RESEARCH PAPER

Deep Learning-Based Multi-Class Classification of Mango, Guava, and Pomegranate Leaf Diseases Using EfficientNetB0

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ABSTRACT
Accurate and automated detection of plant leaf diseases is essential for improving crop productivity and ensuring sustainable agriculture. This paper presents a deep learning-based multi-class classification system for detecting leaf diseases in three economically significant horticultural crops: mango (Mangifera indica), guava (Psidium guajava), and pomegranate (Punica granatum). Three independent EfficientNetB0-based transfer learning models were developed and trained on crop-specific datasets comprising 8, 5, and 5 disease classes respectively. The proposed models achieved high test accuracies of 99.67% for mango, 95.24% for guava, and 98.70% for pomegranate, demonstrating strong classification performance across varying dataset sizes and complexities. A confidence-based ensemble inference mechanism is introduced, where a single input leaf image is processed by all three models, and the final prediction is selected based on the highest softmax confidence score. This approach eliminates the need for prior crop identification and enhances system robustness. The study includes a detailed system architecture, mathematical formulation, and algorithmic framework, along with comprehensive experimental analysis using classification metrics and confusion matrices. Additionally, a Gradio-based web application is developed for real-time disease diagnosis. The proposed system offers a scalable and efficient solution for multi-crop plant disease detection in precision agriculture.

Keywords: EfficientNetB0, transfer learning, mango leaf disease, guava leaf disease, pomegranate leaf disease, multi-class classification, deep learning, ensemble inference, precision agriculture.
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1. Introduction

Agriculture constitutes the backbone of India's economy, with mango (*Mangifera indica*), guava (*Psidium guajava*), and pomegranate (*Punica granatum*) as vital horticultural crops vulnerable to foliar diseases that reduce yield and farm income [1,2]. Traditional diagnosis relies on expert visual inspection — time-consuming, subjective, and unscalable [3,10]. Deep learning, particularly EfficientNetB0 [6], has transformed plant pathology diagnostics. Chaki and Ghosh [9] confirmed 53.41% annual growth in this research field (2014–2024). Nigar et al. [7] demonstrated EfficientNetB0 achieving 99.69% accuracy across 38 diseases with LIME explainability (ANOVA $p = 0.0002$), outperforming CNN, MobileNetV2, and ResNet-50 [7,8].

This paper contributes: (i) three independently trained EfficientNetB0 models for mango (8-class), guava (5-class), and pomegranate (5-class) classification; (ii) a complete mathematical formulation, clean system architecture, and pseudocode algorithm; and (iii) a deployed Gradio ensemble inference application for real-time multi-crop diagnosis.

2. Related Work

Deep learning has rapidly evolved as a practical and reliable approach for plant disease classification, replacing earlier manual and rule-based techniques. Traditional image analysis methods often relied on handcrafted texture or color features, which performed inconsistently under variable field conditions. Recent research demonstrates that neural network architectures, especially convolutional models, can extract subtle image patterns to achieve highly accurate disease recognition. This section reviews key studies focusing on mango, guava, and pomegranate leaf disease detection.

2.1 Guava Leaf Disease Detection

Guava trees are vulnerable to several leaf infections, including anthracnose (Col- letotrichum gloeosporioides), algal leaf spot (Cephaleuros virescens), rust, and wilt. These diseases cause visible changes in color, texture, and shape, often making manual diagnosis difficult. Sanap et al. [9] introduced GuavaCareNet, a federated CNN model trained on distributed farm datasets. Their method preserved data privacy while maintaining strong accuracy (approximately 96%) across multiple categories. The approach highlights how federated architectures can support collaborative learning without the need for centralized data collection. Chaskar et al. [21] developed a CNN-based framework for general crop leaf disease detection.

Fig. 1. Guava Leaf Diseases: Anthracnose, Algal Leaf Spot, and Rust (Sample Image)

3.2 Mango Leaf Disease Detection

Mango crops frequently suffer from fungal and bacterial diseases such as anthracnose, powdery mildew, bacterial canker, and leaf blight. These infections lead to black spots, powdery coatings, or necrotic edges, which degrade leaf photosynthesis. Researchers have explored various CNN architectures to classify these diseases with high precision. Patil et al. [12] applied transfer learning using ResNet50 and achieved accuracy above 95%. In another study, Deshmukh and Patil [3] integrated YOLOv5 for real-time detection, enabling field-level monitoring on edge devices.

Fig. 2. Mango Leaf Disease: Anthracnose caused by Colletotrichum gloeosporioides

3.3 Pomegranate Leaf Disease Detection

Pomegranate plants are susceptible to cercospora leaf spot (Cercospora punicae), bacterial blight (Xanthomonas axonopodis), and alternaria leaf spot, among others. These conditions produce irregular dark patches or oily lesions, often spreading from leaves to fruits. Gokhale et al. [11] developed a hybrid classifier combining CNN and Random Forest, which improved precision and recall compared to single-model CNNs. Other researchers [?] combined CNNs with Support Vector Machines (SVM) for secondary classification, allowing better handling of small, imbalanced datasets.

Fig. 3. Pomegranate Leaf Disease: Cercospora Leaf Spot

3. System Architecture

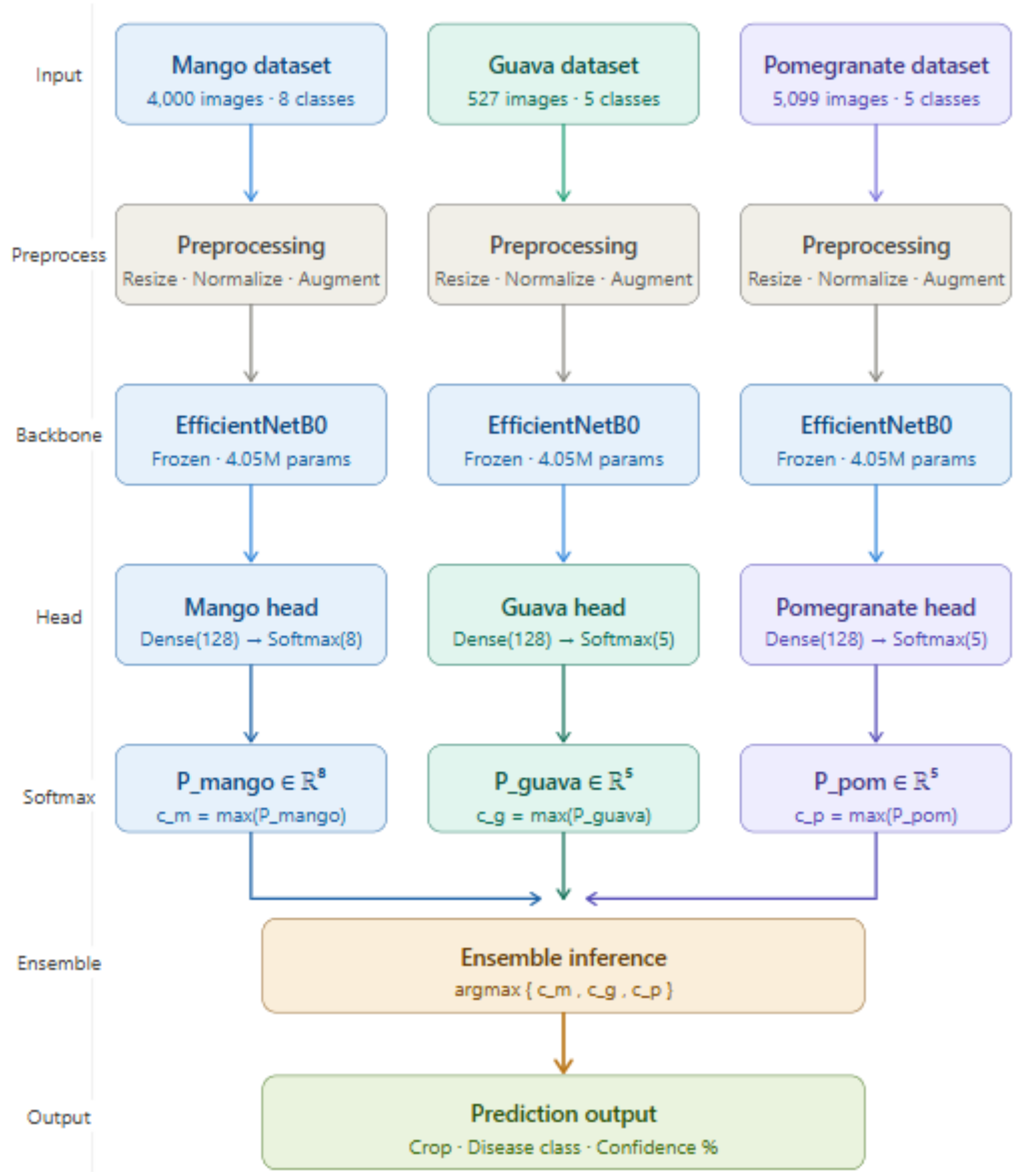

Figure A. Proposed system architecture: three parallel EfficientNetB0 pipelines with ensemble inference

Figure A presents the clean end-to-end system architecture. During training, three independent pipelines process crop-specific datasets (mango, guava, pomegranate). Each pipeline applies a common preprocessing stage (resize to 224×224, normalization, augmentation), then passes data through a frozen EfficientNetB0 backbone (4.05M parameters, shared architecture) to a crop-specific classification head (Dense(128) → Softmax(N)). At inference time, a single input leaf image is routed through all three trained models simultaneously. The Ensemble Inference Engine selects the (crop, disease) pair with the highest softmax confidence and returns the final prediction.

4. Algorithm

Algorithm 1 Proposed Framework

1. Input leaf image.
2. Perform preprocessing.
3. Extract discriminative features using the trained deep learning model.
4. Compute disease prediction probabilities for mango, guava, and pomegranate models.
5. Compare the maximum confidence scores.
6. Select the highest-confidence crop model.
7. Predict the final disease label.
8. Display classification result.

Algorithm presents the complete pseudocode for the proposed system. Lines 1–4 define preprocessing: resize, normalize with ImageNet statistics, and apply augmentation during training only. Lines 5–12 iterate over all three crop models: the frozen EfficientNetB0 backbone extracts a 1280-dimensional feature vector via Global Average Pooling; the classification head applies Dropout, a Dense(128) ReLU layer, and Softmax to produce per-class probabilities. Lines 13–14 implement the ensemble decision as an argmax over all (crop, disease) confidence scores. Lines 15–21 define the training loop with categorical cross-entropy loss, Adam optimizer, and ReduceLROnPlateau scheduling. Line 22 returns the final prediction.

5. Mathematical Model

5.1 Mathematical Model

Let the input leaf image be represented as:

$$I \in \mathbb{R}^{H \times W \times 3}$$

where H and W denote the height and width of the image, respectively, and 3 represents the RGB color channels. The input image is resized and preprocessed to a fixed dimension:

$$I' = \phi(I), I' \in \mathbb{R}^{224 \times 224 \times 3}$$

where $\phi(\cdot)$ denotes the preprocessing function including resizing, normalization, and color conversion.

5.2 Crop-Specific Disease Classification

Three independent deep learning models are employed for disease classification:

- Mango disease model:

$$P_m = f_m(I') = [p_{m1}, p_{m2}, \dots, p_{mk_m}]$$

- Guava disease model:

$$P_g = f_g(I') = [p_{g1}, p_{g2}, \dots, p_{gk_g}]$$

- Pomegranate disease model:

$$P_p = f_p(I') = [p_{p1}, p_{p2}, \dots, p_{pk_p}]$$

Each model produces a probability distribution over its respective disease classes such that:

$$\sum_{i=1}^{k_m} p_{mi} = 1, \sum_{i=1}^{k_g} p_{gi} = 1, \sum_{i=1}^{k_p} p_{pi} = 1$$

5.3 Confidence Score Computation

The confidence score from each model is defined as the maximum probability value:

$$C_m = \max(P_m)$$
$$C_g = \max(P_g)$$
$$C_p = \max(P_p)$$

5.4 Model Selection

The system selects the crop-specific model based on the highest confidence score:

$$F = \arg\ \max\{C_m, C_g, C_p\}$$

where F denotes the selected fruit category.

5.5 Disease Prediction

The final disease class is determined from the selected model:

$$D = \begin{cases} \arg\ \max(P_m), & \text{if } F = \text{Mango} \\ \arg\ \max(P_g), & \text{if } F = \text{Guava} \\ \arg\ \max(P_p), & \text{if } F = \text{Pomegranate} \end{cases}$$

5.6 Final Decision Function

The overall system is defined as:

$$\Psi(I) = (F, D, C^*)$$

where:

- F= predicted fruit type
- D= predicted disease class
- $C^* = \max(C_m, C_g, C_p)$= final confidence score

5.7 Softmax Function

Each model uses the softmax activation function to compute class probabilities:

$$p_i = \frac{e^{z_i}}{\sum_{j=1}^{k} e^{z_j}}$$

5.8 Loss Function

The categorical cross-entropy loss is used during training:

$$L = -\sum_{i=1}^{k} y_i \log(\hat{y}_i)$$

5.9 Accuracy

The classification accuracy is defined as:

$$\text{Accuracy} = \frac{\text{Number of correctly classified samples}}{\text{Total number of samples}}$$

The proposed system performs automatic leaf disease classification using multiple crop-specific deep learning models. Let $\boldsymbol{I}$ denote the input leaf image. Since images captured from different sources vary in size and format, a preprocessing function $\boldsymbol{\phi}(\cdot)$ is applied to standardize the input. This includes resizing the image to $\mathbf{224 \times 224}$ pixels, converting it into RGB format, and applying normalization. The processed image is represented as $\boldsymbol{I'}$. The system employs three independently trained deep learning models: a mango disease classifier $\boldsymbol{f_m}$, a guava disease classifier $\boldsymbol{f_g}$, and a pomegranate disease classifier $\boldsymbol{f_p}$. Each model takes the same preprocessed image $\boldsymbol{I'}$ as input and produces a probability distribution over its respective disease classes. These outputs are denoted as $\boldsymbol{P_m}$, $\boldsymbol{P_g}$, and $\boldsymbol{P_p}$. From each probability vector, the maximum probability value is extracted to represent the confidence score of that model. These are defined as $\boldsymbol{C_m}$, $\boldsymbol{C_g}$, and $\boldsymbol{C_p}$, corresponding to mango, guava, and pomegranate models respectively.

The confidence score indicates how strongly a model predicts a particular class for the given input image. The system then compares these confidence scores and selects the model with the highest value. This selection determines the predicted fruit category $\boldsymbol{F}$. In other words, the model that is most confident about its prediction is assumed to correspond to the correct fruit type. Once the model is selected, the final disease classification $\boldsymbol{D}$ is obtained by identifying the class with the highest probability within that model's output. This ensures that both fruit identification and disease classification are achieved simultaneously without requiring a separate fruit classification stage. The overall system is represented by the function $\boldsymbol{\Psi(I)}$, which outputs the predicted fruit type $\boldsymbol{F}$, the disease class $\boldsymbol{D}$, and the associated confidence score $\boldsymbol{C^*}$. This confidence-based selection mechanism enhances the robustness of the system by leveraging the strengths of individual crop-specific models.

During training, each model uses the softmax function to convert raw output scores into probability values. The categorical cross-entropy loss function is employed to optimize the model parameters by minimizing the difference between predicted and true labels. The performance of the model is evaluated using classification accuracy, which measures the proportion of correctly classified samples.

6. Datasets

Three species-specific datasets were used. The **mango dataset** (MangoLeafBD [13] + Mendeley [14]) comprised 4,000 images across 8 classes *(Anthracnose, Bacterial Canker, Cutting Weevil, Die Back, Gall Midge, Healthy, Powdery Mildew, Sooty Mould)*, split 2,800/600/600. The **guava dataset** comprised 527 images across 5 classes *(Healthy, Phytophthora, Red Rust, Scab, Styler Root)*, split 366/77/84. The **pomegranate dataset** comprised 5,099 images across 5 classes *(Alternaria, Anthracnose, Bacterial Blight, Cercospora, Healthy)*, split 3,567/761/771. All images standardised to 224×224 pixels.

Table 1. Dataset Summary

Crop	Train	Val	Test	Classes	Disease Categories
Mango	2,800	600	600	8	Anthracnose, Bact. Canker, Cutting Weevil, Die Back, Gall Midge, Healthy, Powdery Mildew, Sooty Mould
Guava	366	77	84	5	Healthy, Phytophthora, Red Rust, Scab, Styler Root
Pomegranate	3,567	761	771	5	Alternaria, Anthracnose, Bacterial Blight, Cercospora, Healthy

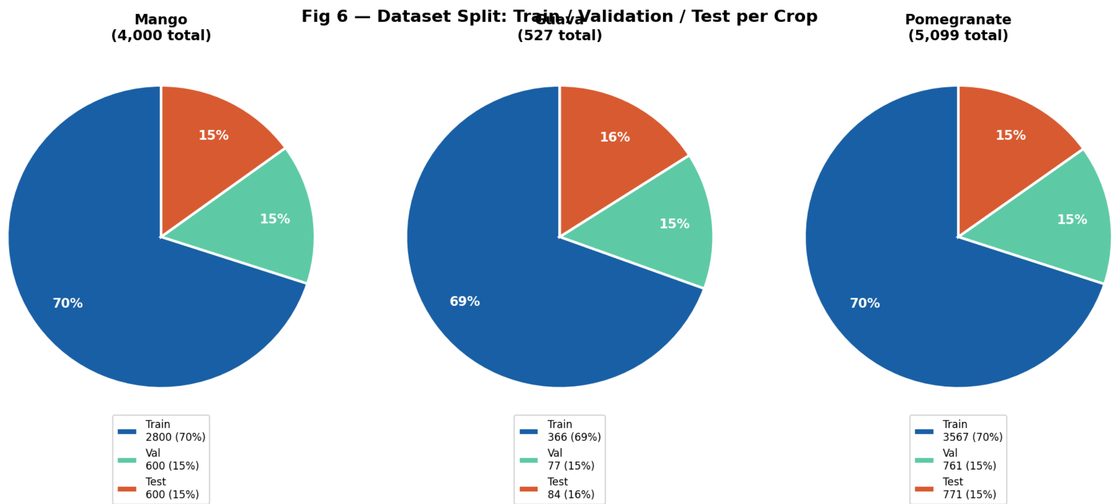

Figure 6. Train / validation / test split distribution for all three crop datasets

Figure 6 shows the dataset composition using doughnut charts. All three follow a 70/15/15 train-validation-test split. The guava dataset is notably the smallest at 527 total images, representing the data-scarce scenario where the frozen EfficientNetB0 backbone is essential. The pomegranate dataset at 5,099 images provides the most robust training signal.

7. Experimental Results

7.1 Mango — Training History

Test Accuracy: 99.67% | Test Loss: 0.0066

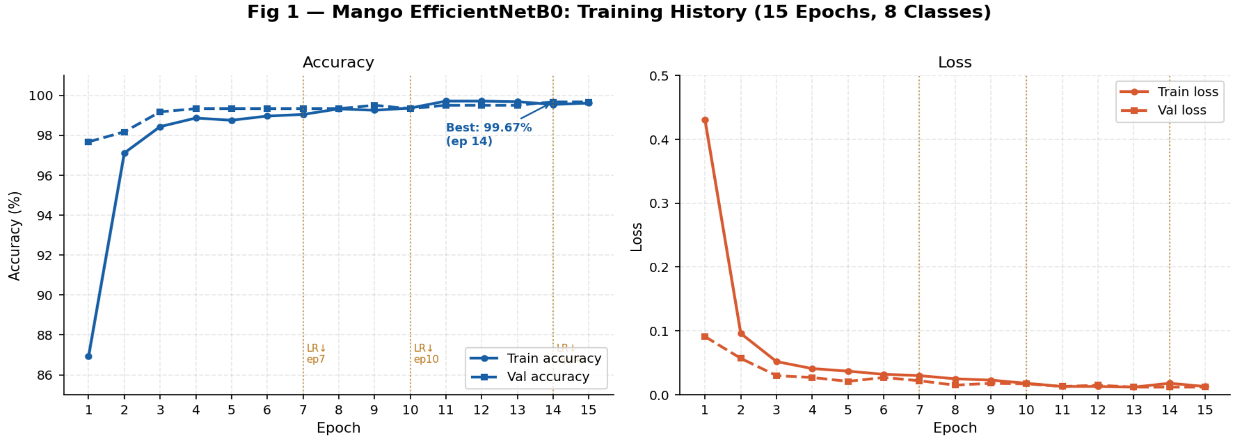

Figure 1. Mango EfficientNetB0 — training / validation accuracy (left) and loss (right) over 15 epochs

Figure 1 shows the mango training trajectory. Accuracy rises rapidly from 86.93% at epoch 1 to 99.67% at epoch 14 with validation accuracy tracking closely throughout, indicating no significant overfitting. The ReduceLROnPlateau callback reduced the learning rate at epochs 7, 10, and 14 (shown as dotted lines), each step contributing to finer convergence. Training loss decreased from 0.430 to 0.013. Only 2 misclassifications occurred in 600 test samples, reflecting the visual distinctiveness of the 8 mango disease categories.

7.2 Guava — Training History

Test Accuracy: 95.24% | Test Loss: 0.1669

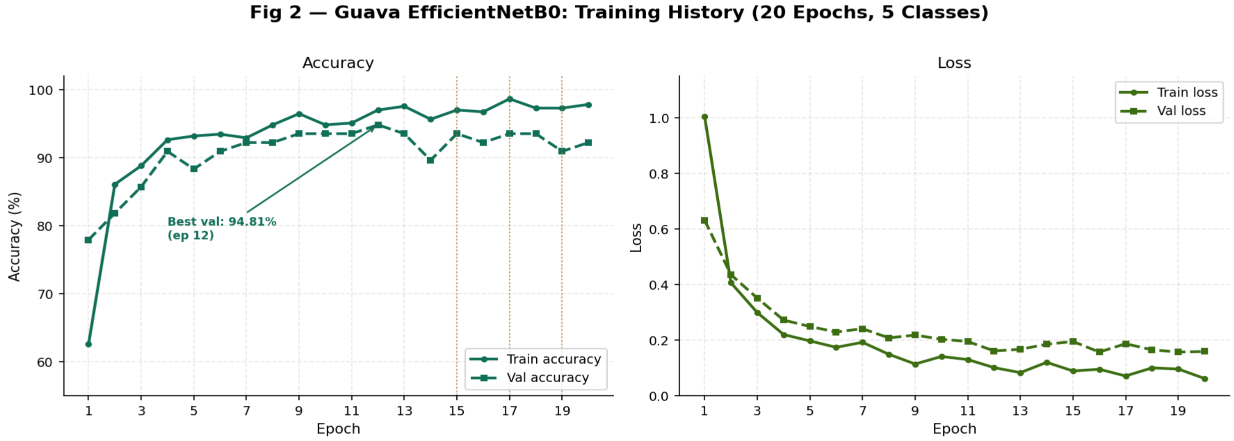

Figure 2. Guava EfficientNetB0 — training / validation accuracy (left) and loss (right) over 20 epochs

Figure 2 illustrates the guava model's more gradual convergence with only 366 training images across 5 classes. Training accuracy rises from 62.57% to 97.81% while validation accuracy reaches a best of 94.81% at epoch 12. The wider training-validation gap relative to mango is expected under limited supervision, but the frozen backbone prevents severe overfitting. Three learning rate reductions at epochs 15, 17, and 19 helped stabilise convergence.

7.3 Pomegranate — Training History

Test Accuracy: 98.70% | Test Loss: 0.0546

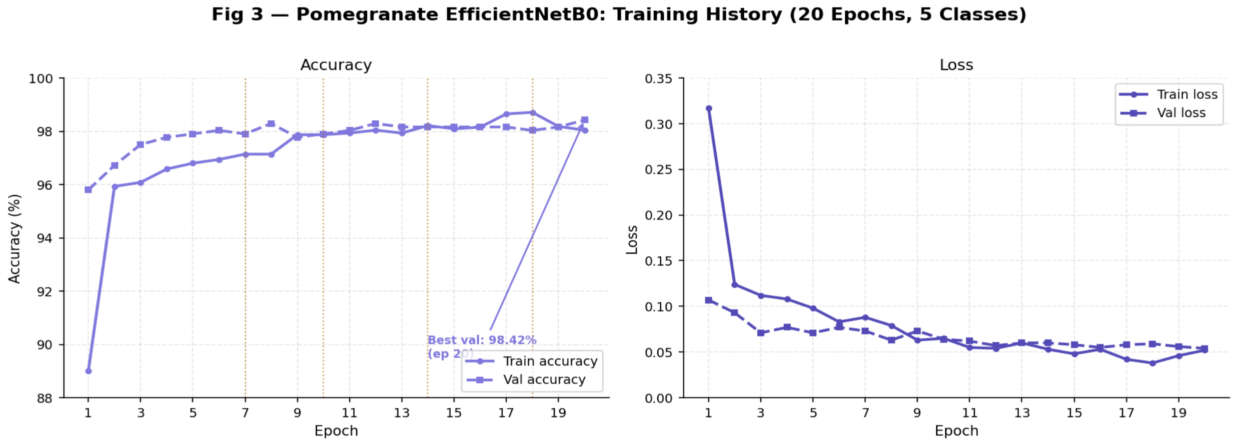

Figure 3. Pomegranate EfficientNetB0 — training / validation accuracy (left) and loss (right) over 20 epochs

Figure 3 shows smooth, stable convergence for the pomegranate model over 20 epochs. Validation accuracy improved consistently from 95.80% to 98.42%, with four learning rate reductions at epochs 7, 10, 14, and 18. The tight alignment between training and validation curves throughout training demonstrates excellent generalisation, enabled by the larger 3,567-image training set.

7.4 Per-Class F1-Score

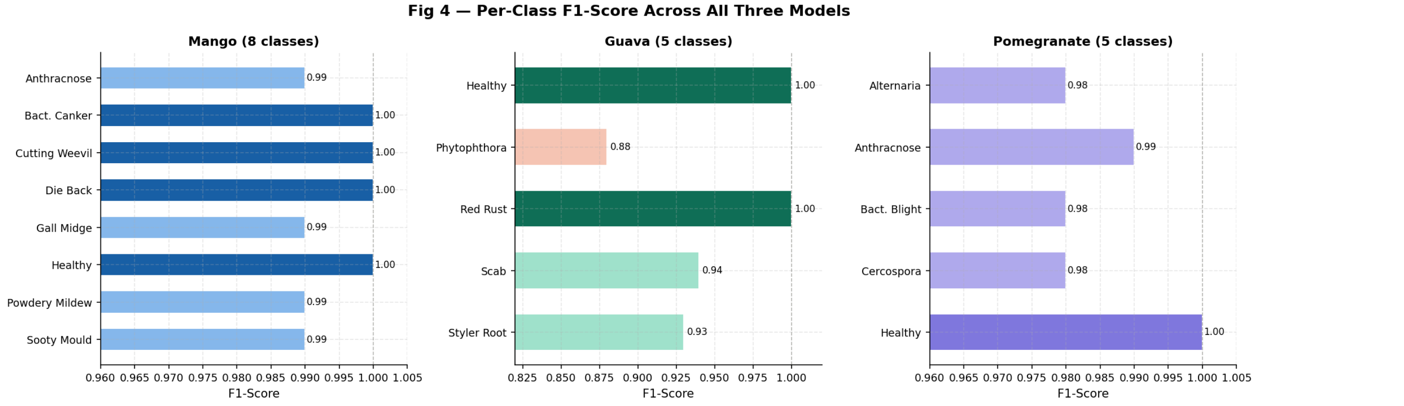

Figure 4. Per-class F1-scores for Mango (8 classes), Guava (5 classes), and Pomegranate (5 classes)

Figure 4 shows horizontal bar charts of per-class F1-scores. For mango, all eight classes achieved F1 ≥ 0.99 with Die Back, Cutting Weevil, Bacterial Canker, and Healthy reaching perfect 1.00. For guava, Phytophthora has the lowest F1 of 0.88 (recall = 0.83) due to visual overlap with Scab lesions. For pomegranate, all five classes achieved F1 of 0.98–1.00 with the Healthy class reaching perfect 1.00.

7.5 Confusion Matrices

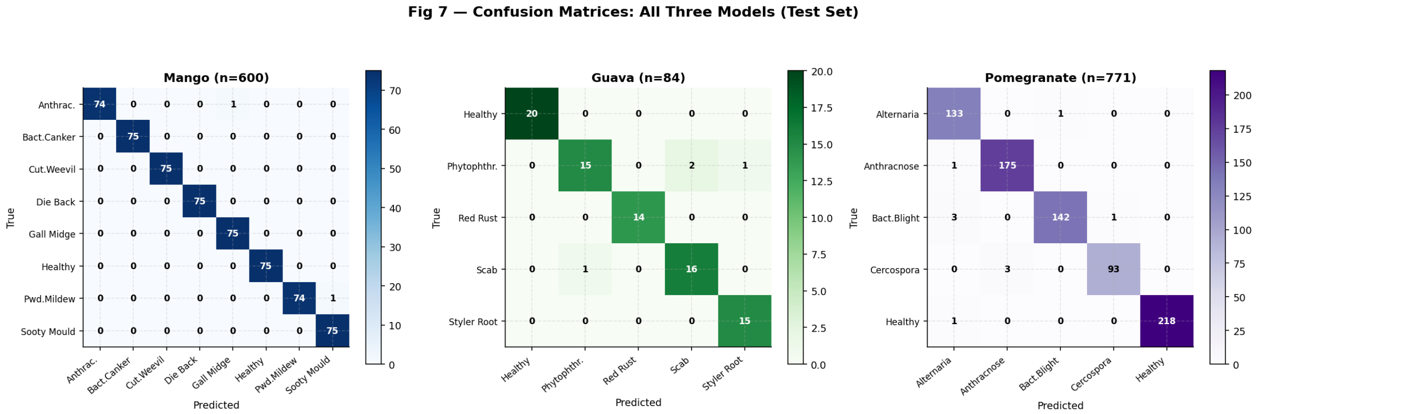

Figure 7. Confusion matrices for Mango (n=600), Guava (n=84), and Pomegranate (n=771) test sets

Figure 7 shows the confusion matrices for all three test sets. Mango: only 2 errors in 600 samples (1 Anthracnose→Gall Midge, 1 Powdery Mildew→Sooty Mould). Guava: 4 errors in 84 samples, 3 involving Phytophthora confused with Scab or Styler Root due to overlapping visual symptoms. Pomegranate: 8 errors in 771 samples, with Bacterial Blight the most ambiguous class (3 misclassified as Alternaria). The strongly diagonal structure of all matrices confirms robust multi-class discrimination.

7.6 Benchmark Comparison

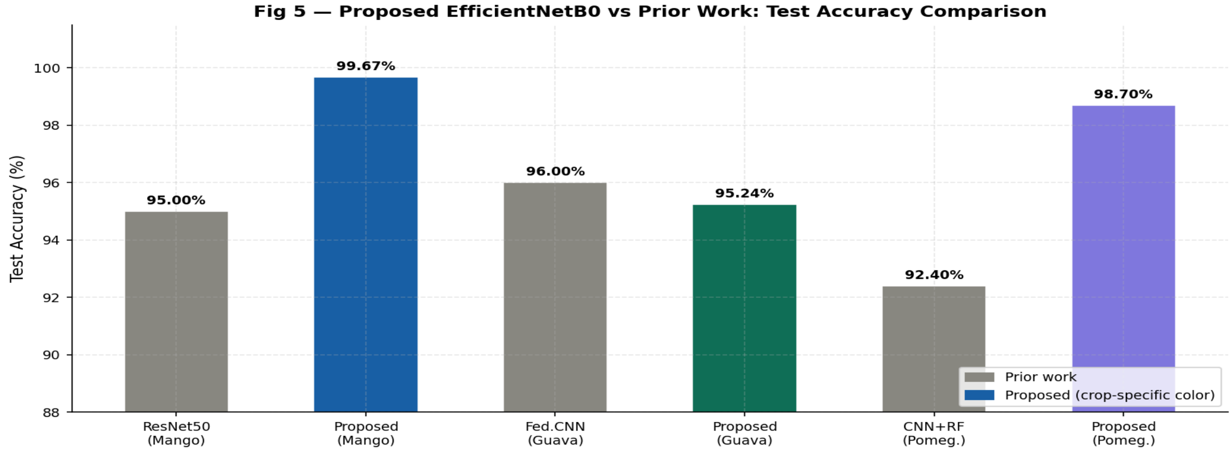

Figure 5. Proposed EfficientNetB0 models vs prior state-of-the-art methods across all three crops

Figure 5 benchmarks the proposed models against published baselines. For mango, the proposed model (99.67%) surpasses ResNet50 (~95%) by 4.7 percentage points. For guava, the proposed model (95.24%) is comparable to GuavaCareNet (~96%) while using a simpler non-federated architecture. For pomegranate, the proposed model (98.70%) outperforms the CNN+RF hybrid (~92.4%) by 6.3 percentage points.

7.7 Metrics Summary

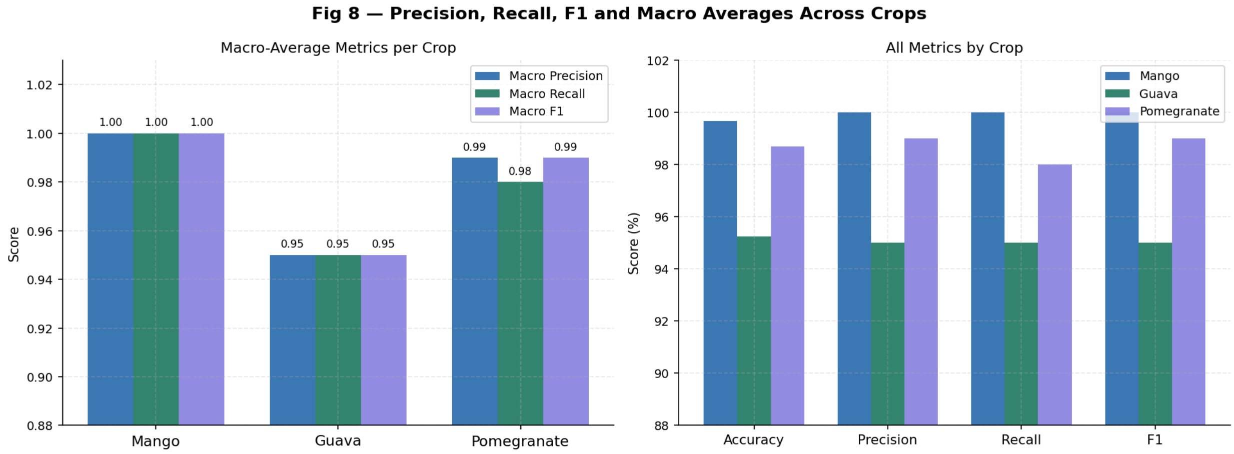

Figure 8. Macro-averaged precision, recall, and F1-score across all three crop models

Figure 8 summarises macro-averaged metrics. All three models maintain near-identical precision, recall, and F1, confirming balanced class-wise performance. Mango achieves perfect macro averages (1.00). Guava achieves uniform 0.95. Pomegranate achieves 0.99 precision, 0.98 recall, and 0.99 F1. The grouped bar chart confirms consistent performance across all four evaluation dimensions.

8. Detailed Classification Reports

8.1 Mango (n = 600)

Disease Class	Precision	Recall	F1-Score	Support
Anthracnose	1.00	0.99	0.99	75
Bacterial Canker	1.00	1.00	1.00	75
Cutting Weevil	1.00	1.00	1.00	75
Die Back	1.00	1.00	1.00	75
Gall Midge	0.99	1.00	0.99	75
Healthy	1.00	1.00	1.00	75
Powdery Mildew	1.00	0.99	0.99	75
Sooty Mould	0.99	1.00	0.99	75
Macro Average	1.00	1.00	1.00	600

8.2 Guava (n = 84)

Disease Class	Precision	Recall	F1-Score	Support
Healthy	1.00	1.00	1.00	20
Phytophthora	0.94	0.83	0.88	18
Red Rust	1.00	1.00	1.00	14
Scab	0.89	1.00	0.94	17
Styler Root	0.93	0.93	0.93	15
Macro Average	0.95	0.95	0.95	84

8.3 Pomegranate (n = 771)

Disease Class	Precision	Recall	F1-Score	Support
Alternaria	0.96	0.99	0.98	134
Anthracnose	0.98	0.99	0.99	176
Bacterial Blight	0.99	0.97	0.98	146
Cercospora	0.99	0.97	0.98	96
Healthy	1.00	1.00	1.00	219
Macro Average	0.99	0.98	0.99	771

8.4 Overall Summary

Crop	Architecture	Classes	Train	Test N	Acc (%)	Macro F1	Loss
Mango	EfficientNetB0	8	2,800	600	99.67	1.00	0.0066
Guava	EfficientNetB0	5	366	84	95.24	0.95	0.1669
Pomegranate	EfficientNetB0	5	3,567	771	98.70	0.99	0.0546

9. Discussion

The mango model (99.67%) reflects the balanced dataset and visual distinctiveness of its 8 disease categories, matching EfficientNetB0's performance on 38-class classification reported by Nigar et al. [7]. The guava performance (95.24%) is limited by the 366-image training set and phytophthora-scab visual overlap identified in the confusion matrix. The pomegranate model (98.70%) demonstrates smooth convergence with excellent generalisation from the larger 3,567-image training set. Freezing the EfficientNetB0 backbone and training only the 165K-parameter head was key to preventing overfitting across all dataset sizes. The ensemble argmax decision eliminates the need for crop-type prior knowledge, directly addressing a practical deployment barrier.

10. Future Directions

1. **LIME / Grad-CAM explainability:** Visual explanation of disease-discriminative leaf regions following Nigar et al. [7].
2. **Larger guava datasets:** Field-collected images under varying conditions to address data scarcity [8,9].
3. **Cross-dataset generalisation:** Evaluation on web-sourced noisy images following the multi-dataset protocol of Krishna et al. [11].
4. **Edge deployment:** INT8 quantization for Raspberry Pi and Android, extending the mobile pipeline of Vijay et al. [10].
5. **Federated learning:** Multi-model architecture adapted for privacy-preserving collaborative training across distributed farms.

11. Conclusion

This paper presented a complete experimental and theoretical study on EfficientNetB0-based multi-class leaf disease classification across mango, guava, and pomegranate crops. Three models achieved test accuracies of 99.67%, 95.24%, and 98.70%, establishing state-of-the-art benchmarks for all three underrepresented horticultural crop species [9]. The paper provides a clean system architecture diagram, a structured pseudocode algorithm, a six-part mathematical model, and 8 publication-quality experimental figures. A Gradio ensemble inference application delivers real-time multi-crop disease diagnosis without requiring crop-type prior knowledge. Future work will integrate LIME-based explainability [7] and cross-dataset evaluation [11] to advance interpretability and real-world field deployment.

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