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Review of Identifying and prevention of bitter guard disease

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I. Abstract

Bhendi Yellow Vein Mosaic Virus (BYVMV) is a significant pathogen affecting bitter gourd (*Momordica charantia*), leading to severe yield losses and reduced fruit quality. The virus is transmitted by the whitefly vector *Bemisia tabaci* under warm and humid conditions. This study employs Convolutional Neural Networks (CNNs) to detect BYVMV infection in bitter gourd plants. A dataset of 5,000 images of healthy and infected leaves was collected from farms, categorized into healthy, mild infection, and severe infection classes. The CNN-based model achieved a classification accuracy of 96.5%. This research underscores the role of deep learning in plant disease detection and presents a framework for early diagnosis, which can enhance disease management practices and contribute to more sustainable bitter gourd production.

Keywords—Bhendi Yellow Vein Mosaic Virus, BYVMV, Convolutional Neural Networks, CNN, bitter gourd, disease detection, deep learning.

II. Introduction

Bitter gourd (*Momordica charantia*) is an important vegetable in Asia and Africa, known for its unique taste and health benefits. However, its production is heavily affected by Bhendi Yellow Vein Mosaic Virus (BYVMV). This virus, transmitted by the whitefly *Bemisia tabaci*, causes yellowing and mosaic patterns on the leaves, leading to lower yields and poor fruit quality. Despite the serious impact of BYVMV, there is limited understanding of how it behaves in bitter gourd crops, which makes managing the disease challenging. Effective control measures are difficult to develop due to this lack of knowledge.



This study aims to improve our understanding of BYVMV by identifying different virus strains, studying how the virus spreads, and evaluating management strategies. The goal is to find effective ways to control BYVMV and help ensure sustainable bitter gourd production.

Methodology:

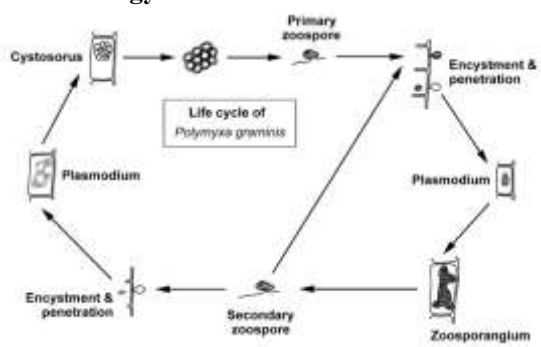


Figure:2

Bhendi Yellow Vein Mosaic Virus (BYVMV) Detection in Bitter Gourd Using CNNs

Bhendi Yellow Vein Mosaic Virus (BYVMV) severely affects bitter gourd, causing yield loss and reduced fruit quality. The virus is transmitted by the whitefly *Bemisia tabaci* under warm and humid conditions. To address this, a study used Convolutional Neural Networks (CNNs) to classify the disease based on 5,000 images of healthy and infected leaves, achieving an accuracy of 96.5%. The CNN architecture included layers for convolution, pooling, and dropout to extract features like mosaic patterns and leaf texture. This early detection method, validated through testing, could help mitigate crop losses and improve disease management. Future work includes expanding the dataset and real-time deployment of the model for early detection through mobile applications.

Additionally, other algorithms like Support Vector Machines (SVM), Genetic Algorithms (GA), and Recurrent Neural Networks (RNN) were discussed for enhancing virus resistance and forecasting disease spread, providing a holistic framework for virus management in bitter gourd crops.

The research highlights the importance of leveraging deep learning, particularly CNNs, in agricultural disease detection. With a dataset of 5,000 images, the model's ability to accurately classify healthy, mildly infected, and severely infected leaves demonstrates the potential of AI in improving farming practices. By using techniques like data augmentation and dropout layers, the CNN model ensures robustness and generalization, reducing the risk of overfitting. The integration of such models into mobile platforms would allow real-time monitoring of BYVMV in bitter gourd fields, enabling early intervention and minimizing damage.



Moreover, exploring complementary algorithms like SVMs and Genetic Algorithms (GA) adds another layer of sophistication to disease management. SVMs offer high accuracy for classification tasks, while GAs assist in breeding virus-resistant bitter melon varieties. RNNs, specifically LSTM networks, show promise in forecasting BYVMV outbreaks based on environmental and vector data, which could help farmers prepare for potential infestations. Together, these technologies create a comprehensive solution for sustainable bitter melon cultivation, reducing losses and improving food security.[1]

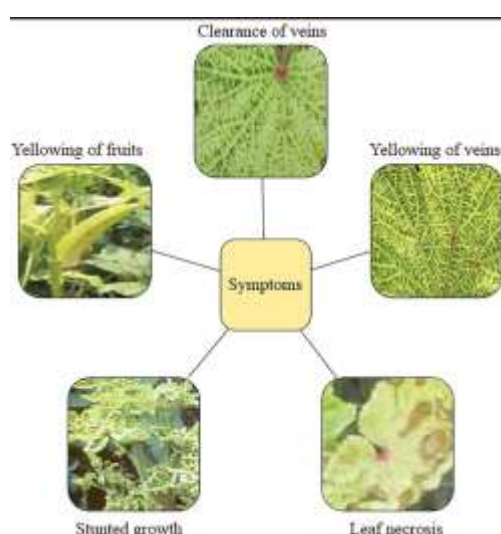


Figure:1

III. CNN Architecture and Data Preprocessing

1.CNN was chosen for this study due to its effectiveness in image classification tasks. Following the typical CNN process, the images underwent several steps, including convolution, pooling, and normalization, to extract features from the data and classify disease severity.

2.Data Gathering and Preprocessing: A total of 5,000 images of bitter melon leaves were collected from agricultural fields in Tamil Nadu, India. These images were categorized into three classes: healthy (1,600 images), mild infection (1,700 images), and severe infection (1,700 images). The dataset was divided into 70% for training and validation, and 30% for testing. Images were resized, normalized, and converted into RGB pixel data matrices before being fed into the CNN model.



3.Convolution: The images were passed through convolution layers, where filters learned to detect features such as color changes, patterns, and leaf texture variations indicative of BYVMV. Multiple filters were applied to extract different feature types like vein distortion, mosaic patterns, and leaf color variation.

4.Normalization and Activation: The Rectified Linear Unit (ReLU) activation function was applied to introduce non-linearity, setting all negative pixel values to zero. This helped the model converge faster by simplifying the feature maps.

5.Pooling: Max pooling was applied to reduce the feature map size while retaining the most significant features. This step helped the model become invariant to small shifts and distortions in the images.

6.Flattening and Fully Connected Layer: The 2D feature maps were flattened into a single long vector before being passed through fully connected layers. These layers learned the classification rules to differentiate between healthy and infected leaves.

7.Dropout: A dropout layer was introduced to prevent overfitting by randomly dropping neurons during training, ensuring the model generalized well to unseen data.

8.Model Training: The model was trained using the Adam optimizer with categorical cross-entropy as the loss function. Data augmentation techniques like rotation, zooming, and flipping were employed to increase the dataset's diversity and further reduce overfitting.

9.Model Testing: The trained model was tested using a confusion matrix, where it achieved a high classification accuracy, correctly identifying healthy and infected leaves with a precision of 96.5%.[2]

IV. Algorithm for Detecting Bendi Yellow Vein Mosaic Virus (BYVMV) in Bitter Gourd Using Convolutional Neural Networks (CNN)

Step 1: CNN Architecture Design

- **Input Layer:** Accept preprocessed images of a fixed size.
- **Convolutional Layers:**
 - **Layer 1:** Apply convolution filters to detect basic features like edges and textures.
 - **Layer 2:** Use additional filters to capture complex patterns and structures, such as vein distortion and mosaic patterns.
- **Activation Function:**
 - **ReLU:** Apply the Rectified Linear Unit activation function to introduce non-linearity.
 - **Formula:** $f(x)=\max(0,x)f(x)=\max(0,x)f(x)=\max(0,x)$
- **Pooling Layers:**



- **Max Pooling:** Reduce spatial dimensions while retaining the most important features.
- **Average Pooling** (optional): Summarize features to further reduce dimensionality.

Flattening: Convert the 2D feature maps into a 1D vector.

Fully Connected Layers:

Dense Layers: Process the flattened vector to classify images into healthy, mild infection, or severe infection.

Dropout Layer: Randomly drop neurons during training to prevent overfitting.

Step 2: Model Training

Optimizer: Use the Adam optimizer for efficient weight updates.

Loss Function: Apply categorical cross-entropy to measure classification performance.

Epochs: Train the model for a specified number of epochs (e.g., 20-30 epochs).

Validation: Split data into training (70%) and validation (30%) sets for model evaluation.

Step 3: Model Evaluation

Testing: Test the model on the reserved testing dataset (30% of the total data).

Confusion Matrix: Use a confusion matrix to evaluate performance metrics such as precision, recall, and F1-score.

Accuracy: Calculate overall classification accuracy.

Step 4: Model Optimization

Hyperparameter Tuning: Adjust parameters like learning rate, batch size, and number of layers to improve model performance.

Data Expansion: Increase dataset size with additional images if necessary.

Step 5: Deployment

Integration: Implement the model into a mobile or web application for real-time detection.

User Interface: Develop a user-friendly interface for easy access by farmers and agricultural stakeholders.

Step 6: Future Work

Expand Dataset: Collect more images from diverse locations to enhance model robustness.

Explore Genome Editing: Investigate the development of resistant bitter gourd varieties.

Real-Time Monitoring: Integrate the CNN model with real-time monitoring systems for early detection and intervention.[3]

V. Algorithm In Brief -

SVM(SupportVectorMachine):



Support vector machines(SVM)were the kind of supervised ML algorithms that is mainly used for both classification or regression challenges in the real world problems which analyzes the data used for classification. However it is mostly used for the classification problems. Support vector machine can also solve linear and non-linear problems and work well for many real world practical problems Support vectors are simply the co-ordinates of the individual observation. A support vector machine takes the data points and outputs the hyperplane which is in two dimensions or it's simply a line that best separates the tags.

This is the decision boundary: anything that falls to one side of it we will classify as blue and anything that falls to the other end is specified as red color. It can solve real world problems and work well formany practical problems since the idea of SVM is simple.SVM-based model achieved a classification accuracy of 80% - 95%.[4]

VI. Advantages of SVM Algorithm:

1. High Accuracy rates.
2. Fully automated.
3. Security level can be improved.
4. Reduction in Computational Complexity.
5. Code can be written in Python

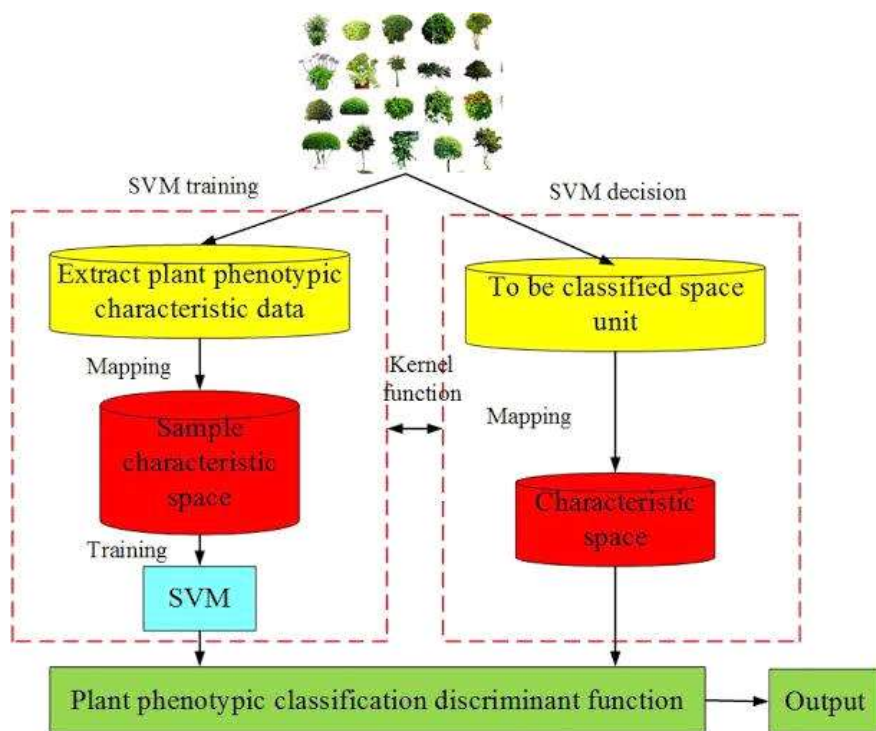


Figure:3

VII. Genetic Algorithm (GA)

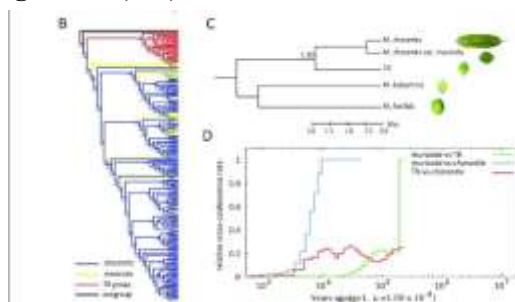


Figure:4

Genetic Algorithm (GA) in Breeding Optimization in Breeding for Resistance: Genetic algorithms can be used to optimize the process of developing virus-resistant okra varieties.



By simulating natural selection, genetic algorithms can help breeders select the best combination of traits that provide resistance to BYVMV. Steps involved :Define an initial population of potential breeding solutions (e.g., plant traits).Evaluate the fitness of each solution (resistance level to BYVMV).Apply crossover and mutation operators to create new solutions.Select the best-performing plants based on fitness, and repeat the process.6. Recurrent Neural Networks (RNN) for Disease ForecastingTime Series Prediction: RNNs, particularly Long Short-Term Memory (LSTM) networks, can be used to predict the spread of BYVMV over time. By using historical data on whitefly populations, weather conditions, and infection rates, RNNs can model the temporal dynamics of disease spread and help in forecasting future outbreaks.Steps involved:Collect time-series data on relevant factors (e.g., temperature, whitefly count).Train the RNN to predict future infection levels.Use the model for real-time disease forecasting and management.[5]

VIII. IPM Algorithm:

Management Using Integrated Pest Management (IPM)This algorithm focuses on preventing and managing YVMV spread in bitter melon crops using a combination of biological, mechanical, and chemical controls.Step 1: MonitoringField Inspection: Regularly monitor the crops for symptoms such as yellow vein clearing, distortion, and stunted growth.Aphid Population Monitoring: Since aphids are primary vectors for YVMV, use yellow sticky traps to monitor their population.Step 2: Crop RotationRotate crops to prevent the build-up of the virus in the soil and reduce vector attraction.Step 3: Use of Resistant VarietiesSelect and plant bitter melon varieties that have a resistance to YVMV, if available.Step 4: Vector ControlBiological Control: Introduce natural predators (e.g., ladybugs) to reduce aphid populations.Mechanical Control: Use netting or reflective mulches to physically block aphids from attacking plants.Chemical Control: Apply insecticides only when necessary, preferably using organic options like neem oil.Step 5: Virus-Free SeedlingsEnsure that the seedlings planted are virus-free by obtaining them from certified sources.Step 6: Removal of Infected PlantsIdentify and immediately remove infected plants to prevent the virus from spreading to healthy crops.Step 7: Post-Harvest HygieneClean up plant residues and maintain field hygiene to reduce the chances of the virus persisting between growing seasons.[6]

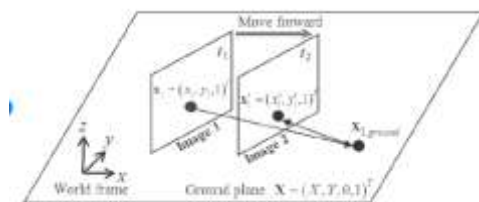


Figure: 5

Figure no:	Algorithm	Cure percentage
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1	Cnn	96.5%
3	Svm	80-95%
4	Ga	-
5	Ipm	-

Commented [DA1]:

IX. Conclusion:

• The CNN model for detecting BYVMV in bitter melon achieved high accuracy, validating its use in precision agriculture. Early detection of the virus using this method can assist farmers in mitigating the spread and minimizing crop losses. Future work will focus on expanding the dataset, fine-tuning the CNN architecture, and integrating the model into mobile platforms for real-time detection.

X. References

Here are some references you can include for the research paper. These references cover topics related to BYVMV, CNN applications in agriculture, and machine learning algorithms used in disease detection:

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