

From images to insights: Using a convolutional neural network to improve powdery mildew severity detection in mungbean

PITCHAKON PAPAN¹, WITSARUT CHUEAKHUNTHOD^{1,4}, CHANWIT KAEWKASI²,
WANPLOY JINAGOOL¹, AKKAWAT THARAPREUKSAPONG³, TEERAYOOT GIRDTHAI¹,
KANLAYANEE SAWANGSALEE¹, PIYADA ALISHA TANTASAWAT^{1*} 

¹School of Crop Production Technology, Institute of Agricultural Technology,
Suranaree University of Technology, Nakhon Ratchasima, Thailand

²School of Computer Engineering, Institute of Engineering, Suranaree University of Technology,
Nakhon Ratchasima, Thailand

³Center for Scientific and Technological Equipment, Suranaree University of Technology,
Nakhon Ratchasima, Thailand

⁴Department of Horticulture, Faculty of Agriculture, Kasetsart University, Bangkok, Thailand

*Corresponding author: piyada@sut.ac.th

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Abstract: To efficiently identify powdery mildew (PM) severity in mungbean leaves, we developed a Convolutional Neural Network (CNN) approach and validated its effectiveness against human evaluation. We fine-tuned an EfficientNet-B3 pre-trained model, which, in our related studies, performed better than re-implemented Inception V3 models. The CNN was trained on 90% of the images (2 880) for training and 10% (320) for validation, with data augmentation applied using Python and TensorFlow. The model obtained 82.10% and 73.03% as training and validation accuracies after 14 epochs, respectively. Further analysis with an additional 15 datasets revealed PM disease indices ranging from 2.03 (resistance) to 6.45 (high susceptibility). The concordance between AI-predicted and human-assessed PM severity was 74.4% (adjusted R^2 : 72.4%), with an average root mean squared error (RMSE) of 0.854 and a mean absolute error (MAE) of 0.715, indicating moderate predictive error. Comparison of our developed AI-based application prototype on smartphones with expert evaluations yielded a strong correlation ($r = 0.992^{**}$, $R^2 = 0.984$), suggesting that this tool can effectively estimate PM severity across mungbean cultivars. The application shows considerable promise, and further optimisation and strategic dissemination efforts will enhance its adoption among farmers.

Keywords: artificial intelligence; deep learning; EfficientNet-B3; machine learning; *Vigna radiata* (L.) R. Wilczek; visual observation

Mungbean [*Vigna radiata* (L.) R. Wilczek] is a leguminous crop of significant economic, nutri-

tional, and environmental values. Originating from the Indian subcontinent, mungbean is cultivated

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extensively across India, Asia, Africa, Australia, and the Caribbean. Globally, it is grown on approximately 7.3 mil. ha, with an average yield of 5 t/ha (Nair & Schreinemachers 2020). Major producers include India, Myanmar, Pakistan, the Philippines, Bangladesh, and Thailand. However, mungbean productivity is severely affected by various biotic and abiotic factors, including environmental conditions, soil health, nutrient management, agricultural practices, and disease management strategies (Parvez et al. 2013). Socioeconomic factors also play a pivotal role in influencing yield outcomes.

Among the biotic constraints, plant diseases, particularly powdery mildew (PM), are primarily caused by *Podosphaera fusca* (Fr.) U. Braun & Shishkoff, are major impediments to global mungbean production, leading to significant yield losses (Hacquard 2014). The pathogen has been reported under several synonymous names, including *Sphaerotheca phaseoli* and *Podosphaera xanthii* (Royal Botanic Gardens, Kew 2025). In Australia, PM of mungbean has been attributed to two distinct species, *Podosphaera xanthii* and *Erysiphe vignae* sp. nov., highlighting the pathogen diversity associated with this disease (Kelly et al. 2021). The pathogens primarily infect green tissues, thereby reducing the photosynthetic efficiency and adversely affecting pod formation and seed size, culminating in diminished productivity. Integrated disease management approaches are crucial for mitigating the adverse effects of PM on mungbean cultivation (Pandey et al. 2018). Traditional disease detection methods rely heavily on visual inspections, which are labour-intensive, time-consuming, and subjective (Dey et al. 2016). This necessitates the development of advanced diagnostic tools for early, precise disease detection to ensure timely management interventions and minimise yield losses. In recent years, artificial intelligence (AI)-based methodologies have gained prominence in plant disease diagnosis, offering new prospects for high-throughput and unbiased phenotypic trait analysis, thereby supporting precision agriculture and breeding programs.

AI techniques, including machine learning (ML) and deep learning (DL), simulate human cognitive functions by processing complex datasets to facilitate disease prediction and classification. Although various ML algorithms have been developed, they often require extensive preprocessing and domain expertise to extract relevant features for classifica-

tion (Dargan et al. 2020). Moreover, traditional ML models may struggle to handle large datasets, resulting in suboptimal accuracy. DL, as a specialised subset of ML, addresses these challenges by utilising multi-layered neural network architectures that autonomously learn discriminative features from raw input data, reducing the need for extensive image preprocessing and improving model efficiency (Albattah et al. 2022).

Convolutional neural networks (CNNs) are the most widely used DL architecture for plant disease classification from leaf images. The evolution of CNN models from AlexNet (Krizhevsky et al. 2017) to VGGNet (Simonyan & Zisserman 2015) and GoogLeNet (Szegedy et al. 2015) has enabled the development of increasingly sophisticated models, often referred to as "deeper" architectures due to their enhanced feature extraction capabilities. Although AI-based plant disease detection is an emerging research field for *Vigna* species, existing studies have primarily focused on disease classification rather than severity quantification. For instance, DarkNet-19 has been used to identify yellow mosaic disease in *V. mungo* (Kumar et al. 2023), and MobileNetV2 has been applied to classify four pest types (bruchids, whitefly, stem fly and aphids) and six foliar diseases [charcoal rot, Fusarium wilt, halo blight, yellow mosaic virus, Cercospora leaf spot (CLS), and PM] in mungbean (Mallik et al. 2023).

In Thailand, PM and CLS represent the predominant mungbean diseases in the winter and rainy seasons, respectively. Our prior study demonstrated the application of CNNs for assessing CLS severity in mungbean (Papan et al. 2025). However, to date, there has been limited research on automated severity assessment of PM in mungbean using DL frameworks. Disease severity is a critical metric for evaluating the extent of infection and is vital for guiding disease management decisions and supporting disease-resistance breeding programs. The present study seeks to address this gap by developing a lightweight CNN model to assess PM severity in mungbean accurately. Utilising the EfficientNet-B3 architecture, the proposed model was trained on a dataset of field-collected mungbean images to achieve robust, scalable performance in PM severity detection. The effectiveness of this approach was subsequently evaluated against conventional visual assessment methods to establish a reliable tool

for high-throughput phenotyping in precision agriculture.

MATERIAL AND METHODS

Data acquisition. A category set of 9 parental cultivars/lines, V4718, V4758, V4785, CN72, CN84-1, CN3, KPS1, SUT1 and KING and 10 promising breeding lines namely O2-31, O2-33, O2-37, O2-39, B1, B2, D5, G1, H3 and H4 were used to collect a meticulous inventory of 3 200 mungbean leaves once the plants reached the age of 65 days for PM severity profiling in this study. The leaves were collected from the fields of Suranaree University of Technology (SUT) Farm, Nakhon Ratchasima, Thailand, from November 2021 to January 2022, during the winter season, when PM is the predominant disease. Most importantly, these PM-infected leaves were naturally infected, without artificial inoculation.

Each mungbean leaf was photographed with a Canon EOS 650D (Canon Inc., Japan) camera at a resolution of 2 480 × 3 507 pixels, and the pictures were saved in Joint Photographic Experts Group (JPEG) format to facilitate further analysis. These images were then classified into 9 different

types as described by Khajudparn et al. (2010): 1 = no symptoms of the disease, 2 = 2–3 lesions on lower leaves, 3 = 2–3 lesions on lower leaves with sporulation, 4 = high number of sporulating lesions spread on lower and middle leaves, 5 = similar to score 4 with leaves beginning to turn yellow or dry and abundant sporulation, 6 = similar to score 5 but visible from distance with heavy sporulation, 7 = lesions found on leaves throughout the plant with leaves dry and brittle but not exceeding 25%, 8 = similar to score 7 with leaves dry and brittle between 25–50% and 9 = leaves very dry and brittle exceeding 50% (Figure 1). Representative images exhibiting PM symptoms were manually extracted from each predefined category, resulting in 300 × 300-pixel image segments. Subsequently, a total of 3 200 cropped images, with no or positive PM symptoms, were classified into 9 severity categories by expert evaluators, thereby establishing a reliable ground truth for subsequent model training.

The complete schematic of the methodology for PM detection is illustrated in Figure 2. The workflow commenced with the systematic collection of infected mungbean leaves from a controlled field experiment, followed by high-resolution image acquisition and segmentation through comprehensive preprocessing, includ-

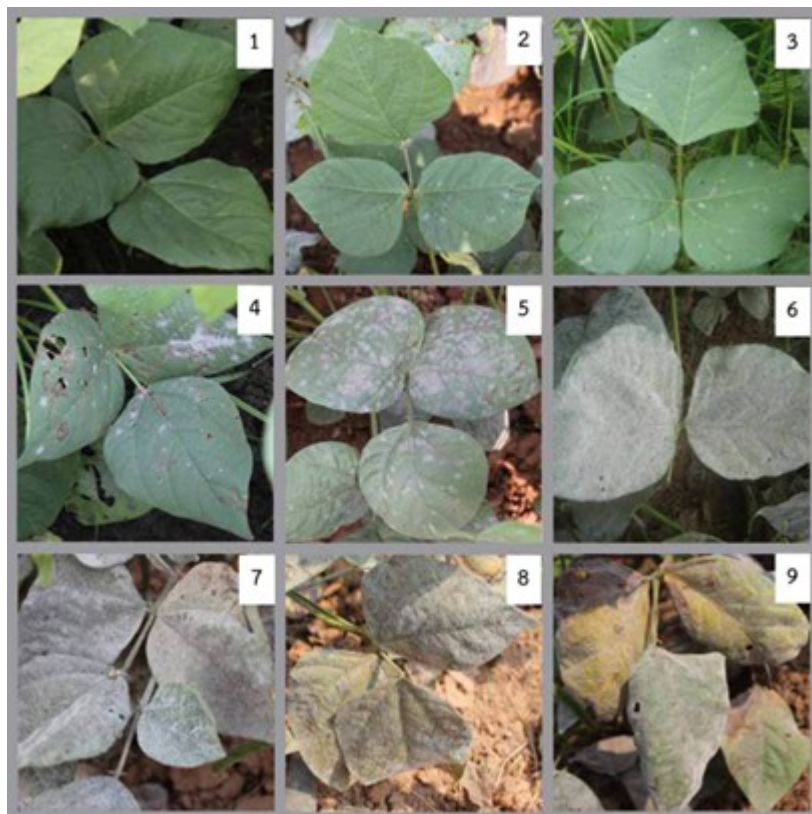


Figure 1. Sample images of powdery mildew (PM) symptoms in mungbean (1) no symptoms of the disease; (2) the presence of 2–3 lesions on the lower leaves; (3) the presence of 2–3 lesions on the lower leaves with sporulation; (4) a high number of lesions on both lower and middle leaves with sporulation; (5) similar to score 4 with leaves beginning to turn yellow or dry and abundant sporulation; (6) similar to score 5 with symptoms visible from a distance and abundant sporulation; (7) lesions found on leaves throughout the plant with leaves dry and brittle but not exceeding 25%; (8) similar to score 7 with leaves dry and brittle between 25–50%; (9) leaves very dry and brittle exceeding 50%

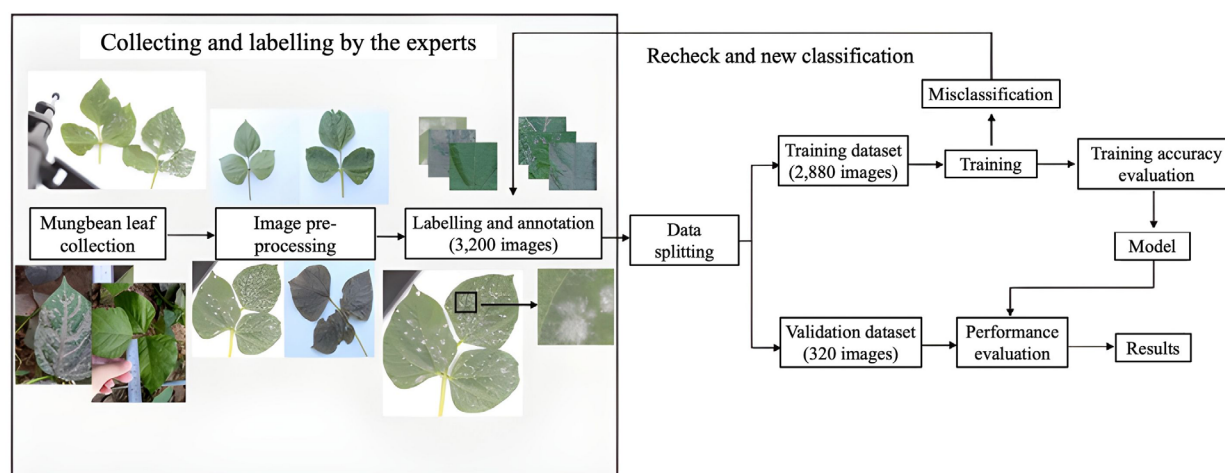


Figure 2. An overview of the method for powdery mildew (PM) detection in mungbean based on deep learning (DL)

ing photography and cropping. Expert annotators then meticulously categorised the segmented images to define the ground truth, which served as a foundation for model training. These annotated samples were subsequently used to develop an artificial neural network (ANN)-based model for precise classification of PM severity levels. The trained model was then applied to classify and predict the severity of PM infections in new mungbean leaf samples, providing an integrated, automated approach for early, accurate identification of PM in mungbean.

System description. Our dataset was divided into two parts: 90% for training and 10% for validation. We employed a neural network architecture based on EfficientNet-B3, which has previously demonstrated strong performance in CLS severity detection (Papan et al. 2025), to train the disease detection classifier. The architecture served as a starting point for training, and we applied the knowledge transfer technique to adapt it to our mungbean datasets.

The configuration parameters were set as follows:

- Solver Type: Stochastic Gradient Descent
- Base Learning Rate: 0.005
- Learning Rate Policy: Step (reduced 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, terminate and revert to the best checkpoint if the last three results are worse
- Image size: EfficientNet-B3 (300 × 300 pixels)

Furthermore, the output layer of each ANN was modified by replacing it with a dense layer with a SoftMax activation function. The net result of this transformation was to produce, for each record, a set of probabilities across all classes. These probabilities were then used to compute a disease index score according to equation 1. Note that a score of 9 was not used due to very few leaves identified with this score.

$$\text{Disease Index Score} = \sum p_i \times c_i \quad (1)$$

Where: p_i – the probability value for each class; c_i – the class itself (ranging from 1 to 8) for PM disease.

Utilisation of optimal architecture for validation of powdery mildew (PM) severity. In this study, we generated a total of 15 datasets, comprising samples from 9 parental and check cultivars/lines including V4718, V4758, V4785, Chai Nat (CN)84-1, CN72, CN3, Kamphaeng Saen (KPS)1, Suranaree University of Technology (SUT)1, KING, and our 6 promising breeding lines including O2-39, B1, B2, D5, H3, and H4. These datasets were created using mungbean leaf samples obtained from 65-day-old plants at the SUT Farm from November 2022 to January 2023. Leaf samples were captured using different smartphones (iPhone 8, Huawei Y7, and Huawei P30 Pro), resulting in 27–125 images per cultivar/line. We then resized all representative images of each leaf to a uniform size of 300 × 300 pixels.

Moreover, to assess PM severity in these datasets, we used the earlier-identified architecture on the validation data, which achieved the highest

performance. We computed a disease index score using a Softmax function based on Equation 1. To evaluate the accuracy of our system in detecting PM severity, we calculated correlation coefficients between the disease index scores generated by the model and the PM scores assigned by SUT experts during their observations of PM responses at 65 days after planting, using the scoring system of Khajudparn et al. (2010).

To enable our technology to run on any device, we created an application prototype in which the ANN is deployed in the cloud, allowing it to run directly on smartphones. Correlation coefficients between PM scores obtained using our developed application prototype in this research and those provided by experts were computed to demonstrate its effectiveness. We conducted this evaluation using 15 mungbean leaf images from 65-day-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 the field conditions at SUT in November 2022–January 2023. These images, depicting natural PM infection, were captured with smartphones (iPhone 8, Huawei Y7, and Huawei P30 Pro) and cropped to 300×300 pixels. The PM index scores were determined by uploading the images to our application prototype and comparing them with expert-assigned scores, following the criteria outlined by Khajudparn et al. (2010).

In our study, all mungbean cultivars/lines were planted in a randomised complete block design with 3 replicates at the SUT Farm. Each block had one 6 m long row for each cultivar/line, with a spacing of 20 cm between plants within the row and 50 cm between rows. Two plants per hill were maintained, resulting in approximately 60 plants per row. Additionally, the susceptible cultivar CN72 was grown around the blocks to serve as a source of PM inoculum.

Performance evaluation metrics for prediction models. Prediction performance evaluation indexes serve as criteria for evaluating the PM disease index prediction model. We employed R^2 , adjusted R^2 , root mean squared error (RMSE), mean absolute error (MAE), and mean squared error (MSE) to evaluate model performance. The predicted values (predicted disease severity scores) and true values (actual disease severity scores) were used as inputs for these metrics, with their equations adapted from Verma et al. (2024).

RESULTS

The objective of this study was to establish an effective methodology for detecting PM severity in mungbean leaves through a DL-based approach. A dataset comprising 3 200 high-resolution images of mungbean leaves with varying PM severity (scored from 1 to 8) was collected and systematically categorised. The images were partitioned into eight distinct groups based on the disease severity index to serve as ground truth for model training. Given the superior performance of the EfficientNet-B3 architecture over Inception V3, as demonstrated in findings by Papan et al. (2025) in the context of CLS in mungbean, EfficientNet-B3 was selected as the core CNN architecture for this study. To mitigate the risk of overfitting, the dataset was split into a training set (90%, 2 880 images) and a validation set (10%, 320 images). Data augmentation techniques were applied to improve the model's robustness. The CNN was implemented and fine-tuned in Python, using TensorFlow as the primary DL framework. Model training and optimisation were performed on a computational setup comprising a GPU (GeForce GTX1060, 6 GB GDDR5) and a CPU (Intel Core i7-8750H, 2.20 GHz, 16 GB RAM). The EfficientNet-B3 model underwent 14 training epochs, and the accuracy metrics for both training and validation sets were recorded at each epoch to monitor model performance (Figure 3). The final model achieved a training accuracy of 82.10% and a validation accuracy of 73.03%, indicating its potential efficacy in distinguishing PM severity levels in mungbean leaves.

The performance of the EfficientNet-B3 model was evaluated using 15 independent datasets representing diverse mungbean cultivars/lines collected under field conditions at SUT Farm between November 2022 and January 2023. These datasets presented multiple real-world challenges, including complex backgrounds, uncontrolled lighting, variable distances, camera differences, heterogeneous field environments, weed presence, variations in leaf colour, and fluctuating weather conditions. Each dataset contained between 27 and 125 leaf images, which were utilised to assess the model's predictive capability without further training. Disease severity indices were calculated for each image, even when imperfections in leaf morphology were present.

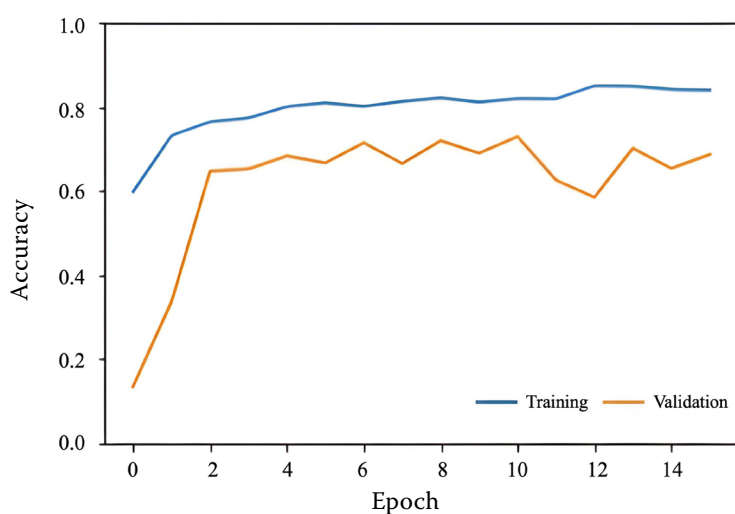


Figure 3. Progression of accuracy through the training of the dataset using EfficientNet-B3. The blue line shows the accuracy of prediction from the training dataset. The orange line shows the accuracy of prediction from the validation dataset.

The disease severity scores for PM across the 15 mungbean cultivars/lines ranged from 2.03 to 6.45. Line V4718 exhibited the lowest disease index (2.03), indicating high resistance, while lines V4758 and D5 displayed moderate resistance with scores of 3.30 and 4.55, respectively. In contrast, cultivars/lines CN72, CN84-1, SUT1, O2-39, B1, B2, H3, and H4 had indices ranging from 4.73 to 6.02, suggesting intermediate susceptibility to PM. The highest disease severity scores were observed in cultivars/lines V4785, CN3, KPS1, and KING, which ranged

from 6.14 to 6.45, indicating they are highly susceptible (Table 1).

The overall accuracy of the EfficientNet-B3 model in predicting PM severity across these diverse field datasets ranged from 62.00% to 84.75%, demonstrating its capability to handle complex field images with significant variability and environmental noise. These results underscore the model's robustness and its potential utility for large-scale phenotyping and field-based resistance screening.

Table 1. Evaluation indicators for validating powdery mildew (PM) severity in 15 cultivars/lines based on EfficientNet-B3

Cultivars/ lines	Number of images	Corrected images	Misclassified images	Accuracy (%)	PM scores			
					EfficientNet-B3		Experts	
V4718	76	62	14	81.58	2.03	R	1.50	R
V4758	38	25	13	65.79	3.30	MR	3.13	MR
V4785	100	62	38	62.00	6.14	MS	5.75	MS
CN84-1	39	33	6	84.62	6.00	MS	7.50	S
CN72	89	68	21	76.40	6.02	MS	7.63	S
CN3	51	39	12	76.47	6.25	MS	7.50	S
SUT1	125	87	38	69.60	6.45	MS	7.25	S
KPS1	76	57	19	75.00	6.02	MS	6.88	MS
KING	27	18	9	66.67	6.29	MS	7.13	S
O2-39	60	40	20	66.67	5.91	MS	6.75	MS
B1	86	65	21	75.58	5.62	MS	5.63	MS
B2	59	50	9	84.75	5.13	MS	5.75	MS
D5	92	63	29	68.48	4.55	MR	4.38	MR
H3	91	73	18	80.22	4.73	MR	5.63	MS
H4	125	93	32	74.40	5.89	MS	6.13	MS

PM response: resistance (R) = 1.0–3.0, moderate resistance (MR) = 3.1–5.0, moderate susceptibility (MS) = 5.1–6.9, and susceptibility (S) = 7.0–9.0; PM scores in the field conditions were averaged across 3 replicates of a randomised complete block design

The performance of the EfficientNet-B3 model was further assessed by categorising its predictive accuracy across defined severity score ranges: 1–2, 3–4, 5–6, and 7–8. Results indicated that the model achieved higher accuracy in the lowest-severity range, with 95.90% for scores 1–2, compared to the highest-severity range (55.40% for scores 7–8). Whereas, the accuracy was moderate in the intermediate severity ranges, 3–4 (68.70%) and 5–6 (78.30%). This discrepancy suggests a tendency for the model to underestimate disease severity at higher scores, potentially due to ambiguities in leaf colour and texture, which could diminish overall performance in complex scenarios.

Despite these limitations, the model demonstrated a strong fit to human assessments, explaining 74.4% of the variance in expert observations. After accounting for model complexity, the adjusted R^2 value was 72.4%, indicating that the model could reliably capture the majority of variability in PM severity classification. The RMSE between AI predictions and human scores was 0.854, indicating the average magnitude of the error. The MAE was 0.715, while the MSE, which emphasises larger deviations, was recorded at 0.729. These metrics suggest that while the model was generally accu-

rate, moderate predictive errors persisted, particularly at higher severity levels.

To facilitate field-level implementation, the EfficientNet-B3 model was subsequently integrated into a cloud-based computing environment, enabling the development of a mobile application prototype for real-time PM disease severity assessment using a smartphone. This application represents a practical tool for rapid phenotyping and disease management of diverse mungbean cultivars under field conditions.

An AI-based application prototype was developed to evaluate PM severity across 15 mungbean cultivars/lines grown under field conditions at SUT Farm between November 2022 and January 2023. The prototype's performance was validated by comparing its outputs with disease severity ratings provided by trained experts in the field. The correlation between the AI-generated scores and human evaluations was exceptionally high ($r = 0.992^{**}$, $R^2 = 0.984$), demonstrating the model's accuracy and consistency (Table 2).

The prototype's predictions were significantly and positively correlated with expert assessments across all cultivars/lines, except for CN72, where the correlation was slightly lower ($r = 0.724^*$;

Table 2. Comparison of powdery mildew (PM) severity evaluations in mungbean by the application prototype developed in this study and human

Cultivars/lines	PM scores				Correlation coefficients	Coefficient of determination
	Application prototype		Human			
V4718	1.00	R	1.10	R	1.000**	1.000
V4758	1.38	R	1.63	R	0.970**	0.941
V4785	3.45	MR	3.60	MR	0.955**	0.912
CN84-1	5.52	MS	6.25	MS	0.960**	0.922
CN72	5.49	MS	6.35	MS	0.724*	0.524
CN3	6.10	MS	7.00	S	0.811**	0.658
SUT1	5.02	MR	5.65	MS	0.840**	0.706
KPS1	5.32	MS	5.65	MS	0.937**	0.878
KING	5.71	MS	6.50	MS	0.980**	0.960
O2-39	5.24	MS	5.35	MS	0.929**	0.863
B1	4.02	MR	4.33	MR	0.915**	0.837
B2	4.15	MR	4.27	MR	0.848**	0.719
D5	3.52	MR	4.00	MR	0.868**	0.753
H3	3.93	MR	4.30	MR	0.825**	0.681
H4	4.81	MR	5.10	MS	0.858**	0.736

PM response; resistance (R) = 1.0–3.0, moderate resistance (MR) = 3.1–5.0, moderate susceptibility (MS) = 5.1–6.9, and susceptibility (S) = 7.0–9.0

$R^2 = 0.524$). For the remaining cultivars, correlation coefficients ranged from 0.811** to 1.000** and R^2 values ranged from 0.658 to 1.000, indicating robust agreement between the AI model and human experts. Notably, the AI-based tool successfully matched the PM response profiles of all cultivars/lines with expert field evaluations, except for three cultivars/lines (CN3, SUT1, and H4), where minor discrepancies were observed.

These findings suggest that the AI-driven application can serve as a reliable tool for quantifying PM severity in mungbean, providing accurate and rapid assessments to support disease management decisions. However, further refinement and validation of the prototype are recommended to enhance its robustness and usability. Future efforts should focus on optimising the tool for broader deployment among mungbean farmers to facilitate real-time disease monitoring and promote precision agriculture practices in diverse field environments.

DISCUSSION

The accurate identification of PM severity levels in mungbean leaves marks a significant advancement in agricultural disease management, laying the groundwork for rapid, precise, and automated diagnostics. This study's use of the EfficientNet-B3 model demonstrates the efficacy of CNNs for classifying PM severity across diverse mungbean genotypes, achieving commendable training and validation accuracies of 82.10% and 73.03%, respectively. These results suggest that the model holds potential for generalizability across varying field conditions, though specific performance metrics indicate areas for further optimisation.

A particularly noteworthy finding is the model's performance across different severity score ranges. The high precision achieved in the low-severity category (95.90% within the score range of 1–2) suggests the model excels at distinguishing between healthy plants and those in the early stages of infection. However, the decline in accuracy across higher-severity ranges highlights the challenge of identifying advanced PM symptoms. This issue likely arises from the increasing visual complexity in severely infected leaves, where extensive tissue damage, colour variations, and textural changes complicate classification. These results are consistent with those of Mohanty et al. (2016), who ob-

served that DL models often struggle to accurately classify advanced disease stages due to overlapping visual features that blur symptom differentiation.

The model demonstrated a satisfactory alignment with expert assessments, as evidenced by an adjusted R^2 value of 72.4%. Nevertheless, approximately 27.6% of the variance remains unexplained, suggesting that the model does not fully capture additional factors contributing to disease severity. The RMSE and MAE values of 0.854 and 0.715, respectively, indicate that while the model's predictions closely mirror expert evaluations, moderate discrepancies persist. To improve performance, future iterations could incorporate additional features, such as environmental variables (e.g., humidity, temperature) and genotype-specific attributes of mungbean cultivars/lines. The importance of integrating such multi-modal data to enhance predictive accuracy is reinforced by Ferentinos (2018), who highlighted the value of combining diverse data sources in ML models. By factoring in these contextual variables, the model could achieve more precise disease classification under complex field conditions.

The development of a smartphone-based application prototype for real-time PM assessment represents a major advancement in the deployment of AI-driven tools for agricultural diagnostics. The application showed a very high correlation with expert ratings ($r = 0.992$, $R^2 = 0.984$), demonstrating its potential as a practical field tool. Its capacity to provide rapid, on-site assessments empowers farmers to monitor crop health more effectively, enabling timely interventions to mitigate disease spread and improve yield outcomes. These findings align with those of Ahmed and Reddy (2021), who reviewed various smartphone applications for rapid and accurate disease detection across multiple crop species, highlighting the transformative potential of mobile technologies in precision agriculture.

This study delivers highly promising results, with great potential for further enhancing both the model and the smartphone application, particularly in boosting accuracy for high-severity classifications. Furthermore, the current application prototype using a CNN-based approach discriminated between symptoms of CLS and PM, the two predominant mungbean diseases in Thailand, and reliably assessed disease severity (Papan et al. 2025; data not shown), underscoring its potential appli-

cability in real-world settings. Successful implementation will also depend on farmer education and training to ensure effective use. Cook (2000) emphasised the importance of engaging farmers in adopting advanced technologies through collaboration with agricultural extension services. In alignment with this, our partnerships with agricultural sectors in Thailand's key mungbean-producing regions – central, northern, and northeastern Thailand – position us to promote this tool and support its adoption among local farmers. Our results establish a proof-of-concept for using CNNs to diagnose PM disease in mungbean, with significant implications for precision agriculture. Continued efforts to enhance model accuracy through integrating additional data, combined with targeted farmer education, will be essential for realising the full potential of this technology in real-world settings. Nevertheless, the current model and application prototype are promising for future deployment as the first AI-based tool for evaluating PM severity in mungbean, providing farmers with a user-friendly solution accessible via standard smartphones. As agricultural challenges become more complex due to climate change and emerging diseases, AI technologies will be crucial for developing resilient and sustainable food systems.

CONCLUSION

In summary, this study demonstrates the feasibility of using CNN models to evaluate PM severity in mungbean, with significant potential for precision agriculture. Although further model enhancement and targeted farmer education are required, the current model and prototype can be deployed in the future, providing farmers with an accessible, easy-to-use tool for assessing PM disease severity. As the agricultural landscape evolves, the integration of AI technologies will be essential for building resilient food systems capable of withstanding the pressures of climate change and emerging plant diseases. The tool can also be effectively used for rapid PM screening in mungbean breeding programs to improve disease resistance.

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