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Research Article

Automated Identification of *Begomovirus* in Tomato and Chilli Plants Using Deep Learning

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ABSTRACT

The purpose of this case was to identify and classify diseases of tomato and chilli plants caused by Begomoviruses using AI-based learning techniques. Along with other viruses, it is one of the most destructive in the plant kingdom in Pakistan. Begomovirus is the most common viral infection in both tomato and chilli plants and lowers their productivity. It is not possible to detect Begomovirus through morphological symptoms observation because it shares many symptoms with other viral infections. Leaves may also exhibit other symptoms, such as yellowing and curling, and the entire plant may become stunted. Pathogen spread needs to be controlled as early as possible to contain the virus. Machine learning and artificial intelligence now have several tools to measure the detection of objects with great precision. This research focused on developing an advanced deep learning algorithm for the early identification and intervention of diseases caused by Begomovirus. Screening of the Visual Geometry Group 16 (VGG-16), Residual Network-50 (ResNet-50), and the third version of the Google Inception CNN (Inception-v3) techniques were applied to diagnose Begomovirus, and possible solutions were suggested. Using VGG-16 yields the highest detection accuracy of 98% for plants infected with Begomovirus, while Inception-v3 and ResNet-50 achieve 95% and 80%, respectively. This technique involves capturing data images from an algorithm for those features that correlate and merge the images to teach the algorithm more efficiently without explicitly instructing it on how to do so. This research aims to train a deep learning model to automatically diagnose Begomovirus based on disease severity measurements.

Keywords: *Begomovirus* Detection, Deep Neural Network, Tomato, Chilli

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INTRODUCTION

Agriculture holds an undeniable importance in nearly all economies worldwide, particularly in Pakistan (Abbas et al., 2025). It serves as a major source of sustenance to a large proportion of the population, with an esoteric percentage of 70% of people being directly or indirectly involved in it. This sector generates approximately 25% of the GDP, which is higher than any other sector in terms of economic activity. Plus, Agriculture single-handedly feeds the Pakistani population of over 200 million and provides raw materials for the industrial sector. The crops mentioned above, particularly tomatoes (*Solanum lycopersicum* L.) and chillies (*Capsicum annuum* L.), are of concern to the population due to their high consumption and economic significance. Multi-crop integrated Farming Systems can improve crop profitability throughout the year (Kaur et al., 2018). McKinsey's projection for all grains and palm oil commodities is 56.6 million tons, which includes a record production of 31.4 million tons of wheat expected in 2024 (FAO, 2025). This unprecedented wheat production is attributed to a significant planting area, excellent crop yields, and sufficient irrigation, as well as the high prevalence of modern seed adopters.

These crops are consumed as vegetables but also processed into various sauces like chilli sauce and tomato sauce. Due to growing populations, economic development, and urbanization, the marketing of these vegetables is expected to become more favorable in the future.

For the year 2024, the production of tomatoes and chilli is an average of 9.2 tons per Tomato (*Solanum lycopersicum* L.) and chilli (*Capsicum annuum* L.) are perhaps the two most popular vegetables consumed by Pakistanis. Annually, Pakistan produces 529,600 tons of tomatoes and chillies.

The production of tomato and chilli is an average of 9.2 tons per hectare (Nozaki et al., 2006). Chillies and tomatoes are also used in Pakistan for making other blends. The demand for these captivators increases with income increases. As populations, economies, and urban areas continue to develop, the demand for these vegetables is expected to increase in the coming years. Numerous cultivated and wild plant species, as well as many economically important species, are susceptible to viruses that can result in partial or total crop loss. One of the most severely affected families by viruses is Solanaceae, which includes crops such as tomatoes, chillies, peppers, and aubergines. Due to their limited yields and unpredictable prices, we stress the importance of these two crop viruses. This research proposes an automated diagnosis of Begomovirus using deep-learning models, with a claimed best result in terms of accuracy after identifying and measuring the disease's severity.

All vegetable crops are now facing the problem of Begomovirus infection. Begomoviruses are defined as one of the most important series of viruses that cause infection to many kinds of plants, a member of the Geminivirus family (Begomovirus). They are composed of geminate particles and have a circular, single-stranded DNA genome. Based on the range of hosts, genomic makeup, and insect vectors, Gemini viruses are classified into nine groups: Begomovirus, Mastrevirus, Curtovirus, Becurtovirus, Topocuvirus, Turncurtovirus, Capulavirus, Grablovirus and Eragrovirus.

Numerous Begmomovirus varieties affect tomatoes such as TYLCV and ToYMV. Along with the Pepper leaf curl virus and the Chilli leaf curl virus, which also infect Capsicum plant species, the family of Begomovirus, which infects pepper, is known to cause extensive damage worldwide (Nalla et al., 2023; Srinivas et al., 2018). Infected plants show a range of available symptoms, including stunting, crinkling, flower bud abscission, leaf deformation, and chlorosis. Variations in symptom expressions may occur due to the host plant and the virus strain in question. CLCuD is one of the most devastating diseases of crops in Pakistan and India, which is caused by whiteflies that are vectors of Begomoviruses (Pechuho et al., 2020). Recently, reports of a new iteration near Multan within the Punjab province appeared to be the latest development. This disease was first reported in this region in 1967, and it was also described in 1985 as CLCuD. The first reports of CLCuV dissemination and prevalence were made at the Central Cotton Research Institute CCRI in Multan (Simpson et al., 2020).

That is when CLCuD effectively decreased cotton production in Pakistan in the early 1990s. Now inflected other southern and western provinces. The impact of CLCuV cannot be overlooked in the context of Pakistan's national economy, as the country has suffered losses of Rs. 50 to 55 billion since 1992. Responding to the disease remains important(Sattar et al., 2013).

Literature Review

Begomovirus is known as one of the most damaging viruses affecting plants, causing significant damage to vegetable crops. They are vector-borne and are caused by whiteflies (Bemisia tabaci), and have a single-stranded, circular DNA genome (Sani et al., 2020). As with other viruses within the Geminivirus family, Begomoviruses are further divided into nine subgenera: Begomovirus, Mastrevirus, Curtovirus, Becurtovirus, Topocuvirus, Turncurtovirus, Capulavirus, Grablovirus, and Eragrovirus, based on a range of host, the structure of the genome, and their vectors (Roumagnac et al., 2022).

So far, the following species of these viruses have been noted in tomato and chilli crops:

- Tomato Yellow Leaf Curl Virus (TYLCV)
- Chilli Leaf Curl Virus
- Pepper Leaf Curl Virus

These viruses have caused severe symptoms, including chlorosis, leaf curling, folding, stunting, abscission of flower buds, and reduced fruit harvest (Srinivas et al., 2018). The impact of CLCuD, which is associated with other Begomoviruses, is known to be devastating in certain areas of Pakistan and India, resulting in an economic loss of more than 50 to 55 billion rupees since the beginning of 1992 (Binyameen et al., 2021). This provides a clue to the necessity of continuous attention and control measures put in place. The Symptoms of Begomovirus will depend on the strain of the virus, the type of host plant, or environmental conditions. Below are some symptoms of tomato and chilli plants affected by Begomovirus infections.

Tomato Symptoms - This study focuses on the impact of Begomoviruses on tomato leaves. The Tomato plant is well known to be infected by multiple varieties of Begomovirus, as it is very prone to Begomovirus infections. The most frequent one being. The Tomato yellow leaf curl virus (TYLCV) is illustrated in Figure 1 (a) (Song et al., 2022). Other types of Begomovirus are also capable of damaging tomato plants. Tomatoes infected with Begomovirus usually exhibit the following symptoms:

Figure 1. a) (TYLCV) on young plants. b) Tomato Leaf Curl Virus (Plant Village Dataset).

Symptoms of Tomato Yellow Leaf Curl Virus – The leaf curl disease caused by the virus in tomatoes belongs to the Geminivirus family and is disseminated by whiteflies. Tomatoes plants that become infected by the virus usually show dramatic upward leaf curling and downward bent on the leaves for a V-shaped or cupped development as indicated by Figure.1 (b). Leaflets may also become a bit thicker*. Yellowing and Venial Chlorosis*- Leaf yellowing is one of the most distinct characteristics of tomato plants infected by the Begomovirus. In most cases, the yellowing affects the lower leaves first and later moves upward. They also often appear as veins turn yellow, while the surrounding areas turn pale, a condition known as venial chlorosis, as depicted in Figure 2 (a).

Figure 2: a) Yellowing and Venial Chlorosis on Tomatoes b) Chilli Leaf Curl Virus

Severe infections of Begomovirus may cause the death of tomato plantations if progression occurs early in the growth stage or in newly germinated seedlings. It should be noted that the symptoms exhibited on infected tomatoes caused by Begomovirus vary depending on the strain, environmental conditions, and age of the tomato plant.

Chilli Plants Symptoms - Begomovirus attack on chilli plants infection features include excessive vertical curling of the leaves, crinkled appearances, puckering, involution, vesicle formation at inters venal regions, banding at the veins, stunting of petioles and internodes, bunching of leaves, and stunted growth of the plant as seen in figure 2 (b). Suppose the disease is not retarded till the later phases of growth development. In that case, diploid flower buds may undergo abscission, and pale-colored pollens may normally form without abnormal pollen grains, leading to low yield and set

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fruits or deformed fruits at the final stage (Kumar et al., 2015). *Chilli Leaf Curling* - Infected Begomovirus chilli plants might show marked curling of the leaves, which is term as Chilli leaf curl disease. The leaves often become fragile and assume a cupped or clawed form, as shown in Figure 3 (a).

Figure 3. a) Leaf Cupping and Curling b) Leaf Spots on Chilli Plants.

Chilli Leaf Spots – Some Begomoviruses produce mosaic patterns on the leaves, which appear as patches of both light and dark green colors. These patterns can be more or less pronounced and may have accompanying veins with chlorosis, as shown in Figure 3 (b). *Yellow stunt–begomovirus–infected* chili plants frequently display chlorosis of the leaves, as seen in Figure 4. Typically, this symptom commences at the leaf edges or tips before radiating inward, resulting in the leaf center becoming entirely yellow or pale (Ferro et al., 2019).

Figure 4. Yellowish Stunting on Chilli leaves.

Plant disease recognition has greatly benefited from the emergence of deep learning as a control method of choice due to its effectiveness and efficiency. Several deep-learning model training sessions focusing on detecting and classifying numerous plant diseases have been conducted. Those works emphasized the potential of deep learning in automating the process of disease identification. Use of Convolutional neural network (CNN) for identification of diseases of tomato. The study differentiated diseased and healthy tomato plants with high accuracy, even with some of them having viral infections. Unfortunately, the precise identification of Begomovirus in tomatoes was not the aim of this study.(Zakir Hossain et al., 2019).

Checking out the application of deep learning models in detecting plant diseases of various crops. The effectiveness of deep CNN architectures in plant disease analysis has been proven. However, this research did not deal with Begomovirus identification in tomato and chilli plants.(González-Pérez et al., 2011), created the Plant Village database, which contains images of both healthy and sick plants. They applied deep learning algorithms, particularly convolutional neural networks (CNNs), to recognize and classify the numerous plant diseases. While this work featured several crops, the primary recognition of Begomovirus in tomatoes and pepper was not emphasized.(Moury et al., 2005).

The objective of the Study:

In the present article, we intend to design a deep learning-based model to automate the detection and classification of Begomovirus infections in chilli and tomato plants. The goals of this study are:

To compile and augment an image dataset of leaves with different parts of Begomovirus, design a deep learning architecture for the detection and recognition of several Begomovirus forms, and evaluate the effectiveness of different deep learning methods for achieving the set objectives in terms of accuracy and validation.

MATERIAL AND METHODS

It is worth mentioning that proactive and prompt action is necessary in cases of Begomovirus. Your crops will sustain less damage if you routinely check on them and take action promptly. An analysis of a range of literature revealed that some machine-learning approaches have been applied primarily for disease monitoring purposes with limited success. The objective of this study focuses on high-performing automatic plant disease detection and diagnosis using different deep learning algorithms. Its effect on the health and productivity of the plants is great. The system will mitigate the economic damage experienced by the farmers.

To address the newly described problems, we designed novel automated methods, such as the one depicted in Figure 5, for the rapid detection of Begomovirus infections in chilli and tomatoes. These methods require further improvement to enhance crop protection and productivity within the agricultural sector.

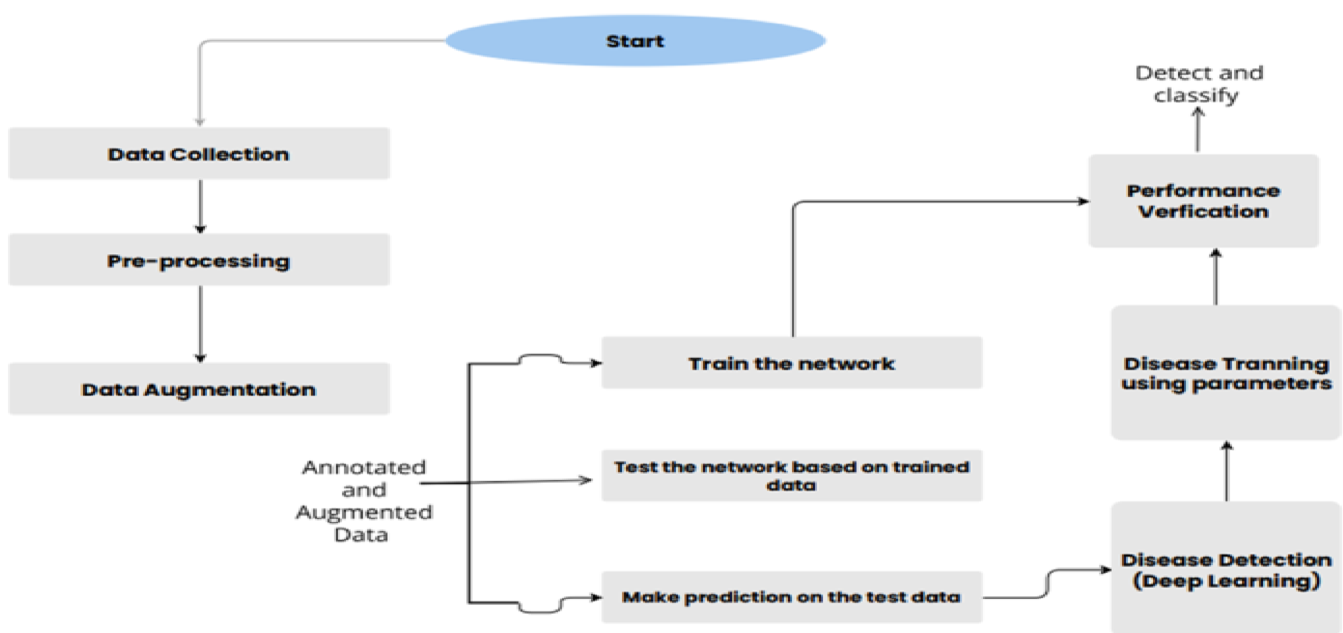

Figure 5. Flow Chart of Proposed Method.

Dataset Collection

We collected a comprehensive dataset consisting of healthy and diseased samples of chilli and tomato plants infected with Begomovirus from the MNSUAM campus and other open resources. This dataset is available on the public repository labelled the Plant Village dataset. We expect this dataset to contain images with different degrees of infection at different stages of the infection process.

For this given analysis, the selected dataset includes 18,000 images of tomato and chilli plants' leaves. Each category has an equal number of images. The dataset contains complete images of plant diseases with no missing images.

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Additionally, a subset of images was taken with a mobile camera and a DSLR in sunlight, with a resolution of 720x1600 pixels. To create a deep learning model that can automatically detect and classify the different variants of Begomoviruses, it is necessary to develop a model that assists farmers by warning them of potential Begomovirus attacks. Some diseases damage crops, just like many other organisms in nature. The manifestations of these disorders can often be recognized by their color, form, and general appearance. A plant disease may manifest in various ways, such as on the leaves or stems. Viruses may cause some of these diseases. Whiteflies can transmit viruses. In this paper, these viruses were detected using VGG-16, ResNet-50, and Inception V3 deep neural networks.

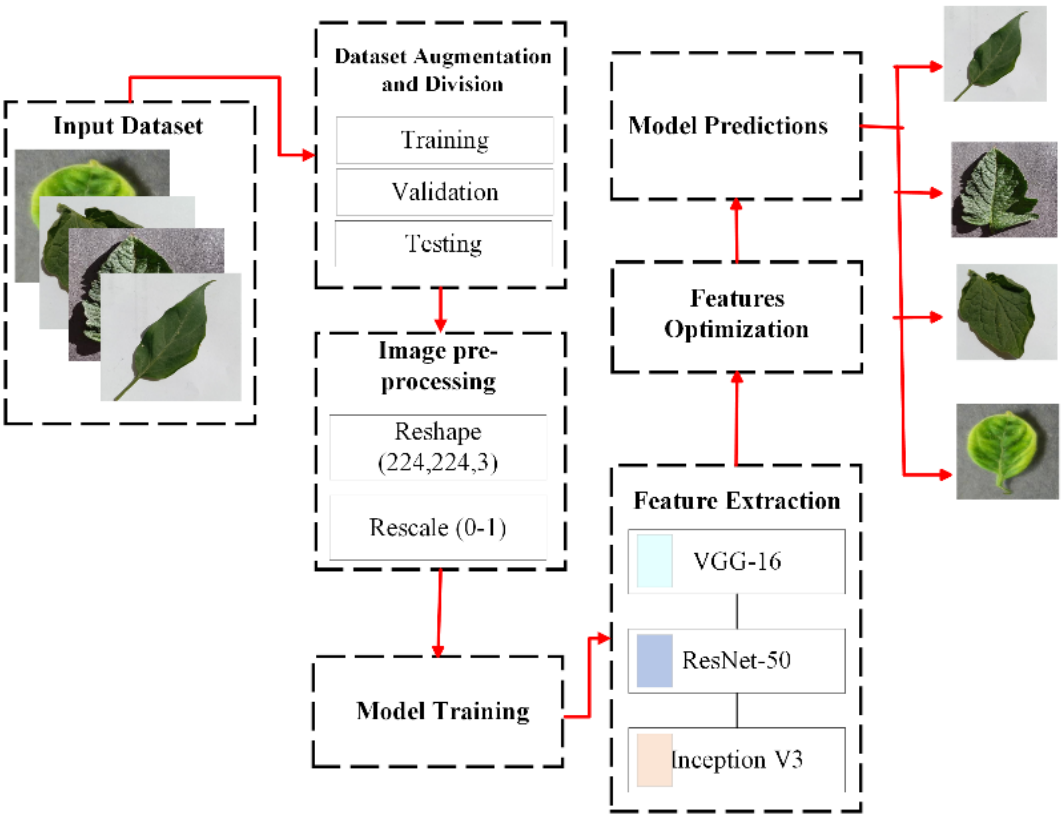

Figure 6. Proposed methodology

The ReLU activation function is commonly referred to as a nonlinear operator used in various image manipulation tasks. As it operates on the feature maps, it performs an activation that can jumpstart the model's learning patterns. We put this evidence in the next convolutional layer for further analyzing. This is what the process looks like.

$$Conv\_layer = (filter, ReLU) \quad (1)$$

The ReLU function follows the equation:

$$f(x)=max(0,x) \quad (2)$$

where *x* is returned as-is if $x \geq 0$, otherwise, it outputs 0.

VGG16

As shown in Figure 9, the first two layers are described as convolutional layers with 3 × 3 filters, each containing 64 filters, resulting in a volume of 224 × 224 × 64 due to uniform convolutions. The filters have a 3×3 kernel while a stride of 1 is maintained. After this, a max-pooling layer with a filter size of 2 × 2 and a stride of 2 is used, which reduces the volume dimensions from 224 × 224 × 64 to 112 × 112 × 64. Then, two more convolutes with 128 filters further increase the volume to 112 \times 112 \times 128. Another pooling layer reduces the dimensions to 56 \times 56 \times 128. This volume is later reduced to 28 × 28 × 256 through the introduction of two additional convolutional layers with 256 filters each. A max-pooling layer splits these two additional stacks, each of which has three convolutional layers. This leaves the volume at 7 × 7 × 512 after the last pooling layer, which is then resized to the fully connected layer. The last layer is a SoftMax output layer, which segments the results into Sitting, Walking, and Standing.

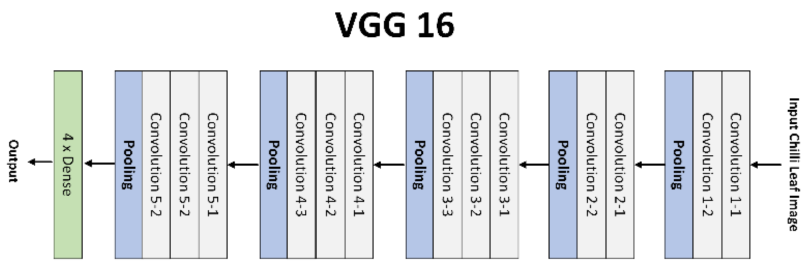

Figure 7. Architecture of VGG 16

ResNet

Microsoft Research presented ResNet in 2015, marking the first use of the residual network architecture to address the performance drop associated with deep networks. Accuracy diminishes with an increase in the depth of the network because of the vanishing gradient problem. The residual network design resolves this problem by using skipping connections whereby lower layers are reached directly from higher layers, and gradients are not significantly reduced during backpropagation.

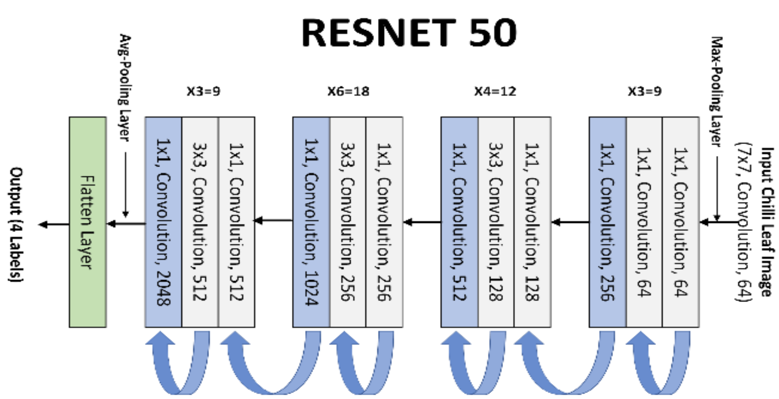

Figure 8. The architecture of the Resnet-50 model

Certain layers are skipped by connecting ahead to later layers, as shown in Figure 11. Because ResNet's ability to work well with accuracy and extremely deep networks, it is frequently employed in computer vision. The network consists of two main blocks: an identity block and a convolution block. Convolution blocks are used when the input set's size does not equal the output set's size, and the identity block is used when these sets are equated to each other. This framework ensures proper training and maximizes the model's accuracy.

A skip connection is defined as a direct access link within a model that leads to different points, changing its output like it was not modified

The ResNet-50 architecture consists of:

- A convolutional layer with 64 distinct kernels of size 7 × 7, a stride of 2, forms the first layer.
- A max-pooling layer with a stride of 2.

A three-layer convolution block, consisting of (1 × 1), 64 kernels, (3 × 3), 64 kernels, and (1 × 1), 256 kernels. This sequence is by layers sequentially. A layer with a skip connection in the model changes the standard input X will be multiplied by the layer's weight and then followed by summation with a bias and applying the activation function F() as represented in Equation (4):

$$F(w * X + b) = F(X) \quad (3)$$

With a **skip connection**, the output is modified as shown in **Equation (5)**:

$$F(X) + X \quad (4)$$

As shown in Figure 13 & 14, in ResNet-50, two types of blocks are used:

1. Convolutional Block
2. Identity Block

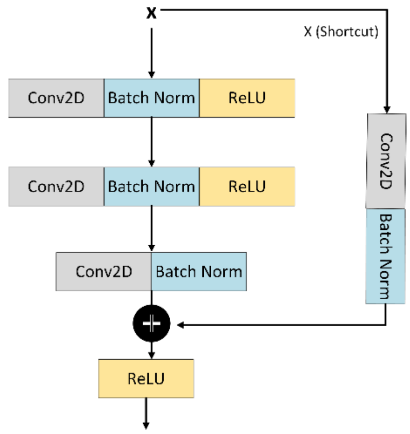

Figure 9. Convolution Block

The value of X is added to the output layer only when the input size matches the output size. If the dimensions differ, a convolutional block is introduced in the shortcut path to ensure that the input and output sizes are equal. There are two methods to achieve this size alignment.

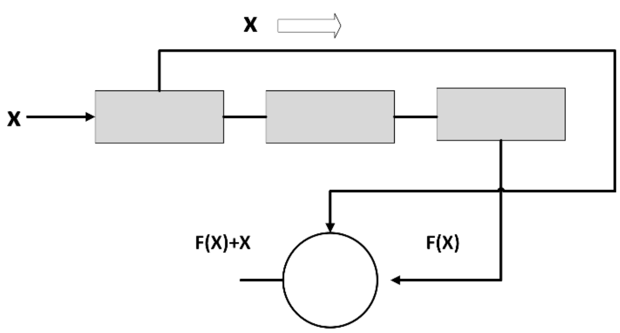

Figure 10. Identity Block

The equation for ensuring equal input and output size becomes:

$$(I + 2P - K) \div S + 1 \times (I + 2P - K) \div S + 1 \quad (5)$$

In convolutional neural networks (CNNs), pooling is typically used to reduce the image size. However, in ResNet-50, a stride of 2 is used instead.

- repeated three times, resulting in a total of nine layers.
- Another block with 1 × 1, 128 kernels, 3 × 3, 128 kernels, and 1 × 1, 512 kernels, repeated four times, adding 12 layers.
- A subsequent block with (1 × 1), 256 kernels, followed by (3 × 3), 256 kernels and (1 × 1), 1024 kernels, repeated six times, resulting in 18 layers.
- A final block with (1 × 1), 512 kernels, followed by (3 × 3), 512 kernels and (1 × 1), 2048 kernels, repeated three times, adding nine more layers.

After these convolutional blocks, an average pooling layer is applied, followed by a fully connected layer with three nodes representing Sitting, Standing, and Walking. A SoftMax activation function is then used to produce the final output.

RESULTS AND DISCUSSION

The results achieved in this study concerning the identification of Begomovirus using deep learning techniques are quite promising. The identification and classification of plants infected with Begomovirus were accurately done after training three different deep-learning models on the labeled datasets. Although there are variations based on the structural design of the method and model used, the following are the results of the general observations made. Visual Geometry Group (VGG-16) - The VGG-16 model is a multi-layered model that was created by the Visual Geometry Group (VGG) from Oxford University, which is known as a deep Convolutional Neural Network. Due to its efficient and effective performance in image classification, this algorithm is widely used. The name VGG-16 refers to a network comprising 16 weight layers, which include both convolutional and fully connected layers.

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The VGG-16 model is organized into modules that include several convolutional layers, along with max-pooling layers that serve to down-sample the spatial dimensions. It features a simple architecture that includes downsized filter sizes of 3x3 and increased depth of layers, enabling it to capture fine details in the input image, as shown in Figure 11.

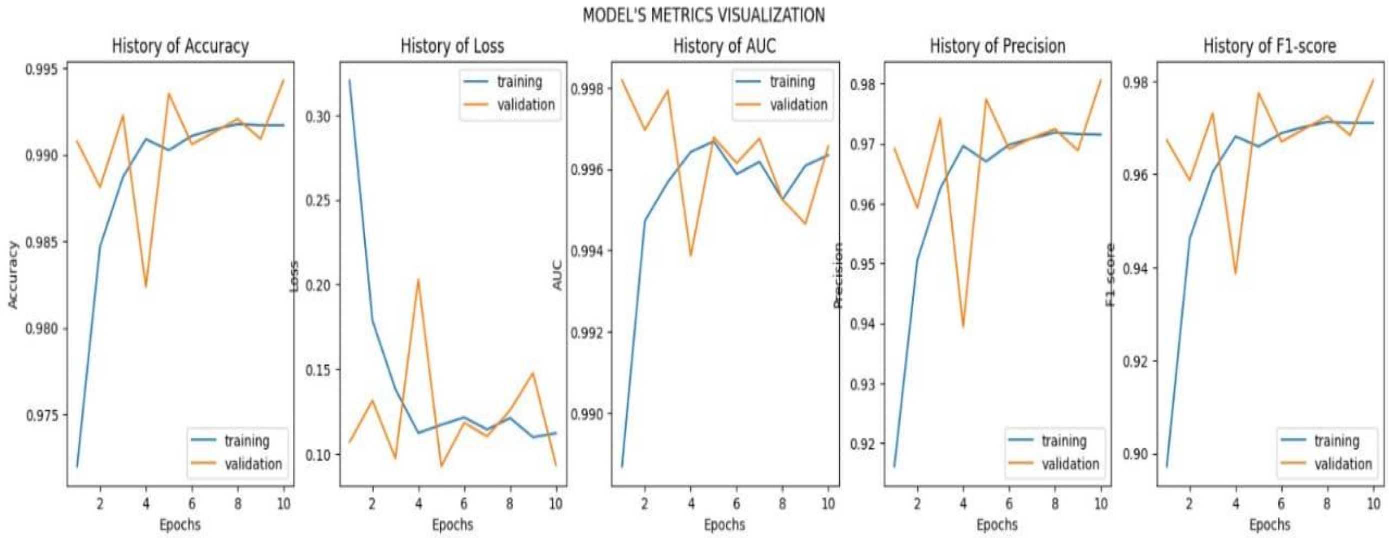

Figure 11. Training Accuracy and Loss of VGG-16.

With ResNet-50, we have yet another deep Convolutional Neural Network (CNN) that features 50 layers. A pre-trained version of this specific neural network is available. It has been trained using a dataset consisting of more than a million images from the ImageNet database. Its image input size is 224 x 224 pixels, and it was trained for 50 epochs in Google Colab. (Zhang et al., 2016)proposed the ResNet-50 model and described how residual connections facilitate the training of deeper neural networks, as illustrated in Figure 17.

Inception-v3: An architecture for deep Convolutional Neural Network (CNN) image classifiers that contain 48 layers can perform computer vision-related tasks. This is the basic enhancement of the 3rd CNN, Google Inception, to achieve state-of-the-art performance in the ImageNet Large Scale Visual Recognition Challenge and competition at the time.

The 3rd CNN Google Inception architecture has been optimized by its inception modules specially designed for the efficient extraction of local and global features simultaneously. These modules enable the network to develop well-defined features across multiple scales and resolutions, facilitating effective representation learning. Every inception module comprises a series of parallel convolutional layers that differ in filter sizes. This parallel configuration enables the extraction of features at different levels of abstraction. As well to these, the inception modules apply 1x1 convolutions for the reduction in cost and count of parameters, which is referred to as “dimensionality reduction,” as shown in Figure 12.

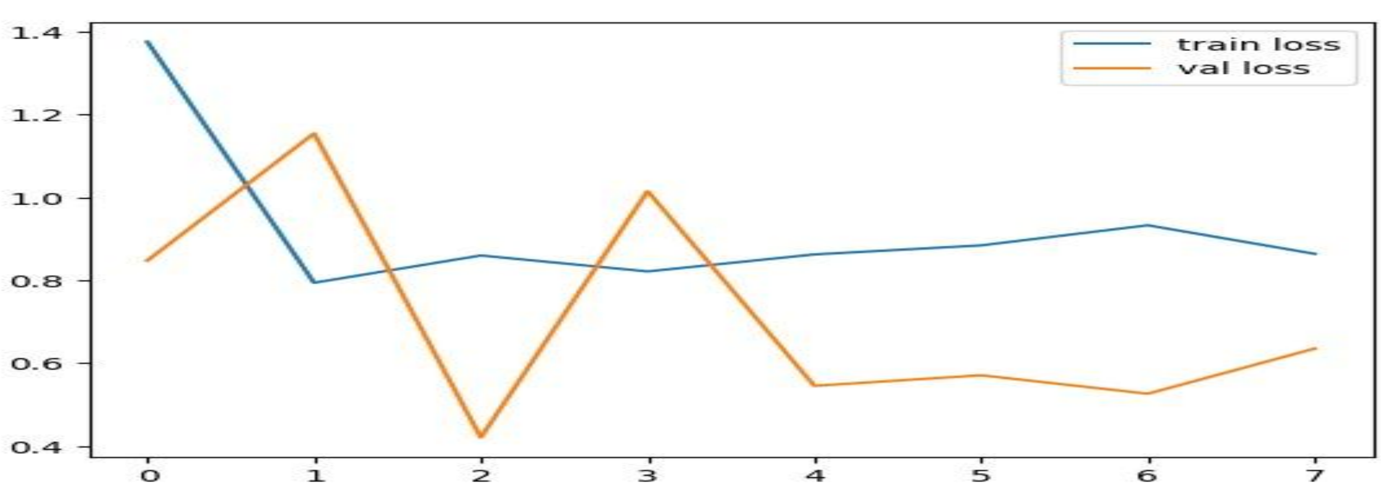

Figure 12. Training Loss and Validation Loss of Inception-v3.

The importance of model comparison should not be neglected. Evaluating a model is crucial in selecting the most effective model for given problem or task. The results comparison of VGG-16 and ResNet-50 can be seen in Table 1

Table 1. Comparing results of models implemented.

Models	Accuracy (%)	Precision (%)	Recall (%)	FI-Score	AUC
VGG-16	98.4	96.7	96.4	96.4	99.4
Inspection-v3	95	95.1	92.4	94.2	95
ResNet-50	80	83	83	85.5	86.1

CONCLUSIONS

The identification of Begomovirus disease for chilli and tomato crops has been investigated in this study through automation with deep learning techniques. This system enhances detection, accuracy, reduces processing time, and improves scalability, functioning as an early response monitoring system for controlling plant diseases. Employing sophisticated and modern deep-learning neural networks enables the system to detect diseased plants accurately and promptly, thereby minimizing crop failure and enhancing global food security. Deep learning facilitates early detection, accurate diagnosis, and informed responsive actions to crop failures and global food security. There is a need for further studies and efforts aimed at fully automating plant disease diagnostic and management systems.
Subsequent studies will require the design of systems optimized for AI model generalization, especially multimodal data sources, and more efficient computational approaches to optimize automation and AI-powered plant disease diagnosis interpretation.

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AUTHOR CONTRIBUTIONS

All authors contributed equally to this research.

COMPETING OF INTEREST

No conflicts of interest have been disclosed by the authors.

REFERENCES

Abbas, S., Haider, A., Kousar, S., et al 2025. Climate variability, population growth, and globalization impacting food security in Pakistan. *Sci. Rep.*, *15*(1), 4225.

Binyameen, B., Khan, Z., Khan, S.H., et al 2021. Using multiplexed crispr/cas9 for suppression of cotton leaf curl virus. *Int. J. Mol. Sci.*, *22*(22). https://doi.org/10.3390/ijms222212543

FAO. 2025. *GIEWS - Global Information and Early Warning System, Country Brief, 2025*. Country Analysis. https://www.fao.org/giews/countrybrief/country.jsp?code=PAK

Ferro, M.M.M., Ramos-Sobrinho, R., Xavier, C.A.D., et al 2019. New approach for the construction of infectious clones of a circular DNA plant virus using Gibson Assembly. *J. Virol. Methods.*, *263*. https://doi.org/10.1016/j.jviromet.2018.10.017

González-Pérez, J. L., Espino-Gudiño, M. C., Torres-Pacheco, I., et al 2011. Quantification of virus syndrome in chili peppers. *Afr. J. Biotechnol., 10*(27), 5236–5250. https://doi.org/10.5897/AJB10.1165

Kaur, K., Singh, J., Kaur, M. 2018. Compressive strength of rice husk ash based geopolymer: The effect of alkaline activator. *Constr. Build. Mater.*, *169*, 188–192.

Kumar, S., Ahlawat, W., Kumar, R., et al 2015. Graphene, carbon nanotubes, zinc oxide and gold as elite nanomaterials for fabrication of biosensors for healthcare. *Biosens Bioelectron*, *70*, 498–503.

Moury, B., Palloix, A., Caranta, C., et al 2005. Serological, molecular, and pathotype diversity of Pepper veinal mottle virus and Chili veinal mottle virus. *Phytopathology*, *95*(3), 227–232. https://doi.org/10.1094/PHYTO-95-0227

Nalla, M.K., Schafleitner, R., Pappu, H.R., et al 2023. Current status, breeding strategies and future prospects for managing chilli leaf curl virus disease and associated begomoviruses in Chilli (Capsicum spp.). *Front. Plant Sci.* (Vol. 14). https://doi.org/10.3389/fpls.2023.1223982

Nozaki, D.N., Krause-Sakate, R., Hasegawa, J.M., et al 2006. First report of Tomato severe rugose virus infecting pepper plants in Brazil. *Fitopatol. Bras.*, *31*, 321.

Pechuho, N., Khan, Q., Kalwar, S. 2020. Cotton crop disease detection using machine learning via tensorflow. *Pak. j. eng. technol.*, *3*(2), 126–130.

Roumagnac, P., Lett, J. M., Fiallo-Olivé, E., et al 2022. Establishment of five new genera in the family Geminiviridae: Citlodavirus, Maldovirus, Mulcrilevirus, Opunvirus, and Topilevirus. *Arch. Virol.*, *167*(2). https://doi.org/10.1007/s00705-021-05309-2

Sani, I., Ismail, S. I., Abdullah, S., et al 2020. A review of the biology and control of whitefly, bemisia tabaci (Hemiptera: Aleyrodidae), with special reference to biological control using entomopathogenic fungi. *Insects*, *11*(9). https://doi.org/10.3390/insects11090619

Sattar, M. N., Kvarnheden, A., Saeed, M., et al 2013. Cotton leaf curl disease - An emerging threat to cotton production worldwide. *J. Gen. Virol.*, *94*(PART4), 695–710. https://doi.org/10.1099/vir.0.049627-0

Simpson, E.L., Sinclair, R., Forman, S., et al 2020. Efficacy and safety of abrocitinib in adults and adolescents with moderate-to-severe atopic dermatitis (JADE MONO-1): a multicentre, double-blind, randomised, placebo-controlled, phase 3 trial. *The Lancet*, *396*(10246), 255–266.

Song, L., Wang, Y., Zhao, L., et al 2022. Transcriptome Profiling Unravels the Involvement of Phytohormones in Tomato Resistance to the Tomato Yellow Leaf Curl Virus (TYLCV). *Horticulturae*, *8*(2). https://doi.org/10.3390/horticulturae8020143

Srinivas, P., Hunt, L.N., Pouch, S.M., et al 2018. Detection of colistin heteroresistance in Acinetobacter baumannii from blood and respiratory isolates. *Diagn Microbiol Infect Dis*, *91*(2), 194–198.

Zakir Hossain, M.D., Sohel, F., Shiratuddin, M. F., et al 2019. A comprehensive survey of deep learning for image captioning. *ACM Computing Surveys*, *51*(6). https://doi.org/10.1145/3295748

Zhang, J., Terrones, M., Park, C.R., et al 2016. Carbon science in 2016: Status, challenges and perspectives. *Carbon*, *98*, 708–732.