



Detection of Potato Tuber Diseases in Türkiye Using a Deep Learning Methodology

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Abstract

Visual inspection performed by experts to diagnose plant disease is time-consuming, labor-intensive, and subject to human error. This study presents a deep learning-based approach for detecting common scab in potato tubers (*Solanum tuberosum*), a disease caused by a group of bacteria known as *Streptomyces* spp., using four different potato varieties: Provento, Othello, Madaline, Bettina. A total of 800 healthy and diseased tubers were collected with detailed records of variety and field of cultivation for each tuber variety. The presence of disease was confirmed through laboratory analysis. RGB and near-infrared (NIR) images were captured in a controlled environment designed to simulate a commercial sorting machine. By applying this approach a cleaned dataset of 1374 images was produced. The data were split into training (70%), validation (15%), and testing (15%) sets, and four datasets (RGB images separated by variety, NIR images separated by variety, RGB images merged across varieties, NIR images merged across varieties) were analyzed. MobileNetV3 achieved the highest test accuracy (90.5%) on the NIR dataset with a loss of 0.415 and training time of 24 min. In comparison, VGG19 reached 95.7% accuracy on RGB images. Analysis of the merged RGB dataset showed a maximum accuracy of 99% for both InceptionV3 and VGG19, while ResNet101 achieved 99.5%. Thus, ResNet101 provides the maximum classification certainty (99.5%) among all tested CNN architectures. Across all datasets tested, MobileNetV3 demonstrated the ideal combination of maximum accuracy (> 99%), optimal low loss (< 0.41), and efficient average training time (24 min). Thus, it is suggested as an optimal candidate for real-time, automated potato disease detection in precision agriculture systems.

Keywords Common scab · Convolutional neural networks (CNNs) · Near-infrared (NIR) imaging · Plant disease detection · RGB imaging · *Solanum tuberosum* · *Streptomyces* spp.

Introduction

Potato (*Solanum tuberosum* L.) is a globally important industrial and food crop. According to Food and Agriculture Organization of the United Nations (FAO) statistics, China, India, Russia, the USA, and Ukraine are the top producers, and potato ranks as the third most important food crop worldwide after wheat and rice (FAO 2022). Potatoes provide a substantial nutritional profile, serving as a rich source of carbohydrates, protein, and various vitamins (Jansky et al. 2019).

Biotic factors, including pests and diseases, are major contributors to annual yield and quality losses in potato production. Potato tubers can be affected by various seed- and soil-borne diseases. Notable bacterial diseases include blackleg and soft rot (*Pectobacterium carotovorum* subsp. *atrosepticum*, *P. carotovorum* subsp. *carotovorum*, and *Dickeya* spp.), bacterial wilt (*Ralstonia solanacearum*), potato common scab (*Streptomyces* spp.), and bacterial ring rot (*Clavibacter michiganensis* subsp. *sepedonicus*) (Charkowski et al. 2019). Important fungal diseases include late blight (*Phytophthora infestans*), early blight (*Alternaria solani*), and powdery scab (*Spongospora subterranea*), all of which can cause significant pre- and post-harvest losses (Campos and Ortiz 2019).

Potato common scab (PCS) is among the most economically significant bacterial diseases of potatoes. Although PCS has a limited effect on total yield, it severely reduces tuber quality and marketability (Uysal et al. 2025). The disease is caused by Gram-positive Actinomycetes in the genus *Streptomyces* and is distributed worldwide in potato-growing soils (Loria et al. 2006). PCS is primarily associated with *S. scabiei* but can also be caused by more than twenty species, including *S. caviscabies*, *S. bottropensis*, *S. europaeiscabiei*, *S. niveiscabiei*, *S. luridiscabiei*, *S. stelliscabiei*, *S. puniscabiei*, *S. turgidiscabies*, *S. brasiliscabiei*, and *S. caniscabiei* (Corrêa et al. 2021; Li et al. 2019; Nguyen et al. 2022; Wanner 2009). The disease manifests as brown to dark lesions on the tuber surface, which may be raised or deeply pitted depending on environmental factors, pathogen activity, and cultivar susceptibility (Karagöz and Kotan 2017).

Symptom similarity with other tuber disorders, such as powdery scab (*Spongospora subterranea*) and patchy russetting (*Rhizoctonia* spp.), can lead to misdiagnosis. As tubers dry, some visual symptoms may fade, making laboratory confirmation essential for accurate PCS identification (Samanta et al. 2012). Traditional visual diagnosis by experts is time-consuming, labor-intensive, and prone to human error. Consequently, the development of automated, high-accuracy disease detection systems has become a critical research priority (Mahum et al. 2023). Rapid and reliable detection is vital for protecting yields, reducing environmental impact, and enabling effective agricultural planning.

Recent advances in deep learning have greatly expanded the range of use and effectiveness of automated agricultural systems through the application of such technologies to the various areas of agricultural system automation (Ayoub et al. 2025). The combination of deep neural networks and optimization algorithms through hybrid model approaches in the context of classifying plant diseases and other applications is an example of this (Elshewey et al. 2024, 2025; Bozdağ et al.

2025). Many recent studies have examined the impact of hybrid model optimization deep learning on the prediction and classification accuracy of many different applications (Elshewey 2025; Umar et al 2025; Elshewey and Osman 2024; El-Rashidy et al. 2025). Deep learning methods are increasingly used to detect plant diseases (Nath et al. 2025; Kant et al. 2025; Han et al. 2025). Extensive reviews comparing Convolutional Neural Networks (CNN) architectures and optimization techniques used for plant disease detection also clearly demonstrate the use of deep learning (Haque et al. 2025; Nizamani et al. 2025). For example, the ability of CNN design to substantially enhance the accuracy of plant disease classification via the capture of fine-grained visual attributes and to produce significant model robustness across varying imaging conditions is supported (Gulzar and Ünal 2025). Likewise, deep learning-based image processing has proven successful for assessing food and crop quality, with optimally designed CNN models providing strong classification performance while maintaining acceptable levels of computational efficiency, supporting their use in post-harvest inspection processes (Ünal 2025). The study has successfully demonstrated that lightweight, computationally efficient deep learning architectures can perform competitively with reduced processor requirements. Numerous studies have explored machine learning and deep learning methods for detecting potato tuber diseases. For example, Samanta et al. (2012) applied K-means clustering to segment scab lesions, achieving 97.5% accuracy. Tarik et al. (2021) trained a seven-layer CNN on 2,034 field images representing seven potato diseases, obtaining 99.23% accuracy. Oppenheim et al. (2019) used the CNN-F algorithm to classify multiple tuber diseases, including common scab, with up to 95.85% accuracy. Leiva et al. (2024) developed *ScabyNet*, a deep learning-based grading system that achieves 99% accuracy on 7.154 images. Yang et al. (2023) combined multispectral imaging with YOLOv3-tiny for defect detection, achieving a mean average precision of 90.26%.

While researchers have demonstrated high degree of accuracy in detecting potato tuber diseases using CNNs, there are still some limitations that need to be addressed. First, many current datasets contain images that were collected in the field, without comprehensive documentation to record all of the necessary information about the potato cultivars grown at a particular location and the environmental conditions. Secondly, many of the disease labels were assigned strictly from the visual symptoms displayed on the potato, and thus did not include laboratory confirmation to validate their accuracy. This raises concerns about both the reliability of the datasets and the ability of the models developed utilizing these datasets to generalise. Third, while many previous publications have emphasized maximizing classification accuracy with CNNs, there remains a need to focus on the real-time capabilities of CNN architectures used in large-scale industrial potato sorting operations. Finally, because very few studies have directly compared the same potato samples imaged with RGB (red-green-blue) and NIR (near-infrared) cameras at the same time using exactly the same procedures, there is still much uncertainty regarding the cost and performance of each system type (RGB vs. NIR). These limitations highlight the need for well-documented, laboratory-verified datasets and systematic evaluations of CNN architectures with respect to both accuracy and real-time applicability.

To address these limitations, an imaging system integrating both RGB and NIR cameras was developed (Zheng et al. 2018). RGB cameras capture visible color information, enabling visual analysis of tuber surface characteristics, while NIR cameras detect wavelengths beyond the visible light, providing insights into internal tissue structure and early disease symptoms (Semyalo et al. 2024). NIR imaging complements RGB by revealing morphological changes associated with disease progression, such as variations in water content, stress responses, or photosynthetic activity (Zahir et al. 2022). Despite the higher cost of NIR imaging, combining both modalities allows evaluation of their complementary effectiveness and cost-efficient diagnostic potential.

To the best of our knowledge, this study is the first to develop a unique RGB and NIR dataset supported by laboratory evidence to detect potato common scab in Türkiye. These images were taken under simulated sorting conditions, and the presence of disease was verified in the laboratory. Previous studies have used field images and assessed diseases visually, whereas our research sampled all tubers systematically, with extensive documentation on the variety and origin of each tuber, and verified their disease status using laboratory methods to isolate the pathogen and perform pathogenicity tests. Finally, this study presents an extensive quantitative comparison of lightweight versus deep CNN architectures applied to RGB, NIR, and merged datasets, providing practical examples for implementing cost-efficient disease detection systems within commercial potato processing lines.

Materials and Methods

This study used a systematic data collection process, labeling potato samples, and comparing different imaging techniques using RGB and NIR cameras. The overall workflow of the study, including data collection, laboratory verification, image acquisition, dataset construction, model training, and evaluation, is illustrated in Fig. 1.

Collection of Potato Tubers

Potato tubers were collected from Niğde province (37°54' N, 34°42' E), in the Central Anatolia Region of Türkiye, during the 2024 harvest season (Fig. 2a). Both tubers exhibiting visible PCS symptoms and healthy tubers of the same varieties were sampled from four major potato-producing districts: Yeşilgölcük, Altunhisar, Konaklı, and Edikli. These districts were selected due to their intensive potato cultivation and their relevance as potential hotspots for the spread of various tuber diseases (Fig. 2b).

A systematic approach was employed to collect and classify the health status of potato tubers. Initially, the sampling fields were georeferenced and marked to document their precise locations and agronomic characteristics. This field marking facilitated a consistent and repeatable data collection process, enabling reliable comparisons of tuber health across different locations.

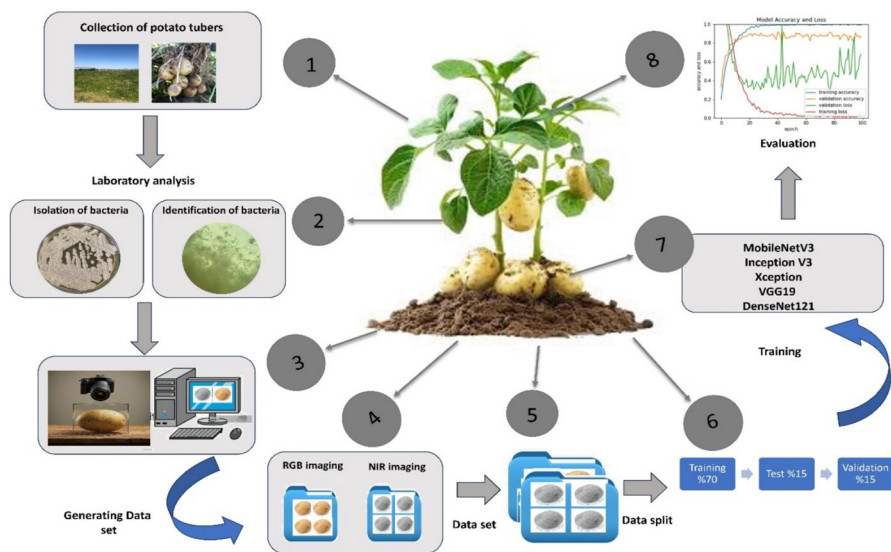


Fig. 1 Flowchart illustrating the complete methodology of the study, including potato tuber collection, laboratory confirmation of potato common scab, RGB and NIR image acquisition under industrially simulated conditions, dataset construction, CNN model training, and performance evaluation



Fig. 2 Survey locations (a) and collection of infected potato tuber samples (b)

Subsequently, four distinct potato varieties—Bettina, Madaline, Othello, and Provento—were identified within the marked fields. Both healthy and symptomatic

tubers were carefully collected from each variety and segregated into designated containers based on their health status. For each variety, 100 healthy and 100 infected samples were gathered, totaling 800 tubers.

Each sample was then labeled with adhesive tags indicating the variety and health class to ensure accurate categorization during subsequent processing. Since laboratory diagnostic procedures render samples unusable for imaging, all tubers were first subjected to image acquisition prior to laboratory analysis. If laboratory tests failed to confirm disease presence in a sample initially classified as infected, its corresponding images were removed from the dataset. This rigorous validation process ensured a balanced, high-quality dataset of healthy and diseased tubers for each variety, thereby enhancing the reliability and accuracy of the model training phase.

Isolation of Bacteria

Streptomyces spp. were isolated from potato common scab lesions following a modified protocol based on Lerat et al. (2009). Briefly, tubers were surface sterilized by immersion in 1% sodium hypochlorite (NaOCl) solution for one minute, followed by rinsing with sterile distilled water (SDW). Lesion tissues measuring approximately 5 × 5 × 5 mm were aseptically excised and subjected to further surface sterilization in 70% ethanol for 30 s, followed by three consecutive washes with SDW.

Homogenized tissue suspensions (50 µL) were plated onto water agar and incubated at 30 °C for 7–10 days. Colonies exhibiting morphology characteristic of *Streptomyces* were subsequently transferred to yeast malt extract (YME) agar and incubated at 30 °C for an additional two weeks. Pure cultures were obtained via single-colony subculturing on YME agar. Spore suspensions from confirmed isolates were prepared and stored in 50% glycerol solution at 80 °C for long-term preservation.

Pathogenicity Assay and Identification of *Streptomyces*

The pathogenicity of *Streptomyces* isolates was assessed using the potato tuber slice assay, following the method described by Loria et al. (1995). Disease-free potato tubers of cultivar Agria, known for its susceptibility to potato common scab (PCS), were surface sterilized with 0.1% sodium hypochlorite and cut into 5 mm thick slices. These slices were placed on moistened filter paper within Petri dishes and inoculated with 5 mm agar plugs containing sporulating colonies of the test strains, previously cultured on yeast malt extract (YME) agar at 30 °C for 5–7 days. The inoculated slices were incubated at 25 °C in the dark for 5 days. Necrosis severity was evaluated on a scale from 0 to 4, where 0 indicated no color change; 1, slight browning; 2, intermediate browning; 3, high browning; and 4, strong browning. *S. scabiei* (PP258033) served as the positive control, and sterile distilled water (SDW) as the negative control.

Morphological characterization of the *Streptomyces* isolates was performed according to the International *Streptomyces* Project (ISP) protocols (Loria et al.

2006; Shirling and Gottlieb 1966). Colony morphology, spore color, and spore chain arrangement were examined on YME agar as described by Shirling and Gottlieb (1966). Spore ornamentation was observed using light microscopy at 40 $\times$ magnification (Leica DM500). Melanin production was assessed by detecting diffusible dark pigment formation on peptone yeast extract iron agar (PYI, ISP medium 6) and tyrosine agar (TYR, ISP medium 7). All plates were incubated at 28 °C, and morphological data were recorded after a 14-day incubation period.

Image Acquisition

Potato tuber images were acquired simultaneously using RGB and NIR cameras in a custom-designed imaging cabinet (Fig. 3) compatible with industrial production lines. The system ensured consistent orientation and optimal viewing angles, enhancing image quality for automated disease detection. RGB images captured visible color information, while NIR images provided insights into internal tissue structure and early disease symptoms. Two-angle imaging was attempted for each tuber, yielding a total of 1421 images from 800 samples.

Dataset Construction

All RGB and NIR images were resized prior to inputting into each of the selected CNN architectures to meet the specific input requirement of each architecture. Through this process, InceptionV3 and Xception models resized their input images as 299 $\times$ 299 pixels while for MobileNetV3, VGG19, DenseNet121, and ResNet101 a 224 $\times$ 224 pixel size was used, which allowed the appropriate input size for both model types and consistent preprocessing across all model groups used in this study.

Next, all images were visually checked before being trained so that any images that were considered low quality or looked blurred were removed before training

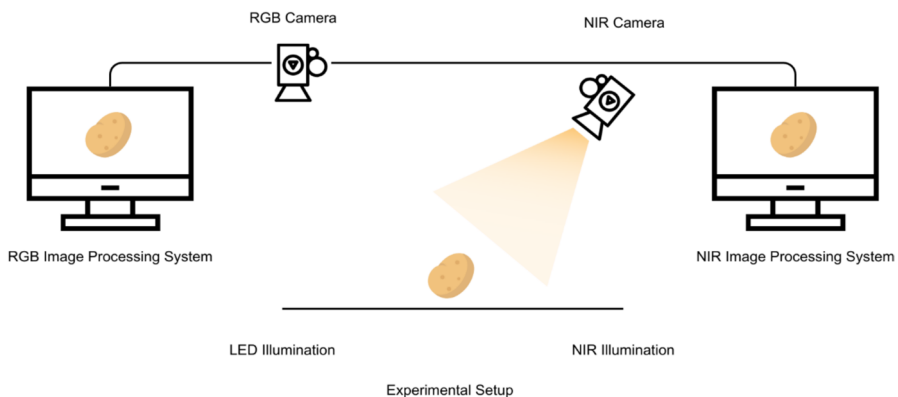


Fig. 3 An imaging cabinet system integrating both RGB and NIR cameras

Table 1 Number of images obtained from potato tubers

Classes	Training	Validation	Test	Total
Bettina infected	52	11	12	75
Bettina healthy	196	42	42	280
Madeleine infected	111	24	24	159
Madeleine healthy	88	19	20	127
Othello infected	104	22	23	149
Othello healthy	130	28	28	186
Provento infected	154	33	34	221
Provento healthy	123	27	27	177
Total	958	206	210	1,374

Table 2 Number of images obtained after merging

Classes	Training	Validation	Test	Total
Infected	422	91	91	604
Healthy	539	115	116	770
Total	961	206	207	1,374

began. The images used in the study were collected under constant lighting conditions and have uniform backgrounds that mimic what a sorting system would look like in an industrial setting. Therefore, no background segmentation or geometric transformation of the images was necessary for the study. In addition to the above, no other image enhancement or filtering techniques were employed in the study to maintain the true appearance of the potato tubers, and to enable a more accurate representation of how the models would perform when deployed in real-world conditions.

Images from samples with diseases other than PCS were excluded. The cleaned dataset was split into training (70%), validation (15%), and test (15%) subsets. RGB and NIR images were analyzed collectively, and all potato varieties were aggregated into two classes: “healthy” and “infected,” as summarized in Tables 1 and 2.

In this study, all CNN models were trained and tested using the original RGB and NIR images acquired under controlled and consistent conditions, without the use of any data augmentation techniques. The primary goal was to maintain the natural appearance of potato tubers, ensuring that the results of the models reflect conditions that will be experienced in the sorting of potatoes using industrial systems. While data augmentation can be beneficial for improving generalization of small and/or highly varied datasets, it can also create artificial images that produce patterns that do not occur in physical-world conveyor-belt inspection. In addition, the lighting, setup, and tuber placement were specifically selected to provide an accurate representation of what could be found within an industrial environment. Because of this, any form of augmentation to prevent bias towards overestimating model performances was intentionally avoided.

CNN Architectures

CNNs are deep learning models designed to capture spatial relationships in images, making them well-suited for agricultural applications such as disease detection (Fig. 4). In this study, six CNNs were selected based on their architectural diversity. MobileNetV3 uses the least amount of system resources (Lin et al. 2024) while still providing similar results when compared to other neural networks, which typically use large amounts of resources. Therefore, this was included in the study as an example of a lightweight CNN, compared with complex, computationally intensive models such as VGG19, DenseNet121, and ResNet101 (Simonyan and Zisserman 2015). Conversely, the InceptionV3 and Xception CNN Models were included due to their use of factorized and depth-wise separable convolutions, which have been shown to improve feature extraction efficiency and performance in visual recognition tasks (Das et al. 2022). The aim was to achieve a better understanding of how each design will process image recognition tasks in real-world situations by performing a direct comparison of the designs of the six models. Together, these architectures provided a spectrum of computational complexities for accurate classification of potato tuber diseases.

Experimental Environment Settings and Evaluation Metrics

The CNN models were trained and tested on a desktop with an Intel i7 CPU (3.6 GHz), 16 GB RAM, and an NVIDIA RTX 2060 GPU using Python 3.8, OpenCV 4.5, Keras 2.5, and Pylon Viewer 6.2. Model performance was evaluated using accuracy, recall, precision, F1 score, and binary cross-entropy loss, calculated as:

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + FP + TN + FN)} \quad (1)$$

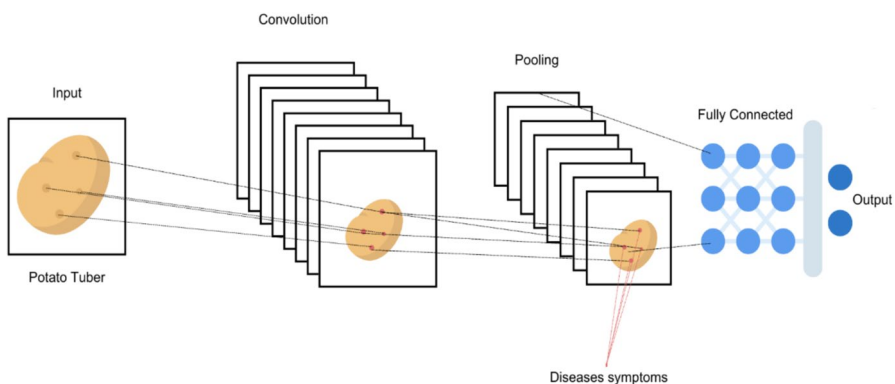


Fig. 4 Convolution neural network architecture

where the initials TP, TN, FP, and FN stand for true positive, true negative, false positive, and false negative, respectively.

Out of all actual positive events, recall is the percentage of true positives that were accurately predicted. As stated in the subsequent Eq. (2)

$$\text{Recall} = \frac{TP}{(TP + FN)} \quad (2)$$

Precision: The percentage of positive data that is correctly predicted is shown here. In other words, higher accuracy leads to fewer false positives, which are calculated using Eq. (3)

$$\text{Precision} = \frac{TP}{(TP + FP)} \quad (3)$$

F1 score: As indicated in Eq. (4), the F1 score is computed by dividing the sum of recall and precision by the product of recall and precision (Gulzar et al. 2024).

$$F1 - score = 2 \times \frac{\text{Recall} \times \text{Precision}}{\text{Recall} + \text{Precision}} \quad (4)$$

A model metric called binary cross entropy monitors when a model incorrectly labels a data class and penalizes the model for deviations in likelihood when classifying the labels. High accuracy values are equivalent to low loss values. The value of binary cross entropy is $-1 * \log(\text{likelihood})$. As indicated in Eq. (5).

$$\text{Binary cross entropy} = -\frac{1}{N} \sum_{i=1}^n y_i \cdot \log(p(y_i)) + (1 - y_i) \cdot \log(1 - p(y_i)) \quad (5)$$

In this case, $\log(p(y_i))$ is the probability of that class, and Y_i is the actual class. The probability of one is represented by $p(y_i)$, and the probability of zero by $1 - p(y_i)$ (Guo et al. 2023).

Model performance was evaluated using a fixed train–validation–test split (70%–15%–15%), which was kept consistent across all CNN architectures to ensure fair comparison. Each model was trained and evaluated once using identical data partitions and hyperparameter settings. Cross-validation was not applied due to the limited size of the laboratory-verified dataset and the high computational cost associated with training multiple deep CNN architectures. Instead, robustness was assessed through comprehensive testing on an independent test set that was not used during training or validation.

Results and Discussions

Laboratory Analysis

Potato tuber samples were collected from Niğde province (Altunhisar, Konaklı, Yeşilgölcük, and Edikli), and exhibited PCS symptoms including deep-pitted,

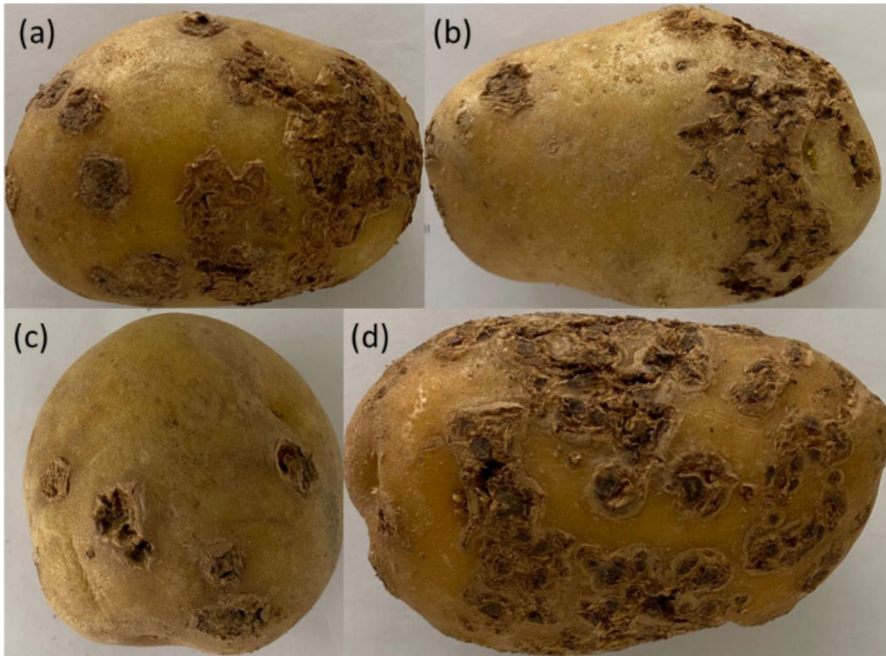


Fig. 5 Potato tubers collected from Niğde province, exhibiting superficial (a), netted (b) deep-pitted (c), and deep-pitted/netted (d)

superficial, and netted lesions (Fig. 5). Fifteen *Streptomyces* strains were isolated, of which ten demonstrated pathogenicity on potato slices (Fig. 6). Morphological characterization showed that all strains cultured on YME agar produced gray spores and yellowish-brown colonies (Fig. 7a). Microscopic examination at 40× magnification revealed spiral-structured spore chains in all strains (Fig. 7b). Additionally, all strains produced soluble pigments on PYI agar (Fig. 7c) and exhibited a minimum growth pH of 5 (Fig. 7d). Based on these characteristics and comparisons with reference strains, all isolates were confirmed to belong to the genus *Streptomyces* and were pathogenic.

PCS, a disease that affects both yield and quality of potato crops, is prevalent in many major potato-growing regions worldwide (Dees et al. 2013; Leiminger et al. 2013). Several *Streptomyces* species are known causal agents of PCS. Earlier research in central Anatolia, Türkiye, identified *S. scabiei*, *S. reticuliscabiei*, and *S. turgidiscabies* using morphological and biochemical methods. Subsequent studies in the Eastern Anatolia (Erzurum province), employing both morphological and molecular techniques, detected *S. scabiei*, *S. bottropensis*, *S. stelliscabiei*, and *S. europaeiscabiei* (Karagöz and Kotan 2017). Further investigations covering Niğde, Nevşehir, Konya, Kayseri, and Hatay provinces revealed the presence of *S. scabiei*, *S. turgidiscabies*, *S. bottropensis*, *S. stelliscabiei*, *S. europaeiscabiei*, and *S. caniscabiei* through combined morphological and molecular characterization (Uysal et al. 2025).

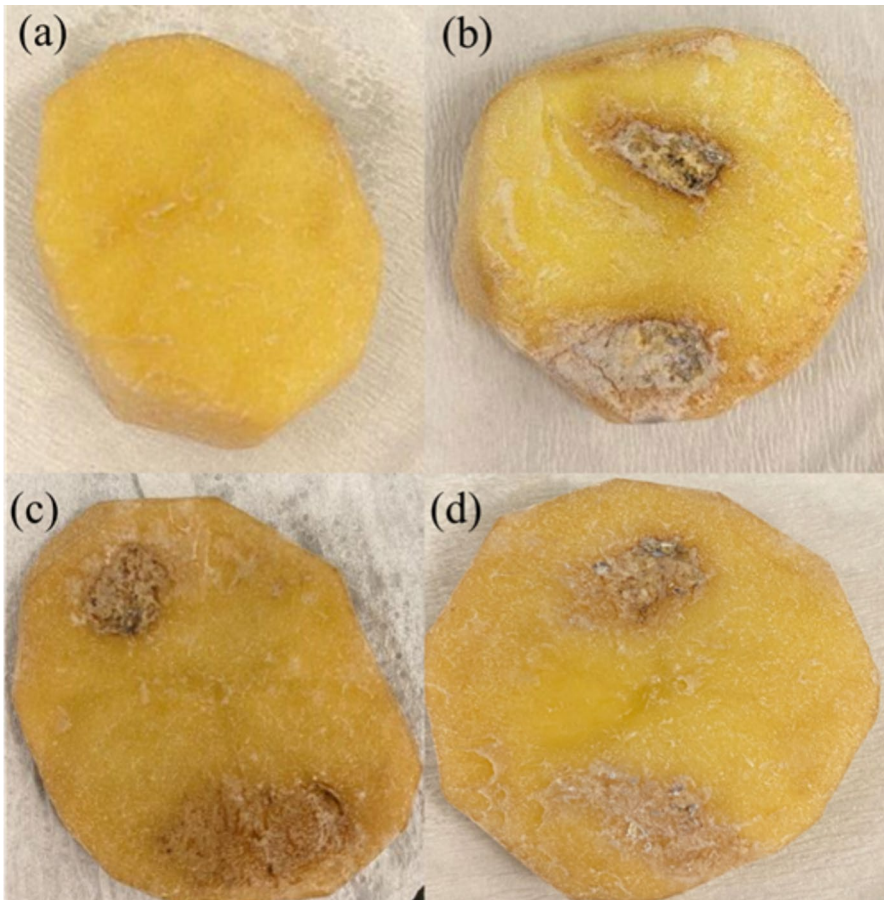


Fig. 6 Potato tuber slice assays for the determination of pathogenicity of *Streptomyces* strains. Negative control (water) (a), positive control (*S. scabiei*) (b), pathogenic *Streptomyces* strain (d, c)

Results of Experimental Study

Before training the models, the process of determining optimal hyperparameters was conducted. This step involves carefully tuning parameters critical for each model's performance. Various hyperparameters, such as learning rate and batch size, were systematically tested to identify the combinations that maximize model accuracy. Initially, all hyperparameters were fixed except for the learning rate. The models were trained with different learning rates, and it was found that a learning rate of 0.00001 minimized the model loss while achieving high accuracy. This result highlights the significant impact of the learning rate on overall model performance. Next, with the learning rate fixed at this optimal value, the effect of batch size on model performance was evaluated. Through this process, a batch size of 8 was determined to be optimal, and subsequent training continued

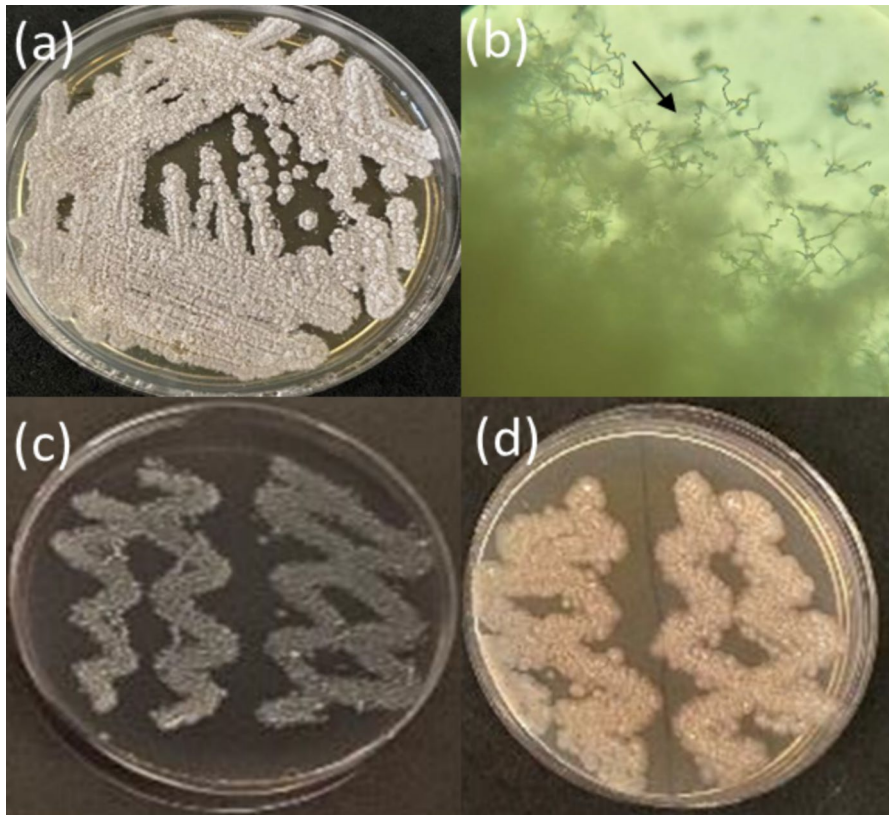


Fig. 7 The observed morphological features of the pathogenic *Streptomyces* strains included gray spores (a), spiral spore chain morphology under a light microscope (b), melanin production on PYI and TYR agar (c), and growth of the strains at pH 5 (d)

using this setting. Several popular optimization algorithms were also compared based on accuracy, loss, and training time. Among these, the Adam optimizer yielded the highest accuracy and was selected as the most suitable optimization function for this study. Briefly, optimal hyperparameters for model training were determined through systematic tuning. A learning rate of 0.00001 and a batch size of 8 minimized loss and maximized accuracy. Among the tested optimizers, Adam yielded the best performance and was selected for model training.

NIR Dataset Results

At this stage, models were trained using the NIR dataset with the previously determined optimal hyperparameters, and their classification performance was evaluated. The classification results are summarized in Table 3. As shown in Table 3, all models achieved high training accuracy above 99%, but their

Table 3 Classification performance of models trained with NIR dataset using optimum parameters

Model	Training accuracy	Training loss	Validation accuracy	Validation loss	Test accuracy	Test loss	Number of epochs	Training time
MobileNetV3	0.998	0.011	0.917	0.381	0.905	0.415	100	0:24:27
InceptionV3	0.997	0.007	0.868	0.691	0.881	0.492	100	0:46:12
Xception	0.999	0.004	0.845	0.513	0.819	0.780	100	0:42:43
VGG19	1.000	0.001	0.893	0.752	0.890	0.900	100	0:40:16
DenseNet121	0.992	0.021	0.908	0.411	0.852	0.656	100	0:50:03
ResNet101	0.994	0.025	0.888	0.649	0.862	0.734	100	1:00:41

performance on the validation and test datasets was comparatively lower. In terms of test accuracy, the Xception model showed the lowest performance with 81.9%. The MobileNetV3 model demonstrated the best performance on this dataset, achieving 90.5% test accuracy and a loss of 0.415. Furthermore, the MobileNetV3 model's training time was 24 min and 27 s, making it the most optimal model by balancing high accuracy, low loss, and relatively short training time.

Evaluating the learning curves (Fig. 8) provides further insights into model behavior. The MobileNetV3 model exhibited rapid improvements in training accuracy, stabilizing near 100%, while validation accuracy plateaued around 90%. The gap between stable validation loss and lower training loss suggests potential overfitting. Loss curves support this observation. Conversely, validation loss curves for all

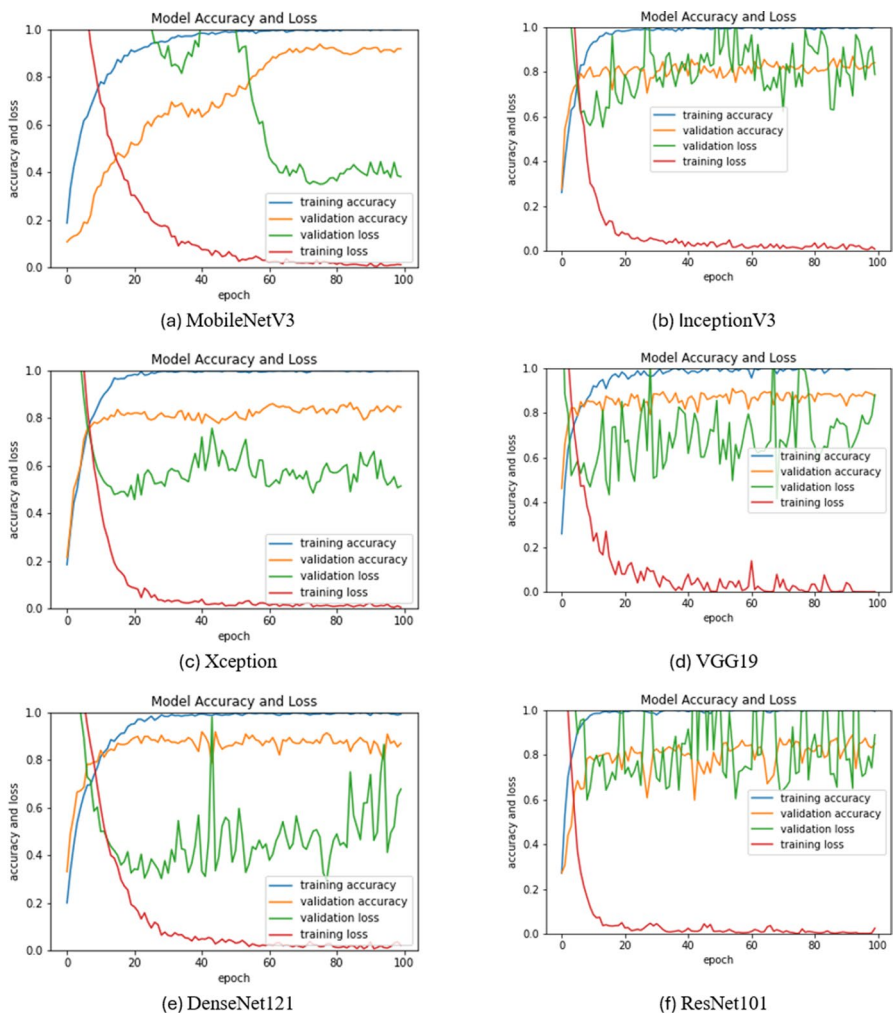


Fig. 8 Learning curves of models trained with NIR dataset

other models, except MobileNetV3, showed significant fluctuations, indicating difficulties in generalizing to the validation set. This suggests that the NIR dataset size may be insufficient for effectively training more complex models.

To address this limitation and improve generalization, additional techniques such as data augmentation or dataset restructuring are necessary. Since the primary goal of this study is to detect infected potatoes rather than differentiate between varieties, a new dataset was created by merging all healthy potato images into one class and all diseased images into another, regardless of variety. This approach provided a more suitable dataset for training and enhanced model performance.

Briefly, models trained on the NIR dataset achieved high training accuracy (> 99%), but validation and test performance were lower. MobileNetV3 outperformed other models with 90.5% test accuracy, low loss (0.415), and the shortest training time (24 min 27 s), while Xception performed worst at 81.9% test accuracy. Learning curves suggested some overfitting, likely due to limited dataset size, highlighting the need for data augmentation or class merging.

RGB Dataset Results

In this stage, models were trained using the RGB dataset with the optimal hyperparameters, and their classification performance was evaluated. The results are presented in Table 4. As shown in Table 4, all models achieved high training accuracy with low training loss, though their performance on the validation and test datasets was comparatively lower. However, the models trained on the RGB dataset performed better than those trained on the NIR dataset, and notable differences among the models were observed. While MobileNetV3 achieved the highest test accuracy of 90.5% on the NIR dataset, the VGG19 model achieved the best test accuracy of 95.7% on the RGB dataset. This was followed by InceptionV3 and DenseNet121, both attaining 93.8% test accuracy.

The superior performance of models trained on the RGB dataset can be attributed to the richer information content in RGB images, which contain three color channels (Red, Green, and Blue), compared to the single-channel NIR images. This increase in data complexity allowed the more sophisticated models to be trained more effectively.

Examining the learning curves (Fig. 9) further highlights the models' behavior. All models quickly reached training accuracy close to 100% and maintained stability. Validation accuracy was also high but remained somewhat lower than training accuracy. However, the validation loss curves for all models exhibited significant fluctuations, indicating difficulty in generalizing to the validation data. This suggests that the dataset size for RGB images is still insufficient for adequately training these complex models.

To address this, instead of duplicating the RGB data, a separate dataset was created by grouping all healthy potato images into one class and all diseased images into another, regardless of variety. This restructuring provided a more balanced and effective dataset for training. Briefly, models trained on RGB images generally outperformed NIR-based models. VGG19 achieved the highest test

Table 4 Classification performance of models trained with RGB dataset using optimum parameters

Model	Training accuracy	Training loss	Validation accuracy	Validation Loss	Test accuracy	Test loss	Number of epochs	Training time
MobileNetV3	0.994	0.016	0.927	0.228	0.914	0.398	100	0:24:24
InceptionV3	0.996	0.017	0.927	0.335	0.938	0.247	100	0:47:27
Xception	0.997	0.008	0.917	0.344	0.886	0.368	100	0:55:01
VGG19	0.985	0.062	0.961	0.148	0.957	0.177	100	0:40:19
DenseNet121	0.993	0.007	0.937	0.275	0.938	0.319	100	0:49:39
ResNet101	0.999	0.005	0.927	0.309	0.919	0.242	100	1:01:16

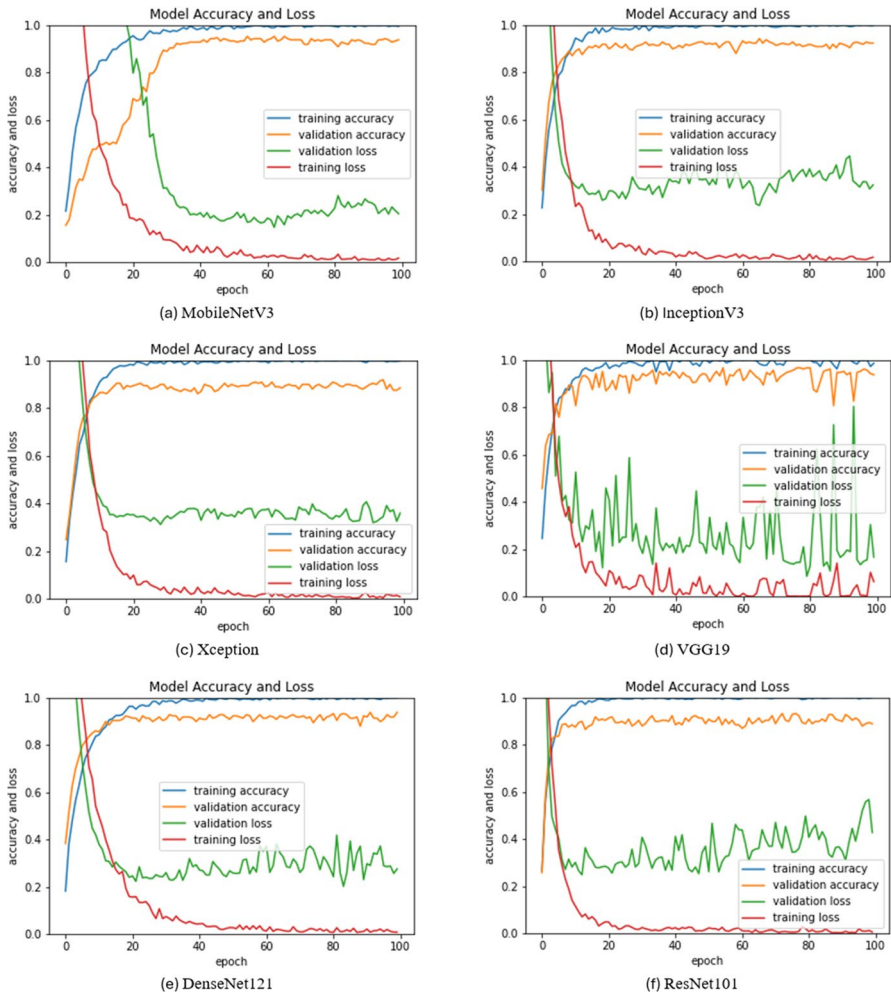


Fig. 9 Learning curves of models trained with RGB dataset

accuracy at 95.7%, followed by InceptionV3 and DenseNet121 (93.8%). The richer color information in RGB images enabled more effective learning, though the fluctuation validation loss indicated room for improved generalization.

Merged NIR Dataset Results

In this step, the models' performances were compared using the tuber dataset acquired with the NIR camera, without distinguishing among potato varieties. The results are presented in Table 5.

According to Table 5, the MobileNetV3 model emerged as the fastest, offering a strong balance of high accuracy and short training time. Both InceptionV3 and

Table 5 Classification performance of models trained with the merged NIR dataset

Model	Training accuracy	Training loss	Validation accuracy	Validation loss	Test accuracy	Test loss	Number of epochs	Training time
MobileNetV3	1.000	0.001	0.985	0.042	0.981	0.051	100	0:24:13
InceptionV3	1.000	0.003	0.990	0.023	0.990	0.026	100	0:46:14
Xception	0.998	0.006	0.976	0.050	0.976	0.037	100	0:42:39
VGG19	1.000	0.001	1.000	0.002	0.990	0.027	100	0:40:16
DenseNet121	0.990	0.037	0.971	0.071	0.966	0.138	100	0:50:34
ResNet101	1.000	0.001	0.990	0.040	0.976	0.061	100	1:01:58

VGG19 achieved the highest test accuracy of 99%, but their training times exceeded 40 min. Xception and ResNet101 also performed well, with test accuracies of 97.6%, while DenseNet121 reached 96.6%. However, the latter three models required longer training times, also exceeding 40 min.

Examining the learning curves in Fig. 10 reveals that all models except VGG19 achieved near 100% accuracy on both training and validation sets. Notably, the VGG19 model's validation accuracy showed a rapid decline after 60 epochs, as seen in Fig. 10(d), with a corresponding erratic pattern in the loss curves—clear indicators of overfitting. In contrast, MobileNetV3 and Xception demonstrated consistent

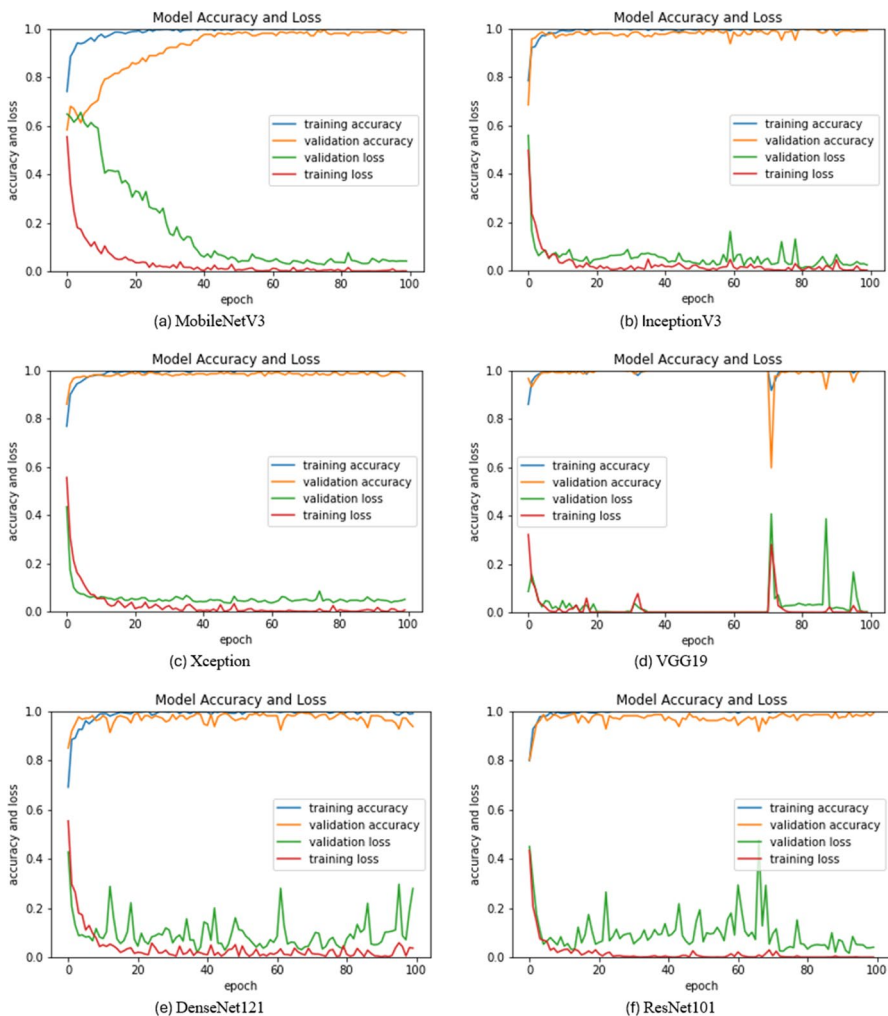


Fig. 10 Learning curves of models trained with NIR merged dataset

trends in both training and validation loss curves, while the remaining models' loss curves showed significant fluctuations.

The confusion matrices in Fig. 11 were analyzed to further assess classification performance. InceptionV3 and VGG19 misclassified only 2 samples each. DenseNet121 achieved perfect detection of scab-infected potatoes, with no false negatives, while MobileNetV3, Xception, and VGG19 each missed only 1 sample. Considering all results, MobileNetV3 was determined to be the optimal model, combining consistent learning behavior, high classification accuracy, and the shortest training time among the models trained on the merged NIR dataset.

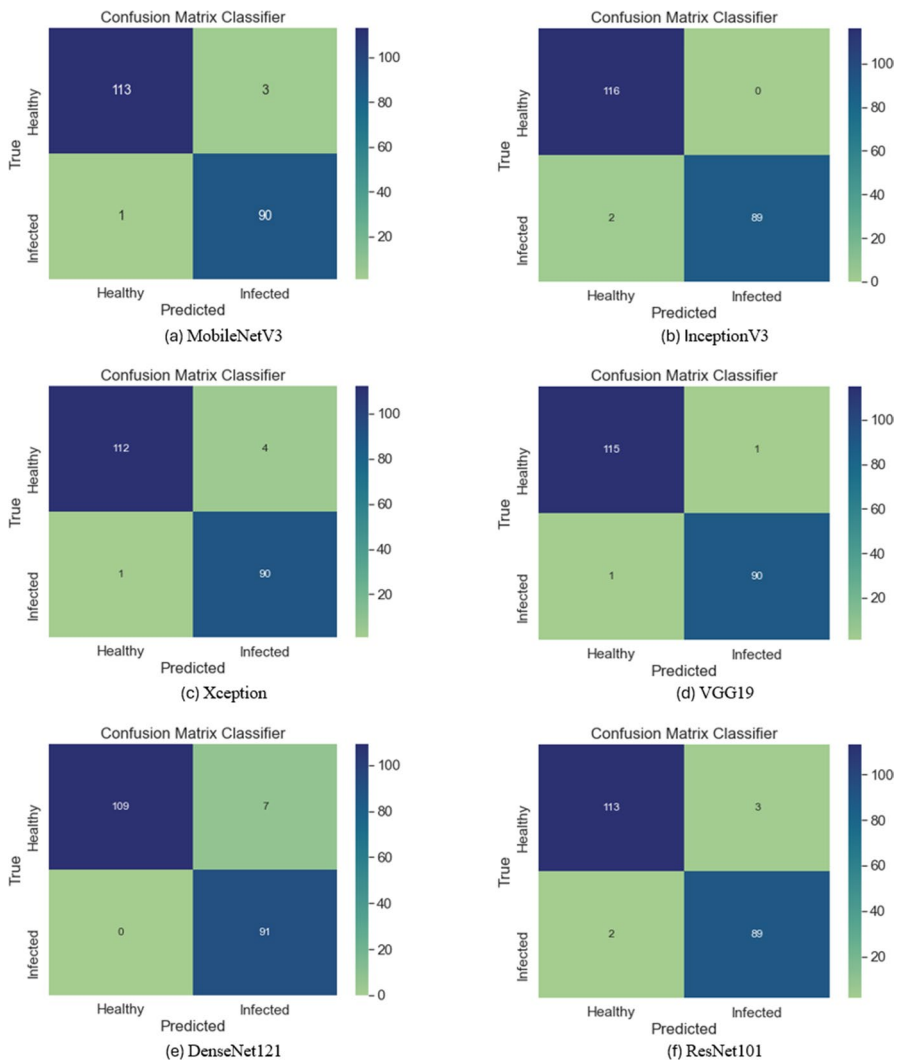


Fig. 11 Confusion matrices of models trained on NIR merged data

Briefly, when healthy and infected tubers were merged across varieties, MobileNetV3 again provided the best balance of accuracy and efficiency, while InceptionV3 and VGG19 achieved 99% test accuracy with longer training times (> 40 min). Confusion matrices confirmed minimal misclassifications, indicating robust performance for merged-class datasets.

Merged RGB Dataset Results

In this step, the models' performances were compared using the tuber dataset acquired with the RGB camera, without distinguishing between varieties. The results are presented in Table 6.

According to Table 6, all models except InceptionV3 and Xception achieved classification accuracies of 99% or higher, with test loss values below 0.046. Although InceptionV3 demonstrated good performance with a test accuracy of 98.1% and Xception achieved 96.1%, these results were lower compared to the other models.

Examining the learning curves shown in Fig. 12, nearly 100% accuracy was attained for both training and validation sets across all models except VGG19. Notably, the VGG19 model exhibited a sharp decline in validation accuracy after 60 epochs, as illustrated in Fig. 12d. Consistent trends in training and validation loss curves were observed for all models except VGG19, which displayed erratic loss patterns throughout training, indicating overfitting.

The confusion matrices in Fig. 13 were analyzed to further assess classification performance. All models, except InceptionV3 (Fig. 13b), achieved 100% accuracy in detecting scab-infected potatoes. It is worth noting that Xception (Fig. 13c) misclassified 8 healthy potatoes as scab-infected.

Overall, ResNet101 demonstrated consistent learning behavior and the highest classification accuracy among models trained with the combined RGB dataset. However, due to its training time exceeding one hour, MobileNetV3 was identified as the optimal choice, balancing accuracy and efficiency.

Comparing the training results from both NIR and RGB datasets, the RGB data consistently yielded superior performance. Consequently, it was concluded that the more economical RGB camera can effectively replace the costlier NIR camera for scab disease detection in potatoes.

Briefly, for merged RGB data, ResNet101 achieved the highest classification accuracy (99.5%), while MobileNetV3 offered a practical balance of speed and reliability. Models trained on RGB data consistently outperformed those trained on NIR data, suggesting that RGB imaging is sufficient for accurate PCS detection in industrial applications.

Traditional diagnosis of plant diseases relies heavily on expert examination, which is time-consuming and prone to human error and inexperience. To overcome these challenges, developing automated, highly accurate methods for tuber disease detection is crucial. Timely and precise diagnosis is essential for maintaining crop yields, minimizing environmental impact, and optimizing agricultural management.

Deep learning has significantly advanced plant classification by enhancing the accuracy and efficiency of visual analysis. In this study, a systematic data collection approach was employed, recording potato varieties and field locations, with careful

Table 6 Classification performance of models trained with the merged RGB dataset

Model	Training accuracy	Training loss	Validation accuracy	Validation loss	Test accuracy	Test loss	Number of epochs	Training time
MobileNetV3	1.000	0.001	0.990	0.066	0.990	0.046	100	0:24:31
InceptionV3	1.000	0.001	0.995	0.019	0.981	0.045	100	0:46:45
Xception	0.999	0.005	0.981	0.035	0.961	0.128	100	0:43:28
VGG19	1.000	0.001	0.995	0.017	0.990	0.039	100	0:40:15
DenseNet121	1.000	0.002	0.990	0.062	0.990	0.025	100	0:50:39
ResNet101	1.000	0.001	0.995	0.090	0.995	0.019	100	1:02:11

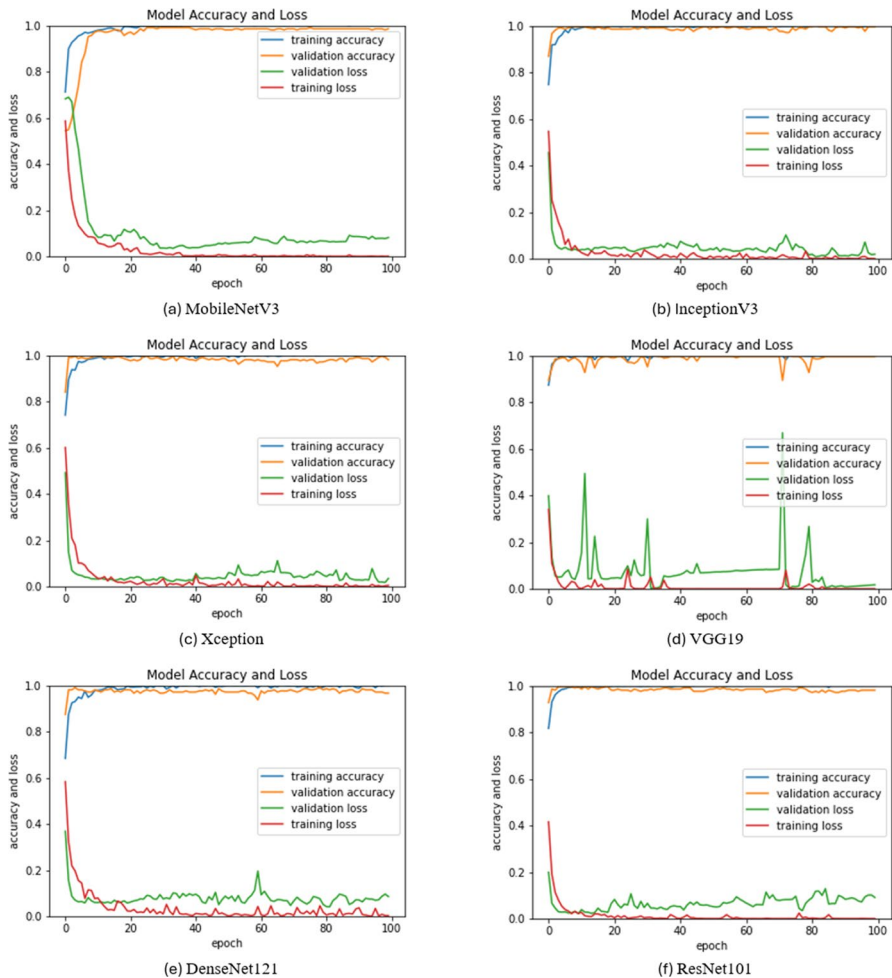


Fig. 12 Learning curves of models trained with merged RGB dataset

labeling of each sample. Imaging was performed using both RGB and NIR cameras within a custom-designed imaging cabinet, simulating conditions suitable for industrial potato sorting systems. Four potato varieties—Provento, Othello, Madeleine, and Bettina—were sampled, with 100 healthy and infected tubers collected per variety, totaling 800 samples and 1421 images.

After data cleaning, 1374 high-quality images were divided into training, validation, and test sets at ratios of 70%, 15%, and 15%, respectively. Four datasets were created: NIR, RGB, merged NIR, and merged RGB. Model performance varied across datasets: In the NIR dataset, Xception had the lowest test accuracy (81.9%), while MobileNetV3 achieved the best balance of 90.5% test accuracy, low loss (0.415), and short training time (24 min 27 s). For the RGB dataset, VGG19 achieved the highest accuracy at 95.7%. Within the merged NIR dataset,

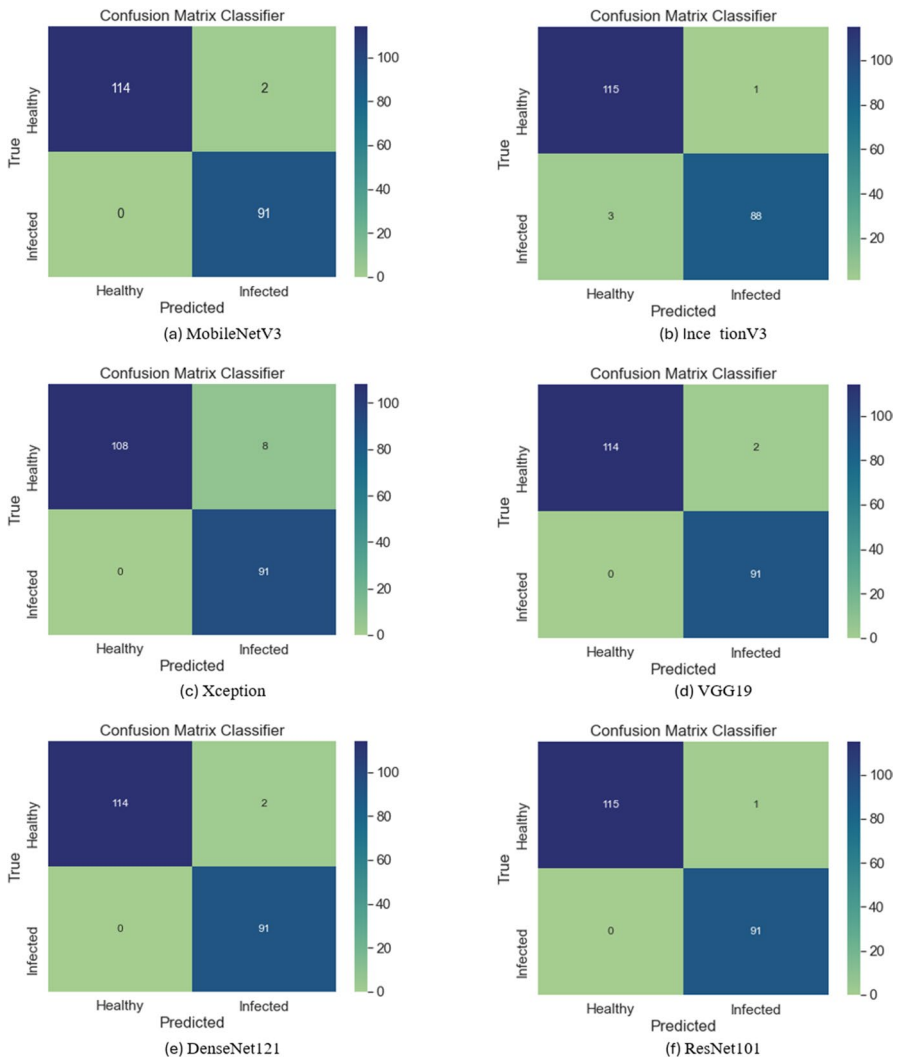


Fig. 13 Confusion matrices of models trained on merged RGB data

MobileNetV3 was the fastest model with strong accuracy, whereas InceptionV3 and VGG19 attained the highest test accuracy of 99%, albeit with training times exceeding 40 min. In the merged RGB dataset, ResNet101 yielded the best test accuracy of 99.5%, while Xception showed the lowest at 96.1%.

This qualitative analysis accompanied the quantitative assessment of correctly and incorrectly classified potato tuber images through visual inspection of representative examples. Figure 14a shows RGB and Fig. 14b shows NIR images from the test set that have true positives (infected tubers accurately identified), true negatives (healthy tubers accurately classified), false positives (healthy tubers inaccurately

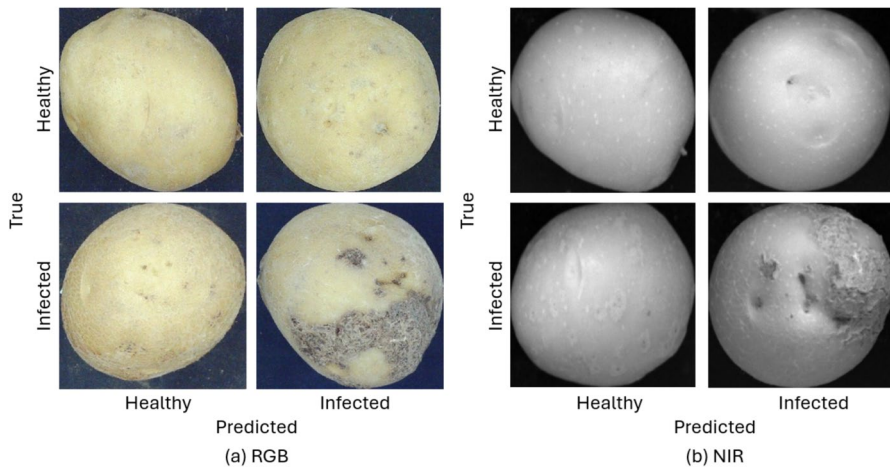


Fig. 14 Samples **a** RGB and **b** NIR images from the test set

classified as infected), and false negatives (infected tubers inaccurately classified as healthy). The clearly defined lesions and irregularities of surface texture associated with potato common scab serve as a strong visual pattern for correctly classified potato tuber samples. On the other hand, misclassified potato tuber samples often correspond to cases where tubers show borderline symptoms of scab or where there is no significant evidence of scab beyond the tuber surface characteristics. This analysis illustrates the difficulties of visually distinguishing among diseases and helps identify the sources of residual classification error in the confusion matrices.

Overall, the results suggest that RGB imaging, combined with efficient CNN architectures like MobileNetV3, provides a cost-effective and reliable approach for automated potato scab detection, offering a promising alternative to more expensive NIR systems.

Inference times were measured for each of the CNN models to determine if they could be realistically deployed within industry potato grading systems (Table 7). Average inference times (ms) are given to calculate the potential for real-time operation within the model. The lower the inference time, the faster predictions can be made on the labelled data. The study found that models that used the lightweight MobileNetV3 model enabled much lower inference times while maintaining high rates of classification accuracy. Therefore, they are well-suited for applications with high throughputs (industrially). On the other hand, heavier models such as the VGG19 had longer inference times, which could hinder their ability to operate in time-sensitive applications despite being marginally more accurate than their speedier counterparts. Hence, the aforementioned comparisons between the classification ability/performance of the models as well as their computational efficiency demonstrate that the overall system could be practically integrated into real-world potato sorting systems.

Table 7 Comparison of inference time performance of the models

Dataset	Model	Test duration (ms)	Number of samples	Inference time (ms)
Merged NIR	MobileNetV3	1,489.79	207	7.20
	InceptionV3	4,730.15	207	22.85
	Xception	2,672.95	207	12.91
	VGG19	11,211.62	207	54.17
	DenseNet121	3,929.39	207	18.98
	ResNet101	2,629.47	207	12.70
Merged RGB	MobileNetV3	1,493.31	207	7.21
	InceptionV3	4,703.84	207	22.72
	Xception	2,575.70	207	12.44
	VGG19	11,243.51	207	54.32
	DenseNet121	3,922.31	207	18.95
	ResNet101	2,628.27	207	12.70

Conclusion

Automated detection of potato common scab using deep learning provides a rapid, accurate alternative to traditional expert-based diagnosis. A systematic dataset consisting of 800 tubers (1421 images), covering four varieties, was developed using both RGB and NIR imaging modalities under industrially simulated conditions and rigorously validated in a laboratory.

Quantitative comparisons across six CNN architectures demonstrated that model performance varied significantly depending on the imaging modality and dataset structure. Across all models and datasets, MobileNetV3 consistently balanced accuracy (more than 99.0%), efficiency, and training time (24 min). MobileNetV3 also achieved the best performance on NIR images with 90.5% accuracy, while VGG19 performed best on RGB images with 95.7% accuracy.

When healthy and infected tubers were merged across varieties, the performance of all models was improved. When models were trained with the merged NIR dataset, InceptionV3 and VGG19 achieved test accuracies of 99%. When models were trained with the merged RGB dataset, all models produced the best overall results and the best was ResNet101, which achieved a test accuracy of 99.5%. Although ResNet101 delivered the top performance in terms of accuracy, it required substantially longer training (1 h).

These findings demonstrate that RGB imaging combined with optimized CNN architectures provides a cost-effective approach that can effectively replace NIR based system without performance loss. The use of data confirmed in the laboratory enhances model robustness and practical applicability.

Along with the improved models, another notable contribution of this study is the establishment of an RGB–NIR Disease Dataset for Potato Tuber Diseases in Türkiye as the first laboratory-verified resource based on established methodologies and

industry practices for imaging potato tubers, making the developed models usable for subsequent research and commercial applications.

Limitations and Future Studies

While the proposed deep learning models exhibited good performance, several limitations should be acknowledged. First, the dataset size was constrained by the requirement for laboratory verification of potato common scab, which limited the number of available samples. Disease validation provided the models with high-quality labeled data, but larger datasets would further enhance model robustness. Another limitation of the proposed models is that even though validation, monitoring and early stopping were implemented to reduce overfitting, the use of controlled laboratory conditions in capturing images may have resulted in optimistic performance evaluations. The images used to train the models were captured under controlled laboratory lighting conditions, a fixed camera viewing position, and a uniform background. Although these conditions were established to simulate an industrial setting, it is important to note that the proposed models were not evaluated for generalization to images obtained under field conditions with variable illumination and occlusions, as well as variable backgrounds and noise. If these models are to be deployed directly in unstructured environments, such as agricultural settings, additional domain adaptation, peripheral images, and model tuning would be required using images collected from field locations.

Future development of the proposed framework is to develop a stronger and widely applicable model that can effectively address and support all of the various situations encountered when applying a model in the real-world setting. In addition, future database expansions will include images of a greater number of tubers, taken under various lighting environments, a greater number of commercially available varieties of tubers and tubers connected to a much broader climatic range to more accurately represent the various forms of agricultural variability. In addition, the integration of XAI methods, such as Grad-CAM and SHAP into the frameworks will provide a means for visual representation of the predictions made by these models and will, therefore, support greater transparency in the models. That will enhance the understanding of errors made by these models as well as the creation of trust in the use of deep learning technology to develop automated systems for disease detection in agricultural applications.

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Author Contribution CUS and ZÜ designed the research, supervised the project, acquired the funding, and analyzed data; MEA, NU, and KSTK performed the experiments, visualized and analyzed data, and drafted the manuscript. CUS and ZÜ revised the manuscript. All authors read and approved the final manuscript.

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Data Availability The data that support the findings of this study are available from the corresponding author, ZÜ, upon request.

Declarations

Competing interests The authors declare no competing interests.

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