

Department of Food, Agricultural and Biological Engineering

Detection of High Plains Wheat Mosaic Virus (HPWMoV) in sweet corn using multispectral imagery and deep learning

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INTRODUCTION

- High Plains Wheat Mosaic Virus (HPWMoV)** is a major phytosanitary concern for sweet corn seed production.
- Disease symptoms include yellow mosaic, streaking, stunting, and necrosis (Fig 1).
- Virus transmission occurs through the wheat curl mite (*Aceria tosichella*) and infected seed.
- Phytosanitary certification is required for sweet corn seed exports to certain countries, such as New Zealand, ensuring they are free of HPWMoV.
- Traditional certification methods – including field inspections, laboratory testing, and using indicator plants – are labor-intensive, time-consuming, and costly.
- Remote sensing approaches offer a promising solution by enabling field-scale detection of HPWMoV infection in a timely and cost-effective manner.



Fig 1. Corn plants showing visual symptoms of HPWMoV infection

OBJECTIVE

Develop an innovative approach using multispectral imagery from Unmanned Aerial Systems (UASs) and deep learning to enable field-scale detection of HPWMoV infections.

METHODOLOGY

The specifics of each step have been provided in the following sections.

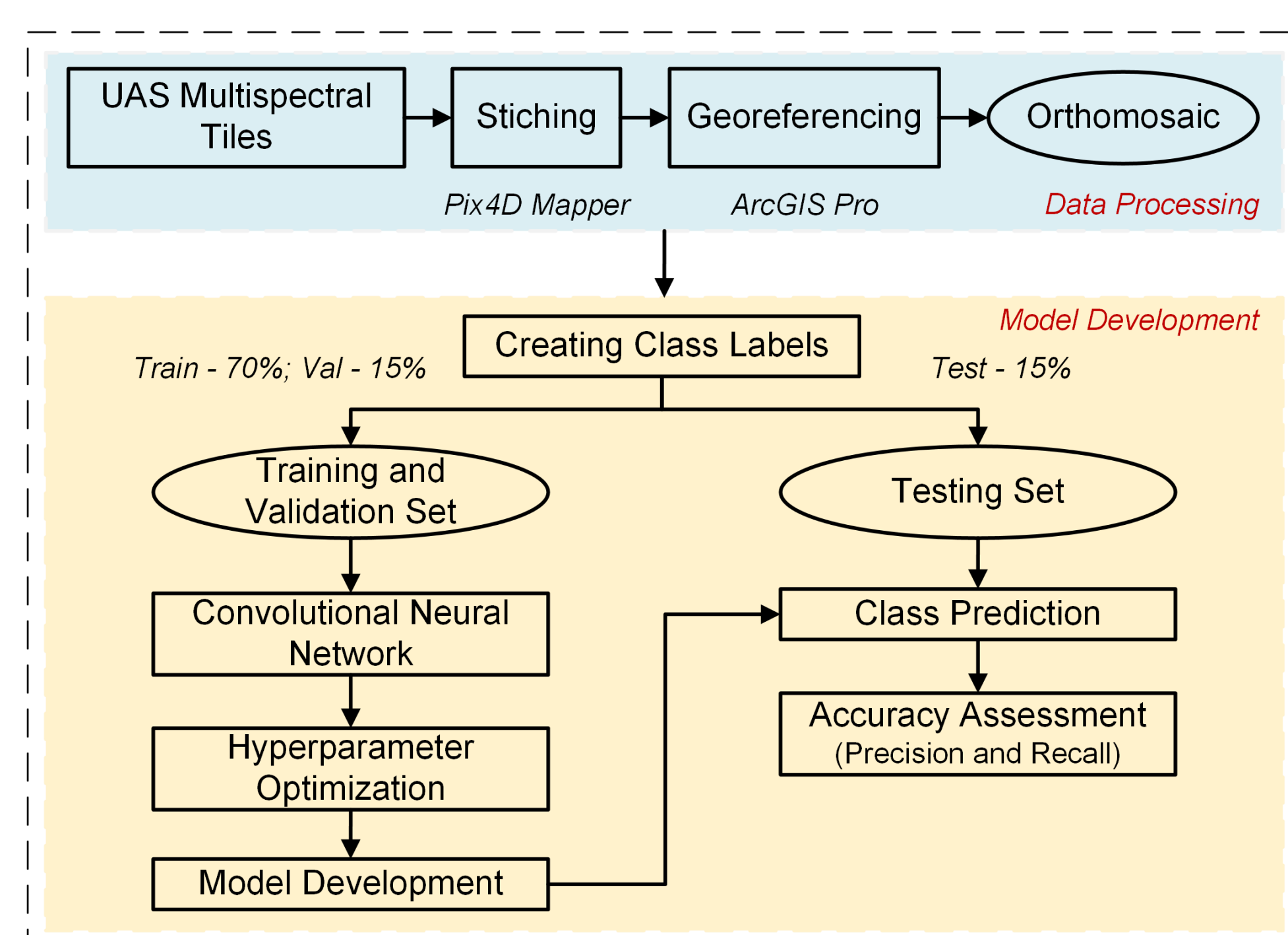


Fig 2. Data analysis workflow for disease detection model

Study area and experimental design

- Experiments were conducted during corn growing season in 2024 on research plots at Snyder Farms of the Ohio State University located in Wooster, Ohio, USA.

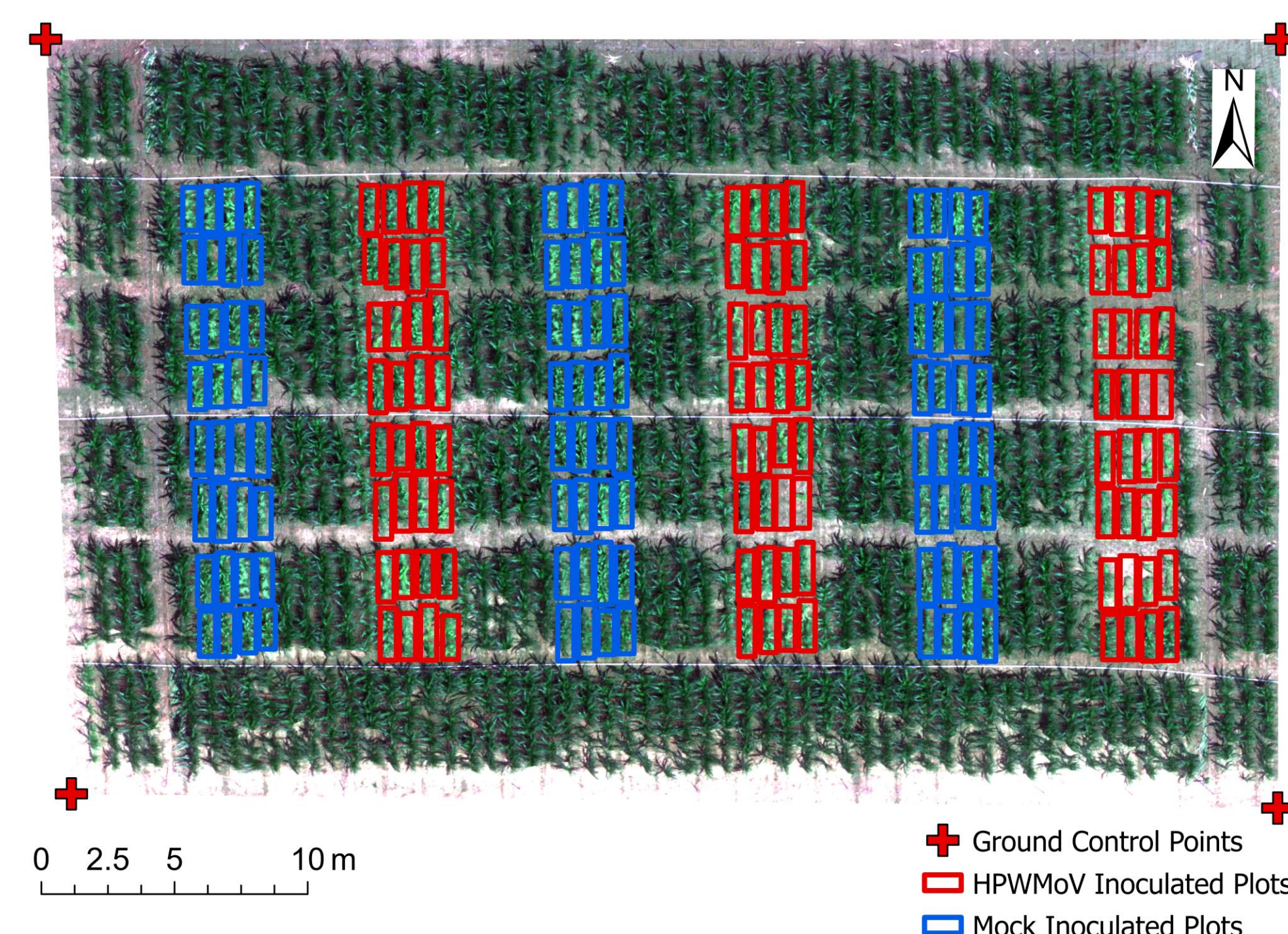


Fig 3. Experimental layout in Snyder field in 2024, overlaid on an aerial image captured on 8 July 2024

- Experimental design: 96 plots consisting of 2 treatments, 16 corn varieties, two rows per plot, 10 plants per row
- Two treatments:
 - HPWMoV Inoculated** - Inoculated plants with HPWMoV
 - Mock Inoculated** - Inoculated plants with mites but without the virus

Data acquisition

Table 1. Flight specifications

Flight height	30 m
UAS	DJI Matrice 200
Sensor	Micasense Rededge MX (5 Bands – RGB, Red Edge, NIR)
Resolution	2.08 cm/pixel
Front overlap	80%
Side overlap	70%
Flight time	18 mins
Flight date	8 July 2024



Fig. DJI Matrice 200

- Four permanent Ground Control Points (GCPs) were used for georeferencing.
- Precise GPS coordinates for GCPs were collected using Trimble Real-Time Kinematic (RTK) GPS system.

Data processing

- Multispectral images were stitched into single orthomosaic image using Pix4D Mapper.
- Image labels for HPWMoV and Mock inoculated plants were created in ArcGIS Pro.
- Convolutional Neural Network (CNN) based deep learning modeling was implemented using Python 3.10 in Google Colaboratory.

Model Development

- Convolutional Neural Network (CNN) architecture
 - Two convolutional blocks with convolution layer followed by batch normalization, Rectified Linear Unit (ReLU) activation, max pooling, and dropout layers.
 - Training images → 672 (70%); Validation images → 144 (15%); Testing images → 144 (15%)
- The model's performance was evaluated using Overall Accuracy, Precision, Recall, and F1-score.

RESULTS

Surface reflectance across different bands

- Healthy cell structures reflect more NIR light, leading to higher reflectance in mock-inoculated plots.
- In contrast, virus infection causes cell damage and structural degradation, resulting in lower reflectance in HPWMoV-inoculated plots.
- The ability of multispectral imagery to capture this subtle physiological difference enables the development of a disease detection model.

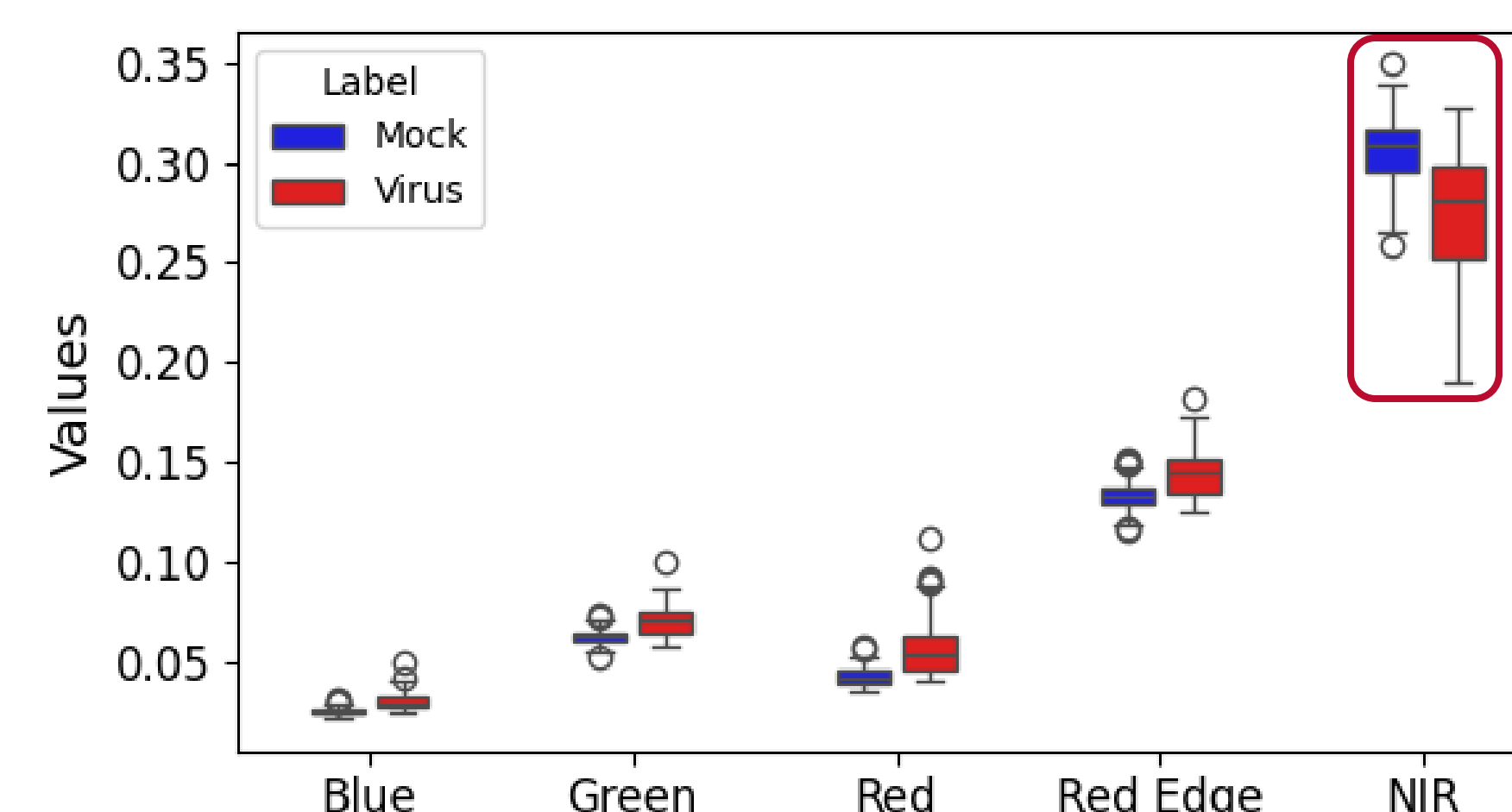


Fig 4. Average reflectance value for mock and virus inoculated plots across different spectral bands

Model performance

- The precision score of 80.3% for "Virus" indicate that the proposed approach accurately represent HPWMoV infected crops on the ground.
- The recall score of 79.1% for "Virus" suggests that the model successfully captured the majority of ground truth HPWMoV-infected crops.
- The overall accuracy of 81% on the unseen test data demonstrates that the model accurately distinguishes mock-inoculated and HPWMoV-inoculated crops.

True Label	Mock	63	13
	Virus	15	53
	Predicted Label	Mock	Virus

Fig 5. Error matrix for the proposed CNN model

Model comparison

The developed CNN-based model outperforms traditional machine learning methods to accurately distinguish mock-inoculated crops from the HPWMoV-inoculated crops.

Table 2. Model comparison

Model	Accuracy Metrics	
	Overall Accuracy	F1-Score
Convolutional Neural Network	81.0	79.1
Multi Layer Perceptron	69.0	74.1
Random Forest	74.3	74.1

CNN Explainer

- In mock-inoculated crops, pixels capturing the green biomass play a key role in classification as "Mock", indicating that the model relies on crop features rather than the background.
- In HPWMoV-inoculated crops, background pixels appear to contribute more significantly to the classification.

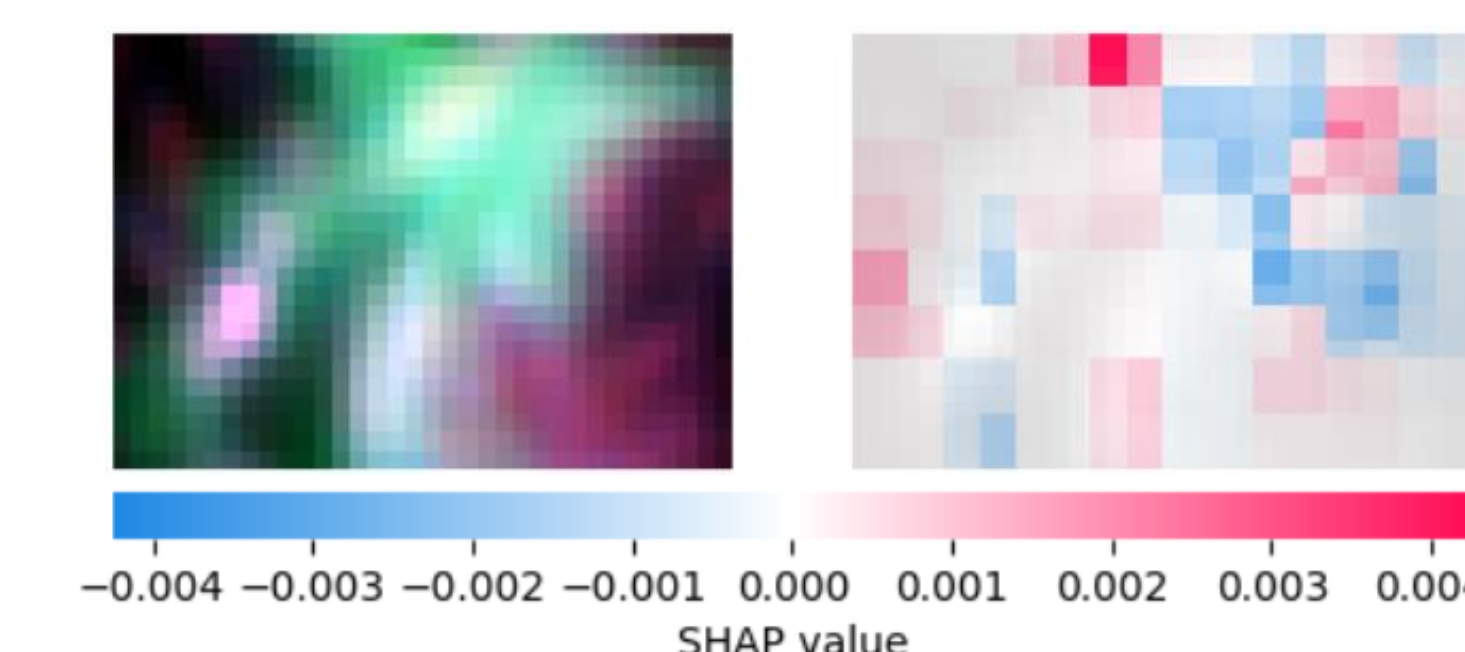


Fig 6. Shap values for mock-inoculated crop

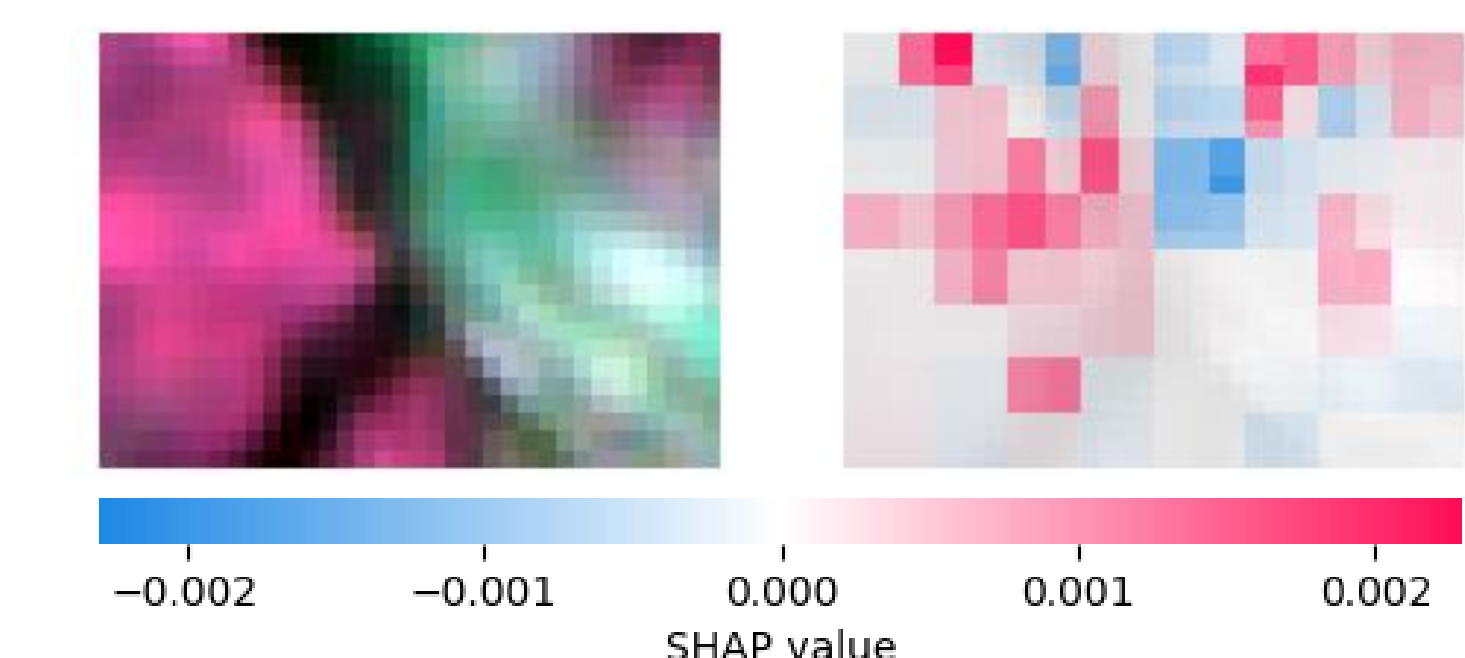


Fig 7. Shap values for HPWMoV-inoculated crop

CONCLUSIONS AND FUTURE WORKS

- A CNN-based deep learning model was developed to distinguish HPWMoV-inoculated crops from mock-inoculated crops.
- Multispectral imagery effectively captures the subtle physiological differences caused by virus infection.
- The CNN-based model outperforms traditional machine learning methods, achieving with an overall accuracy of 81% and an F1-score of 79.1%.
- Significance:** This study establishes a foundation for further research aimed at enhancing the scalability of disease detection models for larger datasets and other crops.
- Future work** will focus on fine-tuning the model's hyperparameters and increasing the training dataset to improve precision and overall performance.

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