

SMART SCREENING: DEEP LEARNING DRIVEN IDENTIFICATION OF FUSARIUM STALK ROT RESISTANT CULTIVARS IN ZEA MAYS L.

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Abstract

Plant breeders and pathologists face the challenge of identifying maize strains resistant to stalk rot at an early stage. This task becomes complicated since the disease reduces crop yields, resulting in higher production costs and environmental pollution as a result of the extensive use of fungicides. The current method used by experts to detect resistant strains has limitations. It is based on phenotypic and genotypic procedures highly depending on the expert skills and experience. Trained algorithms have the ability to detect patterns in images and can be used to identify strains resistant to stalk rot at an earlier stage and with higher accuracy. The current research tested the performance of convolutional neural networks in image-based detection of resistant strains using python and TensorFlow framework. It was observed that the proposed model exhibited 81.25% accuracy on phenotypic images. The F₁ score, recall ratio and precision of phenotypic images were 83.90%, 92.50% and 75.51% for the resistant class while 78.65%, 70% and 90.32% for the susceptible class respectively. The model showed F₁ score, recall ratio and precision of 99.5%, for resistant class of genotypic images. The current study not only helps agriculturists in early identification of the resistant lines against stalk rot in maize but also helps in addressing food security issues worldwide. It also helps in controlling environmental pollution by minimizing the use of fungicides.

Key words: PCR; Stalk rot; Resistant detection; Maize; CNNs

Introduction

Agricultural growth determines the food security in a state. The balance of food demand and supply is being disturbed due to exponential increase in the population (Penuelas *et al.*, 2023). Importance of maize crop can be denied as industry needs raw material from agriculture to contribute in gross domestic production (Bharatkumar *et al.*, 2023; Jin *et al.*, 2023). Diseased free nutritional products are the main demand in national and international markets. The diseases not only decrease food supply but also disturb food chain causing high price in the market (Khatri *et al.*, 2023). Microorganisms open the door for pest and diseases resulting in selection of junk foods by the people that are source of many human diseases. Timely and precise identification of the diseases is very important for sustainable agriculture. Diseases differ in their color, shape and size. Some are similar in color but different in shape or vice versa. So it is difficult to identify the diseases on the visual basis (Alqahtani *et al.*, 2023). A major loss in agricultural production is caused by fungi particularly stalk rot (Elsayed *et al.*, 2023). Early maturity and drying of the plant are the main impact of the disease. The conventional method of crop disease identification relies upon visual observation of the field by experienced farmers, extension

workers or pathologists. The method is laborious and time consuming. Moreover, it requires laboratory studies to properly identify the disease. Pathologists do not recommend any remedial action without physical examination of the infected field (Belisário *et al.*, 2022). Wrong judgment at any stage may cause extensive use of expensive pesticides without any remedy causing environmental pollution. Moreover, extensive use of pesticides may lead to the development of resistant strains of the pathogens causing huge agricultural losses.

The conventional disease identification methods are more time consuming and varies from person to person. Therefore, there is a need of computer-based identification system to address disease occurrence and severity in timely manners. It not only increases the yield per acre but also ensures highly nutritional value of the crop that is not achievable under disease stress (Youwen *et al.*, 2008). A complete understanding of the genetic makeup of the varieties is necessary to be utilized in breeding programs to fulfill food demand globally. The role of genome-based technologies (genotyping and sequencing technology) in modern plant breeding is not denied. Advancement in molecular techniques has shown vital improvement in resistant breeding programs. Genetic composition of maize inbred lines is examined globally (Garg *et al.*, 2023; Liu *et*

al., 2023; Zhang *et al.*, 2022) which helps in minimizing the traditional inbred line selection procedure. It is also believed that maize inbred lines variation against diseases is also linked with the genotypes. Single Nucleotide Polymorphism markers to determine the genetic composition of various plant groups are used in unsupervised artificial neural network algorithms (Yoosefzadeh Najafabadi *et al.*, 2023). The computer software also plays a vital role in accurate determination of genetic diversity of *Olea europaea* (Slobodova *et al.*, 2023).

Deep learning techniques of image processing not only detects weed in vegetable plantation with accuracy but also helps in accurate application of weedicides to the field (Jin *et al.*, 2021). The deep learning algorithms especially CNN has made possible to classify the diseases on image basis (Attallah, 2023; Qian *et al.*, Qureshi *et al.*, 2023, 2024). CNN with minimum number of layers generates accurate results in identification and classification problems (Alhazmi, 2023; Ghosh *et al.*, 2023). It has also shown pronounced impact in taxon identification and examinations of genetic diversity as compare to other traditional classification approaches. The deep learning approach (YOLO-V3 neural network model implemented on a drone) is used to take photographs of pest position for the right and accurate application of pesticide (Al Hiary *et al.*, 2011; Hu *et al.*, 2023; Qian *et al.*, 2025). ConvNet has been explored for classification, localization and image recognition problems where it has shown excellent results (Simonyan *et al.*, 2015). The following goals are set for the current research 1) determination of the role of CNN model in assisting pathologists for resistant and susceptible stalk identification using phenotypic and genotypic images 2) exploring the importance of CNN model in early varietal identification against stalk rot and pollution control.

Materials and Methods

The goal of current research was to assess a neural network model to underline the phenotypic images with genetic images for the detection of healthy/affected lines against stalk rot at seedling stage before cultivating plants in the field. The suggested system was implemented on a computer with an Intel(R) Core (TM) Core i5-8400 CPU running at 3.60 GHz and 8.00 GB of installed RAM. The target model was achieved using TensorFlow, Google Collaboratory hardware and Python.

The phenotypically, healthy and affected images of were gathered from Maize and Millet Research Institute, Yousaf Wala, Pakistan, while the genetic images of these lines were collected by performing polymerase chain reaction in the department of Medicinal Chemistry, University of Minnesota, USA. Resistant source detection on image characteristics largely depends upon five major steps. It includes image acquisition, image preprocessing, image segmentation, feature extraction and classification (Fig. 1). The key success to image processing problems is the selection of reliable image class. Datasets of phenotypic and genotypic images of stalk rot resistant and susceptible were collected using the research of (Sajjad Hussain Qureshi *et al.*, 2015). Before feeding of the image to the proposed model, image preprocessing was performed for better using of memory resources.

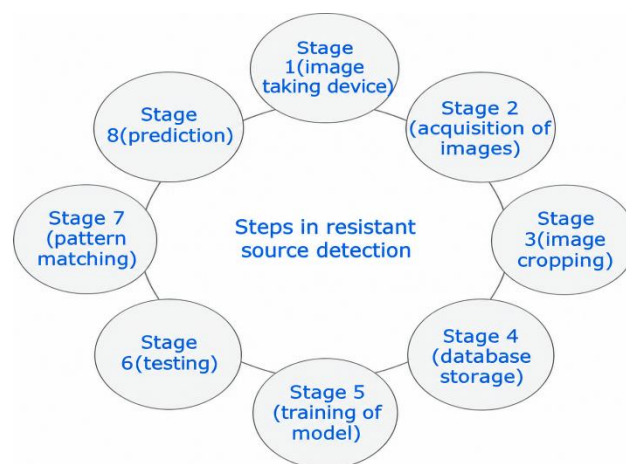


Fig. 1. Steps in resistant source detection using CNN model.

Preprocessing not only eliminates noise from the image but also helps in enhancement and detection of desirable features from the images. It involves background removal, cropping, color transformations, flipping, enhancement, smoothing, rescaling and rotating of infected images. After preprocessing, image segmentation was performed. Segmentation was performed based on similarities and differences. During this step, desirable area from undesirable area was separated. Desirable area contained area of interest having features to be studied. Determination and recognition of lesion area is very essential for correct prediction. This activity was performed in feature extraction step. Feature extraction for crop disease identification and classification mostly depends upon color, shape and texture of lesion area. Color of different diseases varies which helps in detection of accurate diseases. Texture determines the different color distribution of lesion area. Mostly, contrast, cluster shade, cluster prominence, correlation, entropy, energy, homogeneity, sum entropy and sum of squares are used for texture features extraction. Moreover, shape of the diseases on the plant varies in their appearance, which also helps in accurate prediction of plant diseases. The current study explored the CNN which automatically extracted the desirable features. The automatic feature extraction is executed by adjusting the learning weights of the neurons. The conceptual working of CNN model is elaborated in Fig. 2.

Training of the model (CNN): After desirable preprocessing of the raw images, the collected images were divided into train dataset and test dataset at the ratio of 80% and 20% respectively. The training of CNN model was executed on train dataset. Successful training of the model was responsible for accurate identification of the resistant and susceptible classes in the test image. The model consisted of following layers.

Convolutional layer: Trained kernels or filters having the optional trainable bias for each kernel perform convolutional operation on two-dimensional convolution layers. This operation involves the movement of kernels over the input in strides. The size of stride defines the skipped pixels between each convolution. The larger stride results in fewer convolutional operations with smaller output size. The result of each operation is formulated by multiplying each input with kernel weight by adjusting bias. This operation generated feature map which was used as input for next layer by applying activation function.

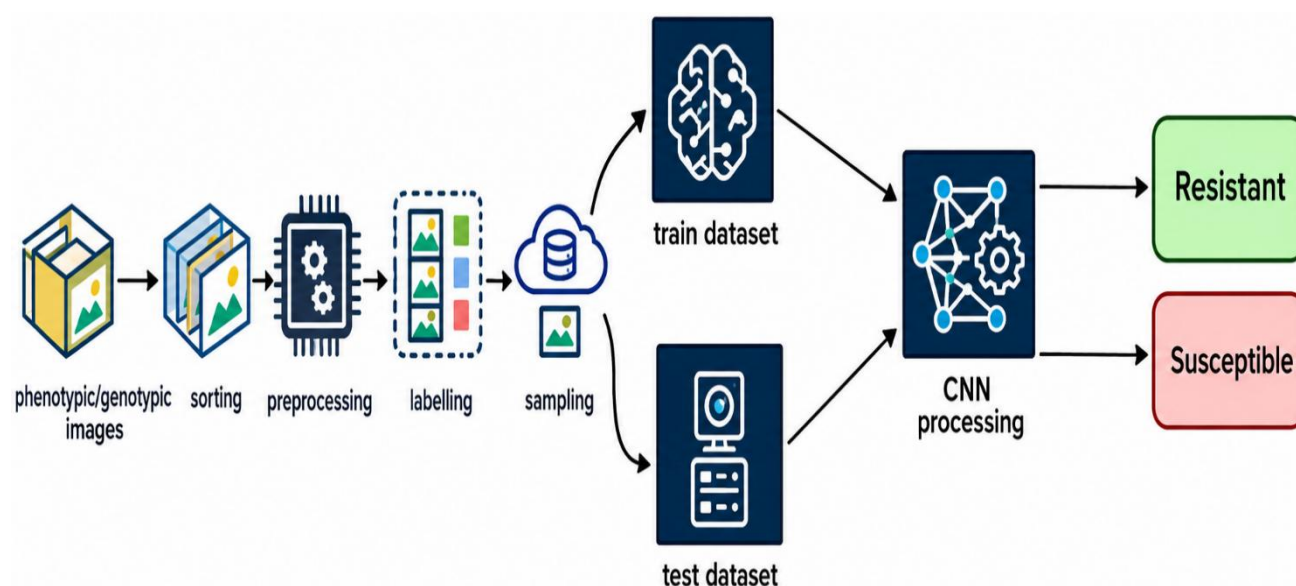


Fig. 2. Conceptual Design of image-based classification model.

Pooling layer: This layer minimizes the size of input attributes. The layer is helpful in identifying and focusing on the area of interest. It performs two operation i.e., maximum and average pooling. These techniques compute maximum or average values of each kernel to be incorporated in the feature map.

Fully connected layer: This layer is used for classification purpose and is placed after convolutional and pooling layers. This layer is among the many hidden layers of network. The layer performs operations by taking input from previous layer by activation function, multiplying it with weighted vector by adjusting bias and giving output as classification. Dropout regularization was used in CNN to avoid overfitting. In this process, neuron is randomly assigned the value of zero during forward and back propagation of learning process. This technique prevents neural network from affecting the problem of overfitting.

RGB images having size of 299×299 pixels were fed to the model. The proposed model had six layers of convolution having filters of 32, 64, 128, 128, 256, and 256. The convolutional layers used a 2×2 kernel size along with average pooling. The padding was same with the stride of 2. Finally, the fully connected layer with a Softmax activation function predicted two classes. The model was trained using a learning rate of 0.0001 for 12 epochs. The adjustment of weights and biases was important activity during training to get predicted values close to actual values.

Results

Most farmers across the world perform a visual inspection to check resistant stem against stalk rot. The experiment was performed to identify the resistant and susceptible lines based on phenotypic and genotypic images using the power of CNN. TensorFlow framework was used for Python programming. Hardware limitations were handled using Google Colaboratory. Two separate simulations were executed to achieve the objectives. The data set was separated into batches in order to solve the computational power issues. A batch size of 32 was maintained for the suggested models. For the current

experiment, learning rate of 0.0001 with twelve number of epochs was selected.

The proposed model phenotypically divided stalk into two classes. Figure 3A and 3B depict the graphical layout of the training and the validation parameters. Figure 3A depicts accuracy measurement during training and validation of the suggested model whereas Fig. 3B depicts the loss measurement. A decent fit of the data is depicted in Figure 3A and 3B. The model exhibited 81.25% accuracy when evaluated on 400 images, with 200 images for each category (Fig. 3A). The F_1 score, recall ratio and precision of the model were further assessed. The F_1 score, recall ratio and precision were 83.90%, 92.50%, and 75.51% for the resistant class and 78.65%, 70%, and 90.32% for the susceptible class respectively (Table 1).

The graphical representation of the relationship between the training and validation parameters on the genotypic images is shown in Figure 4A and 4B. Figure 4A depicts the accuracy measurement found when the suggested model was trained and validated, whereas Figure 4B depicts the loss measurement. Figure 4A and 4B display the best fitting of the data. The model exhibited 99.5% accuracy when evaluated on 400 genetic images (200 from each category) (Fig. 4A). Additionally, the F_1 score, recall ratio, and precision of the model were assessed. For classes (resistant and susceptible), F_1 score, recall ratio and precision were calculated and elaborated in Table 2. Later on, the model was checked using test data. Figure represents the actual and predicted class of the phenotypic and genotypic data fed to the model.

Confusion matrix: Figure 3B details the confusion matrix generated during the categorization of stem into resistant and susceptible classes using phenotypic images. Out of two thousand (2000) images, the model for training picked sixteen hundred (1600) images while four hundred (400) were opted for validation purpose with equal number of resistant and susceptible images. The confusion matrix showed that 185 and 140 images belonged to the resistant and susceptible classes respectively. The model incorrectly classified sixty (60) susceptible and fifteen (15) resistant images.

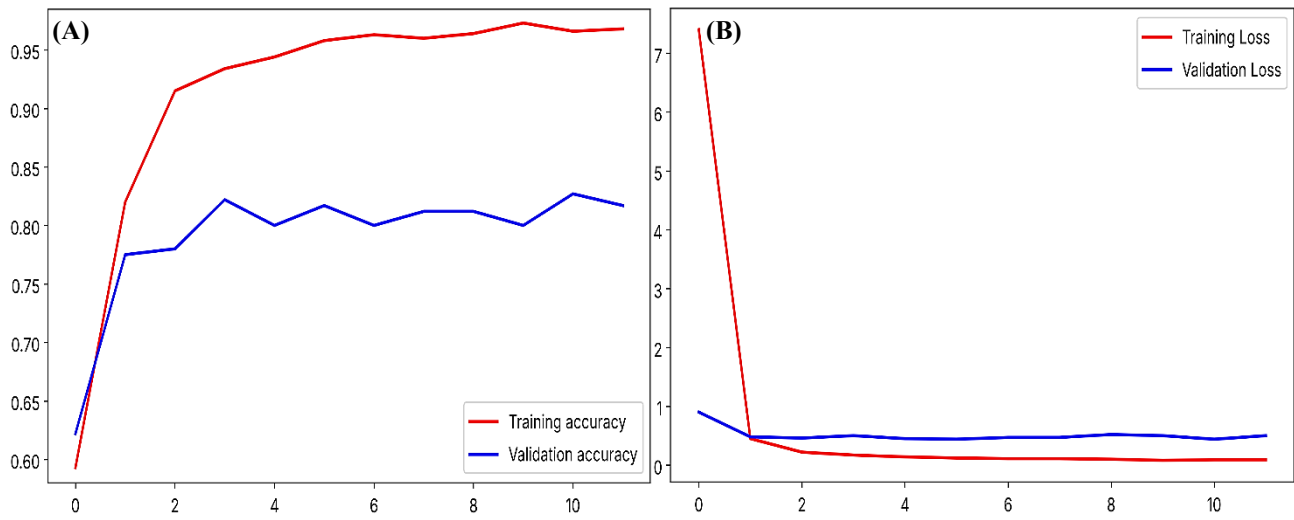


Fig. 3. Phenotypic image based training and validation accuracy (A) and loss (B).

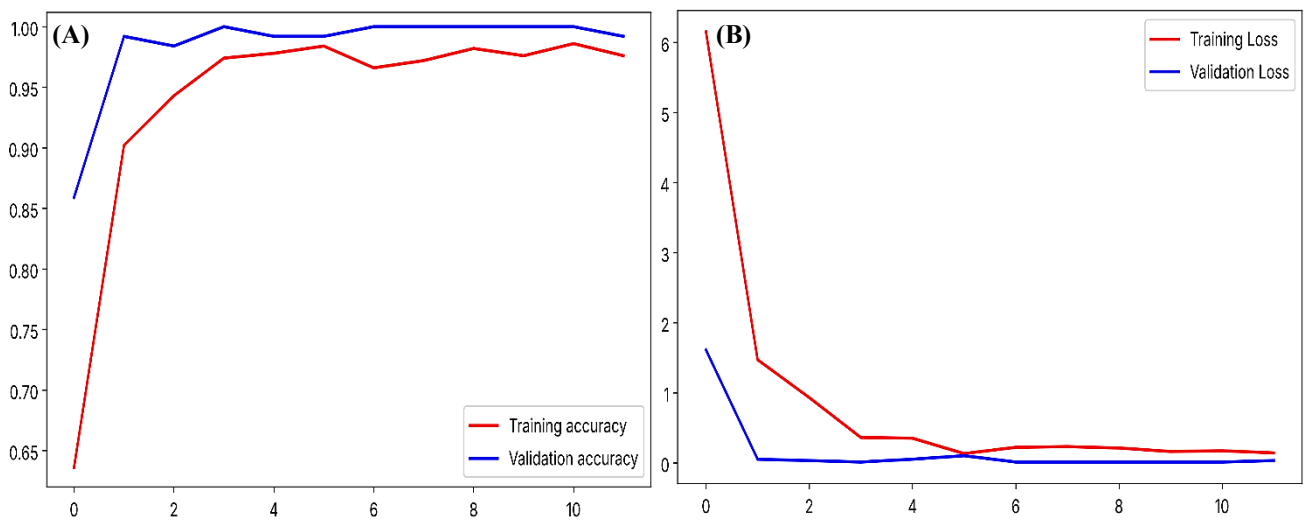


Fig. 4. Genotypic image-based training and validation accuracy (A) and loss (B).

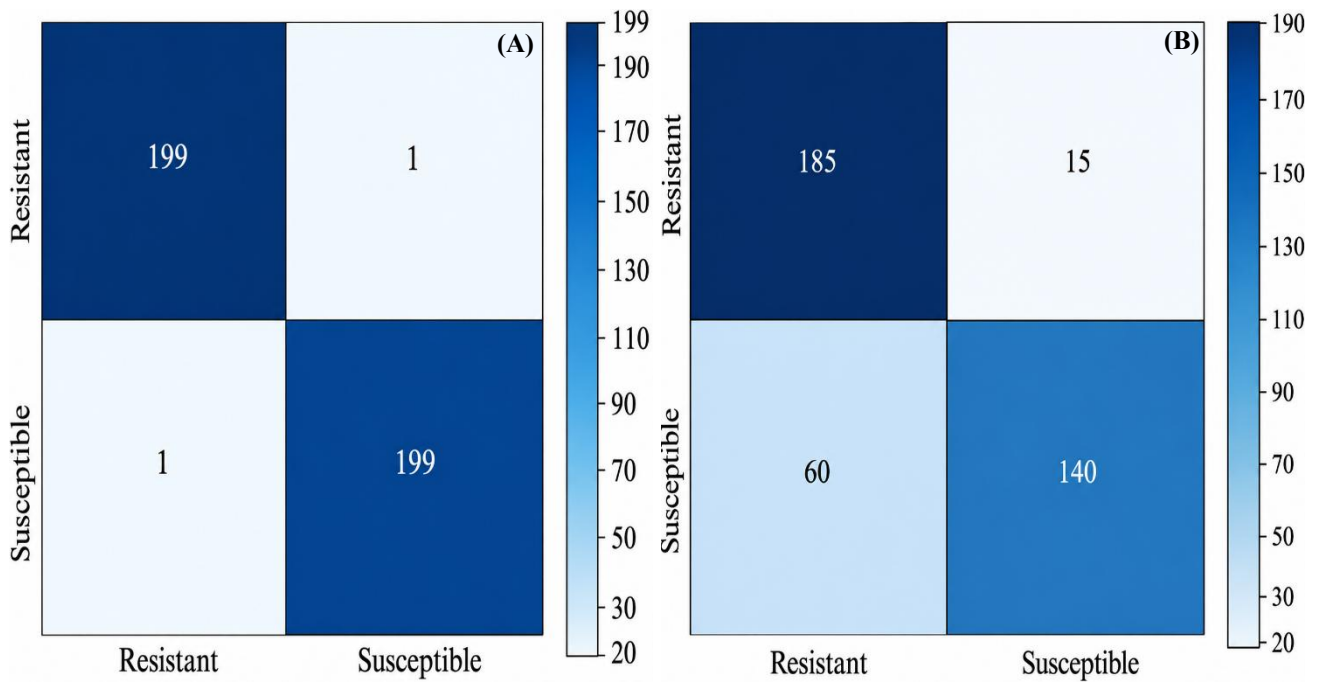


Fig. 5. Confusion Matrix of genotypic (A) phenotypic (B) images of stalk rot.

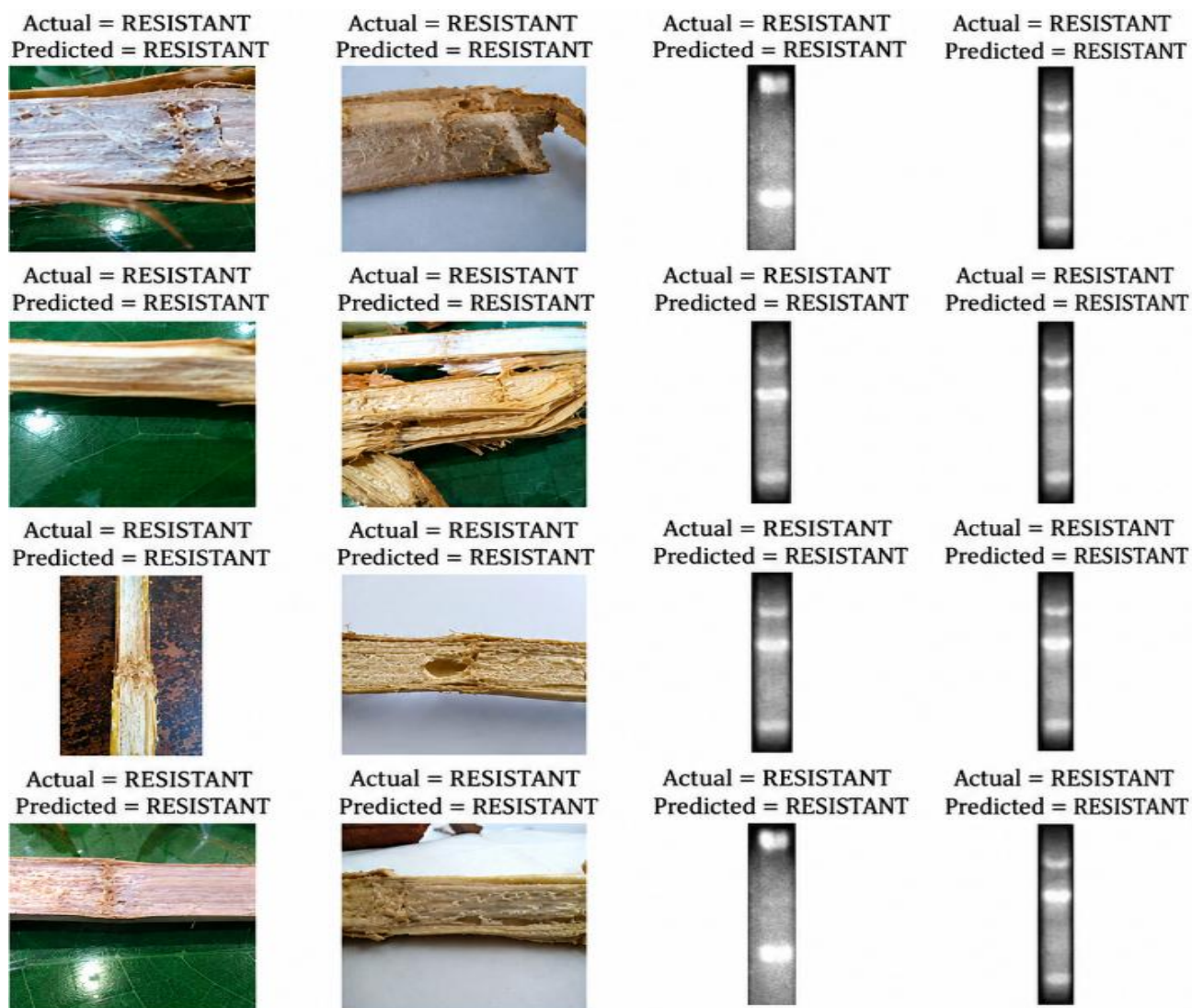


Fig. 6. Results of model predictions.

Table 1. F1 score, recall ratio, precision, and accuracy (%) of phenotypic images of stalk rot.

Severity scale	F1 Score (%)	Recall ratio (%)	Precision (%)	Accuracy (%)
Resistant	83.90	92.50	75.51	81.25
Susceptible	78.65	70	90.32	

Table 2. F1 score, recall ratio, precision, and accuracy (%) of genetic scales of stalk rot.

Severity scale	F1 Score (%)	Recall ratio (%)	Precision (%)	Accuracy (%)
Resistant	99.5	99.5	99.5	99.5
Susceptible	99.5	99.5	99.5	

Figure 5A and 5B displays the confusion matrix for the classes evaluated against stalk rot using genetic and phenotypic images respectively. Similar to phenotypic image-based experiment, sixteen hundred (1600) genetic images out of two thousand (2000) selected for the training of the model. Four hundred (400) images having equal contribution of both classes were decided for validation purpose. The suggested model's confusion matrix revealed that 199 images were correctly classified while one image of each category was wrongly classified. Overall, the results of model predictions are mentioned in Figure 6.

Discussion

Maize has a significant position among the cereal crops due to its consumption worldwide. Low yield per acre due to biotic factors is the main problem faced by the farmers. The lack of best practices may contribute to this problem but stalk rot has shown drastic impact to the productivity (Elsayed *et al.*, 2023). The disease is identified by early maturity and drying, which cause falling of stalk before achieving full maturity. Proper application of the fungicide depends upon the susceptible severity that requires experience to detect (Belisário *et al.*, 2022). Production cost is directly affected by improper use of the pesticides that not only cause environmental pollution but also cause the development of resistant strain of the pests.

To recognize the disease properly, breeders and pathologists have developed many conventional methods but these are tedious and time consuming. Computer aided models have shown remarkable performance in precision agriculture and disease detection. These models not only provide the solution to the farmer's problems at their doorstep but also help in addressing the food security issues worldwide. Performance of CNN models over other conventional machine learning methods cannot be denied

(Hedjazi *et al.*, 2017). Classification accuracy of CNN is much higher as compare to other machine learning models. In spite of its complex structure and the lengthy training process, CNN has more accuracy and detection rate as compare to conventional machine learning models. It includes clustering having ability to handle the dimensionality issues (Goh *et al.*, 2023).

The dataset of phenotypic and genotypic images was prepared manually which reflects the real-world problem. However, it is a lengthy and expensive procedure (Goncharov *et al.*, 2019). Total dataset was divided into the ratio of 80% for training and 20% for validation respectively. (Mohanty *et al.*, 2016) studied five alternative ratios and found that 70% for training and 30% for validation were the best ratio for disease detection problems. Diseased area of plant part is responsible for determining the severity of stalk rot which in turn determines the crop productivity (Vanlalhruaia *et al.*, 2023). The severity determines the amount and time of the particular fungicide for the suitable remedial action (Singh *et al.*, 2023). (Fenu *et al.*, 2021) elaborated the importance of pre-trained models for accurate disease detection. The current study got 92.5% and 70% of the accuracy for resistant and susceptible phenotypic images respectively. (Guerrero-Ibañez *et al.*, 2023) investigated the use of CNN to identify and classify tomato diseases. The authors found that the CNN models outperformed with a classification accuracy of 99%. The study of apple black rot disease using CNN has shown 90.4% of the accuracy (Wang *et al.*, 2017). The accuracy of 99.5% was observed for genotypic images. Similar kind of genetic variations were studied by (Ballesta *et al.*, 2023; Abubakar *et al.*, 2023) and got 91% accuracy by his classification model. Our findings endorsed the results of (Mohanty *et al.*, 2016) who got 99.35% of the accuracy in 26 different plant disease detection. Additionally, they demonstrated the impact of different environments (field and laboratory) on the accuracy of the model. They reported that its impact might decrease accuracy as much as 31%. When (Sibiya *et al.*, 2021) used the deep learning model, they reported the accuracy of 95.63% and 89% in validation and test sets respectively. (Su *et al.*, 2021) investigated the wheat head blight using ResNet-101 and got 77.19% of accuracy by their deep learning model. (Krizhevsky *et al.*, 2012) developed a deep neural network (AlexNet) on ImageNet LSFRC-2010 dataset and their classifier got first position in image classification competition. (Ai *et al.*, 2020) employed the VGG-Net model and achieved a disease detection accuracy of 91.83%. Similarly (Chen *et al.*, 2020) studied the maize diseases using INC-VGGN. They claimed the accuracy of 80.38% of their proposed model. The barley spike disease was studied by (Bao *et al.*, 2021) using spatial attention module. This technique helped them to extract the desirable features by minimizing the impact of background. They got 94.1% accuracy of their proposed classifier. Information about color, texture and structure of the lesion area are useful to detect the diseases. (Jin *et al.*, 2021) used these information using genetic algorithms to identify the weeds in the field. (Zou *et al.*, 2021) employed the DesnseNet model to detect different diseases. They claimed the accuracy of 95% of their proposed model. (Hidayat *et al.*, 2023) exploited CNN to determine the rice seed quality and got precision of 93% from their proposed model.

The development of android phones has replaced the need of cameras. It not only benefits the simpler users but also the developers (Chen *et al.*, 2017). Farmers can take photograph of diseased area and can send it to the main server for timely identification of the diseases (Ranjith *et al.*, 2017; Han *et al.*, 2025). Deployment of the proposed model on smartphone not only will help in the identification of disease at their doorstep but also will help breeders and pathologists in the development of high yielding varieties.

Conclusion

Carefully assessing and monitoring plant diseases determine the potential of cultivars in agricultural output. These criteria guarantee that the crop is handled precisely and shrewdly. The benefits of lowering cost, minimizing environmental pollution, balancing of biotic and abiotic factors and increasing yield have been reported by controlling diseases. The current model may helpful for the early identification of resistant lines against stalk rot by underlining the phenotypic data with genotypic data. The model exhibited 99.5% accuracy for genetic images. The model might be helpful for breeders to identify resistant lines against stalk rot before growing the lines in the field. It also helps breeders to use resistant lines in hybridization programs which in turn helps in controlling environmental pollution and improving the ecosystem. The model on phenotypic images might provide the solution to the farmers at their doorstep if it is shifted to an android mobile application.

Future work

- 1) Incorporation of environmental data and spectral images for more accurate identification.
- 2) Development of mobile application for different diseases of cash crops along with remedial action.
- 3) Development of more generalized systems that work for all crops.
- 4) Integration of model with IoT and Drones for crop monitoring against diseases.

Conflicts of Interest: The authors declared there is no conflicts of interest regarding current study.

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Author's Contributions: Sajjad Hussain Qureshi: designed the study and performed experiments. Mueen Alam Khan: analyzed the data. Abeer S Aloufi: wrote the manuscript. Adel A. Rezk, Hossam S. El-Beltagi, Othman Al-Dossary and Arzu Bakhshaliyeva: review the manuscript. Bader Y. Alsubaie: funding acquisition. All authors read and approved the final manuscript.

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Data Availability Statement: The data related to current study is presented in the manuscript

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