CHILEAN JOURNAL
of AGRICULTURAL RESEARCH

RESEARCH ARTICLE

Artificial intelligence-based detection of Cercospora leaf spot disease severity in mung bean

Pitchakon Papan[1], Witsarut Chueakhunthod[1], Chanwit Kaewkasi[2], Wanploy Jinagool[1], Akkawat Tharapreuksapong[3], Arada Masari[4], Sumana Ngampongsai[4], Kanlayanee Sawangsalee[1], and Piyada A. Tantasawat[1*]

[1]Suranaree University of Technology, Institute of Agricultural Technology, School of Crop Production Technology, 30000 Nakhon Ratchasima, Thailand.
[2]Suranaree University of Technology, Institute of Engineering, School of Computer Engineering, 30000 Nakhon Ratchasima, Thailand.
[3]Suranaree University of Technology, Center for Scientific and Technological Equipment, 30000 Nakhon Ratchasima, Thailand.
[4]Field and Renewable Energy Crops Research Institute, 10900, Bangkok, Thailand.
[*]Corresponding author (piyada@sut.ac.th).
Received: 23 September 2024; Accepted: 19 December 2024, doi:10.4067/S0718-58392025000300396

ABSTRACT

Cercospora leaf spot (CLS), caused by *Cercospora canescens* Ellis and G. Martin, is a significant foliar pathogen impacting mung bean (*Vigna radiata* (L.) R. Wilczek) cultivation. Early and precise detection of plant diseases via advanced digital technologies is pivotal for optimizing disease management strategies and developing cultivars with enhanced resistance. In this study, we employed an artificial neural network (ANN) model to assess CLS in mung bean, utilizing a dataset acquired under field conditions, and benchmarked its performance against traditional visual rating methodologies. Our analysis incorporated a deep learning framework based on the EfficientNet-B3 architecture. This model demonstrated superior performance in detecting CLS symptoms from images, achieving a validation accuracy of 88.70% and exhibiting a reduced overfitting gap between training and validation datasets (4.54%), relative to the Inception V3 model, which achieved 82.21% accuracy and an overfitting gap of 12.47%. Furthermore, the CLS index derived from the EfficientNet-B3 model showed a strong correlation with expert-rated CLS scores in field conditions (r = 0.925**, R^2 = 0.856). The application prototype developed in this research accurately assessed CLS severity, aligning closely with visual evaluations by experts (r = 0.910**, R^2 = 0.828). These findings underscore the potential of integrating deep learning techniques into plant disease management, providing a reliable and efficient tool for assessing CLS severity, which can enhance decision-making processes in crop management and facilitate research advancements.

Key words: Artificial intelligence, artificial neural network, Cercospora leaf spot, machine learning, *Vigna radiata*, visual observation.

INTRODUCTION

Cercospora leaf spot (CLS), attributable to the fungal pathogen *Cercospora canescens* Ellis and G. Martin, represents a highly deleterious foliar disease affecting mung bean (*Vigna radiata* (L.) R. Wilczek) globally (Laosatit et al., 2024). The disease typically manifests from the early blooming stage (approximately 30-40 d post-emergence) through to pod maturity, leading to premature defoliation and a consequent reduction in pod and seed size. While fungicides such as captain, carbendazim, and thiamethoxam + carbendazim have demonstrated efficacy in disease mitigation (Bhat et al., 2015), their indiscriminate or excessive application escalates production costs and poses significant risks, including the accumulation of toxic residues in agricultural products and the environment. Furthermore, the emergence of fungicide-resistant *Cercospora* strains has been documented (Sautua et al., 2020), highlighting the need for judicious use of chemical control. Effective disease management necessitates precise and timely assessments of CLS severity to optimize fungicide application, thereby minimizing both chemical use and economic losses (Cioni et al., 2014). Traditionally, CLS identification in mung bean has relied on expert visual inspections (Chankaew et al., 2011; Tantasawat et al., 2020). However, this method is inherently subjective and may present significant challenges for non-experts. Additionally, visual monitoring requires ongoing, labor-intensive oversight by specialists, which can be economically prohibitive for extensive cultivation. Thus, there is a pressing need for more accurate, scalable, and cost-effective diagnostic methods to facilitate timely and precise disease management decisions.

Recent advancements in artificial intelligence (AI) have significantly enhanced the capabilities of precision agriculture, particularly through the integration of computer vision technologies. Automated detection of plant diseases using digital image processing techniques—such as colorimetric analysis and thresholding (Cynthia et al., 2019)—has transformed the field by enabling more efficient, accurate, and cost-effective diagnostics. This innovation allows for the detection of disease symptoms as soon as they appear on plant foliage, thereby facilitating timely interventions (Mahlein, 2016). Historically, machine learning (ML) approaches, including K-nearest neighbors (KNN) (Bansal et al., 2022), support vector machines (SVM) (Elangovan and Nalini, 2017), and random forests (RF) (Ramesh et al., 2018), have been extensively used for the early and precise identification and classification of plant diseases. These methods, known for their effectiveness with relatively modest training datasets, were initially preferred due to their simplicity and efficacy. However, traditional ML-based techniques often encounter significant limitations, such as slow processing speeds and reliance on complex preprocessing steps. Additionally, they require specialized knowledge for feature extraction and selection, a process that can be labor-intensive and prone to variability (Dargan et al., 2020). Consequently, the limitations of conventional ML-based methods in fully automating plant disease detection have led to a shift towards more advanced AI-driven solutions.

Until recently, deep learning-based approaches have substantially transformed agricultural practices by automating the extraction of discriminative features from input data. This advancement has obviated the need for complex image preprocessing and reduced memory footprint (Albattah et al., 2022). Deep learning models, such as artificial neural networks (ANNs), are inspired by biological neural systems and aim to replicate the cognitive processes of the human brain (Cartwright, 2015). These networks acquire knowledge by identifying patterns and relationships within data and undergoing iterative training with diverse datasets. In the domain of computer vision, various ANN architectures have shown significant efficacy in plant disease classification. Noteworthy models include GoogleNet (Mohanty et al., 2016), MobileNet (Bi et al., 2022), VGGNet (Chen et al., 2020b), EfficientNet (Tan and Le, 2019; Atila et al., 2021), and Inception V3 (Szegedy et al., 2016; Fan et al., 2022). These advanced frameworks have been instrumental in improving the accuracy and efficiency of plant disease diagnostics. Recent studies have investigated the application of deep learning techniques for automated disease detection and pest classification in mung bean. For example, Mallick et al. (2023) introduced an advanced deep learning approach capable of multi-class detection and classification of pests (including bruchids, whiteflies, stem flies, and aphids) and foliar diseases (such as charcoal rot, fusarium wilt, halo blight, yellow mosaic virus, powdery mildew, and CLS). Despite these advancements, a significant gap remains in the research regarding the use of deep learning for quantifying disease severity scores, which are essential for effective disease management and control.

The efficacy of ANNs in plant disease detection is significantly influenced by the quality and breadth of the training dataset. Despite notable advancements in machine learning, the application of ANNs specifically for detecting CLS in mung bean remains relatively underexplored. This study aims to address this gap by developing an ANN-based methodology for evaluating CLS in mung bean crops. The primary objectives are twofold: First, to design and implement an ANN approach utilizing the Inception V3 and EfficientNet-B3 architectures to assess CLS severity, employing a meticulously curated dataset collected under field conditions; and second, to rigorously compare the performance of this ANN-based method with the traditional visual rating scale used for disease assessment. This comparative analysis was intended to elucidate the potential advantages of the ANN approach in terms of accuracy, efficiency, and reliability for the automated detection and quantification of CLS, thereby advancing the field of precision agriculture.

MATERIALS AND METHODS

Data acquisition

A total of 2220 mung bean (*Vigna radiata* (L.) R. Wilczek) leaves, both symptomatic and asymptomatic for Cercospora leaf spot (CLS), were collected from 65-d-old plants of nine parental cultivars/lines—V4718, V4758, V4785, Chai Nat (CN)72, CN84-1, CN3, Kamphaeng Saen (KPS)1, Suranaree University of Technology (SUT)1, and KING—as well as from ten promising breeding lines—O2-31, O2-33, O2-37, O2-39, B1, B2, D5, G1, H3, and H4, varying in CLS and powdery mildew resistance (Tantasawat et al., 2020; 2022). These samples were gathered from experimental fields at SUT Farm, Nakhon Ratchasima, Thailand, between June and August 2022. All cultivars/lines were grown in a randomized complete block design with three replicates under field conditions. In each block, seeds of each cultivar/line were planted in a single 6-m-long row with an intra-row spacing of 20 cm and an inter-row spacing of 50 cm, with two plants per hill (approximately 60 plants per row). The susceptible ‘CN72’ was planted around the blocks to serve as a source of CLS inoculum. The CLS-infected leaves spread naturally throughout the fields without the need for artificial inoculation.

Each mung-bean leaf was scanned using a Fuji Xerox DocuPrint CM305df (Fuji Xerox, Tokyo, Japan) at a resolution of 2480 × 3507 pixels with 24 bits of color depth per pixel, saved in TIFF format. The images were classified into five categories based on disease severity as described by Chankaew et al. (2011): 1 = no visible CLS infection, 2 = 1%-25% leaf area infected, 3 = 26%-50% leaf area infected, 4 = 51%-75% leaf area infected, and 5 = 76%-100% leaf area infected (Figure 1). Additionally, representative examples of CLS symptoms in each category were cropped to 300 × 300 pixels. All 2220 cropped images were manually classified by experts into CLS categories 1 through 5; resulting in 445 images for score 1, 455 images for score 2, 440 images for score 3, 439 images for score 4, and 441 images for score 5.

The framework of our methodology for detecting CLS disease is outlined in Figure 2 and is as follows: First, mung bean leaves were collected from the experimental field. Next, image processing was performed, including scanning and cropping. Subsequently, the sample images were classified into five categories of CLS severity by experts. These classified images were then used to train ANN models. Finally, the trained model was applied to categorize CLS disease in mung bean samples.

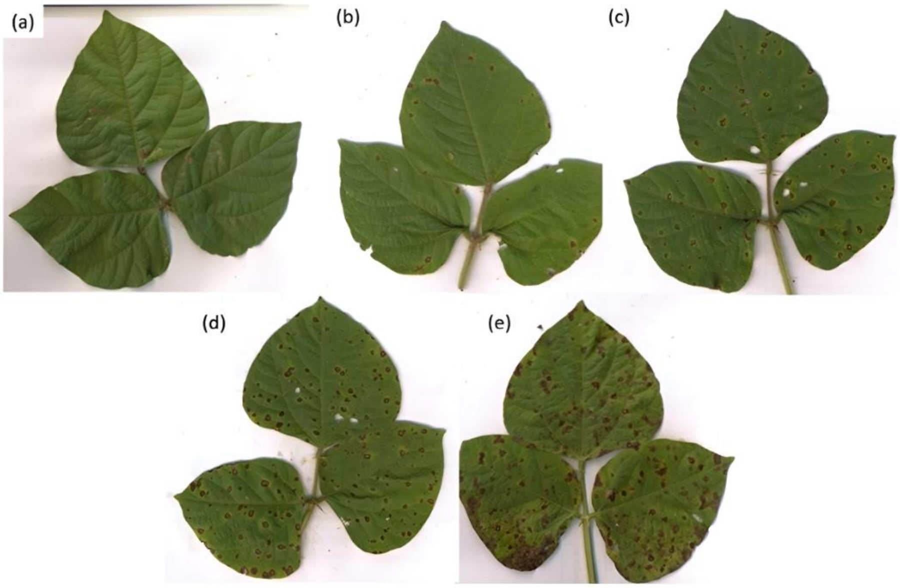

Figure 1. Sample images of Cercospora leaf spot (CLS) symptoms in mung bean: No visual disease infection (a), 1%-25% leaf area infected (b), 26%-50% leaf area infected (c), 51%-75% leaf area infected (d), and 76%-100% leaf area infected (e).

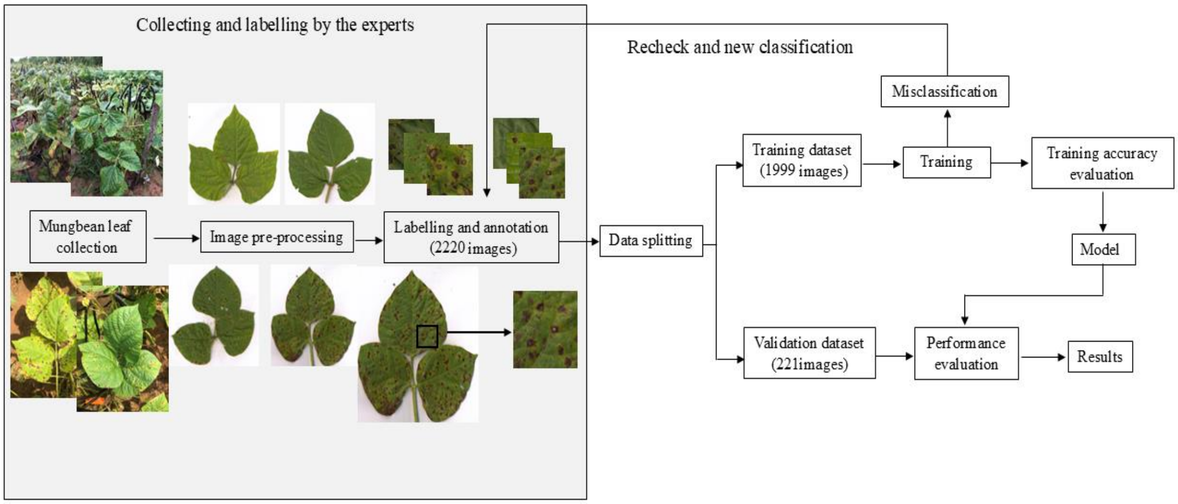

Figure 2. An overview of the method for Cercospora leaf spot (CLS) detection in mung bean based on deep learning.

System description

Our dataset was divided into the following proportions: 90% for training and 10% for validation, respectively. Two ImageNet-based neural network architectures, namely Inception V3 (Szegedy et al., 2016) and EfficientNet-B3 (Tan and Le, 2019), were used as the base networks for training the disease detection classifier. These architectures were re-trained using the knowledge transfer technique with our mung-bean datasets. The parameters were set up as follows:

Solver type: Stochastic Gradient Descent, Base learning rate: 0.005; Learning rate policy: Step (decreases by a factor of 10 every epoch); Momentum: 0.9; Weight decay: 0.0005; Gamma: 0.1; Batch size: 32; Early Stop Policy: Monitoring validation accuracy. Stop and restore the best one, if the last 3 results are worse.

Image size: Inception V3: 299 × 299 pixels; EfficientNet-B3: 300 × 300 pixels.

In addition, the output layer of each ANN was replaced by a dense layer with a Softmax activation function. The output would be a set of probability values for all classes, which were later used to calculate a disease index score, as presented in Equation 1, where p_i represents the probability value of each class and c_i represents a disease severity score class (1-5) of the CLS disease.

$$\text{Disease index score} = \Sigma p_i \times c_i \qquad (1)$$

Utilization of the optimal architecture for validation of Cercospora leaf spot (CLS) severity

A total of 11 datasets were generated from seven parental cultivars/lines, including V4718, V4758, CN72, CN3, KPS1, SUT1, and KING, as well as our four promising breeding lines, including O2-39, B1, D5, and H4. Mung bean leaf samples of 65-d-old plants collected at SUT Farm between June and August 2022, were captured using different smartphones (iPhone 8 and Huawei Y7 and P30 Pro), with 135-150 images per cultivar/line used to create image datasets. Representatives of each leaf image were cropped into 300 × 300 pixels. Additionally, the best architecture from the earlier part was used to evaluate the CLS disease in these datasets using a Softmax function to calculate a disease index score using Equation 1. The correlation coefficients between the disease index score in this study and CLS scores in the field conditions, rated by the experts at SUT, were determined. To ascertain the CLS scores in the field conditions, all 11 cultivars/lines grown at SUT Farm between June and August 2022 were recorded for their CLS responses at 65 d after planting by the experts using the scoring system described by Chankaew et al. (2011).

An application prototype was developed by uploading ANN to the Cloud so that it could be used directly on a smartphone. To evaluate its efficiency, we examined the correlation coefficients between the CLS scores determined by our application prototype developed from this study and those by the experts. Fifteen mung bean leaf images of 65-d-old plants of each of the 15 cultivars/lines (V4718, V4758, V4785, CN72, CN84-1, CN3, KPS1, SUT1, KING, O2-39, B1, B2, D5, H3, and H4) grown in a greenhouse at SUT between October and December 2022, with natural CLS infection, were taken with smartphones (iPhone 8 and Huawei Y7 and P30 Pro) and cropped into 300 × 300 pixels to determine the CLS index scores by uploading the images to our application prototype and having the same images scored by the experts according to Chankaew et al. (2011). The correlation coefficients were calculated using SPSS 16.0 software (IBM, Armonk, New York, USA).

RESULTS AND DISCUSSION

Accuracy metrics from the training dataset

We developed our own datasets consisting of mung bean leaves infected by *Cercospora canescens* with varying severities, as well as healthy leaves. These datasets included a total of 2220 images, categorized into five severity levels of CLS, ranging from 1 to 5. To assess potential overfitting, we randomly selected 90% of the images from each class (396-410 images) for the training set, while the remaining 10% of images (43-45 images) were allocated to the validation set. This 90/10 split helps mitigate the risk of overtraining deep learning networks. Data augmentation and training of the ANNs were performed using Python (Centrum Wiskunde & Informatica, Amsterdam, The Netherlands). The models were re-trained with TensorFlow, developed by Google. Training and validation of the deep ANN models were conducted using a graphics processing unit (GPU; GeForce GTX1060 6 GB GDDR5) and a central processing unit (CPU; Intel Core i7-8750H at 2.20 GHz with 16 GB of memory). The two architectures, Inception V3 and EfficientNet-B3, were trained on our dataset for 9 epochs, with accuracy progression illustrated in Figure 3. As detailed in Table 1, EfficientNet-B3 achieved a higher validation accuracy (88.70%) compared to Inception V3 (82.21%), despite having a lower training accuracy (93.24%) relative to Inception V3 (94.68%). The relatively lower training accuracy of EfficientNet-B3 resulted in a significantly smaller overfitting gap (4.54) compared to Inception V3 (12.47). Furthermore, EfficientNet-B3 achieved accuracies of 83.06% and 81.25% for training and validation, respectively, after just 2 epochs. In contrast, Inception V3's validation accuracy at the 2nd epoch was only 60.34%, despite a training accuracy of 87.45%. Inception V3 required 7 epochs to attain a validation accuracy of 81.25% (Figure 3). Consequently, EfficientNet-B3 was selected for further field evaluation using smartphone images captured under field conditions.

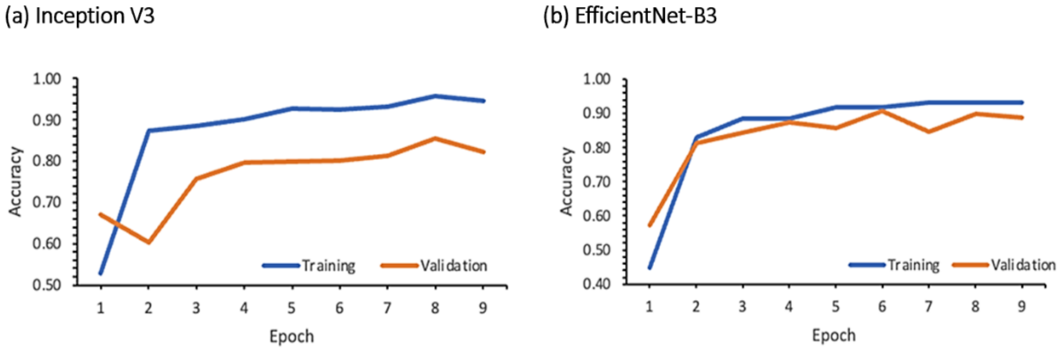

Figure 3. Progression of accuracy through the training of dataset using Inception V3 (a) and EfficientNet-B3 (b). The blue line shows the accuracy of prediction from the training dataset. The orange line shows the accuracy of the prediction from the validation dataset.

Table 1. The training results of two architectures on the mung bean leaf spot disease dataset.

Architecture	Training accuracy	Validation accuracy	Overfitting gap
	%		
Inception V3	94.68	82.21	12.47
EfficientNet-B3	93.24	88.70	4.54

Evaluating the model's performance in predicting the Cercospora leaf spot (CLS) index score

EfficientNet-B3 was employed to assess datasets from 11 mung bean cultivars/lines, collected under field conditions between June and August 2022 to evaluate its practical application. These datasets included images with complex backgrounds and uncontrolled lighting conditions due to varying distances, diverse cameras, surrounding fields, weeds, leaf colors, and differing weather conditions (e.g., overcast or sunny). Each dataset comprised approximately 135-150 leaf images, used to validate the model without additional training and to calculate disease index scores. As detailed in Table 2, the accuracy of this architecture varied from 70.00% to 97.95% across the 11 mung bean cultivars/lines. The dataset for the V4718 line achieved the highest accuracy (97.95%), while the KING cultivar dataset recorded the lowest accuracy (70.00%). Disease index scores, calculated from each leaf image using the Softmax value, ranged from 1.70 (V4718) to 4.30 (D5).

Table 2. Evaluation indicators for validating Cercospora leaf spot (CLS) disease in 11 cultivars/lines based on EfficientNet-B3. [a]CLS response: Resistance (R) = 1.0-2.5, moderate resistance (MR) = 2.6-3.4, and susceptibility (S) = 3.5-5.0. [b]CLS severity scores in the field conditions were averaged across three replicates of a randomized complete block design.

					EfficientNet-B3		Field evaluation by experts	
Cultivars/lines	Number of images	Corrected images	Misclassed images	Accuracy (%)	CLS index scores	CLS response[a]	CLS severity scores[b]	CLS response
V4718	146	143	3	97.95	1.70	R	1.00	R
V4758	148	121	27	81.76	3.08	MR	2.63	MR
CN72	146	123	23	84.25	3.20	MR	2.13	R
CN3	141	106	35	75.18	3.96	S	3.13	MR
SUT1	141	106	35	75.18	3.87	S	3.88	S
KPS1	141	117	24	82.98	3.02	MR	2.75	MR
KING	150	105	45	70.00	3.82	S	3.63	S
O2-39	135	117	18	86.67	2.47	R	1.63	R
B1	140	120	20	85.71	4.03	S	3.75	S
D5	145	133	12	91.72	4.30	S	4.75	S
H4	145	110	35	75.86	2.81	MR	3.13	MR

Among the 11 mung bean cultivars/lines evaluated, V4718 and O2-39 exhibited disease index scores of 1.70 and 2.47, respectively, categorizing them as resistant. The cultivars/lines V4758, CN72, KPS1, and H4, with disease index scores ranging from 2.81 to 3.20, were classified as moderately resistant. In contrast, CN3, SUT1, KING, B1, and D5 were categorized as susceptible, with disease index scores ranging from 3.82 to 4.30. Notably, the field observations of CLS responses for most cultivars/lines, as determined by expert assessments, were consistent with the disease index scores assigned except for CN72 and CN3. Correlation analysis confirmed a significant positive relationship between the disease index scores and the CLS responses rated by experts ($r = 0.925^{**}$, $R^2 = 0.856$), indicating a high degree of congruence between the two metrics. These findings affirm that EfficientNet-B3 is effective for evaluating CLS disease across various mung bean varieties under field conditions. Consequently, the ANN was deployed on the cloud, and an application prototype was developed to facilitate disease index score evaluation via smartphone.

A prototype application for the predictive modeling of CLS severity

When the AI-based application prototype was used to assess CLS severity in 15 mung bean cultivars/lines grown in greenhouses at SUT between October and December 2022, it demonstrated a significant correlation with expert visual evaluations (r = 0.910**, R^2 = 0.828). The application prototype showed that the CLS severity scores for cultivars/lines V4718, V4785, CN84-1, CN72, SUT1, KPS1, KING, O2-39, B1, B2, H3, and H4 were highly significant and positively correlated with expert assessments (r = 0.809**-0.976**, R^2 = 0.654-0.953). Additionally, the scores for cultivars/lines V4758, CN3, and D5 were also significantly correlated between the two evaluation methods (r = 0.742*-0.758*, R^2 = 0.551-0.575). All cultivars/lines were classified with CLS responses consistent with expert scores, except for CN3 and B2 (Table 3). These results validate that the AI-based application prototype provides accurate evaluations of CLS severity in mung bean and suggest that it warrants further development and future recommendations for use by mung bean farmers.

Table 3. Evaluation of Cercospora leaf spot (CLS) in mung bean by the application prototype developed in this study and by human experts. ^{a}CLS response: Resistance (R) = 1.0-2.5, moderate resistance (MR) = 2.6-3.4, and susceptibility (S) = 3.5-5.0.

	Application prototype		Human experts			
Cultivars/lines	CLS index scores	CLS response^a	CLS severity scores	CLS response	Correlation coefficients	R^2
V4718	2.03	R	1.56	R	0.954**	0.910
V4758	2.87	MR	2.80	MR	0.742*	0.551
V4785	2.20	R	2.05	R	0.881**	0.776
CN84-1	3.60	S	3.75	S	0.938**	0.880
CN72	3.75	S	3.90	S	0.960**	0.922
CN3	3.43	MR	3.55	S	0.758*	0.575
SUT1	3.93	S	3.95	S	0.920**	0.846
KPS1	3.26	MR	3.05	MR	0.809**	0.654
KING	3.41	MR	3.36	MR	0.902**	0.814
O2-39	2.34	R	2.25	R	0.835**	0.697
B1	2.62	MR	2.70	MR	0.910**	0.828
B2	2.68	MR	2.45	R	0.850**	0.723
D5	3.50	S	3.50	S	0.749*	0.561
H3	2.96	MR	2.81	MR	0.946**	0.895
H4	2.52	MR	2.56	MR	0.976**	0.953

Implementing an artificial neural network (ANN)-based system for disease detection

Early detection of plant diseases using advanced AI technologies is pivotal for implementing effective disease management strategies and enhancing agricultural productivity. In this study on detecting CLS severity in mung bean, we addressed the absence of publicly available mung bean image datasets by collecting our own images of mung bean leaves infected by *C. canescens* at varying severity levels. The images were acquired using a scanner. We applied an ANN-based disease detection system, which has been extensively studied for its feature extraction capabilities and robustness (Mohanty et al., 2016; Szegedy et al., 2016; Tan and Le, 2019; Chen et al., 2020a; Atila et al., 2021; Bi et al., 2022; Fan et al., 2022). This system enables the assessment, identification, and classification of fine details that are not easily discernible to the naked eye. The dataset was split into training (90%) and validation (10%) subsets, and the ANN model, built on the EfficientNet-B3 architecture, demonstrated high validation accuracy with minimal overfitting between the training and validation sets (Table 1). Similarly, Saputra et al. (2023) highlighted the superior performance of this architecture in capturing critical features across training and validation datasets. Additionally, the model's ability to leverage transfer learning—utilizing pre-existing knowledge from other datasets—further improves the accuracy of disease detection on leaves.

When EfficientNet-B3 was employed to validate CLS reactions in 11 mung bean cultivars/lines, the model accurately classified the early stages of infection, characterized by fewer CLS symptoms and lower scores (e.g., in V4718), as well as the more advanced stages, with severe symptoms and higher scores (e.g., in D5), outperforming its performance at intermediate stages. The validation results demonstrated classification accuracies of 97.95% for V4718 and 91.72% for D5, while for other cultivars/lines, which exhibited a mix of CLS stages, accuracies ranged from 70.00% to 86.67%. Additionally, we compared the CLS index scores generated by the model with expert-assigned CLS severity scores for 11 cultivars/lines under field conditions. The results showed a strong concordance between the model's assessments and the expert ratings ($r = 0.925^{**}$; $R^2 = 0.856$) (Table 2). Notably, despite the model being trained on images scanned with a flatbed scanner, it was able to accurately evaluate CLS severity on images captured by smartphones in field conditions. The evaluation performed by our developed application prototype also showed a high correlation with human expert assessments of 15 cultivars/lines across different growing seasons ($r = 0.910^{**}$; $R^2 = 0.828$) (Table 3). This finding aligns with the observations of El Jarroudi et al. (2015), affirming that human visual ratings, while reasonably accurate, are subject to limitations. Although visual estimation does not require advanced equipment, trained raters may experience fatigue and decreased concentration during evaluations, particularly under challenging climatic conditions, potentially reducing accuracy. In contrast, the EfficientNet-B3 model overcame these limitations, offering consistent CLS severity scores without subjective bias. Furthermore, the model provided decimal scores, which enabled finer discrimination between severity levels, addressing the issue of whether a particular CLS severity should be rated as a 3 or a 4, for example. To the best of our knowledge, this is the first successful application of a deep learning approach for detecting the widespread and destructive pathogen CLS in mung bean.

In this research, we utilized images captured directly with smartphones, without the need for specialized lighting or setup, making the approach highly sustainable. The system's reliance on ANN technology ensures it is user-friendly, providing significant benefits to a wide range of users without the need for advanced technical expertise.

CONCLUSIONS

The findings of this study demonstrate that Cercospora leaf spot (CLS) severity in mung bean can be accurately and efficiently assessed using an artificial neural network (ANN) model, specifically EfficientNet-B3. The severity levels predicted by the model closely aligned with expert evaluations, highlighting its effectiveness. Moving forward, this model holds potential for practical use by mung bean growers in disease management. All that is required is a smartphone to capture images of infected leaves, which can then be analyzed through the application to provide a diagnosis. As a result, users will be empowered to take early preventive measures, offering significant benefits to farmers globally. Additionally, it can be effectively utilized to screen large populations of plants in breeding programs aimed at enhancing disease resistance.

Author contribution

Conceptualization: P.A.T., C.K., P.P., W.C. Methodology: P.P., W.C., C.K. Software: C.K., P.P. Validation: P.P, W.C. Formal analysis: P.P, W.C. Investigation: W.J., A.T. Resources: A.M., S.N. Data curation: P.P., W.C. Writing-original draft: P.P., W.C. Writing-review & editing: W.C., K.S., P.A.T. Visualization: P.P., W.C. Supervision: P.A.T., C.K. Project administration: P.P., P.A.T. Funding acquisition: P.A.T. All co-authors reviewed the final version and approved the manuscript before submission.

Acknowledgements

This research was supported by grants from the Agricultural Research Development Agency (Public Organization) and Suranaree University of Technology. We gratefully acknowledge the World Vegetable Center, Taiwan, and the Chai Nat Field Crops Research Center, Thailand, for providing the seeds used in this experiment.

References

Albattah, W., Javed, A., Nawaz, M., Masood, M., Albahli, S. 2022. Artificial intelligence-based drone system for multiclass plant disease detection using an improved efficient convolutional neural network. Frontiers in Plant Science 13:808380. doi:10.3389/fpls.2022.808380.

Atila, Ü., Uçar, M., Akyol, K., Uçar, E. 2021. Plant leaf disease classification using Efficient Net deep learning model. Ecological Informatics 61:101182. doi:10.1016/j.ecoinf.2020.101182.

Bansal, M., Goyal, A., Choudhary, A. 2022. A comparative analysis of K-nearest neighbor, genetic, support vector machine, decision tree, and long short term memory algorithms in machine learning. Decision Analytics Journal 3:100071. doi:10.1016/j.dajour.2022.100071.

Bhat, F., Bhat, G., Anwar, A., Mohiddin, F. 2015. Cost effective strategies for the management of fungal leaf spot of greengram caused by *Cercospora canescens* Ell. & Mart. under temperate condition of Jammu and Kashmir. Legume Research 38:109-114. doi:10.5958/0976-0571.2015.00018.1.

Bi, C., Wang, J., Duan, Y., Fu, B., Kang, J.-R., Shi, Y. 2022. MobileNet based apple leaf diseases identification. Mobile Networks and Applications 27:172-180. doi:10.1007/s11036-020-01640-1.

Cartwright, H. 2015. Artificial neural networks. Humana Press, Totowa, New Jersey, USA.

Chankaew, S., Somta, P., Sorajjapinun, W., Srinives, P. 2011. Quantitative trait loci mapping of Cercospora leaf spot resistance in mungbean, *Vigna radiata* (L.) Wilczek. Molecular Breeding 28:255-264. doi:10.1007/s11032-010-9478-1.

Chen, H., Chen, A., Xu, L., Xie, H., Qiao, H., Lin, Q., et al. 2020a. A deep learning CNN architecture applied in smart near-infrared analysis of water pollution for agricultural irrigation resources. Agricultural Water Management 240:106303. doi:10.1016/j.agwat.2020.106303.

Chen, J., Chen, J., Zhang, D., Sun, Y., Nanehkaran, Y.A. 2020b. Using deep transfer learning for image-based plant disease identification. Computers and Electronics in Agriculture 173:105393. doi:10.1016/j.compag.2020.105393.

Cioni, F., Collina, M., Maines, G., Khan, M.F., Secor, G.A., Rivera, V.V. 2014. A new integrated pest management (IPM) model for Cercospora leaf spot of sugar beets in the Po Valley, Italy. Sugar Tech 16:92-99. doi:10.1007/s12355-013-0260-7.

Cynthia, S.T., Hossain, K.M.S., Hasan, M.N., Asaduzzaman, M., Das, A.K. 2019. Automated detection of plant diseases using image processing and faster R-CNN algorithm. p. 1-5. In 2019 International Conference on Sustainable Technologies for Industry 4.0 (STI), Dhaka, Bangladesh. 24-25 December. Institute of Electrical and Electronics Engineers (IEEE), New York, USA.

Dargan, S., Kumar, M., Ayyagari, M.R., Kumar, G. 2020. A survey of deep learning and its applications: a new paradigm to machine learning. Archives of Computational Methods in Engineering 27:1071-1092. doi:10.1007/s11831-019-09344-w.

El Jarroudi, M., Kouadio, A.L., Mackels, C., Tychon, B., Delfosse, P., Bock, C. 2015. A comparison between visual estimates and image analysis measurements to determine Septoria leaf blotch severity in winter wheat. Plant Pathology 64:355-364. doi:10.1111/ppa.12252.

Elangovan, K., Nalini, S. 2017. Plant disease classification using image segmentation and SVM techniques. International Journal of Computational Intelligence Research 13:1821-1828.

Fan, X., Luo, P., Mu, Y., Zhou, R., Tjahjadi, T., Ren, Y. 2022. Leaf image based plant disease identification using transfer learning and feature fusion. Computers and Electronics in Agriculture 196:106892. doi:10.1016/j.compag.2022.106892.

Laosatit, K., Yimram, T., Keawwongwal, A., Srichan, M., Amkul, K., Tanadul, O., et al. 2024. Development of pyramided mung bean lines carrying resistance genes for Cercospora leaf spot disease and bruchids. Chilean Journal of Agricultural Research 84:644-652. doi:10.4067/s0718-58392024000500644.

Mahlein, A.K. 2016. Plant disease detection by imaging sensors-parallels and specific demands for precision agriculture and plant phenotyping. Plant Disease 100(2):241-251. doi:10.1094/PDIS-03-15-0340-FE.

Mallick, M.T., Biswas, S., Das, A.K., Saha, H.N., Chakrabarti, A., Deb, N. 2023. Deep learning based automated disease detection and pest classification in Indian mung bean. Multimedia Tools and Applications 82:12017-12041. doi:10.1007/s11042-022-13673-7.

Mohanty, S.P., Hughes, D.P., Salathe, M. 2016. Using deep learning for image-based plant disease detection. Frontiers in Plant Science 7:1419. doi:10.3389/fpls.2016.01419.

Ramesh, S., Hebbar, R., Niveditha, M., Pooja, R., Shashank, N., Vinod, P. 2018. Plant disease detection using machine learning. p. 41-45. In Proceedings of the 2018 International Conference on Design Innovations for 3Cs Compute Communicate Control (ICDI3C), Bangalore, India. 25-28 April. Institute of Electrical and Electronics Engineers (IEEE), New York, USA.

Saputra, A. D., Hindarto, D., Rahman, B., Santoso, H. 2023. Comparison of accuracy in detecting tomato leaf disease with GoogleNet vs EfficientNetB3. Sinkron: Jurnal dan Penelitian Teknik Informatika 7:647-656.

Sautua, F.J., Doyle, V.P., Price, P.P., Porfiri, A., Fernandez, P., Scandiani, M.M., et al. 2020. Fungicide resistance in *Cercospora* species causing Cercospora leaf blight and purple seed stain of soybean in Argentina. Plant Pathology 69:1678-1694. doi:10.1111/ppa.13261.

Szegedy, C., Vanhoucke, V., Ioffe, S., Shlens, J., Wojna, Z. 2016. Rethinking the inception architecture for computer vision. p. 2818-2826. In Proceedings of the 2016 IEEE Conference on Computer Vision and Pattern Recognition, Las Vegas, Nevada, USA. 27-30 June. Institute of Electrical and Electronics Engineers (IEEE), New York, USA.

Tan, M., Le, Q. 2019. EfficientNet: Rethinking model scaling for convolutional neural networks. p. 6105-6114. In Proceedings of the International Conference on Machine Learning, ICML 2019, Long Beach, California. 9-15 June. Proceedings of Machine Learning Research 97:6105-6114.

Tantasawat, P.A., Poolsawat, O., Arsakit, K., Papan, P. 2020. Identification of ISSR, ISSR-RGA and SSR markers associated with Cercospora leaf spot resistance gene in mungbean. International Journal of Agriculture and Biology 23:447-453. doi:10.17957/IJAB/15.1294.

Tantasawat, P.A., Poolsawat, O., Kativat, C., Arsakit, K., Papan, P., Chueakhunthod, W., et al. 2022. Inheritance and identification of ISSR-RGA markers associated with powdery mildew resistance in mungbean for marker-assisted breeding. Chilean Journal of Agricultural Research 82:3-9. doi:10.4067/S0718-58392022000100003.