



Enhancing Agricultural Diagnostics: Tomato Leaf Disease Detection Using Quantum Vision Transformer

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ABSTRACT: The early and accurate detection of plant diseases is vital for ensuring food security and enhancing agricultural productivity. Tomato plants, being one of the most widely cultivated crops, are particularly susceptible to several prevalent leaf conditions. These conditions can lead to significant crop losses and adversely affect both yield and quality, posing a substantial challenge to farmers and the agricultural industry. To identify tomato leaf conditions, traditional methods such as Machine Learning and modern approaches like various Deep Learning architectures have been developed and studied by researchers. This paper presents a novel approach for the detection of ten classes of tomato leaf conditions, encompassing both healthy and diseased leaves. The proposed method leverages a new Quantum Vision Transformer architecture, integrating variational quantum circuits within both the attention mechanism and the multi-layer perceptron. In our study, we conducted extensive experiments comparing the performance of the Quantum Vision Transformer with the Vision Transformer. The experimental results demonstrate that the Quantum Vision Transformer model achieves an Area Under the Curve of 0.928 and an accuracy of 66.85%, while the Vision Transformer model reaches an Area Under the Curve of 0.95 and an accuracy of 72.15%. This highlights the effectiveness and robustness of both models in accurately detecting tomato leaf conditions. The research findings suggest that the Quantum Vision Transformer architecture can serve as a powerful tool for early detection in agricultural applications using quantum computers, contributing to more efficient and sustainable farming practices.

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1- Introduction

Plants are essential because they serve as the primary source of energy production for humanity, providing nutrition, medicinal benefits, and other values. During crop cultivation, diseases affecting plant leaves can cause substantial losses in crop production and economic challenges. Therefore, the identification of leaf diseases is crucial in the agricultural industry [1]. Moreover, rising crop production in agriculture is increasingly threatened by plant diseases, posing a critical global challenge to food security. Modern environmental agriculture emphasizes not only increasing crop yields but also enhancing their quality [2], highlighting the urgent need for effective disease management practices. In recent years, crop occurrence has increased, accompanied by a rise in the complexity of plant diseases and the prevalence of harmful insects, posing significant risks to agriculture. Detecting and diagnosing plant diseases has thus become a pressing concern in recent times. Early identification of diseases is crucial as it enables farmers to take swift action to prevent their spread to other plants [3]. This early detection not only prevents substantial production and economic losses

but also helps maintain the quality and quantity of crops. Therefore, through early detection and effective management strategies, these challenges can be mitigated [4]. Tomatoes are a widely cultivated and seasonal crop known for their high nutrient density. They offer significant health benefits and are used in various edible products like sauces, pastes, canned tomatoes, ketchup, and juices. Additionally, tomatoes possess pharmacological qualities that contribute to their protective effects against conditions such as hypertension, liver inflammation, and gum bleeding [5].

According to the UN Food and Agricultural Organization (FAO), every nation participates in the global tomato market, collectively producing millions of metric tons annually, reflecting significant competition as reported by Our World in Data [6, 7]. Tomato production faces various challenges post-planting, including climate change, soil fertility, water availability, and disease management. Pathogens such as bacteria, fungi, viruses, and viroids pose a significant threat to tomato plants, particularly affecting their leaves. The genetic susceptibility of tomatoes to these diseases necessitates effective management strategies, including addressing climate change impacts, implementing updated phytopathological controls, and considering the influence of the global seed

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industry on tomato crop genetics [8]. The common threats to long-term tomato protection have a significant impact on agriculture worldwide. Additionally, farmers rely on their firsthand experience to identify diseases, which may lead to challenges in categorizing them [9].

Moreover, in contrast to the aforementioned challenges, early detection proves highly beneficial, facilitated by computer-aided technologies that utilize various Machine Learning (ML) techniques and Deep Learning (DL) networks specifically designed for this purpose. These technologies help mitigate damages and losses in the agriculture industry, resulting in significant economic savings. Traditional methods of plant disease detection, which rely on manually crafted classification features, are inadequate for effectively handling the differences between classes and variations within the same class of diseased leaf images in real-world environments. However, with advancements in computing power, big data, the Internet, and artificial intelligence technologies, convolutional neural networks (CNNs) have become popular for plant disease detection. CNNs leverage advantageous features such as local connections, weight sharing, and pooling operations, making them well-suited for this task [10, 11]. The prediction and training times of state-of-the-art plant detection techniques are high due to the large number of training parameters involved [12].

A new network architecture is required to address the issues raised. An innovative architecture called QViT has been developed to classify tomato leaf diseases precisely. This architecture not only facilitates more precise disease classification but also brings several advantages:

Reduced Training Time: Quantum computing's computational prowess enables QViT models to swiftly learn and effectively train with fewer parameters, significantly reducing training time.

Enhanced Feature Learning: Leveraging quantum computing's capabilities, models can rapidly grasp intricate features, thereby improving the accuracy and speed of tomato leaf disease detection.

Optimized Data Utilization: QViT optimizes data utilization and accelerates training processes, diminishing the need for extensive datasets traditionally required for effective model training.

These advancements empower farmers to harness advanced technologies more efficiently to automate tomato leaf disease detection. This potential reduction in costs and increase in productivity underscore the transformative impact of QViT in agriculture.

2- Related Work

Kawsar Ahmed et al. proposed a Deep Convolutional Neural Network (DCNN) model aimed at enhancing the detection and classification of tomato leaf diseases. Their approach also incorporated image pre-processing techniques, such as Gaussian and Median filters, alongside color model transformations (HSI and CMYK) to further improve accuracy. The study identified optimal combinations for enhancing accuracy in disease classification. The results highlighted

significant achievements, with the best-performing DCNN model—ResNet-50—demonstrating a remarkable 99.53% accuracy when using Gaussian Blur and Gaussian Noise filters alongside RGB to CMYK color conversion [13]. Al Amin Biswas et al. emphasized the critical importance of early and accurate diagnosis of tomato leaf diseases to enhance plant productivity and agricultural sustainability. They introduced a lightweight custom convolutional neural network (CNN) model for classifying eleven classes of tomato leaf diseases, including healthy leaves. Through extensive data preprocessing and augmentation, the proposed model achieved a 95.00% accuracy, utilizing transfer learning (TL)-based models VGG-16 and VGG-19. Furthermore, the study integrated the best-performing model into web- and Android-based applications for real-time disease classification, demonstrating its practical utility for farmers [14]. Kakhshani Perveen et al. introduced a multiscale U-network tailored for effective segmentation and diagnosis of tomato leaf lesions. Addressing challenges such as diverse lesion sizes and shapes, the model incorporated multi-scale residual modules to adapt dynamically. A Classifier and Bridge (CB) module connected disease feature extraction with lesion segmentation, utilizing minimal pixel-level annotations through supervised training with binary cross-entropy loss. Evaluation across diverse test sets demonstrated an impressive average accuracy of 99.2%, along with robustness against brightness reduction at 92.4% and resilience to salt-and-pepper noise at 99.2% [15]. Chen CHEN et al. enhanced the AlexNet model with HOG and LBP weighted fusion techniques. Focusing on eight types of tomato leaf diseases and healthy leaves, the research employed transfer learning from the PlantVillage dataset, reducing fully connected layers to optimize classification efficiency. Using the Keras framework in Python, the proposed model achieved a high recognition accuracy of 98.83% with AlexNet [16]. Ledbin Vini et al. introduced TrioConvTomatoNet, a deep convolutional neural network designed for the precise classification of leaf diseases by optimizing feature extraction through layered convolution stages. Employing stochastic gradient descent for enhanced learning, the method integrated both existing and real-time datasets, demonstrating superior accuracy with a 99.39% success rate across varied conditions. This approach not only enabled early disease detection crucial for agricultural management but also promised practical deployment via user-friendly applications [6]. Manjunatha Badiger and Jose Alex Mathew employed advanced DL techniques, specifically the deep batch-normalized eLu AlexNet (DbneAlexnet), for detecting and classifying tomato plant diseases. Initial preprocessing involved anisotropic filtering to refine leaf images, followed by precise segmentation using U-Net optimized through Gradient-Golden search optimization (Gradient-GSO). Augmentation techniques enhanced dataset diversity, while classification utilized DbneAlexnet trained with Gradient Jaya-Golden search optimization (GJ-GSO), achieving a high accuracy of 92.4% in identifying diseases such as bacterial spots and late blight. Identified gaps include the need for broader dataset validation and scalability

Table 1. Summary of Previous Research on Tomato Leaf Disease Detection.

Reference	Year	Dataset Size	Number of Class	Method	Accuracy (%)
Manjunatha and Jose [2]	2023	18161	10	DbneAlexnet	92.40
Ledbin et al. [6]	2024	18160	10	TrioConvTomatoNet	99.39
Ahmed et al. [13]	2023	6794	3	DCNN	99.53
Al Amin et al. [14]	2023	32535	11	Lightweight custom CNN	95.00
Kahkashan et al. [15]	2023	18096	10	Multiscale U-network	99.20
Chen et al. [16]	2024	13038	9	Enhanced AlexNet	98.83
Shanthi et al. [17]	2024	2782	6	CNN	91.20
Neeraj et al. [18]	2024	18162	10	Multiple YOLO	98.80
Santar et al. [19]	2022	1610	7	Modified Mask R-CNN	98.00

assessment in diverse agricultural environments [2]. Shanthi et al. demonstrated that using CNNs, particularly with architectures like AlexNet and VGGNet-16, significantly improves the early detection and classification of tomato leaf diseases. This early detection is crucial for reducing economic losses and improving crop quality and yield. The study achieved an accuracy of 91.2%, but it also recognized the need for a more diverse dataset and further refinement of the model to enhance accuracy and reliability [17]. Neeraj S Kumar et al. used YOLOv5 and YOLOv7 models with transfer learning and ensemble techniques on an open-source tomato leaf disease dataset. The combined YOLO models achieved a high accuracy of 98.8%, along with impressive precision and recall. Challenges included high computational time and limited dataset diversity, which were addressed through transfer learning [18]. Santar Pal Singh et al. demonstrated that the modified Mask R-CNN model effectively detects and segments tomato leaf diseases, achieving a high accuracy of 98% and efficiency. However, the study identified challenges such as misidentification of lesions, dependency on precise annotations, and limited scope in disease identification [19]. Table 1 provides a comprehensive summary of the previous works referenced in this study, highlighting the key findings and methodologies employed in the research on tomato leaf disease detection and classification. In this work, the QViT architecture is employed to detect and classify tomato leaf diseases.

The rest of the paper is ordered in the following manner. The material and method are detailed in Section 3. The evaluation, analyses, and discussions of the experiment performance are presented in section 4. Finally, section 5 provides a comprehensive summary of the article.

3- Materials and methods

This section details the methodologies employed in this investigation, encompassing the structures and the detection process.

3- 1- Preprocessing

Before feeding the images to the model, we resized them to 40×40 for several reasons. First, transformers require fixed-size inputs; hence, by resizing the images, we ensure that all the images have the same dimensions, which is essential for batch processing. Additionally, resizing the images to smaller dimensions yields computational efficiency—the smaller the images, the less memory usage, and the faster the processing. Furthermore, a model that can handle lower-quality images often learns to focus on the important features that are invariant to resolution and noise, leading to better generalization. This means the model can work well with high-quality images as well.

3- 2- Model

We utilized a Quantum Transformer Encoder in our approach, incorporating Variational Quantum Circuits (VQCs) into the multi-head attention (MHA) and multi-layer perceptron (MLP) components. The VQCs conduct sophisticated quantum computations, the MHA enables the model to focus on different regions of the image simultaneously, and the MLP processes the information from the MHA for final prediction. The procedure closely resembles the original classical Vision Transformer (ViT) [20], in such a way that the input image is divided into small patches, which are accompanied by position embeddings. Position embeddings are vectors that encode the patches in the original image; this allows the model to ascertain the spatial position of each patch in the given image. Fig. 1. depicts the architecture of the model.

In this approach, to enhance the functionality of both MHA and MLP within the encoder, the traditional feedforward layers and classical fully connected are replaced with VQCs [21]. To elaborate, VQCs substituted for the classical MHA to compute the linear projections—Query (Q), Key (K), Value (V), and the final output, which are essential for the MHA to simultaneously focus on different parts of the input—during the MHA calculations. Moreover, the replacement of

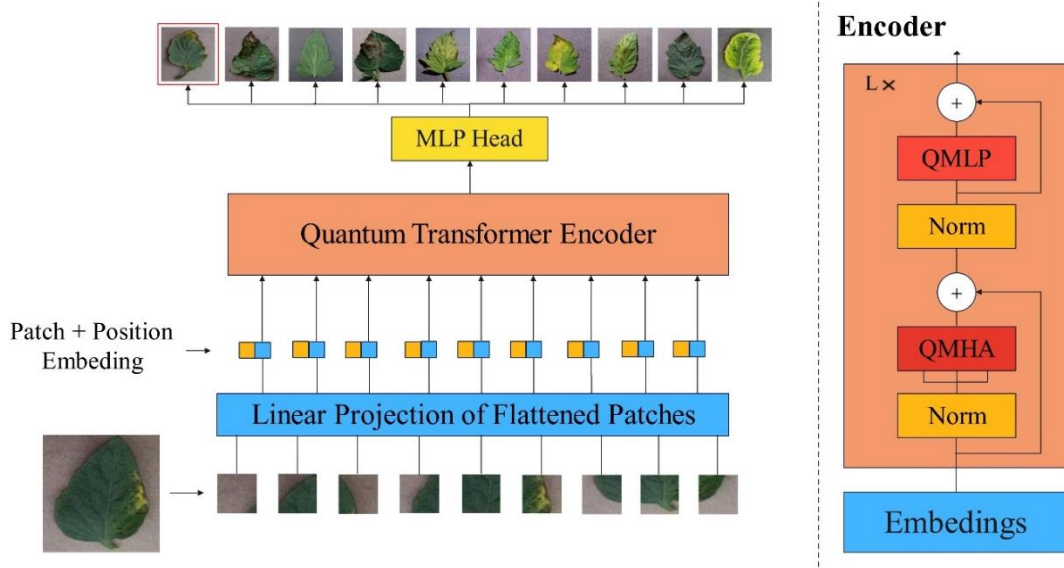


Fig. 1. Model Structure

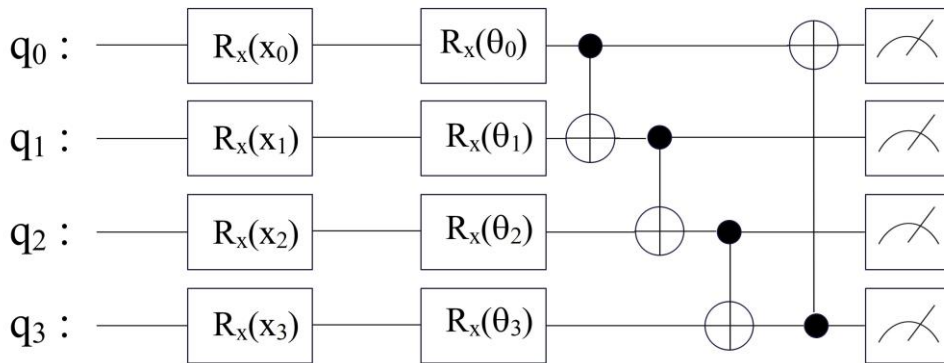


Fig. 2. Implementation of Variational Quantum Circuits in QViT

the classical fully connected layers, in which each neuron applies a linear transformation to the input vector through a weights matrix, with the VQCs in the MLP, has been carried out. Albeit these changes, the activation functions employed in MLP, namely GELU [22], continue to be computed with classical methodologies.

More precisely, the output of the classical multi-head attention layer is calculated by using VQCs to calculate all linear projections in the MHA calculations instead of classical feedforward layers. Similarly, in the MLP module of the encoder, we also apply VQCs to substitute classical fully connected layers. The configuration of the VQCs we utilized [21] can be observed in Fig. 2.

Using rotation angles, every element of the vector $x = (x_0, \dots, x_{n-1})$ is embedded into qubits. Rotation angles,

which allow precise encoding of classical data into quantum states, specify how much each qubit rotates around different axes of the Bloch sphere—a spherical representation used to visualize the quantum state of a qubit. Subsequently, each qubit undergoes one-parameter rotations, which are $\theta = (\theta_0, \dots, \theta_{n-1})$ and are learned alongside other model parameters during training to optimize the qubit states. Afterward, CNOT gates interconnect the qubits, linking the qubits states together to have a functionality akin to matrix multiplication. At the final stage, each qubit is measured, and its output is passed to the next part of the encoder.

4- Experiment Results and Discussion

In this section, we cover the specifics of the experiments, such as data collection, parameters, and experimental results.

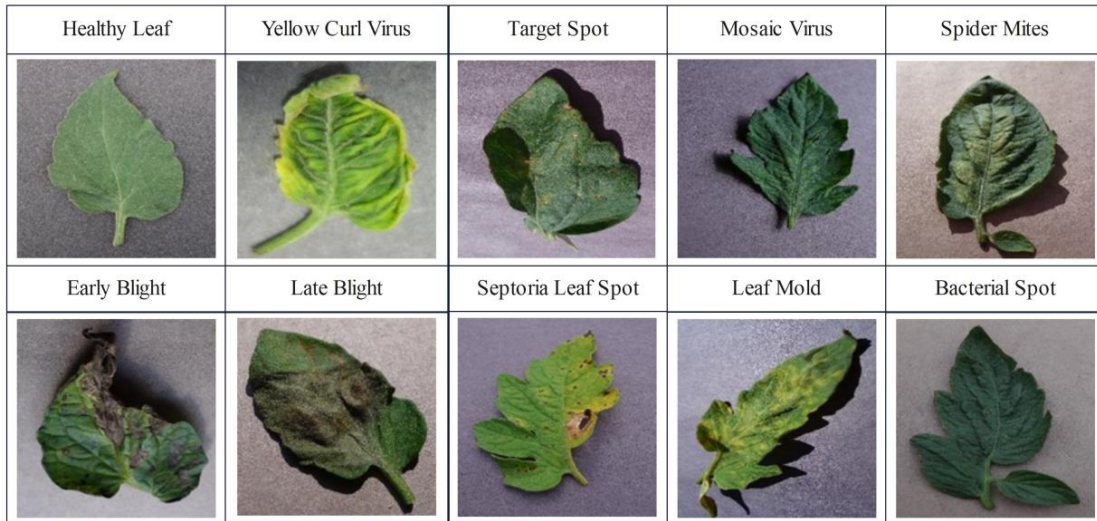


Fig. 3. Examples of 10 different types of tomato leaf diseases

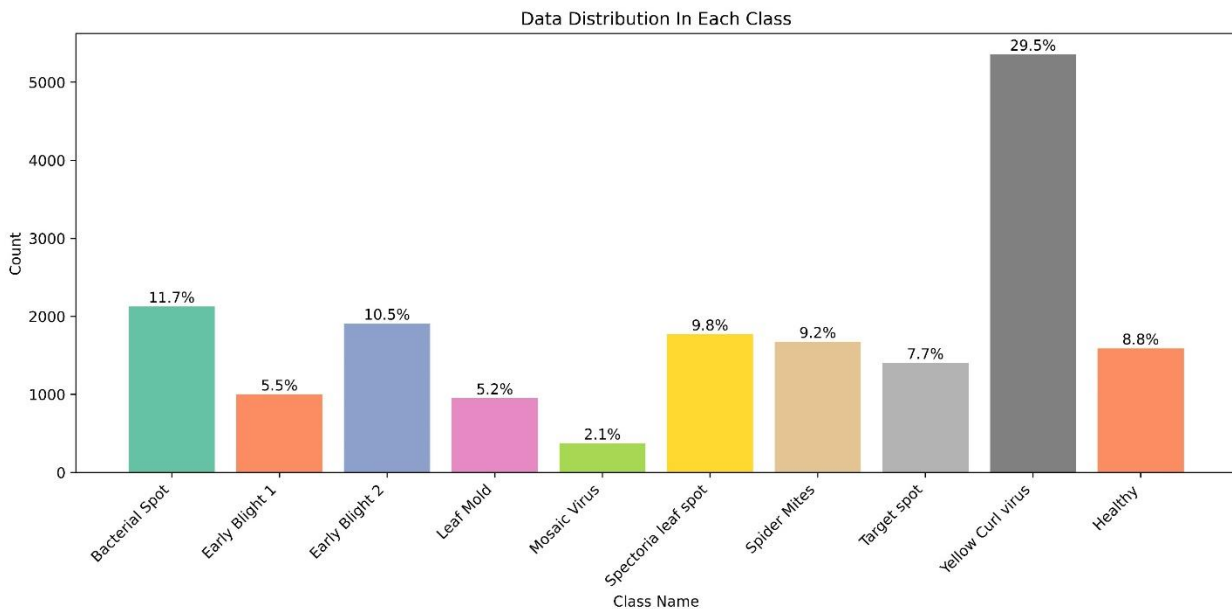


Fig. 4. Bar Chart Illustrating Class Distribution in the Original Dataset of Tomato Leaf Diseases.

We also demonstrate the performance of each model using different data and methods.

4- 1- Dataset

We used the public dataset named PlantVillage Dataset, which consists of plant leaves of 14 crops [7]. For this research, we incorporated a diverse range of tomato leaves, including healthy ones and those affected by nine diseases. The samples can be observed in Fig. 3. Each category of the leaves, with their accompanying briefly explained symptoms, is listed in Table 2. In the analysis of the data set, we have

indicated class distribution, as shown in Fig. 4.

4- 2- Experiment setup

The experiment was conducted on a Windows 10 PC using Google Colaboratory and Google Drive with 8 GB of storage. The setup included a 64-bit operating system, Python 3.10.12, 12.67 GB of memory, and 2 CPUs. Keras 3.4.1 and TensorFlow 2.17.0 were employed to manage the deep neural network training and validation processes.

We trained both the classical ViT and the proposed QViT with the same hyperparameters. These hyperparameters are shown in Table 3.

Table 2. Leaf Categories and Briefly Explained Symptoms

Number	Class	Symptoms	Number of Images
1	Healthy	Total green color	1591
2	Yellow Curl Virus	Leaf curling, yellowing, and stunting [23]	5357
3	Target spot	Necrotic brown lesions with concentric rings on tomato leaves [24]	1404
4	Mosaic Virus	Lighter coloring, bushy appearance, mottled leaves, leaf curling, distorted fruit, and internal browning [25]	373
5	Spider Mites	Speckled leaves, whitish-yellowish discoloration, webbing, brown falling leaves, fruit russetting [26]	1676
6	Early Blight	Dark spots with concentric rings [27]	1000
7	Late Blight		1909
8	Septoria Leaf Spot	Small circular spots, light centers [28]	1771
9	Leaf Mold	Yellow upper spots, fuzzy underside [29]	952
10	Bacterial Spot	Small dark spots, yellow halos [30]	2127
	Total		18160

Table 3. Hyperparameters Used for Training ViT and QViT

Number	Hyperparameter	Value
1	Patch Size	14
2	Hidden Size	6
3	Number of Transformer Block	4
4	Number of Attention Heads	2
5	Hidden MLP Size	3

Table 4. Parameters of the Transformers

Number	Model	Total Parameters
1	ViT	4588
2	QViT	4024

To have a fair comparison, we adhered to a benchmark established by [31]; therefore, we set the same trainable parameters for QViT as the ones for classical ViT. Due to the same dimensionality of the input and output of the VQC, the number of qubits should match the size of the corresponding layer in the classical neural network. Thus, the quantum architecture utilizes circuits of 4 qubits each for both the QMHA layer and the QML layers within each transformer block—16 qubits in total [21]. We compared two types of transformers—ViT and QViT; the parameters of the transformers are listed in Table 4. For each model, the

number of classes was 10, and the number of epochs was 250.

The key point is that the QViT has fewer parameters compared to the classical ViT. The reason is that the proposed VQC has only n free parameters; however, a classical fully connected layer bias has $n^2 + n$ parameters.

The classical model components and baseline were implemented using Jax [32] and Flax [33]. These tools were also used to train both the classical and quantum-based models. The VQCs were implemented, trained, and executed through numerical simulation on the classical computer using Tensor Circuit [34].

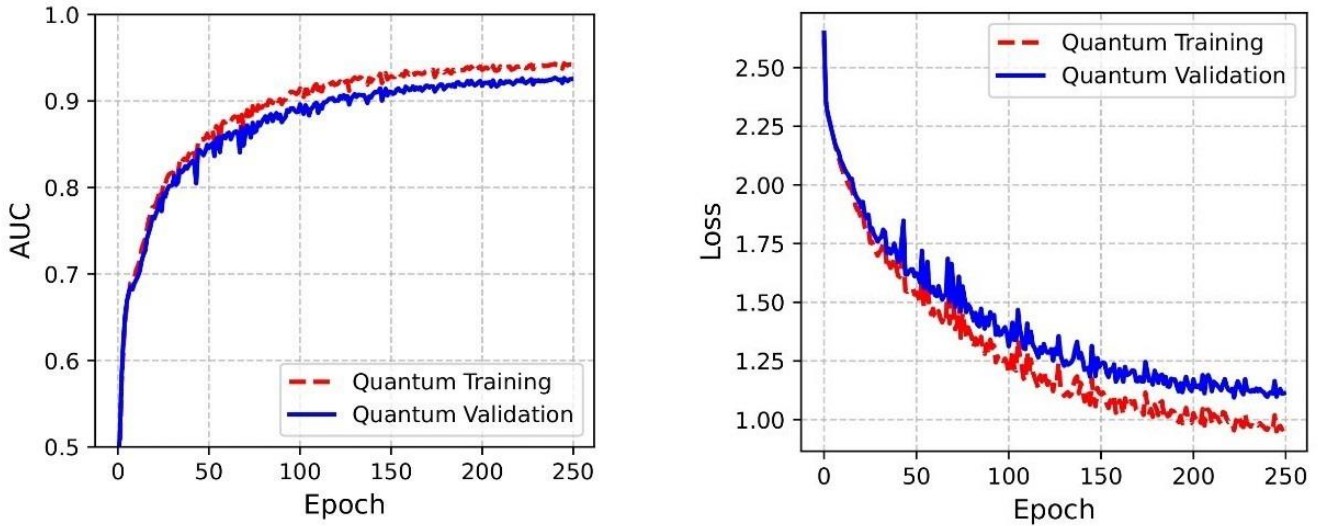


Fig. 5. Performance of the Quantum Model During Training and Validation.

4- 3- Performance Analysis

In this study, the performance of the quantum model during the training and validation process is evaluated using the Area Under the Curve (AUC) metric. Specifically, we adopt the same training-validation-test split utilized by Andrews et al. [34]. Our dataset is divided into 13,620 images for training, 1,816 images for validation, and 2,724 images for testing. Fig. 5 illustrates the training AUC, represented by the red line, and the validation AUC, shown by the blue line. The training AUC exhibits a rapid increase in the early epochs, reaching near-perfect performance by around the 75th epoch and continuing to improve gradually thereafter. In contrast, the validation AUC also shows a steady increase but at a slower rate compared to the training performance. This divergence between the training and validation AUC curves suggests that the model may be overfitting to the training data, a common challenge in ML that requires careful monitoring and mitigation techniques to ensure robust generalization on unseen data. We calculate the AUC for each epoch across all model configurations. At the conclusion of the training, we select the parameters corresponding to the epoch that yields the highest validation AUC and subsequently reassess these parameters on a separate hold-out test set to derive the final test AUC. This approach allows us to gauge our model's proficiency in accurately detecting and categorizing various tomato leaf diseases, which is crucial for facilitating early diagnosis and enhancing agricultural practices. Additionally, it is observed that the training and validation loss curves do not converge throughout the 250 epochs of training. The significant and persistent gap between the two loss curves indicates that the model is unable to generalize well to the validation data, implying that it has overfit to the training data. A confusion matrix, illustrated in Fig. 6, is also employed to further evaluate the model's performance across different classes. In this matrix, each

row represents actual classes, while each column represents the model's predictions, with the main diagonal elements indicating correctly classified samples and the off-diagonal elements showing misclassified samples in other classes. The confusion matrix reveals that the model performs particularly well in classifying yellow leaf curl virus with 473 correct predictions and limited misclassifications, indicating strong feature learning for this disease. It also performs reasonably well for Spider mites and Target spots, though moderate misclassification occurs in classes like Healthy, Late blight, and Septoria leaf spots. However, the model struggles with Early blight and Bacterial spots, frequently misclassifying them as other diseases, possibly due to overlapping visual features. This suggests a need for improved feature extraction or addressing class imbalance, as some underrepresented classes, such as Early blight and mosaic virus, show weaker performance. Incorporating data augmentation may help reduce misclassification and strengthen model accuracy across all classes.

Moreover, it is essential to understand the concepts of Precision and Recall, which are crucial metrics for evaluating classification models. Precision refers to the ratio of true positive predictions to the total predicted positives, indicating the accuracy of the positive predictions made by the model. It is calculated as shown in Eq. (1):

$$\text{Precision} = \frac{TP}{TP + FP} \times 100 \quad (1)$$

where TP (True Positives) is the number of correctly identified positive samples, and FP (False Positives) is the number of incorrectly identified positives. Recall, on the other hand, is the ratio of true positive predictions to the actual positive samples, reflecting the model's ability to identify all

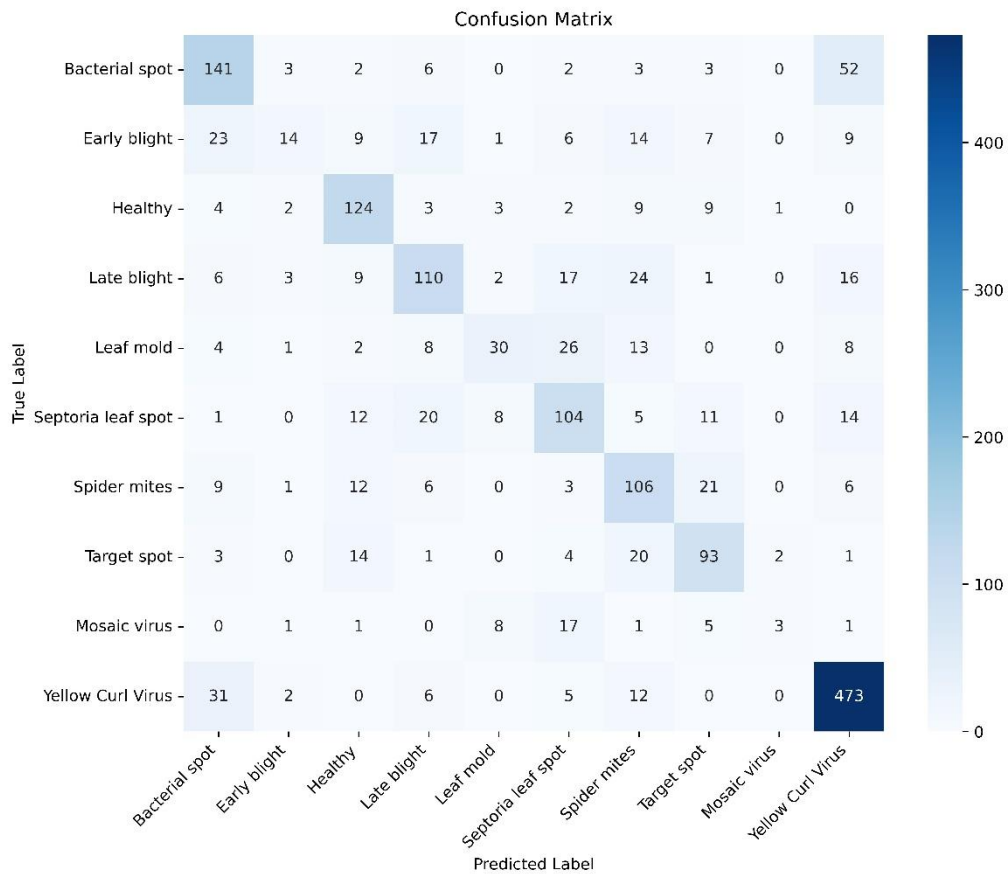


Fig. 6. Confusion matrix illustrating the model’s classification accuracy for tomato leaf diseases.

Table 5. Computed Parameters of Each Model

Number	Model	AUC	Accuracy	Precision	Recall	Loss
1	ViT	0.95	72.15	65.54	61.96	0.84
2	QViT	0.92	66.85	60.29	53.95	0.96

relevant instances. It is expressed as shown in Eq. (2):

$$\text{Recall} = \frac{TP}{TP + FN} \times 100 \tag{2}$$

where FN (False Negatives) represents the number of actual positives that were not identified. There is often a trade-off between precision and recall, where increasing one may decrease the other.

In the context of our study, the ViT model demonstrated superior performance metrics compared to the QViT model. This is reflected in its higher accuracy, AUC, recall, and

precision. High precision and recall values for ViT suggest that it has effectively learned to classify diseases with fewer misclassifications, contributing to its overall reliability in detecting and categorizing tomato leaf diseases.

4- 4- Results

The parameters—AUC, Acc, and Loss—of each model have been computed at the end of each epoch, and they are shown in Table 5.

Moreover, the train time and the total time of each model, calculated at the end of the process, are presented in Table 6.

The QViT model required a total training time of 7792.68 seconds and an overall time of 10456.41 seconds (including

Table 6. Processing Time of the Models.

Number	Model	Train Time (s)	Total Time (s)
1	ViT	686.80s	1031.72s
2	QViT	7792.68s	10456.41s

evaluations), achieving an AUC of 92.76, a loss of 0.96, an accuracy of 66.85%, a recall of 53.95%, and a precision of 60.29%. In contrast, the ViT model trained significantly faster, with a training time of only 686.80 seconds and a total time of 1031.72 seconds, resulting in a higher AUC of 95.11, a lower loss of 0.84, and better accuracy at 72.15%. ViT also showed improved recall (61.96%) and precision (65.54%) compared to QViT.

These findings suggest that ViT outperformed QViT across key metrics, including accuracy, AUC, recall, and precision, while also requiring significantly less computational time. The faster training and evaluation times for ViT can be attributed to its execution on a classical computing platform, which suits its architecture well. In contrast, QViT's slower performance and slightly lower metrics are likely due to the fact that it was executed on classical hardware, which is suboptimal for quantum-inspired models that are designed to benefit from quantum computing environments. Consequently, ViT appears to be more efficient and effective in this classical setting, while QViT may realize its full potential only on a quantum computing platform.

5- Conclusion

Tomato leaf disease identification is a crucial and challenging task due to the variability and complexity of diseased leaf images. By incorporating Variational Quantum Circuits (VQCs) into the attention mechanisms and multi-layer perceptron, a Quantum Vision Transformer model was developed for this purpose. This model leverages quantum computing to enhance the accuracy and efficiency of disease classification. The ViT model achieved an AUC of 0.95 and an accuracy of 72.15%, while the QViT model reached an AUC of 0.928 and an accuracy of 66.85%.

This study demonstrates that incorporating quantum circuits into the QViT model, along with the Multi-MHA mechanism, has the potential to improve accuracy and efficiency in tomato leaf disease identification. The MHA mechanism, by enabling simultaneous focus on different regions of an image, boosts the model's processing speed and provides it with the capability to analyze complex features in a shorter time.

However, it is essential to note that this paper lacks substantial discussion on the practical implications of the QViT approach in real-world agricultural settings, particularly regarding the increased computational resources required for its implementation. Given these challenges,

further research is necessary to explore solutions that can optimize computational efficiency and reduce the resource demands of the QViT model. This is especially pertinent for smaller farms or environments with limited resources, where the adoption of such technologies could be hindered.

Furthermore, the current limitations of the QViT model, particularly in classical computing infrastructure, may significantly impact its practical implementation. The lack of memory for utilizing larger datasets restricts the execution speed of this model, and the inability to balance the dataset may detract from the training quality for each class. Addressing these limitations will be crucial for improving the model's applicability in real-world scenarios.

Finally, framing this research as an exploratory study testing the integration of quantum circuits into DL, rather than asserting superiority over classical models, could provide a more accurate context for our findings. This shift in perspective allows for a more comprehensive understanding of the potential benefits and future directions for integrating quantum technologies into agricultural applications.

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