

2024-10-04

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IJST

<https://doi.org/10.17485/IJST/v17i37.2453>

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RESEARCH ARTICLE



A Deep Learning Model for Classifying Black Sigatoka Disease in Banana Leaves Based on Infection Stages

OPEN ACCESS

Received: 31-07-2024

Accepted: 10-09-2024

Published: 04-10-2024

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Citation: Kambo E, Nyambo D, Leo J, Ally M (2024) A Deep Learning Model for Classifying Black Sigatoka Disease in Banana Leaves Based on Infection Stages. Indian Journal of Science and Technology 17(37): 3889-3897. <https://doi.org/10.17485/IJST/V17I37.2453>

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Funding: None

Competing Interests: None

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Published By Indian Society for Education and Environment ([iSee](https://www.isee.org/))

ISSN

Print: 0974-6846

Electronic: 0974-5645

Abstract

Objective: This research study aims to develop an efficient deep-learning model to detect and classify stages of Black Sigatoka disease in banana plants. **Methods:** In this study, deep learning techniques, specifically the basic Convolutional Neural Network (CNN) and VGG16 models, were used to address the challenge of identifying Black Sigatoka disease in banana leaves early on. The tests were conducted on a dataset containing labelled images of banana leaves, assessing their effectiveness based on criteria such as accuracy, precision, recall, and F1-score after adjusting hyperparameters for optimal outcomes. **Findings:** The results of the trials revealed that the basic CNN model attained a training accuracy of 96% and a validation accuracy of 89%, surpassing the performance of the VGG16 model. The VGG16 model, on the other hand, had a training accuracy of 92% and a validation accuracy of 89%. Across precision, recall, and F1 score measurements, the basic CNN model consistently outperformed the VGG16 model, with scores averaging 0.90 for all three metrics compared to VGG16's precision of 0.80, recall of 0.75, and F1 score of 0.75. The CNN model demonstrated its efficiency by stopping training at 26 epochs, whereas VGG16 completed training in 21 epochs. This demonstrates its effectiveness in detecting Black Sigatoka while utilising minimal resources. **Novelty:** A significant component of this study is its emphasis on identifying the stages of Black Sigatoka disease, which is commonly overlooked in research. By studying disease progression, this study provides insights for early intervention and disease management, aiding efforts to lessen the impact of Black Sigatoka on banana farming.

Keywords: Black Sigatoka; Deep Learning; Disease Stages; Convolutional Neural Network; Classification; Identification

1 Introduction

In recent years, technological innovations have continued to make considerable contributions within different sectors found in society. For example, online business has boomed across the world; in medicine, preliminary self-health diagnosis tools have been developed and are in use. The agriculture sector is not left behind as well. In an

effort to adopt technology in the agriculture sector, a lot has been done. Technology is required to address a number of challenges, such as diseases, one of them being Black Sigatoka which, is said to be a threat to global food security. It is a fungal type of disease caused by *Mycosphaerella fijiensis*. This fungus affects not only banana leaves as well as plantains⁽¹⁾. For this study, both bananas and plantains will be collectively referred to as bananas. The disease is known to significantly affect the quality as well as the quantity of banana yields from the farms. The global economy of farmers is affected at large, with the situation being particularly challenging in developing countries like Tanzania. In Tanzania, around 60% of the population, which is approximately 40 million people, depend on farming for their livelihoods⁽²⁾. Such devastating impact of Black Sigatoka disease could heavily impact not only their food security but also their economic stability.

Black Sigatoka fungus affects the plant's photosynthesis ability, causing it to fail to produce the required amount of food it requires, which may cause the plant to die or produce fruits of lower quality. The disease is characterised by having faint brown streaks in the early stages, evolving to well-defined black spots in the later stages. In general, the earliest stages are very difficult to detect, as observed in other studies as well, for example, the study by⁽³⁾ that tried to address the problem by developing an automated system for early detection. Studies have been carried out that proposed different stages of the disease. Some proposed six stages, and those that have proposed to modify the six stages, turning them into four stages of the disease based on the infection severity. The following terms are used to categorise the stages of the disease: "high", "medium", "early," and "health"^(4,5).

As stated before, technology has continued to play a major role in providing solutions to different problems across different sectors, including agriculture. In recent years, artificial intelligence has continued to rise in providing different solutions. Deep learning has been successful in solving classification tasks across different sectors. Different studies have applied different algorithms. Convolutional neural networks (CNN) have shown promising results in the early detection and classification of diseases accurately through the use of images. For example, the study by⁽⁶⁾ employed a ShuffleNet V2 algorithm which is a variant of a CNN architecture, and compared them to other machine learning architectures, specifically Support Vector Machine (SVM) and K-Nearest Neighbour (KNN). In an attempt to address the challenges brought by Black Sigatoka,⁽⁷⁾ used hyperspectral images in developing models to detect infected banana leaves. Other studies, such as those conducted by^(8,9), have incorporated mobile technology in deploying their classification models.

However, besides these observed solutions, the disease persists. It can be observed that many of the studies that have been carried out have not ventured into the crucial task of classifying the Black Sigatoka disease by its stages of progression. Addressing the problem through its progression stages provides an opportunity to properly manage the disease at its different stages and provide appropriate intervention strategies that are required at each specific stage⁽¹⁰⁾. Most of the literature focusses on dividing cases into infected or healthy, overlooking the journey from initial symptoms to severe infection. This gap, in knowledge is what our research seeks to fill.

In light of these difficulties, this research suggests a learning method to categorize Black Sigatoka disease in banana leaves into different stages: healthy, early, intermediate, and advanced. Using a dataset of banana leaf images gathered from areas in Tanzania, the goal of the study is to create a model that not only identifies the disease's presence but also accurately determines its stage. In this study, the approach used focuses on expanding on the existing CNN architectures by comparing the efficiency of a basic CNN model with that of the pre-trained VGG16 model. The study aims to ultimately help farmers by providing a tool for intervention that may reduce the impact of Black Sigatoka disease on banana production.

Through this research, the study seeks to contribute to the advancement of agricultural practices by providing a valuable solution for combating the destructive impact of Black Sigatoka disease on banana plantations as well as contributing to the ongoing effort to integrate advanced machine learning techniques into agricultural disease management practices that go beyond the traditional methods in use.

The paper is organized as follows: Section 2 provides a thorough explanation of the study's methodology. Section 3 is devoted to results and discussions. The conclusion and future work are explained in Section 4.

2 Methodology

In this section, the details of the different classification algorithms that have been used to classify the four stages of Black Sigatoka disease are described. The focus of this proposed method is to find the best algorithm for the classification task. To that end, the section is divided into the following subsections: data acquisition, data pre-processing, model development, and model evaluation.

2.1 Data acquisition

The Black Sigatoka images used in this study came from a publicly available dataset from ⁽¹¹⁾. The dataset contains 16,092 images of banana leaves and stems, making it the largest publicly accessible dataset for banana-related images in Tanzania. The images from the dataset were collected from different farms in selected regions of Tanzania. The regions are Arusha, Dar es Salaam, Kagera, Kilimanjaro, and Mbeya. The choice of these regions was based on the quantity of banana production and the presence of the disease. Mobile phones were used to collect the images. The agriculture experts were employed to provide the needed supervision. From the dataset, the images of Black Sigatoka-infected banana leaves and healthy banana leaves were considered for this study. A total of 5767 images of Black Sigatoka were present after the initial preprocessing step of removing duplicates. The dataset had images with a size of 1024×768 pixels in jpeg format. Each image was labeled using a number format within a named subfolder as per class name. It is important to note that this dataset did not contain the images of Black Sigatoka that have been grouped based on their stages of infection. The researcher had to undertake meticulous work with three agriculture specialists to separate the images into their respective group stages. Figure 1 shows sample images from the dataset grouped as per their respective stages or classes. A detailed explanation of how the work was done deserves a different paper of its own. The split of the final dataset after data preprocessing for training and testing followed an 80% by 20% approach.

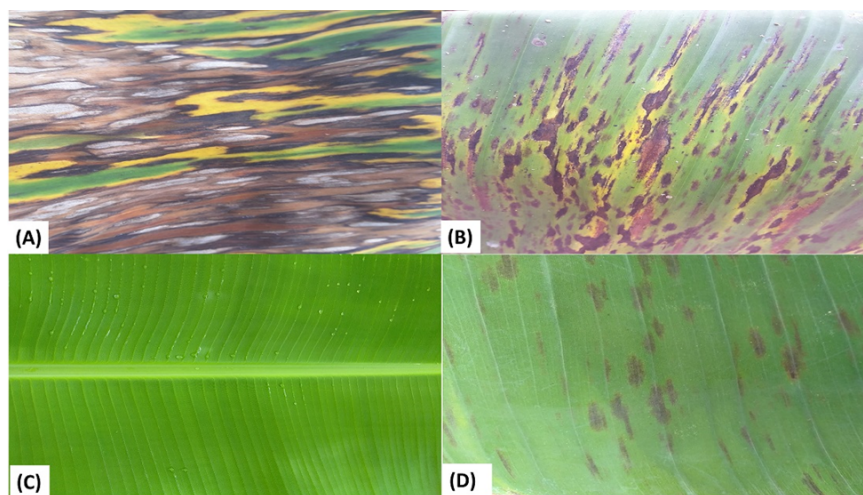


Fig 1. Sample images of Black Sigatoka Disease in Banana Leaves

2.2 Data preprocessing

Preprocessing the data is a necessary task before any model training is carried out. The data collected came in different forms and formats that could not be used as they were. In this study, the following activities were carried out to preprocess the data.

2.2.1 Image resizing

The images that were collected from the different sites had a resolution of 1024×768 pixels. This image quality is considered good for some tasks but not all. In model development, the images may demand more resources and hence cause the model to perform poorly. Thus, the images need to be resized to improve the overall efficiency of the model. Proper methods need to be considered when resizing the images because studies have shown that improper image resizing may cause the deep neural network models to perform poorly. It has also been shown that proper resizing of the images can help models achieve comparable performances even when the images are of smaller sizes. This in turn reduces the complexity of the model without sacrificing the accuracy of the model ⁽¹²⁾. The images were resized to 224×224 pixels in the experiments carried out in this study. It is said that there is no specific image size for all problems; it is a matter of trial and error as the search for better accuracy of the models carries on.

2.2.2 Data augmentation

Data augmentation involves creating new data from the existing data using different transformations or modification techniques. Examples of transformation are rotation, cropping, shear, flipping, scaling, and many others. The images of Black Sigatoka-infected banana leaves present in the dataset were not initially collected with the mindset of grouping them in terms

of their respective stages. In the process of grouping them into their respective stages, a data imbalance was observed; the early-stage images of Black Sigatoka-infected leaves were few compared to the advanced stages and intermediate stages. Thus, to solve this challenge, rotation, flipping, shearing, and cropping transformations were carried out using a Python augmentation package. Table 1 shows the total number of images in each class after augmentation was carried out for training and validation.

Table 1. Distribution of images per class after augmentation for training and validation

Class names	Training images	Validation images	Total images
Health	1600	400	2000
Early	1600	400	2000
Intermediate	1600	400	2000
Advanced	1600	400	2000

2.2.3 Normalization

The min-max normalization technique was applied in this study as a way to scale the pixel intensity value of the images between 0 and 1. Normally, image intensity values range from 0 to 255. 0 represents black color, and 1 represents white colour. This range of intensity values can interfere with the model learning process, especially for those models that are sensitive to feature scales⁽¹³⁾. Thus, there is a need for normalizing the images.

2.3 Model development

In this section, details of the development process of the various models are given. Table 2 provides a summary of the general device specifications and the Google Colab environment configurations employed for executing the experiments. All notebook files were executed on the Google Colab platform to ensure a standardized and efficient computational environment.

Table 2. System specifications for the machine used to run the experiments

Specification Type	Value
OS name	Microsoft Windows 10 pro
System type	x64-based PC
Processor	Intel(R) Core(TM) i5-7200U CPU @ 2.50GHz, 2712 Mhz, 2 Core(s), 4 Logical Processor(s)
Installed Physical Memory (RAM) Google	16.0 GB
Google Colab plan	Colab Pro Plus with a Tesla T4 GPU and 54.8GB of RAM.

2.3.1 The CNN model

The following is the structure of the architecture of the convolutional neural network (CNN) that was employed for training. It used a sequential model that had a total of thirteen layers. It had two initial convolutional layers (conv2d, conv2d1) with 32 filters in each of them. The next was the max pooling layer (maxpooling2d) that was used for downsampling. This pattern was repeated two times. In each repetition, the number of convolutional layers (conv2d2, conv2d3, conv2d4, conv2d5) was increased to 64 and then to 128. The number of filters was maintained to be 32 for the subsequent pooling layers (maxpooling2d11 and maxpooling2d2). In doing this, more complex features were extracted progressively from the images. The next phase of the architecture employed a set of convolutional and pooling layers (conv2d6, conv2d7, maxpooling2d3) with a higher number of filters (256) in the convolutional layers. The last set of layers included two convolutional layers and a pooling layer (conv2d8, conv2d9, maxpooling2d4). The pooling layer had the task of reducing the spatial dimensions of the data. To reduce the risk of overfitting during training, the dropout layers (dropout and dropout1) were placed at strategic points after the fully connected layers. The final part of the model architecture included the flattening layer (flatten) that had the duty to transform the data into a one-dimensional vector, followed by two fully connected layers (dense, dense1) with 1500 and 4 neurons, respectively. The architecture ended with the final layer, which had 4 neurons that corresponded to the four target classes. Table 3 summarises the description of the CNN architecture used in this experiment. In this experiment, a total of 1,771,696 parameters were used as features for the model. Table 4 summarises hyperparameter settings that were used in the training process.

Table 3. CNN model architecture summary

Layer (type)	Output Shape	Param #
conv2d	(None, 224, 224, 32)	896
conv2d_1	(None, 222, 222, 32)	9248
max_pooling2d	(None, 111, 111, 32)	0
conv2d_2	(None, 111, 111, 64)	18496
conv2d_3	(None, 109, 109, 32)	18464
max_pooling2d_1	(None, 54, 54, 32)	0
conv2d_4	(None, 54, 54, 128)	36992
conv2d_5	(None, 52, 52, 32)	36896
max_pooling2d_2	(None, 26, 26, 32)	0
conv2d_6	(None, 26, 26, 256)	73984
conv2d_7	(None, 24, 24, 32)	73760
max_pooling2d_3	(None, 12, 12, 32)	0
conv2d_8	(None, 12, 12, 512)	147968
conv2d_9	(None, 10, 10, 32)	147488
max_pooling2d_4	(None, 5, 5, 32)	0
dropout	(None, 5, 5, 32)	0
flatten	(None, 800)	0
dense	(None, 1500)	1201500
dropout_1	(None, 1500)	0
dense_1	(None, 4)	6004
Total params		1771696
Trainable params		1771696
Non-trainable params		0

Table 4. Model training hyper-parameters for CNN & VGG16 models

Parameters	Value(s)
Batch size	32
Optimizer	Adam with a learning rate of 0.001
Epoch	100 (with early stopping)
Loss	Categorical Cross-entropy
Evaluation metric	Accuracy, Precision, Recall and f1-score

2.3.2 The VGG16 model

In this study, the VGG16 model, a type of network (CNN) design, is employed. It is well regarded for its straightforwardness and efficiency in tasks related to image classification. The Visual Geometry Group at the University of Oxford developed this model architecture. It is a structure with layers dedicated to convolution and max pooling for feature extraction and dimensionality reduction purposes. Unlike the CNN model without predefined layers, VGG16’s deep architecture allows for extracting more intricate features from images. Consequently, the fixed parameters within the VGG16 design simplify both implementation and training processes. In this study, the VGG16 architecture closely resembled a CNN structure with convolutional and max pooling layers followed by fully connected layers. The convolutional layers (block1_conv1 to block5_conv3) were utilized to extract features at abstraction levels, increasing complexity in deep layers. Conversely, max-pooling layers (block1_pool to block5_pool) were employed to downsample feature maps for dimensionality reduction purposes. Additionally, a flattening layer was included towards the end of the architecture to reshape these feature maps into a vector.

Following that, a dense layer with 4 units, each corresponding to a target class, was added to complete the structure. The model had a total of 52,354,192 parameters, with 37,639,504 being trainable. This configuration allowed the model to acquire features for distinguishing between the four study classes. The models’ architecture is outlined in Table 5, while Table 4 details the hyperparameter configurations utilized.

Table 5. VGG16 model architecture summary

Layer (type)	Output Shape	Param #
input_1 (InputLayer)	(None, 224, 224, 3)	0
block1_conv1 (Conv2D)	(None, 224, 224, 64)	1792
block1_conv2 (Conv2D)	(None, 224, 224, 64)	36928
block1_pool (MaxPooling2D)	(None, 112, 112, 64)	0
block2_conv1 (Conv2D)	(None, 112, 112, 128)	73856
block2_conv2 (Conv2D)	(None, 112, 112, 128)	147584
block2_pool (MaxPooling2D)	(None, 56, 56, 128)	0
block3_conv1 (Conv2D)	(None, 56, 56, 256)	295168
block3_conv2 (Conv2D)	(None, 56, 56, 256)	590080
block3_conv3 (Conv2D)	(None, 56, 56, 256)	590080
block3_pool (MaxPooling2D)	(None, 28, 28, 256)	0
block4_conv1 (Conv2D)	(None, 28, 28, 512)	1180160
block4_conv2 (Conv2D)	(None, 28, 28, 512)	2359808
block4_conv3 (Conv2D)	(None, 28, 28, 512)	2359808
block4_pool (MaxPooling2D)	(None, 14, 14, 512)	0
block5_conv1 (Conv2D)	(None, 14, 14, 512)	2359808
block5_conv2 (Conv2D)	(None, 14, 14, 512)	2359808
block5_conv3 (Conv2D)	(None, 14, 14, 512)	2359808
block5_pool (MaxPooling2D)	(None, 7, 7, 512)	0
flatten	(None, 25088)	0
dense	(None, 1500)	37633500
dropout	(None, 1500)	0
dense_1	(None, 4)	6004
Total params		52354192
Trainable params		37639504
Non-trainable params		14714688

2.4 Model evaluation

In this study, the following metrics were used to assess the performance of the model developed. Accuracy, precision, recall, F1-score, and the confusion matrix. From accuracy, the overall measure of the correctness of the model to classify the images can be obtained. Precision is the ratio of correctly identified positive cases to all predicted positive cases. Recall is the ratio of correctly identified positive cases out of all actual positive instances in the dataset. The F1-score provides a balanced assessment of the performance of the model. Lastly, the confusion matrix is used to obtain a detailed breakdown of the model’s performance. It contains the results of the true positive, false positive, true negative, and false negative classifications of the model⁽¹⁴⁾. Using these evaluation metrics together, a robust assessment of the model’s ability to classify Black Sigatoka stages is obtained.

3 Results and Discussion

This section presents the findings from the experiments and explores their implications while incorporating references from relevant studies into our discussions. The evaluation process will use the assessment criteria outlined in Section 2.4. The results of the model training are concise, as seen in Table 6, which includes details like training accuracy, validation accuracy, and key metrics such as precision, recall, and F1 score.

Table 6. Model performance comparison

Metric	basic CNN	VGG16
Training Accuracy	0.95	0.92
Validation Accuracy	0.89	0.89

Continued on next page

Table 6 continued

Macro Avg Precision	0.90	0.80
Macro Avg Recall	0.90	0.75
Macro Avg F1-Score	0.90	0.75

The two models showed differences in performance. In terms of training accuracy, the basic CNN model achieved a score of 0.96, while the VGG16 model reached a score of 0.92. Both models achieved a validation accuracy of 0.89; however, when it comes to precision, recall, and F1 score, the CNN model performed better than the VGG16 model. Specifically, as shown in Table 7, the basic CNN model achieved a consistent score of 0.90 across precision, recall, and F1 score compared to VGG16s scores of 0.80 for precision and 0.75 for recall and F1 score, as indicated in Table 8. These results indicate that the basic CNN model is more effective for classifying Black Sigatoka disease at different infection stages.

Table 7. Detailed multi-class performance for basic CNN model

Class	Precision	Recall	F1-Score
advanced	0.90	0.88	0.89
early	0.95	0.86	0.90
health	0.97	0.98	0.98
intermediate	0.79	0.86	0.82

Table 8. Detailed multi-class performance for basic VGG16 model

Class	Precision	Recall	F1-Score
advanced	0.82	0.65	0.72
early	0.95	0.55	0.69
health	0.91	0.99	0.95
intermediate	0.52	0.81	0.63

Several studies have suggested that a simpler approach can be more effective than more complex models for specialized tasks like identifying and classifying plant diseases. Noteworthy studies by⁽¹⁵⁾ and⁽¹⁶⁾ have explored this idea in depth. This study’s results support this viewpoint, reinforcing the efficacy of simpler models like the basic CNN for disease classification. On the other hand, studies such as⁽¹⁷⁾ suggest that models such as VGG16 excel in scenarios like general image classification tasks, but in this study, the discrepancies in the performance observed could be attributed to the characteristics of the Black Sigatoka dataset and its images favoring a simpler model like the basic CNN architecture developed. This disparity poses a challenge for deep learning models in the sense that the performance of a model is influenced not by its architecture but, by other factors, such as the characteristics of the dataset, hence making it difficult to have consistent results⁽¹⁸⁾.

Moreover, an interesting observation pertained to the utilization of stopping and model checkpoint callbacks during model training was observed. While both the basic CNN and VGG16 models were set to run for 100 epochs, the basic CNN model stopped after 26 epochs and the VGG16 model after 21 epochs. This approach helped to prevent overfitting and promoted generalization. The results depicted in Figure 2, parts **a** and **b**, indicate that the basic CNN model effectively captured features for the classification of Black Sigatoka infected leaves. On the other hand, Figure 2 (**c**) and (**d**) demonstrate that the VGG16 model achieved stability before reaching its intended epoch count. These findings align with studies like that of⁽¹⁹⁾, which highlights the importance of such techniques in achieving optimal performance when working with plant disease datasets such as that of Black Sigatoka.

Furthermore, comparative analysis with recent studies indicates that the developed basic CNN model excels in the detection of Black Sigatoka infection stages. For instance, a recent study conducted by⁽⁸⁾ found that their CNN model achieved an accuracy of 0.91, compared to the accuracy of 0.96 obtained in this study using the basic CNN model. Similarly,⁽²⁰⁾ reported an accuracy of 0.95 using the ResNext50 architecture, which is slightly lower than the basic CNN model of this study. These results suggest that the developed model is not only highly accurate in detecting Black Sigatoka at life stages but also computationally efficient, making it suitable for deployment in environments with limited resources where computational complexity may be of concern.

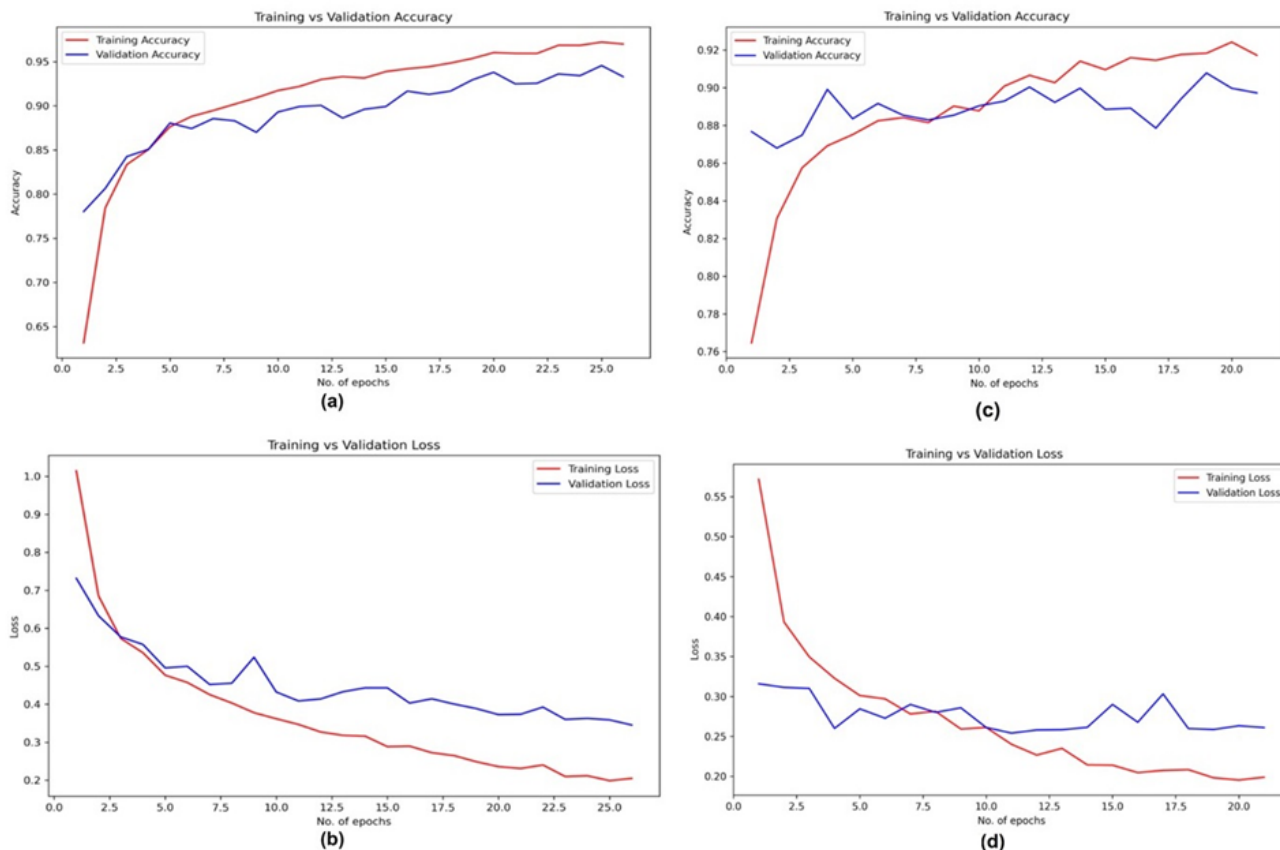


Fig 2. (a) and (b), indicate the CNN model for the classification of Black Sigatoka infected leaves. On the other hand, (c) and (d) demonstrate the VGG16 model

4 Conclusion

In this study, a deep learning model, designed to classify Black Sigatoka disease in banana leaves based on infection stages, is introduced, marking a significant improvement from previous studies that overlooked the distinct progression of the disease. Unlike other studies such as ^(6,8,9), that mainly focused on less detailed classifications, this study’s model categorizes the Black Sigatoka stages into four: healthy stage, early stage, intermediate stage, and advanced stage. This detailed classification is essential for targeted interventions to enable disease management strategies.

Strengths and Weaknesses: One notable strength of our approach is the simplicity and efficiency of the CNN model, which achieved an average precision score of 90% across all stages. The lightweight design of this model makes it ideal for use in settings with low resources, like mobile applications used in the field. However, this simplicity also presents a limitation, as the model may not generalize effectively to complex or diverse datasets compared to the VGG16 model. Despite achieving a precision score of 76%, the experiments showed that the VGG16 model exhibited superior generalization capabilities.

Suggestions for Enhancements: Although our model offers a foundation for categorizing diseases, there are areas that could be improved. One aspect that could be enhanced is incorporating data to enhance the model’s accuracy and adaptability across environmental settings and types of banana plants. Moreover, implementing real-time data augmentation techniques during training could help the model better handle complex situations encountered in field settings.

Unanswered Future Outlook: Many questions still exist about how the model performs in different environmental conditions and its ability to adjust to various types of banana plants. Future studies should address these gaps by exploring deep learning structures or hybrid models. ⁽²¹⁾ proposes an interesting concept of using Artificial Neural Networks (ANN) in analyzing the health of banana plants, the concepts that can be expanded to address the Black Sigatoka disease stage identification. ⁽²²⁾ used an ensemble machine learning approach; the same concept of ensemble techniques can be expanded to incorporate other factors

in disease identification and classification tasks. Also, the study by⁽²³⁾ considered banana fruit and stem in their solution that was not considered in this study. In the future, these other banana products can be further studied.

Acknowledgment

The authors express their sincere appreciation to The Nelson Mandela African Institution of Science and Technology and Mkwawa University College of Education for offering exceptional learning facilities and working environments. Also, great appreciation goes to Dr Neema Mduma and her team for collecting the data that has been used in this study. Their assistance has been crucial to the successful completion of this research.

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