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REVIEW ARTICLE

# A comprehensive review of machine learning and deep learning approaches for fungal classification in plants

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## Abstract

Plant diseases are harmful and common nowadays. These abnormal conditions caused by fungi, bacteria, viruses, nematodes or environmental stress like nutrient deficiencies and drought can damage plant health and reduce productivity. They may cause crop yield losses, threaten food security and adversely impact agricultural economies. This review provides a comprehensive examination of recent machine learning and deep learning technologies in fungal classification for plant disease diagnosis. Instead of focusing on individual models, the survey highlights broader advancement trends across macroscopic field imaging, microscopic analysis, hybrid approaches and attention-enhanced architectures. The analysis reveals that the deep learning algorithms consistently outperform traditional techniques. Particularly when deep learning algorithms are supported by transfer learning and attention mechanisms which improve feature extraction for complex fungal patterns. However, challenges such as limited annotated datasets, high inter-class similarity and variations in environmental imaging conditions continue to hinder model generalisation. Studies addressing these limitations and demonstrating the combination of hybrid models, improved optimisation strategies and domain-specific datasets can significantly enhance classification accuracy. Overall, this review synthesises current progress, identifying persistent gaps and outlining future directions for building more robust, scalable and real-world-ready fungal disease detection systems to support sustainable agricultural management.

**Keywords:** convolutional neural network; deep learning; fungi; image recognition; image classification; machine learning

## Introduction

Fungi, as a remarkably diverse group of organisms, wield significant ecological, agricultural and industrial importance. Their pivotal roles in nutrient cycling, decomposition processes, agricultural productivity, medicinal discoveries and biotechnological innovations accentuate the critical need for precise classification methods. However, traditional classification techniques often encounter challenges stemming from their labour-intensive and subjective nature, thereby impeding accuracy and efficiency. Recent technological advances in deep learning have facilitated the analysis and improved the fungal classification process. This paper explains how the machine learning and deep learning algorithms can be applied for the fungal classification. The steps involved in the process of classification of fungi is as follows: the first step is collection of data and it is obtained from dataset collection from reputed repositories. Following data collection, the data are preprocessed to remove redundant information, cleaning up the dataset and so on. After preprocessing, the data is used to train the model and the accuracy parameters are tested using different algorithms such as convolutional neural networks (CNNs), recurrent neural network (RNN) and long short-term memory (LSTM). These deep learning techniques on fungi classification helps in the field of agriculture, forestry, monitoring biodiversity etc. It can also be used for the identification of poisonous and non-poisonous mushrooms. This review highlights the advantages of the machine learning and deep learning methods over the traditional methods. Furthermore, it also enumerates the pathway in enhancing the fungal research in multidisciplinary domains. Besides discussing the advantages this paper also provides insight into the limitations, challenges and future directions for better enhancement.

## Methodology

### Literature survey

#### Macroscopic field image analysis

These works focus on identification and classification using real-world plant or fungal images captured under natural field conditions.

A classification model was proposed to identify the wild fungi using the ResNet50 architecture showing an enhancement in accuracy to identify the wild fungi (1). The model was trained with a dataset of 13581 images which comprises 27 different types of wild fungi, classified into training and validation datasets for enhanced training of the model to improve accuracy. Spatial pyramid pooling (SPP) was integrated to maximise the image features for better training of the model as the wild fungi images were of different size and varying characteristics. Batch normalisation rectified linear unit (ReLU) module is replaced by EvoNorm-S0 for better performance due to varying batch sizes with different image resolutions. This replacement helps in improving the accuracy. The data preprocessing techniques that were used in this paper are rotation, flipping, contrast adjustments, brightness and after the transformation, mixup augmentation is introduced to enhance the dataset and minimise the overfitting issues. The model is trained on GPU and parameters such as epochs, loss function and learning rate are considered. Adaptive optimisation is performed to modify the learning rate based on the loss incurred during training the model. The proposed model shows an accuracy of 96.54 % as compared with the ResNet50.

The classification of fruit leaf-disease pairs using CNN has been described previously (2). Fruits such as apple, custard apple and guava familiar in Hyderabad and Karnataka regions were focussed. Dataset with 14181 images with 10 different class labels was used for analysis. This dataset were real-time images which was picturised in daylight for better disease identification. Dataset comprised of 3 different colour variations such as colour, black and white, white and gray images. These 3 different colour variations were used for better classification accuracy. AlexNet and SqueezeNet CNN architectures are trained with the above dataset of 3 variants and the parameters such as accuracy is compared for analysis. Analysis reveal that colour images give better accuracy than black and white and gray scale images. This paper emphasises on considering real world images for practical aspects. The major drawback is no pre-processing steps are done for image enhancement. Preprocessing images incurs time delay but adding up this step can improve noise removal and elimination of unwanted background colours.

The banana leaves considered for investigation were affected by leaf spot diseases such as *Cordana* leaf spot, Sigatoka and *Deightoniella* leaf spot (3). The images were captured in real field using Canon EOS 750D and taken from the banana fields in Kerala Agricultural University. The images were pre-processed, cropped and resizing was done in preprocessing which reduced the image size to 128 × 128 pixels. Pre-processing step modifies all the images with uniform sizes and this serves as the input for the CNN models. These datasets were used to train 4 CNN models namely Xception, Inception V3, DenseNet 121, MobileNet V2 and their classification accuracies were evaluated. ImageNet database was used for better training using transfer learning. Hyperparameters such as dropout rate, learning rate, batch size, epochs were optimised for all CNN models. Subsequently, 80 % of the dataset was used for training, 20 % for testing and 20 % for validation. Accuracy was tabulated for the four pretrained models for different stages of evaluation.

A methodology was developed for potato disease classification by earlier research (4). This is achieved by image processing techniques. The dataset consisted of 367 potato images exhibiting various diseases. Pre-processing steps such as bilateral filtering, brightness adjustment, contrast stretching, darkness alteration and contrast limited adaptive histogram equalisation (CLAHE) were applied for the potato dataset. Seven potato images underwent the pre-processing steps. The proposed hybrid model combined MobileNet V2 as a feature extractor with LSTM, gated recurrent unit (GRU) and bidirectional LSTM (BiLSTM) as decoder network. Performance was measured using parameters such as accuracy, F1 score, recall and precision. Optimisers such as Adam, stochastic gradient descent, Adagrad and root mean square propagation (RMSprop) were used for optimisation. Results were presented with the different decoder networks and optimisers. Among the evaluated models, the hybrid MobileNetV2–GRU model with the stochastic gradient descent optimiser achieved the highest test accuracy of 99 %.

Four basic classification methods, namely naïve Bayes, Random Forest, gradient boosting and decision tree, were used for rice leaf disease image classification with the support of the Konstanz Information Miner (KNIME) image filtering mechanism (5). The rice leaf diseases dataset consists of 120 images representing three rice leaf diseases—leaf smut rice disease (LSR), bacterial leaf blight disease (BLB) and brown spot rice disease (BSR). The models are evaluated using the above-mentioned dataset. The dataset is partitioned into 70 % for training and 30 % for testing. The KNIME platform is used for feature extraction with the help of different machine learning algorithms. The proposed models are evaluated using the following evaluation metrics such as precision, recall and accuracy. The above-mentioned metrics were used to classify the rice leaf diseases-based images accurately by using the extracted features. Out of the four-classification model, Random Forest outperforms the other three classifiers with 69.44 % accuracy, good precision and recall values for different disease classes' classification. Gradient boosting and decision tree achieves reasonable results, but naïve bayes hold least accuracy of 36.11 % because of the variations in the rice leaf disease-based features.

The study concentrates on identifying the faults in Okra using the following CNN models such as ResNet101, VGG-19 and ResNet50 (6). The above-mentioned CNN models are created using the following python-based libraries—OpenCV, Keras and TensorFlow. The proposed model is evaluated using the 1913 Okra high resolution images-based dataset. The dataset consists of the following defects such as rotten portions, fungus, healthy samples and blackspots. The dataset is partitioned into 80 % for training and 20 % for testing. Before feeding into the CNN model, the Okra images are pre-processed and scaled properly. The pre-processed images are trained with 10 epochs and classified into different levels of defects. The proposed model is evaluated using the following evaluation metrics such as F1-score, precision, recall and accuracy. Out of the three CNN based architectures, VCG-19 showed the maximum accuracy of 98.63 %. The other two architectures also showed reasonable performance with 92.47 % for ResNet50 and 95.89 % for ResNet101. F1-score, precision and recall are also calculated to evaluate the performance of the proposed models.

In this work, the author concentrates on coffee plant disease classification with the help of gray level co-occurrence matrix (GLCM) features and colour moment by merging the different machine learning methods and some image processing techniques (7). The dataset that is used for training and testing consisted of following type of Arabica coffee leaf images belonging to four categories: Cercospora, rust, healthy and Phoma. In order to maintain the

uniformity in classification and feature extraction, the dataset is pre-processed with scaling of the particular size of 100 × 100 pixels. In both YCrCb (luminance-red chrominance-blue chrominance colour model) and RGB (red, green and blue) images, colour moment features are derived and it is having some of the statistical measures like standard deviation, skewness and mean. In addition to this, GLCM features were calculated on the grayscale images and to extract texture features like dissimilarity, entropy, energy, homogeneity, correlation and contrast. The authors chose the K-nearest neighbour (KNN) for coffee leaf image classification and helps to assign the class labels in the features extracted. In order to increase the classification accuracy, they performed some parameter tuning such as GLCM angle, k-value and colour space. Different configurations were evaluated using colour moment (YCrCb) and maximum accuracy of 83.5 % was achieved using GLCM with k value 10.

In this study, the authors introduced a transfer learning-based method that consisted of 38 deep transfer learning models in order to identify some plant diseases (8). The following three plant disease-based datasets such as cauliflower, Agri-ImageNet and Sunflower were used for training and testing. The datasets consist of many Agri-ImageNet images extracted from ImageNet and some images of cauliflower and sunflower. The above-mentioned datasets are usually used as foundation of deep learning models (both training and testing). Keras is used for training and testing the deep learning models and parameters like early stopping were used to fine-tune the deep transfer learning models. The deep transfer learning models did the early stopping mechanism tuning from 10–16 epochs with the patience value 6. The following evaluation metrics such as F1 score, accuracy, model complexity and a composite metric (N = (F * A) / P) balancing accuracy were used for models' performance evaluation where N is the composite score, F is the F1-score, A is the classification accuracy and P represents model complexity. Out of the 38 models, EfficientNetV2B3 and EfficientNetV2B2 models outperformed the others achieving the maximum accuracy over all three datasets. EfficientNetV2B2 showed the maximum performance in terms of different evaluation metrics such as composite metric, F1 score and accuracy. EfficientNetV2B3 achieves the next best performance and this model is the best alternative model for the previous one.

Different deep learning architectures were accessed for macrofungi image-based classification (9). The authors used 12 deep learning architectures such as EfficientNet, ConvNeXt, MobileNetV2 and DenseNet121 and its adaptations. The above-mentioned architectures are assessed using the following machine learning techniques such as Random Forest and Support Vector Machine (SVM). The above-mentioned dataset consists of six different macrofungi breed-based RGB images. The six species include *Boletus edulis* and *Amanita pantherina*. Out of the 12 models, DenseNet121 achieved the maximum performance of 92 % accuracy and 95 % area under the receiver operating characteristic (ROC) curve (AUC). Even the transformer-based Swin models are not performed well for the macrofungi classification. The authors suggested the CNNs are well-suited for the macrofungi image classification.

The self-supervised vision models utilising ensemble classifiers derived a solution for fungal classification (10). The approach classified poisonous mushroom species with visual features and has achieved accuracy of 78.4 % and a macro F1 score of 0.577. The model has shown improved optimising classifiers with an effective framework for fungi classification rather than the fine tune of backbone models.

The authors proposed a method to improve fungal classification performance by combining vision transformers with data augmentation and weighted sampling approaches using a framework comprising 7000 images representing nearly 2000 fungal species (11). The methodology demonstrated accurate classification with minimum data settings among 74 entries in the Fungi Conference and Labs of the Evaluation Forum (CLEF) 2025 group.

The baseline models have proposed for domain shift classification tasks to improve fungi classification (12). A large-scale dataset of 350000 observations comprising 5000 fungi species including high quality, climate data and DNA verified images has been observed.

The proposed study involved the classification of filamentous fungi species on colony and culture plated morphological images using CNN (13). This framework included taxonomic classification using deep learning with appropriate clinical and environmental settings hence proving promising accuracy over a wide range of fungal genera.

## Microscopic image classification

Deep learning was employed to classify different types of bacteria and fungi using deep neural network models (14). Five DNN models, namely Xception, ResNet-50, Inception-v3, MobileNetV2 and DenseNet201, were selected for training and testing. To enhance the quality before classification, methods such as congo red and modified gram stain were used in this work. Three datasets comprising images of *Candida albicans, Escherichia coli, Pseudomonas aeruginosa* and *Staphylococcus aureus* were used for training of models. These datasets contain different varieties of microorganisms which is quite commonly used in clinical microbiology. Parameters under test include training and testing accuracy for the 3 datasets. The pretrained and non-pretrained ResNet models achieved accuracies of 92 % and 96 % respectively. Previous researchers concentrated on nine different species of *Aspergillus* fungi and the growth of these nine fungal colonies are monitored on potato dextrose agar (PDA) plates (15). These PDA plates were incubated to enhance the growth of fungi. After the incubation process, identification parameters such as morphology, shape, colour size and hyphae are recorded which helps in the characterisation of fungi. A specialised equipment with a Nikon DS-2 digital camera and microscope is used for recording the morphometric data. Several images exhibiting the characteristics of fungi are listed and this forms the dataset. This dataset is used for macroscopic classification. Data set undergoes data augmentation as the dataset samples are minimal. The CNN architecture with ReLU activation function with RMSprop optimiser for optimised performance is used in this work. A dataset comprising 3600 images was used, with 900 images for validation and 45 images for testing. The model achieved an accuracy of 90.06 % during the training phase and 96.43 % during the validation phase after 10 epochs. This work focuses on formation of one raw microscopic image dataset consisting of microscopic images of nine different *Aspergillus* fungal species (16). Once the image dataset created, some pre-processing methods and data augmentation methods were used to maintain the diversity of dataset and to prepare the dataset for training step. The following data augmentation methods such as zoom-in, zoom-out, horizontal flipping, shear, width and height shifting were

used to mimic and augment the dataset. This augmentation step is used to maintain the diversity in dataset and increase the generalisation ability of the model. In the proposed work, the authors have used the CNN architecture with one densely connected neural network layer, one output layer, one input layer and three 2-dimensional convolutional layers. The above-mentioned CNN model is trained using the dataset containing different *Aspergillus* species and the same dataset is used for testing and validation. The model is trained for upto 20 epochs with some other parameter variations such as various activation functions, RMSprop optimiser and different rate of dropouts to increase the robustness of the model. The proposed CNN model learned the weights to perform fungi image prediction and thereby improving classification accuracy of the fungi. The proposed model also facilitated the monitoring of fungal growth for both crops and plants. The proposed CNN model is undergoing some adjustments and re-computations in training to improve the validation and training accuracies. The major problem with the fungi image classification is the quality and variations in the real-time fungi images. The authors acknowledge the utility of the culture media for providing the platform to perform the experiments in the detailed manner.

In a previous study, the authors presented a graph-based neural network model tailored for classifying fungal species directly from microscopic images, bypassing the need for culturing (17). By using morphological graph representations, the model effectively distinguishes between fungal taxa with high accuracy, representing one of the first automated approaches to handle raw microscopic fungi data.

### Hybrid and ensemble methods

A methodology was proposed using the principles of image acquisition, feature extraction and pre-processing (18). This paper has used a dataset of black fungus-related eye photographs as there are no existing datasets which emphasises on collecting dataset to train the model. After data collection, the pre-processing stage involved applying a 2D Gaussian filter to improve the fungal features. This paper uses the support vector machine as primary classifier followed by an adaptive boosting–support vector machine (ADaboost SVM) as a main classifier in the iterative process. The predictive capability is improved by changing the weights of misclassified samples. Parameters such as accuracy, precision, recall and F1 score are compared with the classification models such as SVM, adaptive support vector machine (ASVM), Bagging KNN and proposed ASVM. On comparison, proposed ASVM shows better performance in accuracy, precision and F1 score.

The authors combine the bagging ensemble along with K-nearest neighbour (BKNN) for black fungus disease prediction and classification (19). The black-fungus eye-based images collected from google were used for both training and testing. These images are pre-processed in order to increase the signal clarity and to decrease the noise. The pre-processed images were used to convert the black fungus images to grayscale image using median filter and then it is assigned for extracting the features. Feature extraction was performed to extract the needed information for black-fungus image classification. The KNN algorithm was used for classification. It used the Euclidean distance to identify the similarity between the training images and new query images. Various KNN classifiers are introduced along with the bagging ensemble method and results of all KNN classifiers are combined to calculate the final accuracy. The performance of the proposed model is evaluated using the following metrics such as recall, F1-score and precision. The BKNN achieved the maximum accuracy of 96.4 %. Complete classification reports give complete details about the recall, F1-score and precision values for each class. The final accuracy of BKNN is 96 % and it is showing the essence of using BKNN for black fungus disease prediction.

### Advanced architectures and attention mechanisms

The Danish fungi dataset termed as DF20 was used, fine grained dataset for the classification of fungi (20). The special features of this dataset include low error rate, rich observation metadata, taxonomy based accurate classification. DF20 has 295938 images of 1604 species of fungi with additional species of protozoa and chromista. DF20 has rich metadata with substrate, habitat, geographic location and this metadata provide better data reliability. The CNN and vision transformers (ViT) were used for training and testing the datasets. The ViT shows better accuracy of 80.45 % and F1 score of 0.743 when compared to CNN. Species level observations were carried out based on the species rareness, phenology, geographical distribution etc.

The fungal recognition approach combined the coordinate attention (CA) module with the EfficientNetV2 CNN-based architecture to address the challenges of fine-grained fungal recognition (21). EfficientNetV2 was considered the baseline architecture and the CA module was incorporated into the first layer to aggregate spatial information. When compared to the other attention mechanisms, the aforementioned CA module encrypts spatial information by breaking down the channel attention into two side-by-side one-dimensional features with their width and height directions and helps to acquire previous location details and long-range dependencies concurrently. DF20-mini dataset is used for evaluating the above-mentioned module. The mini dataset consists of the elongated tail distributions and difficult backgrounds. Different augmentation methods, cosine annealing and stochastic gradient descent-based optimiser were used to adjust the learning rate and PyTorch was used for training the model. The proposed CA-based model was compared with the different deep learning and machine learning classifiers such as ViT, ResNet50, MobileNetV2, InceptionV3 and EfficientNet using the same DF20-mini dataset achieved 78.41 % accuracy. The proposed work outperformed the above-mentioned classifiers. For comparison, the key evaluation metrics like accuracy, Floating-point operations (FLOPs), image size and parameters of the models were used.

### Sequential and DNA-based classification

The convolutional neural networks were compared with traditional sequence analysis tools such as basic local alignment search tool (BLAST) and the ribosomal database project (RDP) classifier for classifying fungal internal transcribed spacer (ITS) and rRNA sequences (22). Exemplary performance is given by the CNN model which shows a considerable reduction in classification time from 50–2 secs for each sample. It also shows improvement in processing time.

The Fig. 1 illustrates a systematic pipeline for image classification using CNNs, starting from dataset preparation to final model selection. The process begins with collecting the dataset, specifically the De-fungi dataset, which contains labelled images used for training and evaluation. Then all dataset classes are visualised and balanced to understand the preliminary data analysis. The dataset is divided into training and testing subsets, typically in a ratio 80 : 20. To improve model generalisation and avoid overfitting, augmentation techniques are followed. Multiple deep learning

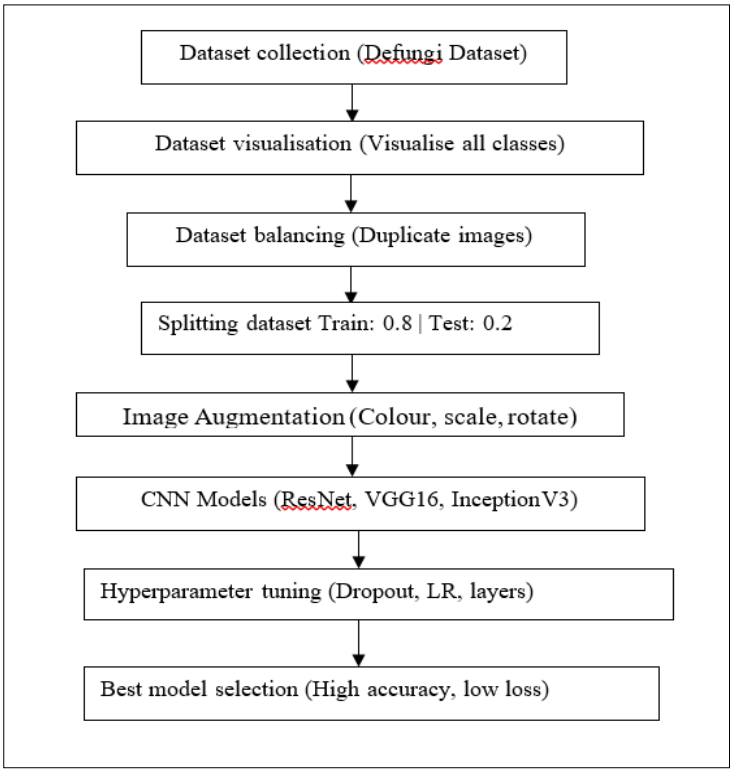



**Fig. 1.** Proposed convolutional neural networks (CNN) workflow for dataset processing, model building and evaluation.

architectures are implemented and compared, including ResNet, VGG16, InceptionV3 and evaluation metrics are analysed.

### Zero-shot and few-shot learning

A vision-language model, contrastive language–image pre-training (CLIP) for zero shot fungal classification has been proposed, comprising the classification of unseen fungal species, through generation of synthetic images and descriptions using large language models (LLMs) (23). The system improves generalisation across growth stages and species do not present in the training set, showcasing the utility of synthetic multimodal data in zero-shot settings.

FungiLT is a dual-channel deep learning model designed for taxonomic classification of fungal ITS sequences (24). The model combines transformer encoders and BiLSTM layers to process over 93000 fungal species with high accuracy. The proposed approach outperformed traditional tools like BLAST and QIIME2, achieving a species-level classification accuracy of 98.77 %, setting a new benchmark in DNA-based fungal taxonomy.

## Results and Discussion

The fungal disease over various plants have been identified and classified using various techniques including artificial intelligence. The diversified study of fungal classification over various plant species using traditional learning algorithms as machine learning and deep learning, has provided various identifications. High accuracy rates using different models have been demonstrated by incorporating many agricultural sectors such as coffee plants, bananas, potatoes, rice and wild fungi. For instance, a proposed learning framework for potato fungal disease has achieved 99 % accuracy with the deep learning model compared to other classifiers. Further for coffee plant disease detection and classification the combination of colour moment and gray level co-occurrence matrix (GLCM) features with the KNN algorithm achieved an accuracy of about 83.5 %. Even many transfer learning frameworks with EfficientNet families have yielded notable performances of about 90 %, in various plant disease detection with enormous datasets. In spite of these advancements there are certain challenges like model sensitivity, parameter choices, diverse disease features handling and typical architectures for agricultural datasets (Table 1).

The performance analysis of various machine learning models is summerised in Table 2, which describes the accuracy, validation accuracy, precision, recall and F1 score in percentage values for various batch sizes.

## Conclusion

The review provides an analysis of various deep learning and traditional machine learning methodologies used in automation and plant disease classification, with the aim of supporting advancements in agricultural management and food security. Several methodologies, including hybrid deep learning architectures integrated with transfer learning, have achieved high accuracy across multiple agricultural applications of fungal disease classification. However, several challenges still remain, such as effective hyperparameter tuning and managing diverse disease characteristics over heterogeneous datasets. Optimised solutions have been proposed by many researchers to address these issues through advanced disease-identification automation systems and improved model performance and enhanced dataset quality. With continued development and streamlined practices, the automation of plant disease detection can be strengthened further to support sustainable agricultural progress. Further research should focus to enhance optimisation and further challenges and applicability for automation of disease identification and classification systems.

**Table 1.** Comparative results based on the key outcome for dataset with models

| Ref | Author | Dataset / Domain | Model / Technique | Key outcome |
|---|---|---|---|---|
| 1 | Jiaxi et al. | 13581 wild fungi images (27 classes) | ResNet50 + SPP + EvoNorm-S0 | 96.54 % accuracy |
| 2 | Zawadzki | Microorganisms (*Candida, E. coli*, etc.) | Xception, ResNet50, InceptionV3, MobileNetV2, DenseNet201 | 92–96 % accuracy |
| 3 | Gaikwad et al. | 14181 fruit leaf images | AlexNet, SqueezeNet CNN | Colour images gave best accuracy |
| 4 | Charan & Ramkumar | Black fungus eye images | SVM + AdaBoost SVM | Improved accuracy, precision, F1 |
| 5 | Billones et al. | 3600 *Aspergillus* colony images | CNN + ReLU + RMSProp | 96.43 % validation accuracy |
| 6 | Mathew et al. | Banana leaf disease dataset | Xception, InceptionV3, DenseNet121, MobileNetV2 | Transfer learning comparison |
| 7 | Picek et al. | DF20 (295938 images, 1604 species) | CNN vs Vision Transformer | 80.45 % accuracy (ViT) |
| 8 | Faria et al. | 367 potato disease images | MobileNetV2 + GRU/LSTM/BiLSTM | 99 % accuracy |
| 9 | CA-EfficientNet study | DF20-mini dataset | EfficientNetV2 + CA | 78.41 % accuracy |
| 10 | CNN Aspergillus study | Microscopic fungi dataset | CNN (3 conv layers) | Improved classification performance |
| 11 | Mekha et al. | 120 rice leaf disease images | Random Forest, NB, DT, GB | 69.44 % accuracy (RF) |
| 12 | Okra disease study | 1913 okra images | VGG19, ResNet50, ResNet101 | 98.63 % accuracy (VGG19) |
| 13 | BKNN study | Black fungus eye images | Bagging + KNN | 96.4 % accuracy |
| 14 | Coffee disease study | Arabica coffee leaf images | KNN + GLCM + Colour Moment | 83.5 % accuracy |
| 15 | Transfer learning study | Cauliflower, Sunflower, AgriImageNet | 38 DL transfer learning models | EfficientNetV2B2 best |
| 16 | Ozsari et al. | Macrofungi RGB images | DenseNet121, EfficientNet, MobileNetV2 | 92 % accuracy (DenseNet121) |
| 17 | Chiu et al. | Poisonous mushroom dataset | Self-supervised vision + ensemble | 78.4 % accuracy |
| 18 | Tam et al. | 7000 fungi images (~2000 species) | Vision Transformer + augmentation | High FungiCLEF performance |
| 19 | Picek et al. | 350k observations, 5000 species | Baseline DL models | Large fungi benchmark |
| 20 | Rani et al. | Synthetic multimodal fungal data | CLIP vision-language model | Zero-shot classification |
| 21 | FungiLT study | 93k fungal ITS sequences | Transformer + BiLSTM | 98.77 % accuracy |
| 22 | Vu et al. | Fungal ITS and rRNA sequences | CNN vs BLAST/RDP | < 2 sec classification time |
| 23 | Graph NN study | Microscopic fungi images | Graph Neural Network | High classification accuracy |
| 24 | CNN culture study | Filamentous fungi colony images | CNN | Promising results |

SPP: spatial pyramid pooling; CNN: convolutional neural network; SVM: support vector machine; ViT: vision transformers; GRU: gated recurrent unit; LSTM: long short-term memory; BiLSTM: bidirectional long short-term memory; CA: coordinate attention; NB: naïve bayes; DT: decision tree; GB: gradient boosting; KNN: K-nearest neighbors; GLCM: gray-level co-occurrence matrix; RGB: Red, Green and Blue; CLIP: contrastive language–image pre-training; ITS: internal transcribed spacer; BLAST: basic local alignment search tool; RDP: ribosomal database project.

**Table 2.** Evaluation metrices of model performances

| Model name | Learning rate | Batch size | Accuracy (%) | Validation accuracy (%) | Precision | Recall | F1-score |
|---|---|---|---|---|---|---|---|
| | 0.0015 | 32 | 91.56 | 87.45 | 0.88 | 0.87 | 0.87 |
| Resnet | 0.0015 | 256 | 98.90 | 87.45 | 0.76 | 0.76 | 0.76 |
| | 0.00015 | 128 | 92.29 | 90.46 | 0.90 | 0.90 | 0.90 |
| | 0.00015 | 32 | 79.00 | 72.39 | 0.83 | 0.84 | 0.83 |
| VGG | 0.0010 | 256 | 89.93 | 84.27 | 0.84 | 0.84 | 0.83 |
| | 0.0001 | 32 | 90.43 | 84.48 | 0.84 | 0.84 | 0.83 |
| | 0.001 | 64 | 58.52 | 59.98 | 0.33 | 0.39 | 0.34 |
| IncV3 | 0.001 | 64 | 65.50 | 64.86 | 0.64 | 0.64 | 0.60 |
| | 0.0015 | 256 | 65.71 | 65.90 | 0.64 | 0.65 | 0.63 |

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## Authors' contributions

PK and JJ were involved in the collection of survey papers and framing the first draft. AN and KN was responsible for drafting and reviewing. KK, KT and MS were responsible for editing, drafting as per the template. MS took charge of including the citations of all the papers included in reference. All authors contributed to providing suggestions for the quality enhancement of the paper. All authors have read and approved the final manuscript.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interest to declare.

**Ethical issues:** None

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