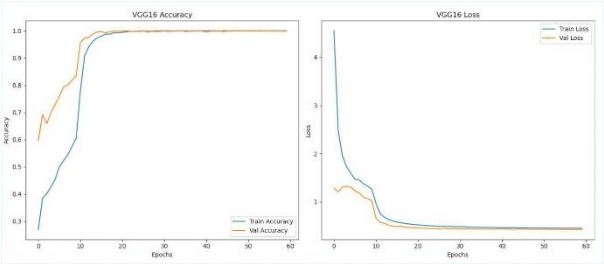

Fig 3: Training and validation accuracy and loss graph of the proposed model.

The confusion matrix was produced, as seen in Figure 4, to assess the proposed model's classification performance across all tomato leaf disease categories. It makes it abundantly evident that the model produced few incorrect classifications and had a high forecast accuracy. The majority of these misclassifications were between visually comparable illness classes, where feature extraction was complicated by overlapping color patterns, texture similarities, and illumination differences in the input photos. The model successfully learnt the distinctive characteristics of each disease type, demonstrating its robustness and dependability for tomato leaf disease diagnosis in spite of these small errors, as evidenced by the overall distribution of properly identified occurrences.

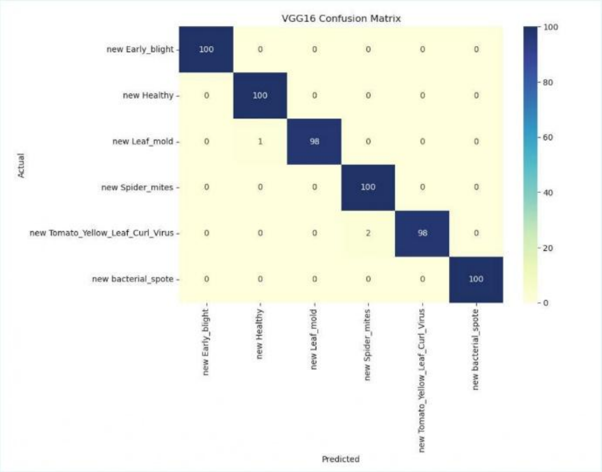

Fig 4: Confusion matrix of the proposed model.

The AUC-ROC (Area Under the Receiver Operating Characteristic Curve) for the proposed model's evaluation is shown in Figure 5. At different threshold levels, the True Positive Rate (sensitivity) is shown compared to the False Positive Rate (1-specificity) using the ROC curve. An AUC-ROC value of 100 (or 1.0) indicates that the proposed model achieved perfect classification performance, meaning it can completely distinguish between the positive and negative classes without any errors. In practical terms

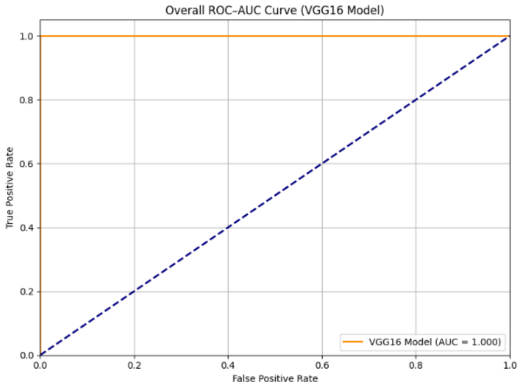

Fig 5: AUC-ROC curve of the proposed model.

To contextualize the performance of proposed VGG16-based model, conducted a comparative evaluation of five alternative deep learning architectures. The Basic CNN achieved a commendable accuracy of 97.16%, demonstrating the potential of traditional convolutional layers when paired with sufficient preprocessing. The Lightweight CNN, optimized for efficiency, delivered a slightly lower accuracy of 94.82%, making it suitable for scenarios with limited computational resources. Among pre-trained transfer learning models, MobileNetV2 balanced speed and performance effectively with 97.16% accuracy, while DenseNet121 outperformed MobileNetV2, achieving 97.83% accuracy and a 97.84% F1-score, indicating strong class-wise consistency. Notably, InceptionV3 yielded superior results among the comparison models, with an accuracy of 98.83% and an F1-score of 98.84%, reaffirming its strength in complex feature extraction.

To contextualize the performance of proposed VGG16-based model, conducted an extensive experimental evaluation comparing it with five other deep learning architectures. The Basic CNN achieved a commendable accuracy of 97.16%, showcasing the effectiveness of traditional convolutional layers when combined with appropriate preprocessing techniques. The Lightweight CNN, designed for resource-constrained environments, delivered a slightly lower accuracy of 94.82%, indicating its suitability for real-time applications with limited computational capacity. Among the transfer learning models, MobileNetV2 offered a balanced trade-off between computational efficiency and performance, also achieving an accuracy of 97.16%. DenseNet121 surpassed MobileNetV2 with a higher accuracy of 97.83% and an impressive F1-score of 97.84%, reflecting strong consistency across all disease classes. The most notable performance came from InceptionV3, which recorded the highest accuracy among the comparison models at 98.83%, along with an F1-score of 98.84%, highlighting its strength in extracting complex features.

The performance metrics derived from these experimental results are summarized in below Table 2, offering a clear comparison with proposed VGG16 model.

Table 3: Comparative Table of Model Performance on Tomato Leaf Disease Classification.

Models	Accuracy	Precision	Recall	F1-Score
Basic CNN	0.9716	0.9735	0.9733	0.9715
Lightweight CNN	0.9482	0.9489	0.9483	0.9482
MobileNetV2	0.9716	0.9725	0.9716	0.9717
DenseNet	0.9783	0.9791	0.9783	0.9783
InceptionV3	0.9883	0.9887	0.9866	0.9867
Proposed VGG16	0.9983	0.9983	0.9983	0.9983

Above table 3 presents a comparative analysis based on experimental study, showcasing the performance of various deep learning models for tomato leaf disease classification. The results are derived from practical implementation, where each model was trained and evaluated on the same dataset. The proposed VGG16 model demonstrated superior accuracy, precision, recall, and F1-score, outperforming all other models considered in the study.

To visualize the comparative performance of all models, an accuracy-based bar graph is presented in Figure 6, highlighting the superior results of VGG16.

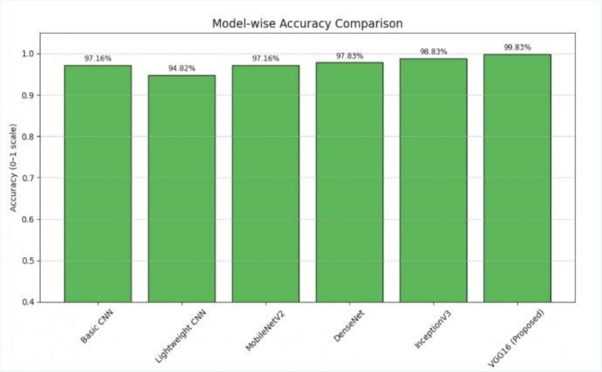

Fig 6: Accuracy comparison of various deep learning models

Figure 7 presents a comparative analysis of all models using precision, recall, and F1-score metrics, offering deeper insights into the classification consistency and reliability across tomato leaf disease classes

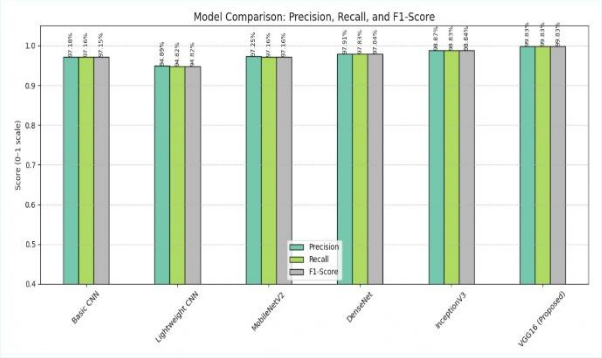

Fig 7: Comparison of precision, recall, and F1-score across all models for tomato leaf disease classification.

Table 4: Comparative Table of Tomato Leaf Disease Detection Approaches.

Author	Year	Models Used	Reported Accuracy	Best Performing Model
Agarwal et al. [40]	2020	Lightweight CNN (3 Conv + Pool layers)	91.20%	Lightweight CNN
Uzma Farheen et al. [19]	2022	InceptionV3 (Transfer Learning)	88.32%	Inception V3
Kokate et al. [21]	2023	Basic CNN (Custom, 14,000 images)	95.53%	Basic CNN
Nazmun Nahar et al. [22]	2023	Ensemble (MobileNet V2 + DenseNet)	98.12%	MobileNetV2 + DenseNet (Ensemble)
Chakraborty et al. [12]	2024	VGG16	99%	VGG16
Tiwari et al.	2025	Proposed VGG16	99.83%	Proposed VGG16

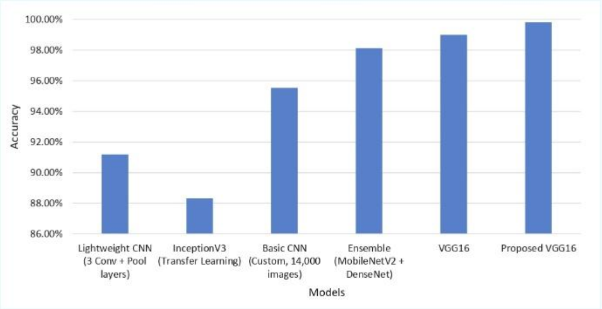

Fig 8: Comparative Table of Tomato Leaf Disease Detection Approaches.

In Table 4, and Figure 8 present a comparison of the proposed method and recent approaches for tomato leaf disease detection, highlighting the models and their accuracy performance metrics across different studies. This table offers a consolidated view to better understand the strengths and limitations of each method.

These results align with findings from previous literature where transfer learning significantly enhanced plant disease classification accuracy. However, most of those studies relied on curated datasets and lacked real-field validation. In contrast, comparative analysis was performed on an augmented, field-like tomato dataset with six classes, making the evaluation more robust. Figure 7 represents the comparative study of tomato leaf disease classification models. The proposed VGG16 model outperforms all other models, demonstrating that the improved architecture achieves the highest accuracy and is the most suitable for tomato leaf disease detection. Overall, while all tested models performed well, the VGG16-based architecture remained the most effective in terms of accuracy, generalization, and deployment suitability.

5. CONCLUSION AND FUTURE WORK

This research delivers a comprehensive evaluation of various deep learning models for tomato leaf disease classification, demonstrating the effectiveness of architecture selection and data preparation. The proposed VGG16-based model, trained with transfer learning and supported by strong augmentation techniques, significantly outperformed other models in terms of precision, recall, and overall accuracy. Its ability to classify visually similar diseases with 99.83% accuracy showcases its practical applicability.

Unlike earlier studies that used limited datasets or heavy models unsuitable for deployment, this work achieves a balance between accuracy and scalability. It shows that complex architectures aren’t always essential; effective fine-tuning and data preparation can yield strong results. Although this study focused on six tomato leaf diseases, future work can extend to more diseases, different crops, and IoT-based environmental data. Deploying the model on mobile or edge devices can enable real-time detection, helping farmers make faster, data-driven decisions. In the future, integrating this approach with smart farming tools and predictive analytics could lead to a fully intelligent, sustainable agriculture system.

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