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MobiTran-SE: Hybrid MobileNetV3Small-Transformer architecture with squeeze-and-excitation for tomato leaf disease classification

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ABSTRACT

Diseases affecting tomato leaves represent a major risk to worldwide agricultural output and overall food security. In this study, we propose a innovative, lightweight and efficient deep learning (DL) approach for the classification of tomato leaf disease. Our architecture integrates the MobileNetV3Small backbone to extract multi-level features from input images, while Squeeze-and-Excitation (SE) blocks strengthen the focus on channel-wise features. A key component of our model is the incorporation of a Transformer-based module, which is applied to the fused features to extract long-range spatial interactions and contextual relationships. This hybrid approach enables the model to better distinguish between complex disease patterns in categories. The experimental findings indicate that the proposed model attains a high classification accuracy of 99.02%. The model also exhibits fast convergence and strong generalization, making it highly applicable for real-time deployment and resource-constrained agricultural environments. This work contributes a powerful and efficient solution to intelligent plant disease monitoring in the field of precision agriculture.

1. INTRODUCTION

The tomato is a vital crop that plays a central role in global agriculture. Not only are tomatoes a daily staple in countless diets around the world, but they also help ensure food security in both developed and developing countries. Rich in vitamins, minerals, and antioxidants, tomatoes offer significant health benefits. Studies have shown that people who consume tomatoes on a regular basis have a reduced risk of developing serious diseases - including multiple cancer types, osteoporosis, and cardiovascular diseases (Palozza et al., 2011; Bhowmik et al., 2012; Martí et al., 2016). This impressive nutritional profile has earned tomatoes a reputation as a "superfood", making them essential for maintaining a healthy diet. Despite its many benefits, tomato crop faces numerous challenges during cultivation. One of the most critical issues is the occurrence of leaf diseases. Such diseases, resulting from infections by bacteria, fungi, or viruses, can cause significant yield losses and deteriorate the quality of the harvest. For tomato growers around the world, and especially in countries such as Vietnam, early and reliable identification of these diseases is crucial (Choi et al., 2020; Rivarez et al., 2021; Yan et al., 2021). When a disease outbreak is detected in its early stages, farmers can take immediate action to control its spread, preserving both the quantity and quality of their crops. This not only helps protect farmer income but also ensures that consumers continue to have access to nutritious produce. Tomato leaf disease classification is not only vital for diagnosis and treatment but also significant due to its economic implications. Tomato diseases can cause substantial financial losses for farmers, driven by decreased yields and increased management costs. Efficient disease control strategies, such as cultivating resistant cultivars and applying integrated pest management, are essential to minimize these impacts and ensure sustainable tomato production (Zheng et al., 2020; Panno et al., 2021). In light of these challenges, there is a pressing need for innovative and automated methods for early disease detection in tomato plants. Advances in DL (Wang et al., 2020; Wani et al., 2025) and computer vision (Hassaballah et al., 2019) have paved the way for the development of state-of-the-art diagnostic systems. Using the power of modern neural network architectures, researchers can now build models that are capable of accurately classifying and diagnosing tomato leaf diseases (Basavaiah & Arlene Anthony, 2020; Trivedi et al., 2021; Thangaraj et al., 2022).

This paper presents a novel hybrid model that integrates MobileNetV3Small as a lightweight backbone with SE blocks and a Transformer Encoder. The aim is to develop an efficient and effective system for the early diagnosis of tomato leaf diseases. By blending the strengths of these components, the proposed model offers both high accuracy in detecting diseases and the potential for faster and more accessible implementation in real-world scenarios. Ultimately, this work contributes to improved disease management strategies, protecting crop yield and quality, and thus supporting both the agricultural community and consumers worldwide.

This paper is organized as follows: Section 2 presents an overview of prior studies on tomato leaf disease detection using DL methods, highlighting existing methods. Section 3 describes the dataset used in this research, including data sources, pre-processing, and class distribution. Section 4 introduces the proposed model architecture, which combines MobileNetV3Small, Squeeze-and-Excitation (SE) blocks, and a Transformer Encoder to improve classification accuracy. Section 5 details the experimental setup and discusses the results obtained, including evaluation metrics and comparative performance. Finally, Section 6 provides the conclusion of the paper and highlights potential future directions for the deployment of the model in real-world agricultural applications.

2. RELATED WORK

Utilizing Convolutional Neural Networks (CNNs) in plant leaf disease detection highlights a substantial improvement in agricultural research and technology, which combines artificial intelligence (AI) with image analysis to enhance crop health monitoring. As global demand for efficient agricultural practices grows, the automation and precision offered by CNNs have become increasingly notable for their ability to identify plant diseases in the early stages, ultimately leading to better yield and resource management. Early research indicates that CNNs outperform traditional detection methods, providing accurate classifications and information on disease severity, transforming the conventional approach to plant health assessment and management (Jafar et al., 2024; Rastogi et al., 2024). CNNs leverage DL techniques to extract features autonomously from images, allowing them to differentiate effectively between healthy and diseased plant leaves. Studies have shown that CNN-based models can achieve highly accurate results, often exceeding 90% - in classifying various plant diseases, making them a preferred choice over traditional machine learning (ML) approaches, for example, SVM or KNN, which typically produce lower accuracy (Agarwal et al., 2020; Sakkarvarthi et al., 2022; Padhi et al., 2025). However, despite their advantages, challenges including the need for large, high-quality datasets, the risk of overfitting, and significant computational requirements pose hurdles for real-world implementation and accessibility in agricultural settings (Alzubaidi et al., 2021; Sarkar et al., 2023; Shah & Sureja, 2025). Prominent datasets such as PlantVillage have facilitated the training and evaluation of CNN models, yet issues of class imbalance and environmental variability continue to complicate the detection process. To resolve these challenges, researchers have explored the development of lightweight deep neural architectures, including MobileNet and EfficientNet, which are optimized for deployment on mobile devices and IoT systems. For example, several studies (Ferentinos, 2018; Mukti & Biswas, 2019; Chen et al., 2020; Hassan, 2021) utilized transfer learning with CNN to achieve high accuracy in the detection of plant diseases, highlighting the potential of these methods in practical applications.

Moreover, integrating these advanced models into practical applications, such as mobile devices and IoT systems, remains an ongoing challenge for researchers aiming to bridge the gap between theoretical performance and field efficacy Addressing these limitations and improving the robustness of the model will be crucial to the continued evolution of plant leaf disease detection technologies, further solidifying the role of CNNs in modern agriculture.

In recent years, hybrid models - combinations of multiple ML or DL techniques - have emerged as a promising direction in the detection of plant disease. These models aim to take advantage of the strengths of different algorithms to improve classification accuracy, generalization, and robustness under real-world conditions. For example, several studies (Sultana & Reza, 2022; Lamba et al., 2023; Prince et al., 2024; Barman et al., 2024) have integrated CNNs with traditional classifiers such as SVM or Random Forests, where CNNs serve as automatic feature extractors and the classical models handle the final classification task. This approach can mitigate overfitting issues often associated with deep neural networks, especially when working with small or imbalanced datasets.

Other hybrid architectures combine multiple deep learning model, such as CNNs and RNNs, enabling the system to capture both spatial and temporal patterns in datasets with time-sequenced or multi-angle images (David et al., 2021; Pandey et al., 2025). In addition, some frameworks incorporate attention mechanisms (Pandey & Jain, 2022; Duhan et al., 2024; Wang et al., 2024) to enrich the input representation, thus enhancing the model's interpretability and robustness.

Building upon the insights and limitations identified in previous studies, this paper introduces a novel hybrid model that combines MobileNetV3Small as a lightweight and efficient backbone, SE blocks for channel-wise attention, and a Transformer Encoder to capture global contextual dependencies. The proposed architecture is designed to achieve early and accurate detection of tomato leaf diseases while preserving computational efficiency, thereby enabling operation on low-resource hardware. By leveraging the complementary strengths of these components, our model aims to bridge the gap between high-performance disease classification and practical field deployment. Ultimately, this work seeks to contribute to improved disease management strategies, safeguard crop productivity and quality, and promote more resilient and sustainable agricultural practices.

3. DATASET AND METHODOLOGICAL APPROACH

3.1. Data collection and preparation

The "Tomato Leaf Disease Classification" dataset (ARUN, 2022) comprises more than 32,500 leaf images of tomato plants, capturing a wide variety of scenarios obtained from both controlled laboratory settings and in-the-wild environments. This extensive dataset encompasses 11 classes, including 10 distinct disease categories. The primary objective is to facilitate the development of a lightweight yet robust classification model capable of accurately predicting tomato leaf diseases for offline deployment in mobile applications.

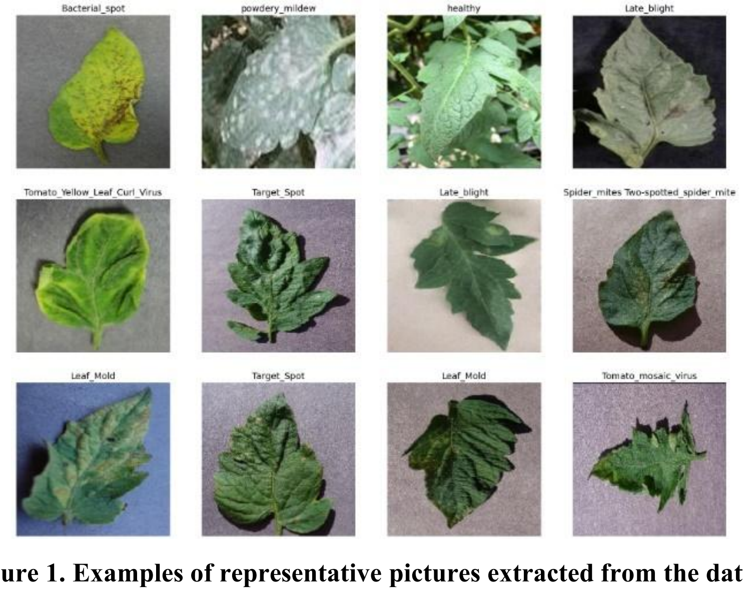


Figure 1. Examples of representative pictures extracted from the dataset

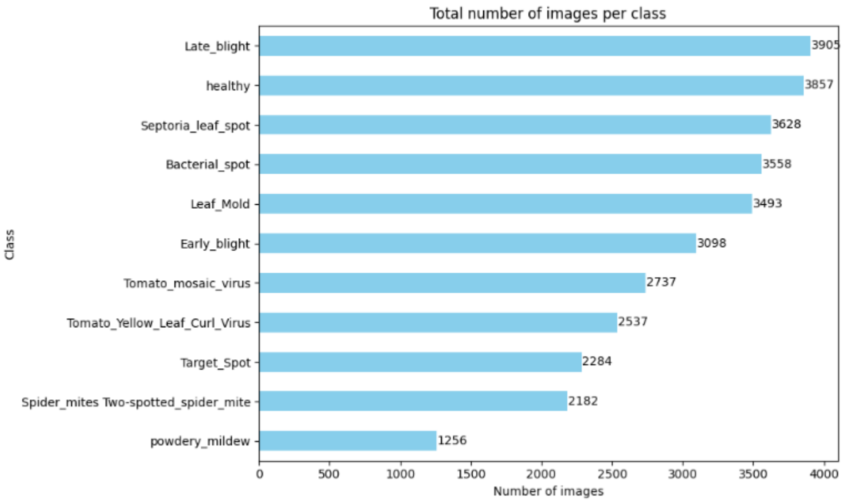


Figure 2. Total number of images per class

The majority of the initial images are derived from the PlantVillage dataset. In order to improve both the variability and resilience of the dataset, a wide range of offline augmentation methods was employed. The applied techniques comprised flipping, gamma adjustment, noise addition, PCA-based color transformation, as well as rotation and scaling. Moreover, recent additions to the dataset have been generated using Generative Adversarial Networks (GANs). A specific subset of the dataset, comprising images of Taiwanese tomato leaves, underwent additional augmentation processes such as multi-angle rotations, mirroring, and brightness reduction. These meticulous augmentation strategies have significantly enriched the dataset, thus improving the generalizability and performance of classification models developed using this resource. Figure 1 presents representative images drawn from the dataset, and Figure 2 presents the total number of images per class.

3.2. The overall methodology

The proposed model (Figure 3) is a hybrid deep learning architecture that leverages both convolutional and attention-based mechanisms to improve feature representation and improve classification performance for the recognition of tomato leaf disease.

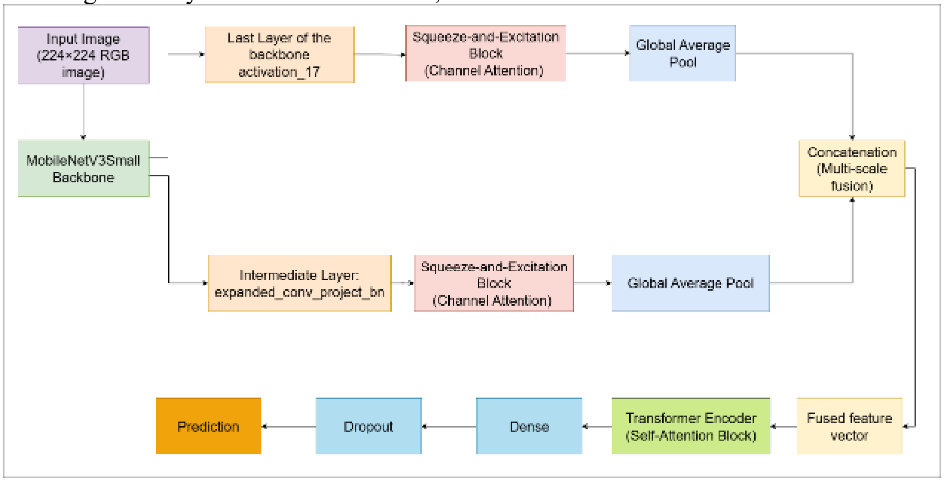


Figure 3. The overall methodology for tomato leaf disease classification

The architecture is based on a MobileNetV3Small backbone, which processes input RGB images of size 224×224. Two key feature maps are extracted from this backbone: one from the final layer (activation-17) and another from an intermediate layer (expanded-conv-project-bn) to enable multiscale feature learning. Each of these feature maps is passed through a SE block to apply channel attention, thereby emphasizing the most informative features. Following this, Global Average Pooling (GAP) is applied to decrease the spatial dimensions and retain the most salient global information. The results generated by both branches are concatenated to perform multiscale feature fusion, combining fine-grained and high-level semantic information. The fused feature vector is then fed into a Transformer Encoder block, which introduces self-attention to capture global dependencies and contextual relationships between features. Subsequently, the enriched feature representation is passed through a Dense layer. Finally, a prediction layer outputs the classification results, identifying the type of tomato leaf disease present in the input picture.

This multi-branch, attention-augmented architecture effectively captures both local and global feature interactions, leading to improved robustness and accuracy in classifying visually similar disease symptoms under varying environmental conditions.

3.3. Mathematical representation of the proposed model

Let the input image be denoted as $I \in R^{224\times 224\times 3}$. This image is fed into the MobileNetV3Small backbone $f_{\text{MobNet}}(\cdot)$, which extracts multilevel features from two specific layers:

Final layer feature map:

$$F_{\text{high}} = f_{\text{MobNet}}^{\text{final}}(I) \in R^{H_1\times W_1\times C_1}$$

Intermediate layer feature map:

$$F_{\text{low}} = f_{\text{MobNet}}^{\text{inter}}(I) \in R^{H_2\times W_2\times C_2}$$

These feature maps are passed through SE blocks to apply channel attention. For a feature map $F \in R^{H\times W\times C}$, the SE block computes:

Squeeze operation:

$$z_c = \frac{1}{H\cdot W}\sum_{i=1}^{H}\sum_{j=1}^{W} F_{i,j,c} \quad \text{for } c = 1, \dots, C$$

Excitation operation:

$$s_c = \sigma\big(W_2 \cdot \delta(W_1 \cdot z)\big)_c$$

Where W_1, W_2 are learnable parameters of the fully dense layers, σ is the sigmoid function, and δ is the ReLU activation function.

Recalibration:

$$F'_{i,j,c} = s_c \cdot F_{i,j,c}$$

where · denotes scalar multiplication, applying channel-wise attention to enhance informative features.

Next, a GAP is applied to both recalibrated features F'_{high} and F'_{low}:

$$f_{\text{high}} = \text{GAP}\big(F'_{\text{high}}\big), f_{\text{low}} = \text{GAP}(F'_{\text{low}})$$

These vectors are then concatenated to form a fused feature vector using multi-scale fusion:

$$f_{\text{fused}} = \text{Concat}\big(f_{\text{high}}, f_{\text{low}}\big)$$

To capture long-range dependencies, the fused vector is passed through a Transformer Encoder:

$$f_{\text{trans}} = \text{TransformerEncoder}(f_{\text{fused}})$$

Finally, the model performs classification using fully connected layers and softmax activation:

$$\hat{y} = \text{Softmax}\Big(\text{Dense}\big(\text{Dropout}(f_{\text{trans}})\big)\Big)$$

4. RESULTS AND DISCUSSION

Figure 4 illustrates the performance of the proposed model on training and validation sets across 20 epochs. The left section of the figure presents the training and validation accuracy, while the right subfigure presents the corresponding loss curves. As observed, both accuracy metrics show a steady increase during the training process, with validation accuracy aligning closely with training accuracy, which implies robust generalization. The highest validation accuracy was achieved at epoch 20, reaching approximately 99.1%. However, the loss curves demonstrate a consistent downward trend, with both training and validation loss converging steadily. The lowest validation lows was recorded at epoch 19, suggesting minimal overfitting. In general, the learning curves confirm that the model converges effectively and maintains high performance in the training and validation datasets.

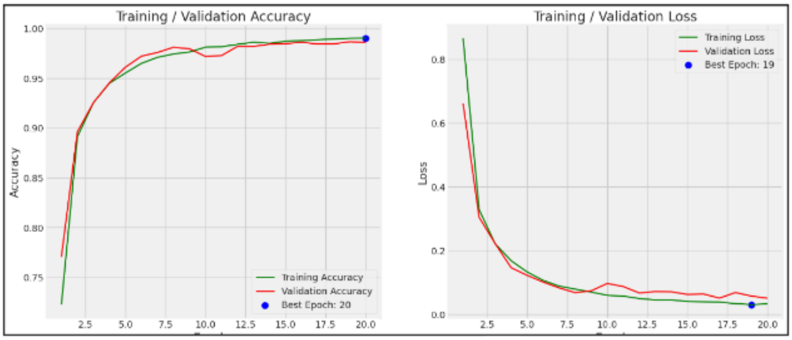
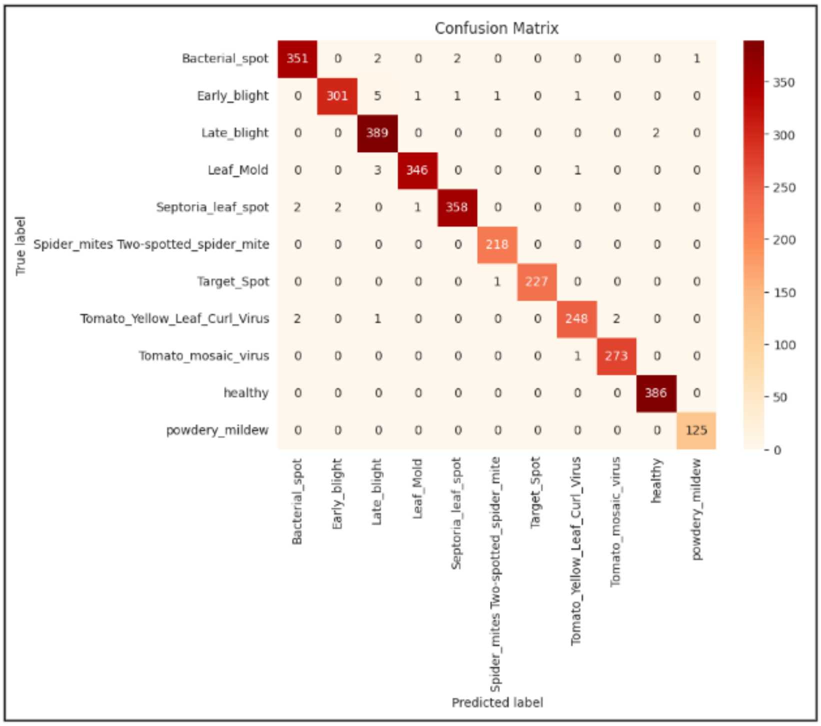


Figure 4. Curves of training and validation accuracy and loss across 20 epochs

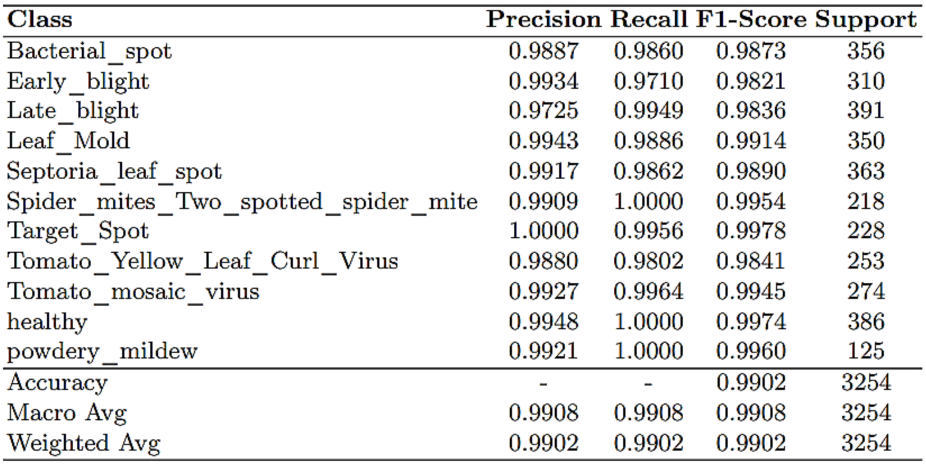
Figure 5 illustrates the confusion matrix for the proposed classification model, which was evaluated on a multi-class plant disease dataset comprising 10 distinct classes and 1 healthy class. The model demonstrates high overall classification performance, with most samples correctly classified along the main diagonal. In particular, the classes Late blight, Tomato mosaic virus, and Healthy achieved near-perfect classification accuracy, with 389, 273, and 386 correct predictions, respectively.

Misclassifications are relatively infrequent but present in some categories. For example, a small number of Early blight samples were misclassified as Late blight (5 instances) and Leaf Mold (1 instance), suggesting a minor confusion between visually similar symptoms. Similarly, the class Tomato Yellow Leaf Curl Virus exhibited some confusion with Late blight and Early blight, with 2 and 1 misclassified samples, respectively. Overall, the confusion matrix indicates that the model is effective in distinguishing between most types of disease, although further improvements could be made to enhance its discriminative capacity among closely related conditions.



	Bacterial_spot	Early_blight	Late_blight	Leaf_Mold	Septoria_leaf_spot	Spider_mites Two-spotted_spider_mite	Target_Spot	Tomato_Yellow_Leaf_Curl_Virus	Tomato_mosaic_virus	healthy	powdery_mildew
Bacterial_spot	351	0	2	0	2	0	0	0	0	0	1
Early_blight	0	301	5	1	1	1	0	1	0	0	0
Late_blight	0	0	389	0	0	0	0	0	0	2	0
Leaf_Mold	0	0	3	346	0	0	0	1	0	0	0
Septoria_leaf_spot	2	2	0	1	358	0	0	0	0	0	0
Spider_mites Two-spotted_spider_mite	0	0	0	0	0	218	0	0	0	0	0
Target_Spot	0	0	0	0	0	1	227	0	0	0	0
Tomato_Yellow_Leaf_Curl_Virus	2	0	1	0	0	0	0	248	2	0	0
Tomato_mosaic_virus	0	0	0	0	0	0	0	1	273	0	0
healthy	0	0	0	0	0	0	0	0	0	386	0
powdery_mildew	0	0	0	0	0	0	0	0	0	0	125

Figure 5. Confusion matrix for tomato leaf disease classification



Class	Precision	Recall	F1-Score	Support
Bacterial_spot	0.9887	0.9860	0.9873	356
Early_blight	0.9934	0.9710	0.9821	310
Late_blight	0.9725	0.9949	0.9836	391
Leaf_Mold	0.9943	0.9886	0.9914	350
Septoria_leaf_spot	0.9917	0.9862	0.9890	363
Spider_mites_Two_spotted_spider_mite	0.9909	1.0000	0.9954	218
Target_Spot	1.0000	0.9956	0.9978	228
Tomato_Yellow_Leaf_Curl_Virus	0.9880	0.9802	0.9841	253
Tomato_mosaic_virus	0.9927	0.9964	0.9945	274
healthy	0.9948	1.0000	0.9974	386
powdery_mildew	0.9921	1.0000	0.9960	125
Accuracy	-	-	0.9902	3254
Macro Avg	0.9908	0.9908	0.9908	3254
Weighted Avg	0.9902	0.9902	0.9902	3254

Figure 6. Performance metrics for various tomato leaf disease classes

Figure 6 presents the classification efficacy of the proposed approach across 11 classes of tomato leaf disease. The results indicate that the model attains consistently robust classification metrics, indicating its robustness and generalization capability. Notably, the class Target-Spot attained perfect precision (1.0000) and near-perfect recall (0.9956), resulting in an F1-score of 0.9978. Similarly, the classes healthy and powdery-mildew achieved perfect recall (1.0000) with corresponding F1-scores of 0.9974 and 0.9960, respectively. The overall accuracy of the model on the test set reaches 99.02%, while the macro-averaged and weighted-averaged F1-scores are also consistently high at 99.08% and 99.02%, respectively. These metrics highlight the model's effectiveness in accurately distinguishing between various categories of tomato leaf disease, even those with relatively few samples, such as powdery mildew (125 images).

Table 1. Comparison of recent methods for tomato leaf disease classification

Paper	Model	Samples	Classes	Accuracy
Paul et al., 2023	Custom model	32,535	11	95.00%
Osmenaj et al., 2025	Ensemble models	11,000	10	98.00%
Rashid et al., 2025	A Light Weighted Method	18,835	10	98.77%
Chen et al., 2022	AlexNet	22,390	10	98.00%
Das et al., 2025	XLTLDisNet	16,011	10	97.24%
Zhao et al., 2021	ResNet50+SeNet	22,925	10	96.81%
Our model	MobiTran-SE	32,535	11	99.02%

Table 1 summarizes a comparison of recent deep learning-based approaches for predicting tomato leaf disease. The models vary in terms of architectural complexity, dataset size, number of target classes, and accuracy achieved. Among the reviewed works, the ensemble-based method in (Osmenaj et al., 2025) and the lightweight model in (Rashid et al., 2025) demonstrated high performance, achieving accuracies of 98.00% and 98.77%, respectively, on datasets ranging from 11,000 to 18,835 images. Traditional architectures such as AlexNet and ResNet50 combined with SE blocks (Zhao et al., 2021) also reported competitive results in moderately sized datasets. Our proposed approach, MobiTran-SE, utilizes the complete dataset of 32,535 images in 11 disease categories and outperforms all previous methods, achieving a state-of-the-art accuracy of 99.02%. This highlights the effectiveness of combining MobileNetV3Small, Squeeze-and-Excitation blocks, and a Transformer-based encoder in a lightweight framework tailored for plant disease classification tasks.

5. CONCLUSION

In this paper, we present a novel, lightweight, and effective deep learning architecture designed for the classification of tomato leaf diseases. The model employs the MobileNetV3Small backbone to extract hierarchical features from input images and incorporates Squeeze-and-Excitation (SE) blocks to enhance channel-wise attention and emphasize informative features. An essential component of the model is the integration of a Transformer-based encoder, which operates on the fused feature representation to capture long-range spatial dependencies and enrich contextual understanding across the input. The experimental results demonstrate the effectiveness of the proposed model, achieving a classification accuracy of 99.02% on the test set. In addition, high precision, recall, and F1-scores were observed in all classes, including those with relatively limited sample sizes. The training and validation curves further confirm the stability and generalization capability of the model, with minimal overfitting observed throughout the training process. These results confirm the potential of the proposed architecture as a practical solution for real-world agricultural applications, particularly in scenarios where computational efficiency and accurate disease identification are essential. Future work will explore the integration of this model into mobile or edge devices to support in-field real-time plant health monitoring systems.

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