Prickly Pear Disease Classification Using Deep Convolutional Neural Networks: A Case Study

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Abstract—**Prickly pear (Opuntia ficus-indica) is a member of the Cactaceae family. Because of its anti-inflammatory, anti-oxidant, antibacterial, hypoglycemic, and neuroprotective properties, prickly pears are a magical fruit. Both the fruit and its stem are utilized in value-added products. Deep learning (DL) applications are required for prickly pear disease detection and classification. To the best of our knowledge, no previous study has investigated prickly pear disease classification using convolutional neural networks. In this study, we propose the use of deep convolutional neural networks MobileNetV2 and DenseNet121, to classify prickly pear disease. A locally collected dataset from Tunisia was divided into two classes: healthy and cochineal. Data augmentation techniques were applied to increase the number of images. These augmented data were then fed as input into MobileNetV2 and DentNet121 networks. The experimental results show that MobileNetV2 achieved a precision, recall, and F1-score of 96.55% for healthy plants. For diseased plants, precision, recall, and F1-score reached 97.14%. Overall, the model obtained a classification accuracy of 96.88%. DenseNet121 achieved precision, recall, and F1-score values of 90.62%, 100%, and 95.08%, respectively, for healthy plants. For diseased plants, the precision, recall, and F1-score were 100%, 91.43%, and 95.52%, respectively, resulting in an overall classification accuracy of 95.31%. Our proposed deep learning models, MobileNetV2 and DenseNet121, perform well and demonstrate strong performance on the prickly pear dataset.**

Keywords*—*Plant disease classification; data augmentation; deep learning; prickly pear disease; MobileNetV2; DenseNet121

I. INTRODUCTION

Opuntia ficus-indica is commonly known as prickly pear and belongs to the Cactaceae family. It originates from Mexico, because of its unique adaptations and great capacity for biomass production, which enable it to thrive in harsh environments like hot weather and eroding, nutritionally deficient soils [1]. The prickly pear plant is utilized for a variety of purposes, such as food, feed, health, and nutrition, as well as for the production of prepared products like cosmetics, tea, juice, jam, and oil that is derived from the seeds [2]. Prickly pear has spread widely throughout the world, such as in Mexico, Africa, the American continent, and the Mediterranean Basin. It is utilized in a variety of medications due to its important function in disease treatment, anti-inflammatory, hypoglycemic, and stomach ulcer prevention properties. It is used as an antioxidant in many countries to treat burns, diabetes, bronchitis, asthma, and indigestion [3]. Early diagnosis of plant diseases is crucial to avoid crop losses. Traditional plant disease detection methods, which rely on manual feature extraction with the help of agricultural experts, are time-consuming, require labor, and are prone to errors. In contrast, deep learning methods have demonstrated impressive results across various fields, including agriculture [4], [5]. This research aims to classify prickly pear diseases using deep convolutional neural networks (CNNs), specifically MobileNetV2 and DenseNet121. The performance of the proposed models was evaluated using metrics such as precision, recall, F1-score, and accuracy. However, the use of well-known pretrained architectures like MobileNetV2 and DenseNet121 may limit the perception of technical novelty. Therefore, this work aims to provide a baseline evaluation of lightweight and efficient deep learning models under real-world conditions for prickly pear disease classification.

To the best of our knowledge, no prior studies have investigated the prickly pear plant, despite its importance. The main contribution of this work lies in its application to prickly pear disease classification using a real-field dataset, which presents unique challenges compared to commonly used plant disease datasets. Unlike controlled datasets, prickly pear images collected from the field exhibit high variability in background, lighting conditions, plant structure, and symptom appearance, particularly due to the irregular shape of cladodes and the diverse visual manifestations of cochineal infection at different stages. In addition, publicly available datasets for this crop are extremely limited or nonexistent, further emphasizing the relevance of this study.

Several studies have emphasized the efficiency of MobileNetV2 and DenseNet121 in early and automatic plant disease detection and classification.

Gatla et al. [6] aimed to develop an efficient edge AI framework for tomato leaf disease detection. They employ lightweight pre-trained models, particularly MobileNetV2, integrated with convolutional neural networks (CNNs), trained on the Plant Village dataset consisting of 18,160 images across ten tomato disease categories. The proposed method accomplished high performance, with MobileNetV2 attaining an accuracy of 98.99%. Joseph et al. [7] aimed to develop an accurate, real-time dataset and detection system for plant diseases affecting rice, wheat, and maize using deep learning. The study fine-tuned eight pre-trained CNN models, achieving test accuracies of 96.32% and 96.28% for MobileNetV2 and MobileNet, respectively, while recognizing the wheat leaf diseases. Taha and Badawy. [8] proposed a deep learning-based system for early plant disease detection to enhance sustainable agriculture. They utilized the MobileNetV2 CNN model, fine-tuned on the Plant Village dataset comprising 31,718 training and 4,514 test images across 20 disease categories. The model attained a high validation accuracy of 99.4%, with precision, recall, and F1-score metrics each around 99.3%, 99.2%, and 99.3%, respectively. Naveed et al. [9] developed AgriSage, an

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Android-based application for plant disease detection. They employed two deep-learning models: a MobileNetV2 classifier for binary classification and a custom CNN for multiclass disease classification. The MobileNetV2 model achieved a precision, recall, and F1-score of 1.00 for both classes on the test set. Duhan et al. [10] propose RTR_Lite_MobileNetV2 for developing a lightweight, accurate deep-learning model for plant disease detection and classification suitable for resource-constrained devices. The method is based on an enhanced MobileNetV2 architecture that integrates multiple attention mechanisms. The model is evaluated on seven publicly available datasets (Plant Disease/PlantVillage, PlantDoc, PaddyDoctor, Coffee, Wheat, Soybean, and Sugarcane). The results demonstrated high performance on the Plant Disease dataset, achieving an accuracy of 99.92%.

Ayyappan et al. [11] aimed to detect several rice plant diseases, such as blast, brown spot, and bacterial blight, using deep learning approaches. The authors trained and evaluated four state-of-the-art Convolutional Neural Network (CNN) models—DenseNet121, Xception, EfficientNet B4, and MobileNet V3 Large—on a dataset containing 10,407 images across 10 classes. Among the evaluated models, DenseNet121 achieved the highest performance with a test accuracy of 97.50%, followed by Xception at 96.32% and both EfficientNet B4 and MobileNet V3 Large at 96.25%. Simangunsong et al. [12] modified the DenseNet architecture to develop an optimized deep learning model for tomato disease classification. DenseNet-SEGR integrates the Squeeze-and-Excite (SE) block and utilizes a customized growth rate of 48 to optimize feature selection and classification. A dataset containing 12,246 images across 10 disease categories was used to train and evaluate the model. Compared to DenseNet-121, DenseNet-201, and MobileNetV2, DenseNet-SEGR achieved superior performance with accuracy of 98.22%, precision of 98.25%, recall of 98.22%, and F1-score of 98.22%. Ahad et al. [13] conducted a comparative study to assess the performance of deep learning architectures for classifying nine epidemic rice diseases in Bangladesh. It compared six models (DenseNet121, Inceptionv3, MobileNetV2, ResNet152V, ResNext10, and Seresnext101), transfer learning applied to four of these, and an ensemble model called DEX (DenseNet121, EfficientNetB7, and Xception). The dataset used combines the Rice Leaf Disease Dataset from Machine Learning Repository, as well as a dataset from the Bangladesh Rice Research Institute. The ensemble framework (DEX) achieved the highest accuracy of 98%, outperforming all individual networks, while Densenet121 achieved 97%. Belattar et al. [14] developed an effective and optimized CNN architecture (OP-CNN) to diagnose strawberry plant diseases in Morocco. To enhance performance, the proposed model was trained on a dataset of 2,000 images from Kaggle, with images preprocessed and augmented. The proposed model achieved an accuracy of 100%, precision of 100%, recall of 100%, and F1-score of 100% in the test set, outperforming DenseNet121, VGG19, and ResNet50, whereas DenseNet121 achieved an accuracy of 99%, precision of 100%, recall of 99%, and F1-score of 99%. Radhika and Kannan. [15] propose a model to enhance early detection of bell pepper leaf diseases using BPCCBAMIV3 (Bit direction and Positional Context Convolutional Block Attention Module) with InceptionV3 by integrating three attention mechanisms—Channel, Bit-level, and Positional—to capture irregular disease patterns and texture features. Using the PlantVillage dataset and a custom bell pepper dataset, we trained and tested the model. It achieved high accuracy, scoring 97.04% and 95.16%, respectively, outperforming others such as AlexNet, VGG16, ResNet50, DenseNet121 and EfficientNetB7. An accuracy of 94.62% was achieved by DenseNet121 on a custom bell pepper dataset.

There are no prior studies addressing prickly pear disease detection and classification using deep learning models. Therefore, the related work was expanded to include relevant studies on plant disease detection using MobileNetV2 and DenseNet121 architectures across other crops, in order to highlight the performance of these models. Compared to existing methods applied to other crops, our approach addresses an unexplored crop using a publicly available real-field dataset and demonstrates promising results for prickly pear disease classification.

The rest of this study is organized as follows. Section II presents a detailed description of the methodology. In Section III, the experimental results of the proposed method are presented and discussed. Section IV concludes the study and discusses future work.

II. METHODOLOGY

This section describes the CNN models employed, the dataset used, and the data augmentation techniques applied. The first and second subsections present the MobileNetV2 and DenseNet121 deep learning models, respectively, for classifying prickly pear plants as healthy or diseased. The third subsection describes the dataset structure and class distribution in detail. The final subsection presents the data augmentation techniques applied during training, including rotation, zoom, shift, and shear transformations.

A. MobileNetV2

The Google team developed MobileNetV2 as an improved version of MobileNetV1 [16]. This lightweight convolutional neural network architecture provides a good balance between model accuracy and inference speed, which makes it suitable for many applications, including object detection, image classification, and semantic segmentation. MobileNet divides the convolution into two layers: depth-wise and point-wise. Depth-wise convolution performs a single convolutional filter per input channel, whereas point-wise convolution calculates a linear combination of the input channels to build new features. MobileNetV2 introduces inverted residual blocks, where residual connections link low-dimensional representations rather than expanded feature spaces, and employs linear bottlenecks by removing nonlinear activations in the final projection layer to prevent information loss in compact feature representations [17]. MobileNetV2 basic structure is shown in Fig. 1.

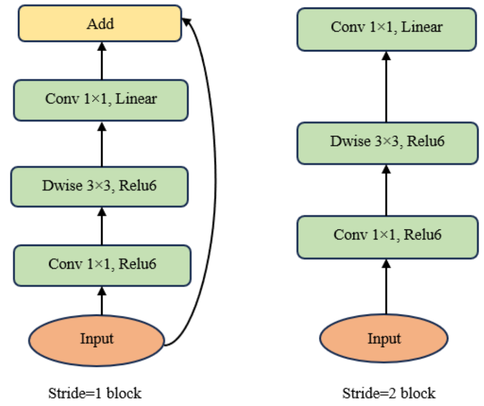

Fig. 1. MobileNet-V2 basic structure.

B. DenseNet121

In a traditional convolutional network with L layers, there are L connections—one between each layer and its subsequent layer. The Dense Convolutional Network (DenseNet) connects each layer to every other layer in a feed-forward fashion; it has L(L+1)/2 direct connections. DenseNet-121 is a densely connected convolutional neural network composed of 121 layers, where each layer receives as input the feature maps of all preceding layers and passes its own feature maps to all subsequent layers. There are several advantages of DenseNet, including the mitigation of the vanishing gradient problem, better feature propagation, and the ability to reuse features [18]. The structure of the dense block is shown in Fig. 2.

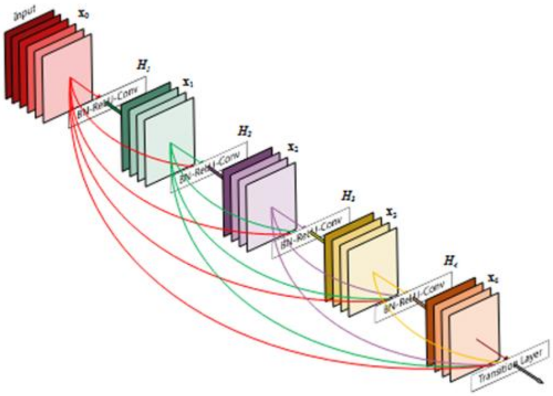

Fig. 2. Dense block structure.

C. Dataset

This research used a dataset of cactus (Prickly Pear), which comprised a total of 628 original images, including 285 images of healthy cacti and 343 images of cacti infected with the cochineal insect. All images were captured in Sidi Bouzid, Tunisia, with a pixel density of 72 pixels per inch, standardized, and saved in PNG format. The dataset was obtained from Mendeley data [19]. Due to the limited dataset size (628 images), the dataset was divided into 80% for training, 10% for validation, and 10% for testing, with data augmentation applied only to the training set to improve generalization. The details of the dataset split are presented in Table I. Images of healthy and diseased prickly pear plants, collected from the field of Sidi Bouzid, Tunisia, are shown in Fig. 3 and Fig. 4, respectively.

TABLE I. IMAGES USED IN THE TRAIN, VALIDATION AND TEST SETS.

Classes	Total images	Training images	Validation images	Testing images
Healthy	285 images	228 images	28 images	29 images
Cochineal	343 images	274 images	34 images	35 images

Fig. 3. Healthy prickly pear.

Fig. 4. Examples of the prickly pear diseases.

D. Data Augmentation and Model Hyperparameters

Data augmentation was used to meet the large data utilization challenge and to address model overfitting issues. This was achieved using the ImageDataGenerator class of the Keras library. Augmented and enhanced images were given to the MobileNetV2 and DenseNet121 predefined architectures. Data augmentation techniques applied during the training phase are presented in Table II. Model hyperparameters for MobileNetV2 and DenseNet121 are provided in Table III and Table IV, respectively. Hyperparameter values were determined through a series of experiments in which multiple configurations were evaluated using the validation set. Parameters such as learning rate, batch size, dropout rate, and regularization were adjusted iteratively to obtain stable convergence and improved validation performance while minimizing overfitting.

TABLE II. DATA AUGMENTATION METHODS AND VALUES

Data Augmentation Methods	Values
Rotation	±25°
Shift	±20%
Shear	±15%
Zoom	±20%
Horizontal Flip	True
Vertical Flip	True
Brightness	80-120%

TABLE III. HYPERPARAMETERS SELECTION FOR MOBILENETV2

Hyperparameter	Value
Batch Size	16
Initial Epochs	40
Fine-tuning Epochs	8
Total Epochs	48
Initial Learning Rate	0.001
Fine-tuning Learning Rate	0.00001
Optimizer	Adam
Dropout	0.5 and 0.3
L2 Regularization	0.0001
Activation Function	ReLU and Sigmoid
Loss Function	Binary crossentropy
Image_Size	224 × 224
Early Stopping	Patience: 7 epochs, Min Delta: 0.001

TABLE IV. HYPERPARAMETER SELECTION FOR DENSENET121

Hyperparameter	Value
Batch Size	32
Initial Epochs	21
Fine-tuning Epochs	12
Total Epochs	33
Initial Learning Rate	0.001
Fine-tuning Learning Rate	0.0001
Optimizer	Adam
Dropout	0.5 and 0.3
L2 Regularization	0.00001
Activation Function	ReLU and Sigmoid
Loss Function	Binary crossentropy
Image_Size	224 × 224
Early Stopping	Patience: 8 epochs, Min Delta: 0.0001

III. RESULTS AND DISCUSSION

This study utilized a publicly available dataset collected in Sidi Bouzid, Tunisia, for prickly pear disease classification. The dataset consists of 628 images of healthy and diseased prickly pear plants, which were used to train, validate, and test the MobileNetV2 and DenseNet121 models. Transfer learning was employed for both models by initializing the networks with ImageNet-pretrained weights, followed by fine-tuning to improve model performance. To mitigate overfitting, early stopping, dropout, and L2 regularization were applied during training. The performance of the MobileNetV2 and DenseNet121 models was evaluated using precision, recall, F1-score, and accuracy. These metrics are defined as follows.

$$\text{Precision} = \frac{TP}{TP+FP} \quad (1)$$

$$\text{Recall} = \frac{TP}{TP+FN} \quad (2)$$

$$\text{F1} - \text{score} = \frac{2.Precision.Recall}{Precision+Recall} \quad (3)$$

$$\text{Accuracy} = \frac{CorrectPredictions}{TotalPredictions} \quad (4)$$

$$\text{PrecisionMacroAvg} = \sum_{i=1}^{n}\left(\frac{Precisioni}{n}\right) \quad (5)$$

$$\text{RecallMacroAvg} = \sum_{i=1}^{n}\left(\frac{Recalli}{n}\right) \quad (6)$$

$$\text{F1} - \text{scoreMacroAvg} = \sum_{i=1}^{n}\left(\frac{F1-scorei}{n}\right) \quad (7)$$

$$\text{WeightedAvg F1—score} = \sum_{i=1}^{N}(Wi \times F1 - scorei) \quad (8)$$

where,

$$\text{Wi} = \frac{Number\ of\ samples\ in\ each\ classi}{Total\ number\ of\ samples} \quad (9))$$

The weighted average precision and recall are computed in the same manner.

The classification results of MobileNetV2 are presented in Table V. They demonstrate strong performance for both classes. For the Cochineal class, the model achieved precision, recall, and F1-score values of 97.14%. For the Healthy class, the precision, recall, and F1-score reached 96.55%. The overall classification accuracy of the model was 96.88% on the test set (64 samples). In addition, the macro-average (96.85%) and weighted-average (96.88%) scores are nearly identical, indicating balanced performance across classes without bias toward either category.

The classification results of DenseNet121 (Table VI) indicate strong performance on the prickly pear dataset. For the Cochineal class (35 samples), the model achieved a precision of 100%, a recall of 91.43%, and an F1-score of 95.52%. For the Healthy class (29 samples), the model obtained a precision of 90.62%, a recall of 100%, and an F1-score of 95.08%. The overall classification accuracy was 95.31% on the test set (64 samples), corresponding to three misclassified images. The macro-average F1-score (95.30%) and weighted-average F1-score (95.32%) are nearly identical, indicating relatively balanced performance across both classes without significant class bias.

TABLE V. Detailed Classification Results of Mobilenetv2 Model on the Prickly Pear Dataset

	Precision	**Recall**	**F1-score**	**Support**
Cochineal	0.9714	0.9714	0.9714	35
Healthy	0.9655	0.9655	0.9655	29
accuracy			0.9688	64
macro avg	0.9685	0.9685	0.9685	64
weighted avg	0.9688	0.9688	0.9688	64

TABLE VI. Detailed Classification Results of Densenet121 Model on the Prickly Pear Dataset

	Precision	**Recall**	**F1-score**	**Support**
Cochineal	1.0000	0.9143	0.9552	35
Healthy	0.9062	1.0000	0.9508	29
accuracy			0.9531	64
macro avg	0.9531	0.9571	0.9530	64
weighted avg	0.9575	0.9531	0.9532	64

The final test set contains only 64 images across two classes, which may affect the stability of the reported performance, as small changes in predictions could influence the evaluation metrics. This limitation is mainly due to the relatively small size of the available dataset. To the best of our knowledge, the dataset used in this study is currently one of the few, if not the only, publicly available real-field datasets for the prickly pear plant. However, we acknowledge that the dataset was collected from a single location in Tunisia, which may limit the generalization of the models to different farms, seasons, cameras, lighting conditions, or plant growth stages. Future work will focus on expanding the dataset by collecting additional images from diverse environments to further evaluate the robustness and generalization capability of the proposed models.

The MobileNetV2 and DenseNet121 models were chosen based on their proven effectiveness in plant disease detection and classification reported in previous studies (Table VII). They demonstrated outstanding results across various datasets and crops, achieving accuracy levels of up to 99% in some cases. However, other computer vision architectures, such as ResNet, EfficientNet, Inception, and Vision Transformer–based models have also shown strong performance in plant disease detection and classification tasks and may be explored for prickly pear disease classification.

The training and validation accuracy graphs for both models (Fig. 5) demonstrate a rapid increase during the initial epochs, which indicates the quick learning features. After this early phase, the curves progressively stabilize, reflecting convergence and effective learning. For MobileNetV2, training and validation accuracies show good generalization with minor fluctuations. After the fine-tuning phase, a small temporary decrease in training accuracy appears, but the validation accuracy continues to improve slightly. For DenseNet121, the training accuracy increases steadily from the first epochs and reaches a high value (≈0.96) toward the end. However, the validation accuracy shows noticeable fluctuations. After the fine-tuning phase (≈ epoch 21), both curves become closer and more stable, but the validation accuracy does not continuously increase; instead, it slightly decreases and then stabilizes around ~0.90–0.92 while the training accuracy continues to improve, which indicates mild overfitting.

TABLE VII. TMobileNetV2 and DenseNet121 Models For Plant Diseases Detection And Classification.

References	**AI model**	**Dataset**	**Crop**	**Accuracy**
[20]	MobileNetV2	Publicly available dataset	Multi-Crop	99.57 %
[21]	MobileNetV2 MobileNet-SE (Squeeze and Excitation)	Fig leaf dataset	Fig	90.74% 92.90%
[22]	MobileNetV2	Secondary publicly available datasets	Apple	97.13 %
[23]	DenseNet121	Maize leaf dataset	Maize	97.14%
[24]	Fine-tuned DenseNet121	Plant leaf dataset from the PlantVillage dataset	Apple	98.9%
[25]	DenseNet121	Cherry Dataset	Cherry	99.9%

The training and validation loss graphs (Fig. 6) for MobileNetV2 and DenseNet121 demonstrate strong generalization performance. MobileNetV2's training and validation loss curves both exhibit a strong decline in the first epoch. After this first stage, losses continue to decrease more gradually with minor variations. Around epoch 40, there is a discernible brief rise in training loss, while validation loss keeps declining before leveling off. In the last epochs, validation loss stays low or close to training loss, indicating that there isn't any significant overfitting. The DenseNet121 loss curves decrease smoothly from the beginning, demonstrating stable and efficient convergence. The validation loss decreases quickly in the early epochs and remains close to or slightly below the training loss for most of the training process. Around the fine-tuning phase (≈ epoch 21), only minor fluctuations are observed in both curves, but they quickly stabilize again. In the final epochs, the training loss continues to decrease slightly while the validation loss levels off with small fluctuations.

As shown in Fig. 7, the confusion matrices of MobileNetV2 and DenseNet121 demonstrate robust classification performance. MobileNetV2 indicates balanced classification, with only one misclassification in each class, while DenseNet121 achieves the best classification performance for healthy samples but misclassifies a small number of infected images as healthy (three images). These few misclassifications are mainly due to variations in lighting, background, glare, and image quality, which can obscure important features and affect model predictions. From a biological perspective, the variability in the manifestation of cochineal infection—including early-stage or partial symptoms—can increase classification difficulty.

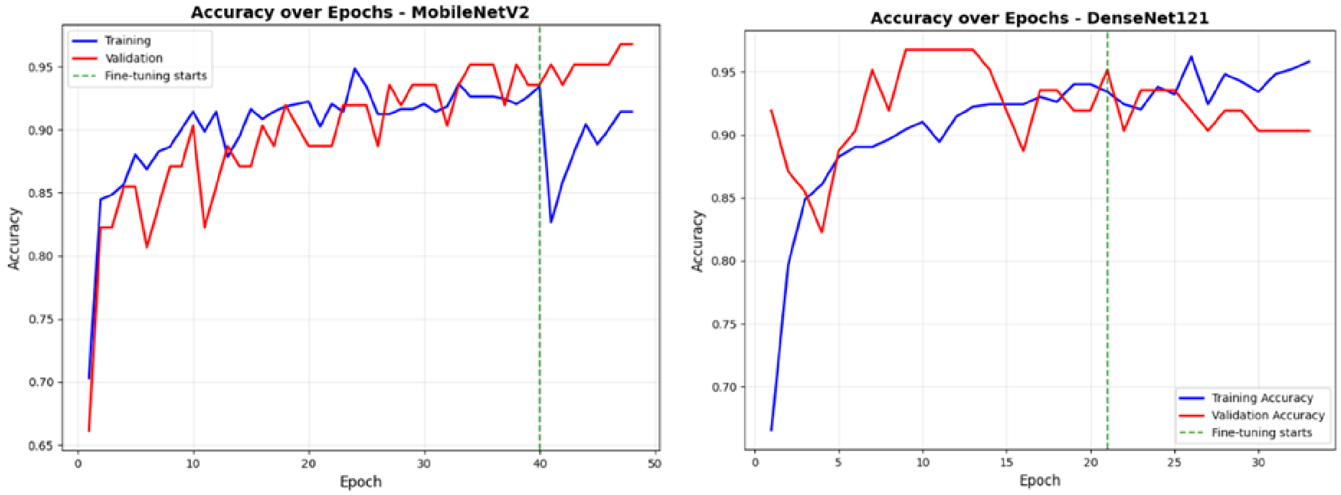

Fig. 5. Training and validation accuracy of MobileNetV2, and DenseNet121.

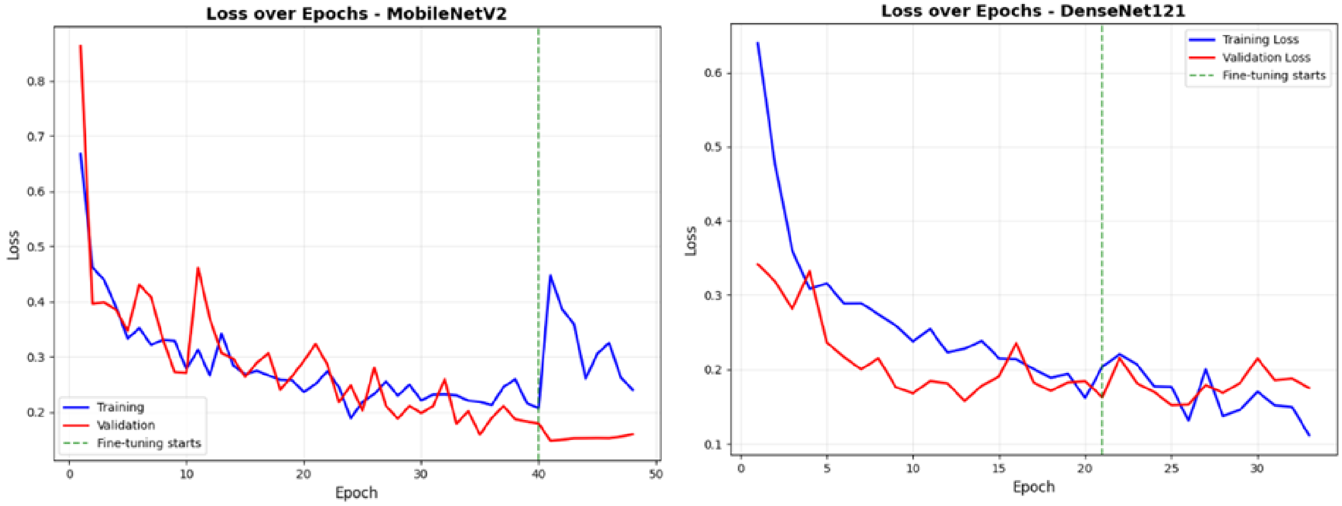

Fig. 6. Training and validation loss of MobileNetV2, and DenseNet121.

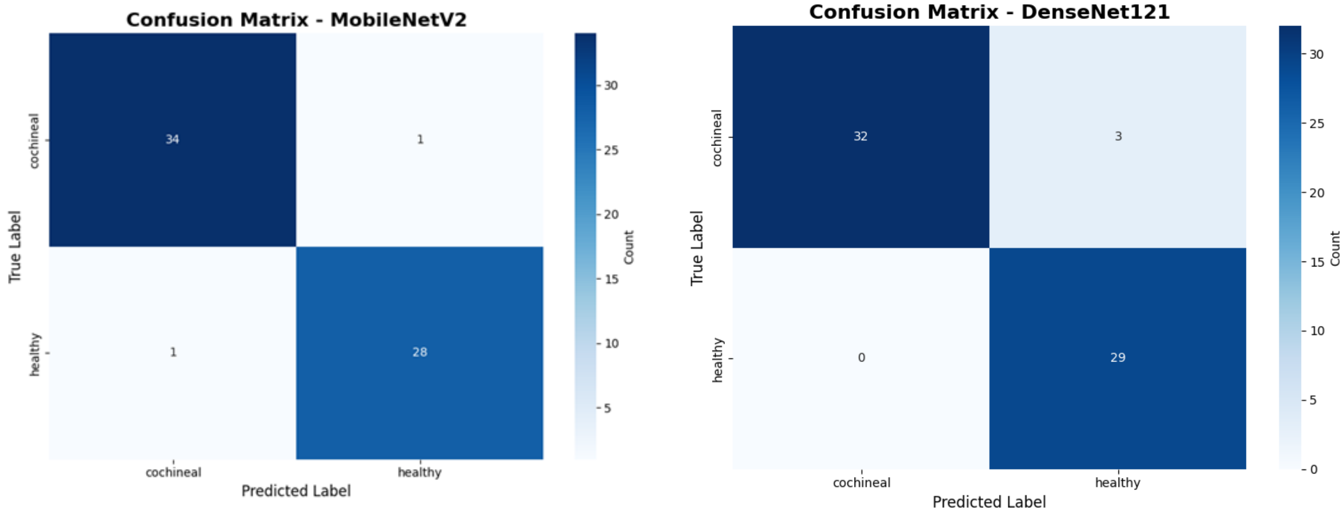

Fig. 7. Confusion matrices of MobileNetV2, and DenseNet121 on the prickly pear dataset.

Finally, both MobileNetV2 and DenseNet121 show strong overall performance for prickly pear disease classification on the cactus dataset.

IV. CONCLUSION

This study evaluates, through a case study, the performance of MobileNetV2 and DenseNet121 for prickly pear disease classification. A publicly available dataset collected in Sidi Bouzid, Tunisia, was used to assess the effectiveness of the models. The results demonstrate strong model performance for classifying prickly pear plants using MobileNetV2 and DenseNet121, achieving comparable classification accuracies of 96.88% and 95.31%. respectively. This study successfully demonstrates that convolutional neural network models can be effectively applied to prickly pear disease classification, despite the limited availability of prickly pear datasets. This highlights the adaptability of deep learning approaches to new agricultural contexts. The main contribution of this work lies in being, to the best of our knowledge, the first study to address disease classification in prickly pear plants using deep learning techniques. In future work, we intend to collect a large, balanced dataset from diverse environments for prickly pear plants and use it to train and evaluate a new reliable deep learning (DL) model, along with other DL models, to identify and classify additional prickly pear diseases, as well as to assess the generalization capability of these models.

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