



Machine Learning-based Automated Detection and Multi-class Classification of Faba Bean Leaf Diseases using a VGG16 based Deep Convolutional Neural Network

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ABSTRACT

Background: Faba bean is an important legume crop valued for its nutritional and soil-enriching benefits, yet its productivity is severely affected by foliar diseases. Automated image-based detection using deep learning provides a rapid and reliable approach for early disease identification and improved crop management.

Methods: This study developed a machine learning-based automated framework for multi-class classification of Faba bean leaf diseases using transfer learning with the VGG16 convolutional neural network. A dataset of 8,021 RGB images collected under natural field conditions was used, comprising four classes: healthy, rust, gall and chocolate spot. Images were resized to 224 × 224 pixels and normalized prior to training. The pretrained convolutional layers of VGG16 were frozen and a custom classification head with global average pooling and dropout regularization was added. Model performance was evaluated using classification metrics.

Result: The proposed model achieved an overall classification accuracy of 92.34% and a macro-averaged F1-score of 0.9227 on the test dataset. Strong classification performance was observed across all disease categories, with particularly high predictive accuracy for healthy and rust classes. The findings demonstrate the effectiveness of transfer learning for plant disease detection and highlight its potential for scalable, automated crop health monitoring in precision agriculture.

Key words: Agricultural artificial intelligence, Automated disease diagnosis, Convolutional neural networks (CNN), Foliar pathology, Plant health monitoring.

INTRODUCTION

As global agriculture faces mounting pressure from climate change, population growth and the demand for sustainable production systems, resilient legume crops such as Faba bean are gaining renewed attention (Dave *et al.*, 2024; Carlini *et al.*, 2025). Faba bean is not only a vital source of plant-based protein for human and animal consumption but also plays a crucial ecological role through biological nitrogen fixation, enhancing soil fertility and reducing dependence on synthetic fertilizers (Khan *et al.*, 2025). Despite its agronomic and environmental benefits, Faba bean production remains highly vulnerable to foliar diseases that compromise both yield and grain quality (Cormack *et al.*, 2025).

Major diseases, including chocolate spot, rust and gall disease, frequently occur under favorable environmental conditions and can spread rapidly across fields (Martineau-Côté *et al.*, 2022). Their early symptoms are often subtle and visually similar, making reliable identification challenging, especially for smallholder farmers who may lack access to expert diagnostic services. Delayed or inaccurate diagnosis can lead to improper pesticide use, increased production costs, environmental contamination and significant economic losses (Singh *et al.*, 2025). Plant diseases are among the major constraints to agricultural productivity and foliar infections can adversely affect plant growth and yield. Leaf diseases caused by bacterial and fungal pathogens can produce characteristic

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symptoms and substantial damage, emphasizing the importance of timely disease identification and management (Chatterjee, 2023; Kumar *et al.*, 2021).

In recent years, advances in computer vision and deep learning have opened new opportunities for precision agriculture. Automated image-based disease detection systems offer the potential to transform traditional crop monitoring by providing rapid, objective and scalable diagnostic tools (Ghazal *et al.*, 2024; Kumar *et al.*, 2025). By using convolutional neural networks and mobile imaging technologies, these systems can detect disease symptoms directly from leaf images, enabling early intervention and data-driven decision-making (Devarajan *et al.*, 2026). Among deep architectures, VGG16 is widely used due to its simple structure and strong feature

extraction capability. When combined with transfer learning, it can achieve high classification accuracy even with limited agricultural datasets (Neelakandan *et al.*, 2025).

From this perspective, integrating artificial intelligence into Faba bean disease management represents not only a technological innovation but also a step toward more sustainable and resilient agricultural systems (Yakkala *et al.*, 2024). Developing accurate and robust deep learning models for foliar disease detection could significantly enhance crop protection strategies, support farmers in real-time field conditions and ultimately contribute to improved food security and environmental sustainability (Mudgil *et al.*, 2024).

However, most plant disease detection research focuses on major commercial crops such as tomato, potato and maize, while Faba bean remains relatively under-explored in deep learning studies (Chohan *et al.*, 2025; Jain and Rathour, 2025). Existing automated disease detection systems are usually crop-specific and models trained on other crops cannot be directly applied to Faba bean because disease symptoms differ in appearance, color and texture (Salau *et al.*, 2023; Kottelenberg *et al.*, 2025). Several works address only binary classification, such as healthy versus diseased, rather than multi-class disease identification.

This study developed an automated deep learning framework for multi-class classification of Faba bean leaf diseases. The research aims to construct and utilize a field-collected, expert-annotated dataset that reflects real agricultural conditions. Transfer learning will be implemented using the VGG16 architecture to enable efficient feature extraction and accurate classification. The proposed model will categorize Faba bean leaves into four classes: healthy, rust, gall disease and chocolate spot. Model performance will be evaluated using classification metrics on an independent test dataset. Furthermore, the study seeks to assess the effectiveness of transfer learning for crop disease detection and to provide a scalable, practical solution for precision agriculture and automated plant health monitoring.

MATERIALS AND METHODS

Experimental environment

The experimental pipeline was implemented using Python 3.11. Model development and training were carried out with TensorFlow 2.x through the Keras high-level API and all

experiments were conducted within a Jupyter Notebook environment. To ensure reproducibility and consistency of results, random seeds were fixed for NumPy, TensorFlow and Python's built-in random module. Training was performed on a workstation equipped with an Intel Core i7-8700T CPU, 32 GB RAM, an NVIDIA GeForce GT 740 GPU (4 GB) and a 512 GB SSD. Hardware acceleration was enabled through the NVIDIA GPU, while primary computational processes were executed on the Intel processor, ensuring efficient model training and evaluation.

Dataset collection

Data collection was conducted across multiple farms located in Hengchun, Taiwan. Specifically, images were collected from farms located in Hengchun regions of Taiwan, between March and June 2024. Images were captured using portable handheld devices, including smartphones integrated with the Open Data Kit (ODK) platform, at varying angles and illumination levels to reflect realistic agricultural environments. Image acquisition was performed using smartphone cameras with resolutions ranging from 12 to 48 MP. Environmental conditions during image acquisition included natural daylight, partial shading and varying background complexity typical of real field settings. Disease labeling was performed and verified by agricultural experts to ensure annotation reliability. Permission for data collection was obtained from the respective farm owners and all images were collected solely for research purposes.

A comprehensive dataset comprised 8,021 RGB images collected under natural field conditions during the active cropping season. Image acquisition was conducted across multiple farms using a portable digital data collection device and agricultural experts supervised the process to ensure accurate disease labeling. All images were captured at a standardized resolution of 512 × 512 pixels to maintain uniformity for model training. The dataset was organized into four categories: healthy leaves (2,019 images), rust disease (2,000 images), gall disease (2,000 images) and chocolate spot disease (2,002 images). The nearly balanced distribution across classes helped minimize training bias and enhanced the reliability and generalization capability of the proposed model.

Faba bean leaf disease categories

The dataset included four visually distinct categories of Faba bean leaves. Chocolate spot disease is characterized

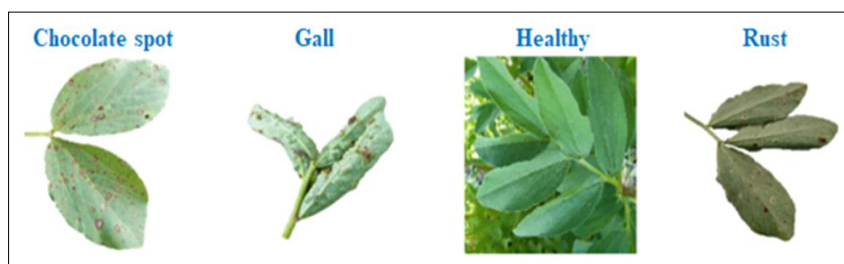


Fig 1: Representative samples of faba bean leaf disease categories.

by dark brown to black lesions scattered across the leaf surface, which may enlarge and merge under severe infection. Rust disease appears as orange to reddish-brown pustules, typically forming powdery spots on the underside of leaves. Gall disease causes abnormal swelling, thickening and deformation of leaf tissues, often resulting in distorted growth patterns. In contrast, healthy leaves exhibit uniform green coloration, intact structure and no visible symptoms of infection. Fig 1 shows representative examples of each category.

Data preprocssing

Prior to model training, all images were resized from 512×512 pixels to 224×224 pixels to satisfy the input dimensional requirements of the VGG16 architecture. The resizing operation can be represented as:

$$X_{\text{resize}} = R(X, 224, 224)$$

Where,

$R(\cdot)$ = Denotes the image resizing function.

X_{resize} = Resized image.

Pixel intensity values were normalized to the range $[0, 1]$ to stabilize gradient updates and accelerate convergence during optimization. The normalization process can be mathematically expressed as:

$$X_{\text{norm}}^{(i,j,k)} = \frac{X^{(i,j,k)} - X_{\min}}{X_{\max} - X_{\min}}, \text{ where } X_{\min} = 0, X_{\max} = 255$$

Where,

$X^{(i,j,k)}$ = Represents the pixel intensity at spatial location (i, j) and channel $k \in \{R, G, B\}$.

The dataset was partitioned into training, validation and test subsets using an 80:10:10 ratio to ensure unbiased model evaluation. Formally, if N denotes the total number of samples, the split is defined as:

$$N_{\text{train}} = 0.8N, N_{\text{val}} = 0.1N, N_{\text{test}} = 0.1N$$

The proportions satisfy the constraint

$$N_{\text{train}} + N_{\text{val}} + N_{\text{test}} = N$$

Categorical class labels were transformed using one-hot encoding to convert discrete class indices into binary vector representations. For a four-class problem, the encoded label vector $y \in \mathbb{R}^4$ is defined as:

$$y_c = \begin{cases} 1, & \text{if the sample belongs to class } c \\ 0, & \text{otherwise} \end{cases}$$

For example, a sample belonging to the second class is represented as $y=[0,1,0,0]$. This preprocessing pipeline ensured numerical stability, compatibility with the deep learning architecture and reliable performance evaluation.

Proposed VGG16 model architecture

The proposed model was implemented using the functional API and is based on the VGG16 convolutional neural network architecture with transfer learning. The input layer accepts images of shape $(224, 224, 3)$. The convolutional base consists of five sequential convolutional blocks. The

first block contains two Conv2D layers with 64 filters followed by max pooling, reducing the spatial dimension to 112×112 . The second block includes two convolutional layers with 128 filters and a pooling layer, producing 56×56 feature maps. The third block comprises three convolutional layers with 256 filters and pooling, generating 28×28 feature maps. The fourth and fifth blocks each contain three convolutional layers with 512 filters, followed by pooling operations, ultimately producing feature maps of size $7 \times 7 \times 512$. The convolution operation within each layer can be mathematically expressed in a generalized multidimensional form as:

$$Z_{i,j}^{(l,k)} = \sigma \left(\sum_{m=1}^{C_{l-1}} \sum_{p=0}^{F-1} \sum_{q=0}^{F-1} W_{p,q,m}^{(l,k)} X_{i+p,j+q,m}^{(l-1)} + b^{(l,k)} \right)$$

Where,

$Z_{i,j}^{(l,k)}$ = Denotes the output activation at spatial location (i,j) of the k^{th} filter in layer l , W represents the convolutional kernel weights of size $F \times F$, C_{l-1} is the number of input channels, $b^{(l,k)}$ is the bias term and $\sigma(\cdot)$ denotes the nonlinear activation function. After feature extraction, a global average pooling 2D layer compresses the spatial dimensions into a 512-dimensional feature vector, followed by a Dropout layer for regularization. The final Dense layer with four neurons applies the softmax function for multi-class classification, defined as:

$$\hat{y}_c = \frac{\exp(w_c^T x + b_c)}{\sum_{r=1}^4 \exp(w_r^T x + b_r)}, \quad C \in \{1, 2, 3, 4\}$$

Where,

$x \in \mathbb{R}^{512}$ = Represents the pooled feature vector.

w_c and b_c = Denote the weight vector and bias for class.

c and $\hat{y}_c$ = predicted probability for each disease category.

The total number of parameters in the model is 14,716,740, of which 14,714,688 are non-trainable (frozen convolutional base), while only 2,052 parameters in the final classification layer are trainable, ensuring computational efficiency and improved generalization. Fig 2 shows architecture of the proposed VGG16-based deep learning model used for multi-class classification of Faba bean leaf diseases, showing convolutional layers, pooling operations, fully connected layers and the final softmax output for four-class prediction.

Model training and evaluation metrics

The model was compiled using the Adam optimizer with a learning rate of 5×10^{-5} . This optimizer provides adaptive gradient updates for stable training. Categorical cross-entropy was used as the loss function for multi-class classification. Accuracy was selected as the primary performance metric. Early stopping was applied to prevent overfitting. Training was stopped when the validation performance no longer improved. Model performance was evaluated using classification metrics and confusion matrix. These metrics were calculated on the independent test dataset to ensure unbiased

assessment. The performance of the proposed model was evaluated using classification metrics and the confusion matrix.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + EN}$$

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Recall} = \frac{TP}{TP + FN}$$

$$F1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

RESULTS AND DISCUSSION

The model was trained for 50 epochs with early stopping enabled. At the final epoch (50/50), the training accuracy reached 86.82% with a training loss of 0.3520. The validation accuracy at epoch 50 was 92.52%, with a validation loss of 0.2144. However, the highest validation accuracy of 92.83% was achieved at epoch 49. Since validation performance did not improve further, the model restored the weights from the best-performing epoch (epoch 49).

The training and validation curves show steady improvement in accuracy over epochs (Fig 3). Training accuracy increased gradually and stabilized near the final epochs. Validation accuracy followed a similar trend and

remained consistently high, indicating good generalization. The validation accuracy being slightly higher than training accuracy suggests effective regularization, likely due to dropout and transfer learning.

This phenomenon can occur when regularization techniques such as dropout are applied during training but are disabled during validation and testing. Consequently, the model is evaluated under more stable conditions on the validation set, which may result in slightly higher validation accuracy than training accuracy. Furthermore, transfer learning from pretrained ImageNet weights provides robust feature representations that enhance generalization performance, particularly when the validation data distribution closely matches the training data. The relatively small difference between training and validation accuracy indicates good model generalization rather than overfitting.

The loss curves demonstrate a consistent decrease in both training and validation loss. Validation loss remained lower than training loss in later epochs, indicating stable convergence and minimal overfitting. The absence of sharp divergence between the curves confirms that early stopping successfully prevented performance degradation.

Fig 4 presents the confusion matrix of the proposed VGG16-based model evaluated on the independent test dataset for four-class classification. The diagonal elements show a strong concentration of correctly classified samples, indicating high predictive performance across all categories. For chocolate spot, 319 samples were correctly

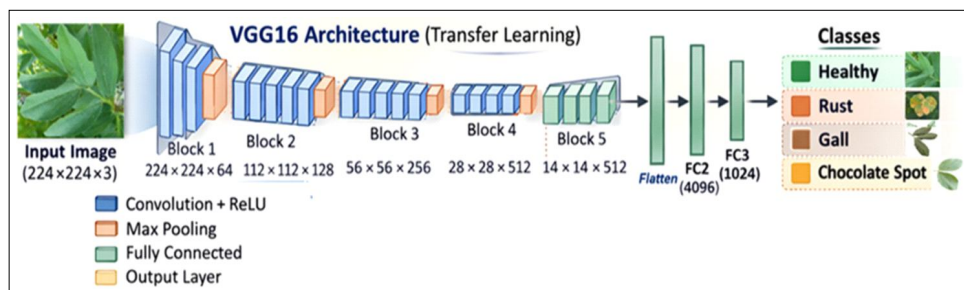


Fig 2: Architecture of the proposed VGG16-based deep learning model for faba bean leaf disease classification.

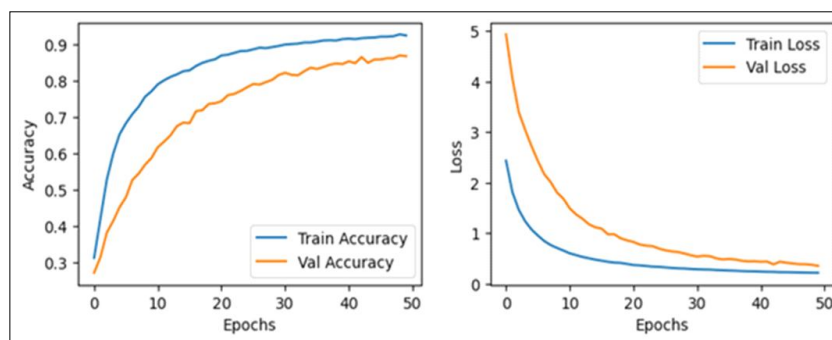


Fig 3: Training and testing measurements over epochs.

identified, with most misclassifications occurring as rust (65 samples), suggesting some visual similarity between lesion patterns. Gall disease achieved 312 correct predictions, with a moderate number of samples misclassified as chocolate spot (56) and rust (32), but none as healthy, indicating clear differentiation from non-diseased leaves. Healthy leaves were correctly classified in 326 cases, with limited confusion mainly toward chocolate spot (58) and rust (17). Rust demonstrated the highest correct classification rate, with 355 true positives and minimal confusion with other classes.

The classification report indicates strong overall performance of the proposed model across all four disease categories (Table 1). For chocolate spot, the model achieved a precision of 0.8939, recall of 0.8404 and an F1-score of 0.8663 based on 401 samples, indicating slightly lower recall compared to other classes. The gall class showed balanced and reliable performance, with precision of 0.9206, recall of 0.9275 and an F1-score of 0.9240 across 400 samples. The healthy class achieved the highest performance, with precision of 0.9470, recall of 0.9728 and an F1-score of 0.9597 from 404 samples, reflecting excellent model discrimination for healthy leaves. Similarly, rust classification demonstrated strong predictive capability, with precision of 0.9293, recall of 0.9525 and an F1-score of 0.9407 across 400 samples. Overall, the model achieved an accuracy of 0.9234 on 1,605 test images. The macro-averaged precision, recall and F1-score were all approximately 0.923, indicating consistent performance across classes, while the weighted averages further confirmed balanced classification effectiveness.

Fig 5 presents representative examples of model predictions for each of the four classes. In all cases, the predicted label matches the true label, indicating correct classification across different disease conditions. The model shows very high confidence for chocolate spot (99.79%) and gall (99.87%), demonstrating strong feature recognition for these disease patterns. The healthy leaf is also correctly identified with a confidence of 97.24%, reflecting reliable discrimination between diseased and non-diseased foliage. The rust sample is classified correctly with a confidence of 86.75%, which is slightly lower than the other classes but still indicates strong predictive capability.

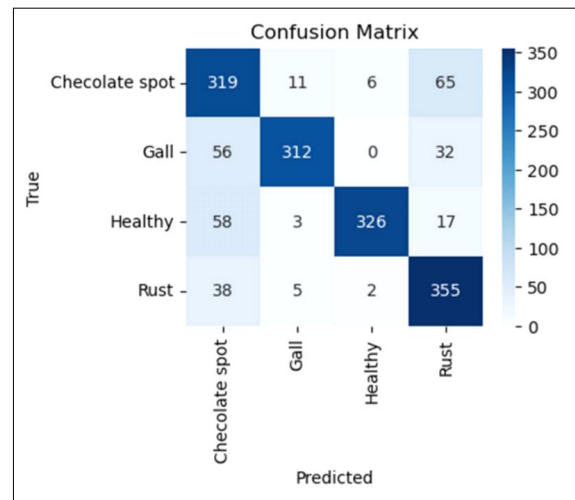


Fig 4: Confusion matrix after testing.

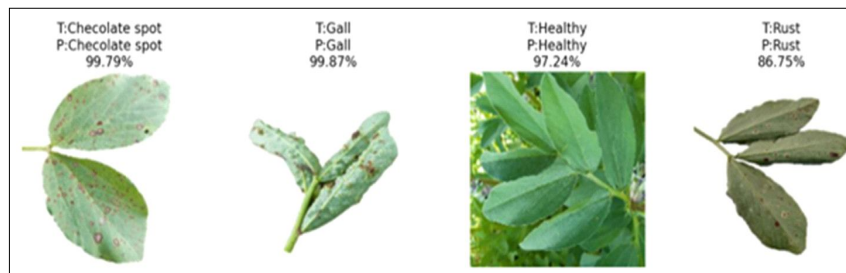


Fig 5: Representative examples of model predictions for faba bean leaf images.

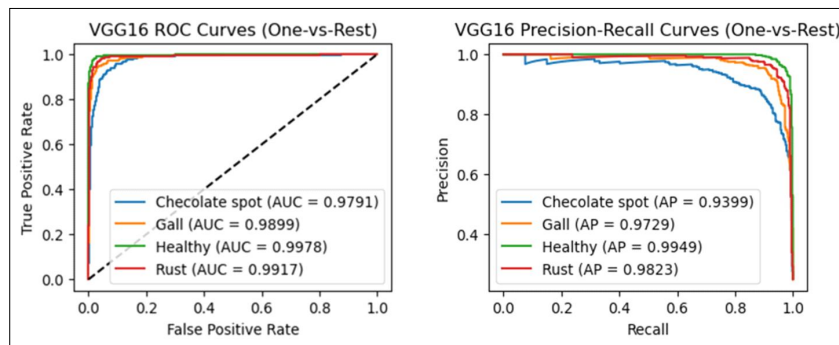


Fig 6: ROC and precision-recall curves of the proposed VGG16-based model for one-vs-rest multi-class classification.

Fig 6 presents the receiver operating characteristic (ROC) curves and precision-recall (PR) curves of the proposed VGG16 model for one-vs-rest multi-class classification of Faba bean leaf conditions. The ROC curves demonstrate the model's ability to distinguish each class from the others across different threshold settings. All curves are positioned close to the top-left corner, indicating excellent discrimination performance. The Area Under the Curve (AUC) values are very high for all classes, ranging from 0.9791 for chocolate spot to 0.9978 for healthy leaves, confirming strong separability between classes. The Precision-Recall curves further evaluate model performance under class imbalance by measuring the trade-off between precision and recall. High Average Precision (AP) scores across all categories indicate that the model maintained high precision even at increasing recall levels. Healthy leaves achieved the highest AP (0.9949), followed by rust (0.9823), gall (0.9729) and chocolate spot (0.9399). Previous studies have widely applied VGG16-based deep learning models for plant disease detection across different crops, including grapevine, tomato, maize, mango, rice, cotton and mixed plant species (Table 2).

Alatawi *et al.* (2022) applied VGG16 to 15,915 PlantVillage images covering 19 plant disease classes and achieved 95.2% accuracy, showing the feasibility of large-scale automated diagnosis. Mousavi and Farahani (2022) further enhanced VGG16 by integrating Faster R-CNN and drone-based image acquisition for grapevine

disease detection, achieving 99.6% accuracy and outperforming several standard deep learning architectures. Paul *et al.* (2024) implemented a pretrained VGG16 model within a mobile application to detect maize leaf diseases using 3,024 field and public images, achieving 93% testing accuracy and supporting real-time disease monitoring.

Similarly, Sofiane *et al.* (2024) used VGG16 to classify tomato leaf diseases across ten categories using 16,012 PlantVillage images, achieving approximately 98.3% accuracy. Kaur *et al.* (2024) applied VGG16 to mango leaf disease classification using 4,000 images across eight classes and reported 94% accuracy. Suseno *et al.* (2023) combined a pretrained VGG16 model with image segmentation techniques, including thresholding and k-means clustering, to classify three rice leaf diseases, achieving 91.66% accuracy after data augmentation and hyperparameter tuning. In another study, Kaur *et al.* (2024) fine-tuned VGG16 for cotton leaf disease classification using an augmented dataset of 5,000 images, achieving 95.5% accuracy and demonstrating improved performance with data expansion strategies.

Salau *et al.* (2023) highlighted the importance of image preprocessing in Faba bean disease detection by training an end-to-end CNN on both raw and enhanced images, achieving a substantial improvement in classification accuracy from 92.1% to 98.14% following preprocessing. Similarly, Jeong and Na (2024) developed a deep convolutional neural network incorporating multiple

Table 1: Classification performance of the VGG16 Model.

Class	Precision	Recall	F1-score	Support
Chocolate spot	0.8939	0.8404	0.8663	401
Gall	0.9206	0.9275	0.9240	400
Healthy	0.9470	0.9728	0.9597	404
Rust	0.9293	0.9525	0.9407	400
Overall accuracy			0.9234	1605
Macro average	0.9227	0.9233	0.9227	1605
Weighted average	0.9227	0.9234	0.9228	1605

Table 2: Comparison of VGG16-based plant disease detection studies.

Author	Crop / Dataset	Model	Accuracy
Alatawi <i>et al.</i> (2022)	15,915 plant leaf images	VGG16 CNN	95.2%
Mousavi and Farahani (2022)	Drone-captured grapevine leaf images (3 diseases)	Enhanced VGG16 + Faster R-CNN	99.6%
Paul <i>et al.</i> (2024)	3,024 maize leaf images	Pretrained VGG16	93%
Sofiane <i>et al.</i> (2024)	16,012 tomato leaf images	VGG16 CNN	98.3%
Kaur <i>et al.</i> (2024)	4,000 mango leaf images	VGG16 CNN	94%
Suseno <i>et al.</i> (2023)	Rice leaf disease images	Pretrained VGG16 +	91.66%
Kaur <i>et al.</i> (2024)	5,000 cotton leaf images	Fine-tuned VGG16	95.5%
Salau <i>et al.</i> (2023)	End-to-end CNN	Faba bean leaf images	98.14
Jeong and Na (2024)	Deep CNN	Faba bean leaf diseases	91
Mostafa <i>et al.</i> (2025)	Sequential CNN	Faba bean leaf images	98.92
This study	8,021 Faba bean leaf images	VGG16	92.34%

convolutional, pooling and dropout layers and trained the model using a balanced 80:20 dataset split, demonstrating the effectiveness of deep feature extraction and regularization for disease classification. More recently, Mostafa *et al.* (2025) and Mohammad *et al.* (2026) employed a sequential CNN trained on expert-labeled and preprocessed Vicia faba leaf images and reported an accuracy of 98.92%, indicating that high-quality annotations and carefully curated datasets can significantly enhance classification performance.

The present study applied transfer learning with VGG16 to classify Faba bean leaf diseases. The proposed model achieved 92.34% accuracy with a macro-averaged F1-score of 0.9227, demonstrating reliable multi-class classification under natural field variability. Collectively, these studies confirm that VGG16-based architectures provide robust and adaptable solutions for automated plant disease detection across different crops, datasets and deployment scenarios.

CONCLUSION

This study demonstrated the effectiveness of deep learning techniques, particularly the VGG16 architecture, for accurate plant disease classification using image-based analysis. The fine-tuned VGG16 model showed strong performance and successfully captured complex visual patterns associated with different disease conditions. The results highlighted the capability of deep learning to support precision agriculture through reliable and early disease detection. However, several limitations were identified. The dataset size was relatively limited, which may have reduced model generalization across diverse environmental conditions. Variations in lighting, background complexity and real field scenarios were not fully represented. In addition, the computational demands of VGG16 could restrict deployment in resource-constrained environments. Future research should focus on collecting larger and more diverse datasets, validating models under real field conditions and developing lightweight optimized architectures. Integration with mobile and drone-based monitoring systems could further enhance practical agricultural applications.

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Authors' contributions

All authors contributed toward data analysis, drafting and revising the paper and agreed to be responsible for all the aspects of this work.

Disclaimers

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Data availability

The data analysed/generated in the present study will be made available from corresponding authors upon reasonable request.

Availability of data and materials

Not applicable.

Use of artificial intelligence

Not applicable.

Declarations

Authors declare that all works are original and this manuscript has not been published in any other journal.

Conflict of interest

Authors declare that they have no conflict of interest.

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