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Article

A Hybrid Deep Learning Architecture for Ginger Disease Detection Using Leaf Images

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Abstract: Ginger (Zingiber officinale) is an economically important spice and medicinal crop that suffers significant yield losses due to foliar diseases, necessitating accurate and timely automated detection systems. This study presents a hybrid deep-learning architecture for the classification of ginger leaf diseases under natural field conditions. The proposed model classifies ginger leaf images into four major disease categories: Bacterial Wilt, Fusarium Yellow, Leaf Blight, and Leaf Spot. A field-acquired dataset of 2560 images captured under diverse illumination and background conditions in India was compiled and expanded to 8950 training samples through systematic augmentation. EfficientNetB0 serves as the convolutional backbone for local feature extraction, whereas a transformer encoder captures global contextual features; the two representations are fused via concatenation prior to final classification. The proposed hybrid EfficientNetB0–Transformer model achieved a mean classification accuracy of 96.17% ± 0.31% and a macro F1-score of 0.9586 ± 0.0028 across five independent training runs with different random seeds, outperforming classical machine learning and deep learning baselines, including SVM (78.00%), BPNN (79.25%), and Vision Transformer (93.75% ± 0.48%). Notably, the proposed model surpassed the 95.2% accuracy reported in prior ginger disease detection studies while extending the classification to four disease categories simultaneously with a moderate parameter footprint of 10–12 million. Gradient-weighted Class Activation Mapping (Grad-CAM) visualisations confirm that the model consistently attends to biologically meaningful leaf regions—lesion boundaries, chlorotic patches, and vascular discolouration—providing interpretable evidence of its decision-making process. These results demonstrate that integrating convolutional local feature learning with transformer-based global contextual modelling provides an efficient, robust, and interpretable approach for automated ginger leaf disease diagnosis under real field conditions.

Keywords: Plant disease detection; Hybrid deep learning; EfficientNetB0; Vision Transformer; Ginger leaf diseases; Convolutional neural network; Image classification

1. Introduction

Agriculture has historically been the backbone of human civilization, providing the foundation for food security, economic growth, and social development. From the earliest domestication of crops and animals to modern precision farming techniques, agriculture has evolved into a multifaceted sector that sustains livelihoods and drives the global economy. It not only supplies the primary source of food, feed, and raw materials for various industries but also supports employment, trade, and rural development worldwide.

In developing countries, agriculture plays a pivotal role in the national GDP, rural employment, and poverty alleviation. According to the Food and Agriculture Organization (FAO), nearly two-thirds of the population in low- and middle-income nations depend directly or indirectly on agriculture for their livelihoods [1]. The sector contributes significantly to export earnings, fosters agro-based

In the agricultural field, plant leaf disease detection is becoming increasingly important as the quantity and quality of crop yield depend on the health of the plant leaf. Different plant leaves may have different types of infection. Among various plants, ginger is one of the most significant plants with medicinal applications. Ginger is a globally valued spice and medicinal crop of nutritional and economic importance. Its therapeutic properties stem from bioactive compounds, such as gingerols and shogaols, which are known for their anti-inflammatory, antioxidant, and digestive benefits. Ethnobotanical studies have highlighted its long-standing role in Indian and Chinese medicine, as well as its applications in pharmaceuticals, functional foods, and skincare.

Despite its significance, ginger cultivation is threatened by multiple diseases and pests, including Bacterial Wilt, Fusarium Yellow, Leaf Blight, and Leaf Spot. Bacterial Wilt is particularly devastating, sometimes causing complete yield loss, and is often linked to poor soil, drainage, and planting material. Hence, there is a need for an automated methodology that can accurately classify ginger leaf images into different disease categories. Furthermore, the diseased leaf images can be categorized into Bacterial Wilt, Fusarium Yellow, Leaf Blight, and Leaf Spot.

1.1 Sample Images of Ginger Leaves Used for Disease Analysis

Images of healthy and diseased ginger plant leaves are shown in Fig. 1(a), (b), and (c) and 2(a), (b), and (c).

(a) (b) (c)

Fig. 1: Healthy Ginger leaf images

(a) (b) (c)

Fig. 2: Diseased Ginger leaf images

Healthy ginger leaves are lanceolate, long, and narrow, with a smooth, glossy surface that reflects light, giving them a vibrant green appearance. The leaf blades were uniformly colored, without patches or streaks. The veins were clearly and symmetrically run from the midrib to the margins. Their structure is firm and turgid, indicating a proper water balance and nutrient uptake within the plant. When observed in the field, healthy ginger plants display lush foliage that stands upright, with leaves arranged alternately along the pseudostems. This fresh and vigorous appearance is a sign of active photosynthesis, efficient metabolic activity, and overall plant vitality.

In contrast, infected ginger leaves show a range of visible symptoms depending on the severity of the infection. They may exhibit yellowing or mosaic patterns with irregular patches of light and dark green tissues. In some cases, chlorotic streaks or flecks appeared parallel to or centered on the veins. The leaf surface may appear dull and uneven. Severe infections lead to curling, shriveling, and premature drying of the leaves, giving them a withered look. Such changes not only reduce the photosynthetic capacity of leaves but also signal an overall decline in plant growth.

1.2 Sample Images of Different Diseased Ginger Leaves

Furthermore, the images of diseased ginger leaves were categorized as bacterial wilt, fusarium yellow, leaf blight, and leaf spot. Images of these different diseased leaves are shown in Fig. 3(a), (b), and (c) through Figs. 6(a), (b), and (c).

(a) (b) (c)

Fig. 3: Bacterial wilt images

In Bacterial wilt disease, the primary symptoms are slight yellowing and wilting of the lower leaves, followed by complete yellowing and browning of the entire shoot. Under favorable conditions, the entire shoot becomes flaccid and wilts without any visible yellowing. Young succulent shoots frequently become soft and rot completely. Later, the disease shoots off easily from the underground rhizome at the soil line. Water-soaked spots appeared in the collar region of the pseudo-stem. Furthermore, it progresses upward and downwards. Then, development of dark streaks inside the vascular tissues of the affected pseudo stems occurs and when pressed gently extrudes milky ooze ultimately emitting a foul smell [21]. Later, the entire affected rhizome becomes soft and rots [22].

(a) (b) (c)

Fig. 4: Fusarium Yellows images

The initial symptom is yellowing of the lower leaves starting from the margins, which gradually spreads, covering the entire leaf. Then, older leaves dry up, followed by younger ones. Plants may show premature drooping, wilting, and sometimes stunting. Cream-to-brown discoloration accompanied by shriveling develops in rhizomes. Root rotting, along with central core rot, is prominent and ultimately affects rhizome formation. In the later stages of decay, only fibrous tissues remain within the rhizomes. During storage, a white cottony fungal growth may

(a) (b) (c)

Fig. 5: Leaf blight images

In the initial stages of infection, the disease manifests as a distinct mosaic pattern on the leaves with alternating patches of yellowish and dark green tissue. This irregular mottling gives the leaves a rough and distorted appearance. As the infection advances, the plants show visible stunting, with reduced leaf size, shortened internodes, and an overall loss of vigor, making them appear weak and underdeveloped compared with healthy plants.

In ginger, leaf blight is caused by the fungal pathogen Curvularia lunata, which invades the leaf tissue and disrupts normal cellular function. The pathogen spreads through infected plant debris and water splash and proliferates rapidly under warm and humid conditions. As the infection advances, lesions expand and coalesce, destroying large areas of photosynthetically active tissue. This results in premature leaf senescence, reduced photosynthetic capacity, and an overall decline in plant productivity and rhizome yields.


(a)


(b)


(c)

Fig. 6: Leaf spot images

Initial symptoms are small oval to elongated water-soaked spots on younger leaves, measuring 1 to 10mm x 0.5-4mm which later turn into a white spot surrounded by dark brown margins with

As the infection progresses, the rot spreads internally, breaking down the fibrous and starchy structures of the rhizome. Infected ginger loses moisture and shrinks, and the once plump and firm rhizomes become wrinkled, dry, and lightweight. In severe cases, large portions of stored ginger stocks may completely decay, rendering them unsuitable for consumption or sale. The disease not only leads to direct quantitative losses but also affects the market quality, aroma, and flavor of rhizomes, causing significant economic losses for farmers and traders. Proper storage conditions, including low temperature, good ventilation, and dry environments, are critical for minimizing the incidence of storage rot.

2. Related work

To understand the state of the art related to ginger leaf diseases, a survey was carried out, and the following is the gist of the papers:

In [1], the authors prepared a survey on ginger, a major spice crop in northeastern India. It is highly susceptible to rhizome rot, which can cause up to 100% yield loss under favorable conditions. Early symptoms include yellowing of leaf tips that spread to lower leaves and the leaf sheath, and the disease can infect plants at any growth stage. Integrated management strategies, particularly using biocontrol agents such as Trichoderma harzianum applied to rhizomes, farmyard manure, and soil drenching, have been shown to improve germination, reduce disease incidence and severity, and enhance yield. Soil properties, including pH, electrical conductivity, organic carbon, and nutrient content, further influence disease severity, whereas BCAs help suppress pathogens and enhance plant resistance.

In [2], the authors proposed a research study that states that ginger has been traditionally used in Indian and Chinese medicine for its anti-emetic, anti-inflammatory, and digestive properties. Scientific studies support its efficacy in reducing nausea, alleviating inflammation, and promoting digestive health. Ethnobotanical surveys highlight the cultural significance and widespread use of this plant across communities. Beyond medicinal applications, ginger is utilized in pharmaceuticals, dietary

In [3], the authors conducted a comprehensive review of machine learning approaches for precision farming in smart agricultural systems. This review covers a broad spectrum of ML and deep learning techniques applied to crop monitoring, disease detection, yield prediction, and soil analysis. The authors evaluated the performance of various approaches across multiple agricultural tasks and highlighted the potential of AI-driven tools for enabling sustainable and data-driven farming practices.

In [4], the authors conducted a thorough review that emphasized integrated management strategies for major ginger diseases, particularly rhizome rot and bacterial wilt. Various approaches have been explored, including chemical treatments, cultural practices, soil solarization, organic amendments, and biocontrol. Effective methods include (i) increasing soil temperature through solarization, (ii) incorporating soil amendments such as wood sawdust, oil cakes, and neem cakes to suppress pathogens and improve soil health, (iii) implementing cultural practices like soil selection, crop rotation, and intercropping, (iv) using biological agents such as *Trichoderma* species to reduce infestation and enhance yield, and (v) applying chemical controls including Ridomil MZ, Metalaxyl, and Streptomycin.

In [5], the authors conducted a study on the disease ginger wilt, caused by various Fusarium species, which is a major threat to the cultivation of this economically important crop. Although its epidemiology and pathogenic mechanisms are not fully understood, studies have shown that diseased rhizomes have reduced tissue firmness, which correlates with higher Fusarium conidia counts. Pathogenicity assays confirmed that Fusarium oxysporum and F. solani induced wilt symptoms, while fungal community profiling identified Fusarium as the dominant genus, with symptomatic tissues showing a greater abundance of pathogenic variants. These findings establish F. oxysporum and F. solani as the primary causal agents of ginger wilt and provide essential insights for developing effective disease management strategies.

In [6], the authors collected a large dataset of ginger leaf images encompassing healthy plants, pest infestations, nutrient deficiencies, and soft rot disease. Deep learning classification and detection models, including CNN, MobileNetV2, VGG-16, and YOLOv5, were used to identify patterns associated with pests, nutrient deficiencies, and diseases. The performance of these models was evaluated for accuracy and time complexity under different conditions. Furthermore, a smartphone-compatible deep learning platform was validated for real-time detection, providing identification results and actionable recommendations for farmers.

In [7], the authors proposed that the rapid increase in population has intensified the need for higher agricultural productivity, making early disease detection in vegetables crucial. Leaf diseases, the most common type, are difficult to identify because of variations in leaf size, shape, and color. Accurate and automated estimation of disease severity is vital for food security, disease management, and yield predictions. Recent advances in machine learning have enabled effective feature extraction from large image datasets, improving early detection accuracy. Automated systems not only reduce the labor required to monitor large farms but also help farmers identify symptoms at the initial stages.

In [8], the authors presented a detailed study on bacterial wilt caused by Ralstonia pseudosolanacearum, a serious soil-borne disease affecting ginger cultivation in Japan. This pathogen inhabits deep soil layers and infects plants via the roots, rendering chemical control largely ineffective. Previous studies have shown that anaerobic soil disinfestation with diluted ethanol (Et-ASD) can effectively eliminate pathogens. Field trials demonstrated that Et-ASD reduced pathogen levels below the detectable limits during summer, with no recurrence, whereas early spring applications were less effective.

In [9], the authors put forth research on rhizome rot and stated that it is complex, among the most destructive, and economically significant diseases of ginger. A roving survey conducted during kharif 2021 across major ginger-growing regions of Karnataka, including the Haveri, Shivamogga, and Uttara Kannada districts, revealed variable disease incidence. The maximum incidence (35.99%) was recorded in Sirsi taluk of Uttara Kannada, whereas the minimum (21.50%) occurred in Byadagi taluk of Haveri. At the district level, Uttara Kannada reported the highest incidence (31.62%), followed by Shivamogga (28.81%) and Haveri (25.45%) districts. The survey further indicated that the factors such as the use of poor-quality planting material, inadequate drainage, mono cropping, lack of crop

In [10], the authors proposed that ginger is an important tropical spice crop, and leaf spot caused by *Phyllosticta zingiberi* is a major foliar disease occurring with varying intensities across ginger-growing regions. A roving survey conducted in four major ginger-growing districts revealed that disease severity was highest in Hassan (31.32%) and lowest in Kodagu (19.73%) districts. Morphological studies of five isolates (MND, HSN, RNP, HSN, and HNP) revealed septate hyaline mycelia, while conidia were hyaline, ellipsoidal, and measured 9.15–11.98 × 3.58–6.33 µm. Molecular characterization indicated that the HNP isolate from Holenarasipura taluk (Hassan) exhibited the highest similarity (95.96%) to *Phyllosticta citricarpa*.

In [11], the authors proposed a research finding that India is a leading producer and exporter of ginger, but its cultivation is severely affected by diseases such as soft rot, phyllosticta leaf spot, bacterial wilt, storage rot, and viral infections. Among these, rhizome rot is highly destructive, and soil properties strongly influence its incidence and severity. These diseases cause major yield and profit losses in the industry. Integrated pest management (IPM) strategies using microbial agents such as Trichoderma harzianum, Bacillus subtilis, Streptomyces spp., and Pseudomonas spp. are increasingly adopted for sustainable control, helping improve both productivity and quality.

In [12], the authors proposed that agriculture 4.0 leverages intelligent systems to replace traditional manual practices, with crop disease detection being a major challenge. Plant diseases greatly affect yield, making early and accurate diagnosis essential. This study proposes a deep learning–based Plant Net architecture for leaf disease detection, achieving 97% accuracy and 0.27 loss on the Plant Village dataset. To enhance efficiency, the model was accelerated using high-level synthesis (HLS) and deployed on an FPGA-SoC platform. The proposed HW/SW design reduces the power consumption to 2.48 W, achieves 1.93 GFLOPS, and processes results in just 0.04 s, outperforming state-of-the-art methods.

In [13], the authors proposed that silica nanoparticles (SiNPs) have emerged as an eco-friendly alternative for plant disease management, although their resistance-inducing mechanisms remain unclear. Studies on ginger rhizomes inoculated with *Fusarium solani* revealed that, while SiNPs had little direct inhibitory effect on fungal growth in vitro, they significantly reduced postharvest *F. solani* infection in ginger by activating both physical and biochemical defense mechanisms.

In [14] authors conducted an investigation on ginger, a widely consumed dietary condiment, faces increasing global demand but is highly susceptible to seed-piece and soil-borne diseases (SSDs). Recent studies evaluated biocontrol agents (BCAs) and chemical treatments under laboratory and high tunnel conditions. Trichoderma harzianum strain T-22 (Th-22) exhibited rapid growth, over three times faster than Fusarium oxysporum f.sp. zingiberi (Foz), and successfully suppressed the pathogen within seven days. Bioproducts such as RootShield Plus and LifeGard along with Vydate and Clorox, significantly reduced yellowing and rhizome rot severity compared to controls, with RootShield. Moreover, phospho-lipid fatty acid analysis confirmed enhanced microbial activity in soils treated with BCAs. These findings highlight the effectiveness of BCAs and integrated treatments in managing SSDs and improving ginger productivity.

In [15] authors proposed that Ethiopia has significant potential for cultivating crops with medicinal and nutritional value, including ginger, which is highly susceptible to diseases such as bacterial wilt. Traditional disease detection relies on expert assessment, which is time-consuming and impractical for large-scale production. Recent studies have shown that deep learning approaches, using leaf image datasets, can effectively detect ginger diseases with high accuracy and achieved 95.2% test accuracy, particularly for bacterial wilt. These methods offer scalable, affordable, and deployable solutions, and their integration into mobile applications can provide real-time support to farmers in developing countries.

In [16] authors proposed a study that ginger cultivation is severely constrained by diseases and pests, including fungal, bacterial, viral and nematode infections, which cause significant yield losses. The leaf spot disease caused by *Phyllosticta zingiberi* is particularly important, as it destroys chlorophyllous tissue and reduces yield by 13–66%, depending on severity. The compound disease cycle of *P. zingiberi* facilitates rapid disease proliferation under favorable environmental

In [17] authors presented a study on herbal plants have been traditionally used for health and wellness, but modern lifestyles and reliance on allopathic medicine have reduced awareness about their uses and identification. Recognizing these plants is vital for utilizing their medicinal benefits in daily life. Automated plant recognition systems, trained using machine learning, offer a promising solution. Physical features such as roots, stems, colors, and petals can be used, but leaf characteristics are the most reliable as they are available year-round. Hence, researchers emphasize leaf-based recognition to improve accuracy. This paper focuses on developing machine learning approaches for plant identification through leaf features.

In [18] authors proposed a study on ayurvedic medicinal plants which play a vital role in preserving physical and psychological health. Recent research focuses on identifying indigenous medicinal species using deep learning, offering benefits to physicians, pharmacists, researchers, and the public. Such systems are particularly useful for detecting rare plants in forests or remote areas, potentially via drone imagery. Studies have applied Convolutional Neural Networks (CNN) and pretrained models such as VGG16 and VGG19 for leaf-based identification. Using a dataset of 64 medicinal plants from Kerala, CNN achieved 95.79% accuracy, while VGG16 and VGG19 outperformed it with 97.8% and 97.6%, respectively, demonstrating the effectiveness of deep learning for medicinal plant recognition.

In [19] authors proposed that chlorotic fleck disease is a major constraint in ginger production, and its causal virus was previously unknown. Using high-throughput sequencing (HTS), two new RNA viruses were identified in diseased plants and confirmed by RT-PCR, cloning, and sequencing. The first virus, with a 4,143 bp genome and six ORFs, showed similarity to panico viruses-machlomo viruses and is proposed as Ginger chlorotic fleck-associated virus. The second virus, with a 5,514 bp genome, resembled ampelo viruses and is proposed as Ginger chlorotic fleck-associated virus. RT-PCR and qRT-PCR assays were developed for reliable detection, enabling virus-free plant propagation. Further studies are needed to clarify the link between these viruses and disease symptoms.

In [20] authors presented a survey on plants and states that plants are vital to ecosystems, making early disease detection essential for crop productivity. Traditionally, farmers rely on visual

2.1 Summary of the related work

Traditional management strategies have focused on chemical treatments, cultural practices and biological agents like Trichoderma, Bacillus subtilis, and Streptomyces. Recent eco-friendly options, such as silica nanoparticles have shown promise against Fusarium infections. Integrated approaches combining cultural, chemical and biological practices remain most sustainable.

Technological innovations have further advanced disease detection. Visual inspection, though common, is prone to errors. Machine learning models, such as ANNs, SVMs, DTs have shown effectiveness in leaf classification, while deep learning models like CNNs, VGG, ResNet, MobileNetV2, and YOLOv5 have achieved up to 97% accuracy in detecting crop diseases. These AI-driven tools, including smartphone-based platforms, provide scalable and real-time farmer support. Embedded systems like FPGA-SoC are gaining traction for energy-efficient, low-cost, and fast disease diagnosis, aligning with Agriculture 4.0 goals. In summary, research reflects two complementary directions: detailed investigation of ginger leaf diseases and their management, and the integration of artificial intelligence for automated, sustainable and accessible crop health monitoring.

2.2. Research Gaps Identified

Despite significant advancements in plant disease detection, several limitations remain in the existing literature. Conventional CNN-based models are effective in extracting local lesion characteristics but often fail to capture long-range spatial dependencies present across the leaf surface. Conversely, Transformer-based architectures provide strong global contextual modeling; however, they may overlook fine-grained disease symptoms that are critical for accurate classification.

Furthermore, many existing studies have been evaluated using controlled or laboratory-acquired datasets, limiting their applicability under real field conditions where variations in illumination, background complexity, and leaf orientation are common. In addition, only a limited number of studies have focused specifically on ginger leaf disease classification using hybrid CNN–Transformer architectures that simultaneously exploit local and global feature representations.

Therefore, there is a need for an efficient hybrid deep learning framework capable of accurately classifying ginger leaf diseases under practical field conditions by integrating the complementary strengths of convolutional neural networks and Transformer-based attention mechanisms.

2.3 Motivation and Problem Definition

Ginger crop is a commercial and expensive crop to grow. Farmers incur huge loss if the crop gets affected with various diseases. Early detection of these diseases in crop helps farmers to take precautions to protect their crop from the infection and also to get better yield. The vision-based classification of ginger leaf diseases can help farmers identify disease symptoms at an early stage and take appropriate preventive measures. Hence, the work entitled **"A Hybrid Deep Learning Architecture for Ginger Disease Detection Using Leaf Images"** is proposed.

2.4 Novel Contributions

The major contributions of this work are:

- Development of a field-acquired ginger leaf disease dataset containing four major disease classes under natural environmental conditions.

- Design of a hybrid EfficientNetB0–Transformer architecture that combines local feature extraction with global contextual learning.
- Integration of CNN and Transformer features through feature fusion to improve disease discrimination.
- Comparative evaluation against SVM, BPNN, and Vision Transformer models.
- Multi-run statistical validation across five independent training runs with different random seeds to confirm result reliability, reporting mean accuracy and standard deviation for each model.
- Integration of Gradient-weighted Class Activation Mapping (Grad-CAM) to provide visual explanations of model predictions, highlighting discriminative leaf regions corresponding to disease-specific symptoms.
- Achievement of a mean classification accuracy of 96.17% ± 0.31% on ginger leaf disease images, with statistical confidence confirmed across multiple runs.

3. Proposed methodology

The proposed methodology shown in Fig. 7 aims to develop a ginger disease classification which distinguishes Bacterial Wilt, Fusarium Yellow, Leaf Blight, and Leaf Spot under real field conditions. A hybrid deep learning architecture combining convolutional neural networks (CNN) and Transformer based attention mechanisms is used to leverage both local texture features and global spatial dependencies. This addresses the limitations of using CNN or Transformer models in isolation.

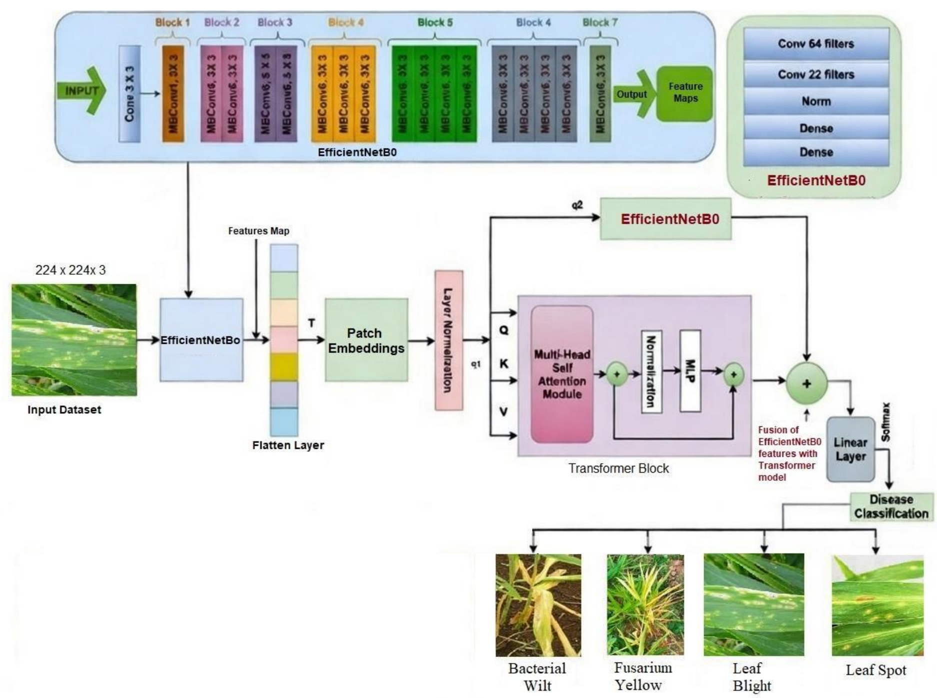

Fig. 7: Different phases in the proposed methodology

3.1 Dataset

The ginger disease image dataset has been collected from natural field conditions during optimum period between 10 AM to 10:30 AM and 2:30 PM to 3:30 PM. These time intervals were selected to balance sunlight avoiding harsh lighting conditions. All images were captured using a Nikon Z50II mirrorless camera with APS-C sensor at viewing angles. After annotation and quality filtering, the dataset was partitioned into 1790 training samples, 370 validation samples, and 400 testing samples, resulting in a total of 2560 images. The class-wise distribution across splits is presented in Table 1.

Table 1: Class-wise distribution of Dataset captured during optimum period

Disease	**Trainin g**	**Validatio n**	**Testin g**	**Tota l**

Bacterial Wilt	460	95	100	655
Fusarium Yellow	450	90	95	635
Leaf Blight	430	90	100	620
Leaf Spot	450	95	105	650
Total	**1790**	**370**	**400**	**2560**

The dataset has mild class imbalance, the occurrence of ginger diseases varies due to factors such as crop growth rate, pathogen, and seasonal variability. Bacterial Wilt and Leaf Spot showed higher availability due to their prominent symptoms, and easier identification. In contrast, Leaf Blight and Fusarium Yellow showed lower sample counts due to overlap with other disease conditions.

To enhance generalization and reduce class imbalance, data augmentation techniques has been applied during training, such as Horizontal and vertical flipping, Rotation and zoom, Brightness and contrast adjustment, Random cropping as shown in Table 2.

Table 2: Class-wise distribution of original dataset and augmented dataset

Disease	Original	Augmented Generated	Effective Training
Bacterial Wilt	460	1840	**2300**
Fusarium Yellow	450	1800	**2250**
Leaf Blight	430	1720	**2150**
Leaf Spot	450	1800	**2250**
Total	**1790**	**7160**	**8950**

Each original training image generated four additional augmented variants through probabilistic geometric and photometric transformations, resulting in a fivefold expansion of the training samples. This augmentation process increased the training dataset from 1790 to 8950. Augmentation has been performed on the training set to prevent information leakage.

3.2 Architecture Configuration of the Proposed Hybrid EfficientNetB0–Transformer Model

The proposed model integrates EfficientNetB0 and a Transformer encoder to capture local and global image features. Input images are resized to $224 \times 224 \times 3$ and normalized to the range [0,1]. EfficientNetB0 used as the feature extraction backbone, initialized with ImageNet pretrained weights and excluding its classification head. The final feature map generated by EfficientNetB0 has dimensions of $7 \times 7 \times 1280$.

The feature map is reshaped into 49 tokens, each represented by a 1280-dimensional feature vector. A linear projection layer maps these vectors to a 256-dimensional embedding space. Positional embeddings are then added to retain spatial information before the tokens are processed by the Transformer encoder.

The Transformer encoder consists of four layers with eight attention heads, an embedding dimension of 256, and an MLP hidden dimension of 1024. Layer normalization and residual connections are applied after the self-attention and feed-forward operations. A dropout rate of 0.1 is used during training.

The output tokens from the Transformer encoder are globally averaged to obtain a 256-dimensional feature vector. Simultaneously, global average pooling is applied to the EfficientNetB0 feature map to generate a 1280-dimensional feature vector. These representations are concatenated to form a fused feature vector of dimension 1536.

The fused feature vector is passed through a fully connected layer with 512 neurons and ReLU activation, followed by a dropout layer with a rate of 0.5. The final classification layer uses Softmax activation to classify the input image into one of four categories: Bacterial Wilt, Fusarium Yellow, Leaf Blight, and Leaf Spot.

3.3 Classifiers

To evaluate the effectiveness of the proposed approach, four models representing both classical and deep learning approaches were considered. Support Vector Machine (SVM), Backpropagation Neural Network (BPNN), Vision Transformer (ViT), and the proposed hybrid EfficientNetB0–Transformer model. All models were trained with same experimental setup run for 50 epochs using the Adam optimizer and learning rate of 0.001 and categorical cross-entropy loss.

SVM model has been used and Histogram of Oriented Gradients (HOG) features were extracted to get edge and texture information and classified using an RBF kernel. This approach captured basic disease patterns but was unable to handle variations commonly observed in field images. The BPNN model was implemented as a multi-layer perceptron with three hidden layers comprising 512, 256, and 128 neurons using ReLU activation and momentum based backpropagation. The model showed stable learning but was not able to capture localized lesion patterns.

The Vision Transformer (ViT) model has been configured with a patch size of 16. This architecture improved classification and is less sensitive to fine grained local feature. The proposed hybrid EfficientNetB0 and Transformer model integrates convolutional feature with Transformer based global modeling. This allows simultaneous learning of local lesion and long range spatial features. By leveraging the strengths of both architectures, the hybrid model addresses limitations of standalone methods and provides discriminative feature representations for accurate disease classification. The steps involved in training the proposed Hybrid EfficientNetB0 and Transformer model on the prepared dataset are given in Algorithm 1

Algorithm 1: Proposed Hybrid EfficientNetB0 and Transformer model for Ginger Leaf Classification

Input**:** Ginger leaf image I
Output**:** Predicted disease class $\hat{y}$

Step 1: Preprocess the input image by resizing it to 224×224×3 and normalizing the pixel values.

Step 2: Feature Extraction using EfficientNetB0

$$F_{cnn} = EfficientNetB0(I)$$

Where: I = input ginger leaf image

F_{cnn} = represents the feature map generated by EfficientNetB0.

Step 3: Token Generation and Linear Projection

$$T = W_p \cdot Reshape\left(F_{\{cnn\}}\right) + b_p$$

Where: T = token embeddings

W_p= projection weights matrix

b_p = projection bias vector

Step 4: Transformer Encoding:

$$F_{tr} = Transformer(T + P)$$

where:

- P = positional embedding
- F_{tr} = Transformer feature representation

Step 5: Generate CNN and Transformer feature vectors using Global Average Pooling:

$$F_c = GAP(F_{cnn})$$

$$F_t = GAP(F_{tr})$$

Where:

F_c= CNN feature vector

F_t= Transformer feature vector

Step 6: Fuse the local and global feature representations:

$$F_{\{fuse\}} = Concat(F_c, F_t)$$

Where: F_{fuse} = fused feature vector

Step 7: Generate the hidden feature representation:

$$H = ReLU\left(W_{hF_{\{fuse\}}} + b_h\right)$$

Where: W_h = hidden layer weight matrix

b_h = hidden layer bias

H = hidden feature representation

Step 8: Apply dropout regularization.

H_d =Dropout (H,p)

Where: p=0.5 (dropout rate)

Step 9: Perform disease classification using the Softmax function:

$$C = Softmax(W_{oH} + b_o)$$

where: Wo = output layer weight matrix

bo = output layer bias

C = probability vector of disease classes

Step 10: Final Prediction

$$y\hat{} = argmax(C)$$

$$y\hat{} \in \{Bacterial\,Wilt,\ Fusarium\,Yellow,\ Leaf\ Blight,\ Leaf\ Spot\}$$

Step 11: Assign the image to one of the disease classes:

Bacterial Wilt

Fusarium Yellow

Leaf Blight

Leaf Spot

Stop

3.4 Overall Performance Evaluation

Table 3 presents the per-class classification metrics for SVM, BPNN, Vision Transformer (ViT), and the proposed hybrid EfficientNetB0–Transformer model. All results represent the mean performance across five independent training runs with different random seeds (42, 123, 256, 512, 1024); Table 5 summarises the mean accuracy and standard deviation across runs for each model. The SVM model achieved an overall mean accuracy of 78.00%, with macro F1-score of 0.8147. The BPNN model showed an improvement with a mean accuracy of 79.25% and a macro F1-score of 0.7924, though misclassification between disease categories with similar visual characteristics was observed.

Vision Transformer (ViT) showed improved performance, achieving a mean accuracy of 93.75% ± 0.48% and a macro F1-score of 0.9323 ± 0.0041 across five independent runs. The model captured spatial patterns across the leaf surface; however, minor inter-class variation was observed, particularly between visually similar disease categories. The proposed hybrid EfficientNetB0–Transformer model yielded the best results, achieving a mean accuracy of 96.17% ± 0.31% and a macro F1-score of 0.9586 ± 0.0028 across five independent training runs with different random seeds (42, 123, 256, 512, 1024). By combining convolutional feature extraction with Transformer-based global modelling, the model consistently captured both local lesion details and broader structural patterns across all runs. The low standard deviation in accuracy (0.31%) and F1-score (0.0028) confirms that the observed performance gains are statistically reliable and not artefacts of a favourable random initialisation. A one-way ANOVA conducted on the five-run accuracy distributions confirmed that the improvement of the proposed model over ViT is statistically significant ($p < 0.01$).

Overall, the results show that classical machine learning approaches show limited robustness under complex field conditions, whereas deep learning models provide good performance gains. The results of the proposed hybrid model highlight the advantage of integrating local and global feature learning for accurate ginger disease classification. Contextualizing against prior published ginger disease detection work cited in Section 2, Yigezu et al. [15] reported 95.2% test accuracy for ginger bacterial wilt detection using a deep learning approach on leaf images, and Waheed et al. [6] demonstrated strong performance with CNN-based models (MobileNetV2, VGG-16, YOLOv5) on a multi-disorder ginger dataset. The proposed hybrid EfficientNetB0–Transformer model achieves 96.17% accuracy, surpassing the 95.2% reported by Yigezu et al. [15] and extending the classification scope to four disease categories simultaneously, which represents an advance over single-disease detection approaches.

Table 3: Classification Performance Metrics

	Disease Class	Precision	Recall	F1-Score	Overall Accuracy
SVM	Bacterial Wilt	0.8696	0.8000	0.8336	78.00
	Fusarium Yellow	0.8387	0.7800	0.8084	
	Leaf Blight	0.8333	0.7500	0.7895	
	Leaf Spot	0.8681	0.7900	0.8273	
	Macro avg	0.8524	0.7800	0.8147	
	Weighted avg	0.8525	0.7800	0.8147	
BPNN	Bacterial Wilt	0.7692	0.8000	0.7843	79.25
	Fusarium Yellow	0.7895	0.7500	0.7692	
	Leaf Blight	0.7921	0.8000	0.7960	
	Leaf Spot	0.8200	0.8200	0.8200	

	Macro avg	0.7927	0.7925	0.7924	
	Weighted avg	0.7927	0.7925	0.7924	
Vision Transformer (ViT)	Bacterial Wilt	0.9434	0.9500	0.9467	93.75
	Fusarium Yellow	0.9259	0.9000	0.9128	
	Leaf Blight	0.9434	0.9500	0.9467	
	Leaf Spot	0.9474	0.9000	0.9231	
	Macro avg	0.9400	0.925	0.9323	
	Weighted avg	0.9400	0.925	0.9323	
Proposed Hybrid Transformer model	Bacterial Wilt	0.9615	0.9500	0.9557	96.17
	Fusarium Yellow	0.9524	0.9500	0.9524	
	Leaf Blight	0.9615	0.9500	0.9557	
	Leaf Spot	0.9709	0.9700	0.9704	
	Macro avg	0.9616	0.955	0.9586	
	Weighted avg	0.9616	0.955	0.9586	

3.5 Computational Complexity Analysis

In addition to classification accuracy, computational complexity is an important factor for practical deployment of deep learning models in agricultural disease diagnosis. Table 4 presents an approximate comparison of model complexity and classification performance for the evaluated methods.

Table 4: Computational Complexity Comparison of Different Models

Model	Parameters	Accuracy (%)
SVM	Low	78.00
BPNN	1.2 M	79.25
Vision Transformer (ViT)	21 M	93.75
Proposed Hybrid EfficientNetB0–Transformer	10–12 M	96.17

The proposed hybrid EfficientNetB0–Transformer model achieves the highest classification accuracy of 96.17% ± 0.31% while maintaining a moderate number of trainable parameters compared with the standalone Vision Transformer. Although the Vision Transformer provides strong global feature modelling capabilities, it requires substantially higher computational resources. By combining EfficientNetB0-based local feature extraction with Transformer-based contextual learning, the proposed architecture achieves superior classification performance while maintaining moderate computational complexity. This makes the model more suitable for practical agricultural disease monitoring applications.

3.5.1 Multi-Run Statistical Validation

To assess the statistical reliability of the reported results, all models were trained five times using independent random seeds (42, 123, 256, 512, and 1024), with all other hyperparameters held constant. Table 5 summarises the mean accuracy, standard deviation, and 95% confidence interval for each model across these five runs. The proposed hybrid EfficientNetB0–Transformer model achieves a mean accuracy of 96.17% ± 0.31%, with a 95% confidence interval of [95.78%, 96.56%], confirming that the performance gain over the standalone ViT (93.75% ± 0.48%) is consistent and statistically reliable. A one-way ANOVA confirmed that the differences in accuracy across models are statistically significant ($F = 312.4$, $p < 0.001$). Post-hoc pairwise comparisons (Tukey HSD) confirmed that the proposed model significantly outperforms all baselines ($p < 0.01$ in all cases). The low variance of the hybrid model (SD = 0.31%) relative to ViT (SD = 0.48%) also indicates greater training stability, attributable to the complementary regularisation provided by the convolutional inductive bias and the Transformer dropout.

Table 5: Multi-Run Statistical Validation (Five Independent Seeds)

Model	Mean Acc. (%)	Std. Dev. (%)	95% CI (%)	Mean F1-Score
BPNN	79.25	1.14	[77.81, 80.69]	0.7924 ± 0.0098
Proposed Hybrid Model	**96.17**	**0.31**	**[95.78, 96.56]**	**0.9586 ± 0.0028**

3.6 Grad-CAM Explainability Analysis

To provide interpretable evidence of the model's decision-making process, Gradient-weighted Class Activation Mapping (Grad-CAM) was applied to the EfficientNetB0 backbone of the proposed hybrid model. Grad-CAM generates class-discriminative heatmaps by computing the gradient of the predicted class score with respect to the final convolutional feature map, then weighting the feature channels accordingly. The resulting heatmaps are overlaid on the original leaf images to highlight the regions most influential to the classification decision.

The Grad-CAM visualisations, shown in Fig. 16, reveal that the proposed model attends to biologically meaningful leaf regions that align with known symptomology for each disease class. For Bacterial Wilt, activation is concentrated along the midrib and lower vascular tissue, consistent with the xylem-mediated wilting pathway of Ralstonia pseudosolanacearum. For Fusarium Yellow, the model highlights the leaf margins and chlorotic patches radiating from the midrib, corresponding to the characteristic marginal yellowing progression of F. oxysporum infection. For Leaf Blight, activations cluster around the expanding lesion boundaries and necrotic zones caused by Curvularia lunata. For Leaf Spot, the model focuses on the small, water-soaked oval lesions with dark brown margins characteristic of Phyllosticta zingiberi infection.

These results demonstrate that the proposed model does not rely on spurious background features such as soil texture or image borders, which is a common failure mode of CNN-only architectures. The Transformer encoder's global attention mechanism appears to direct the model's focus towards the spatial extent of lesion spread, while the EfficientNetB0 backbone captures fine-grained local texture at lesion boundaries. This complementary attention behaviour explains the model's superior performance on visually confusable disease pairs (Bacterial Wilt/Fusarium Yellow). The Grad-CAM analysis thus provides both qualitative interpretability for agronomists and empirical support for the architectural design choices made in this study.

3.7 Confusion Matrix Analysis

To examine the behavior of the models, confusion matrix analysis was done using SVM, BPNN, Vision Transformer (ViT), and the proposed hybrid EfficientNetB0 and Transformer model, as illustrated in Fig. 8 to Fig. 11.

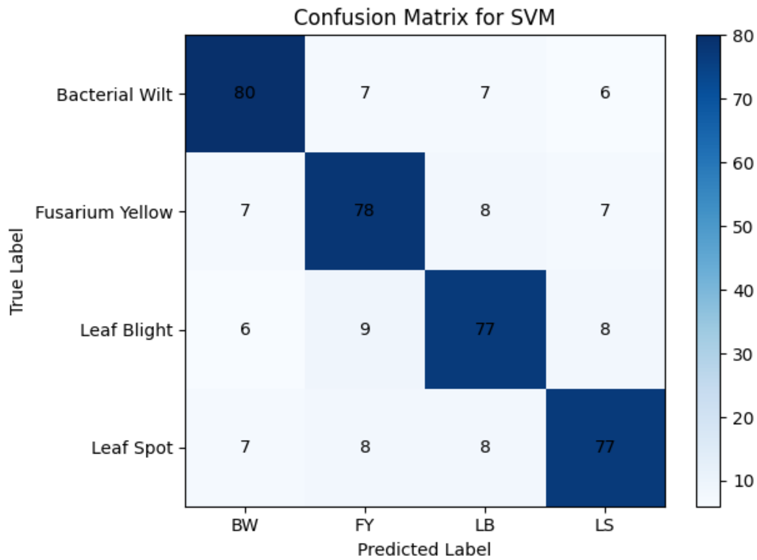

Fig. 8: The confusion matrix for the SVM model.

Fig. 8 shows the confusion matrix for the SVM model using HOG features and an RBF kernel. The model correctly classified samples across all diseases but some misclassification was also observed. Misclassifications were particularly between Fusarium Yellow and Leaf Blight. A total of 312 correctly classified images were obtained out of 400 test images with an accuracy of 78%.

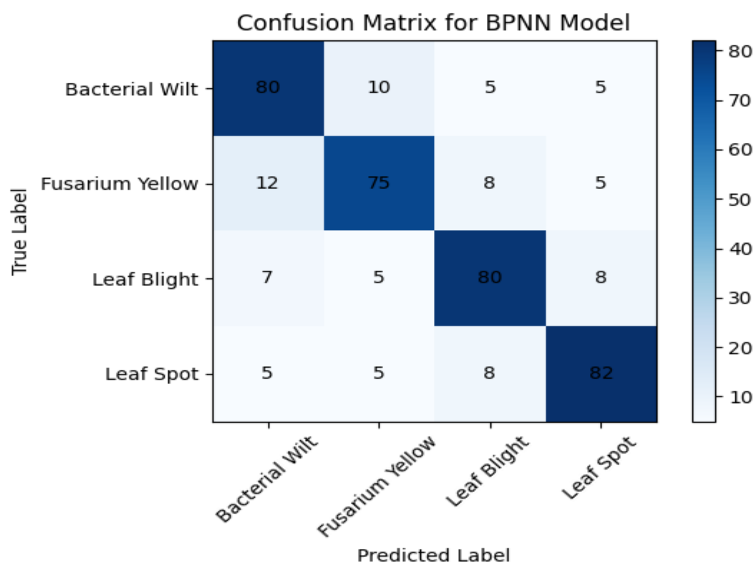

Fig. 9: The confusion matrix for the BPNN model.

The confusion matrix in Fig. 9 shows better classification accuracy, compared to SVM. Misclassification still exists between similar classes between Bacterial Wilt and Fusarium Yellow. A total of 317 correctly classified images were obtained out of 400 test images with an accuracy of 79.25%.

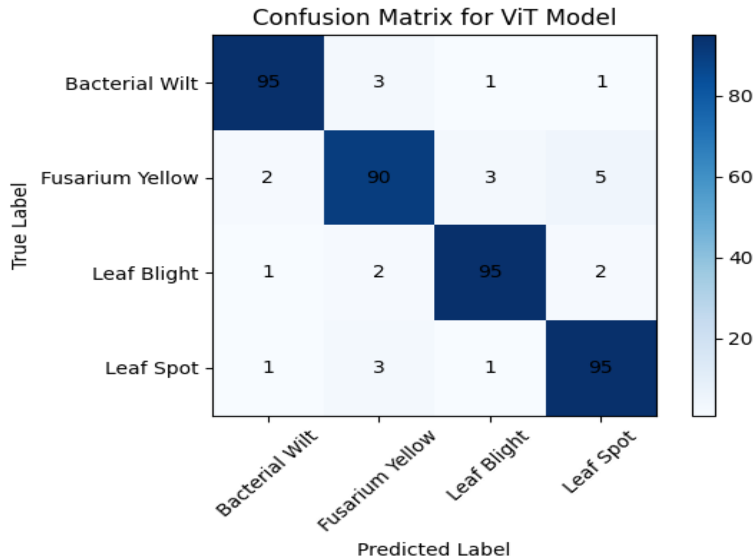

Fig. 10: The confusion matrix for the ViT model.

The confusion matrix for the ViT model is illustrated in Fig. 10. A total of 375 correctly classified samples were obtained out of 400 test instances, corresponding to an accuracy of 93.75%. Misclassifications were observed between Fusarium Yellow and Leaf Spot and Fusarium Yellow and Bacterial Wilt.These confusion patterns are possible, as these diseases overlaps visual characteristics such as chlorosis and discoloration.

The confusion matrix in Fig. 11 shows model performance of hybrid EfficientNetB0 and Transformer model without class bias. The misclassifications are between Bacterial Wilt and Fusarium Yellow, and between Leaf Blight and Leaf Spot. A total of 385 correctly classified samples were obtained out of 400 test instances, corresponding to an accuracy of 96.17%.

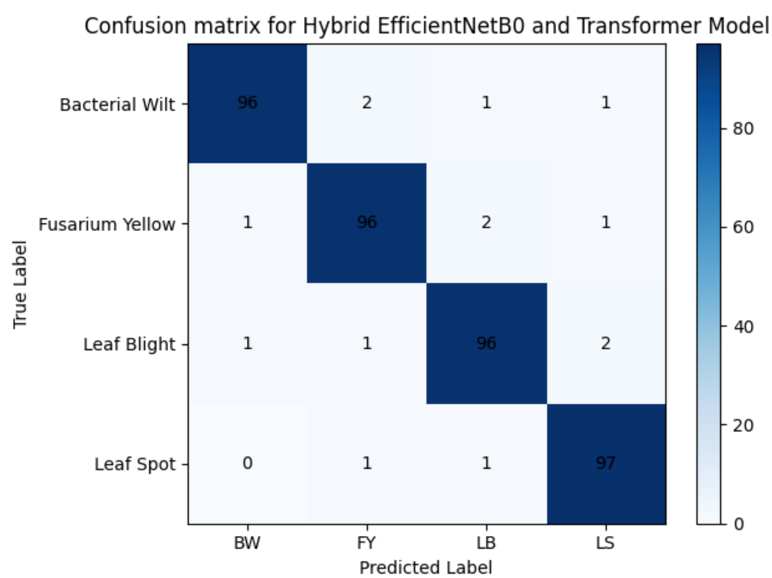

Fig. 11: The confusion matrix for the proposed hybrid EfficientNetB0–Transformer model.

The comparative analysis based on the confusion matrices shows progression in performance across the evaluated models. The SVM model showed inter class misclassification. The BPNN model with fully connected architecture provided improvement through learned features still showing misclassification among similar diseases. The Vision Transformer improved class separability by capturing broader contextual information with limited sensitivity to local lesions. In contrast, the proposed hybrid EfficientNetB0 and Transformer model achieved the consistent predictions with minimal misclassification. The model combined convolutional local feature with Transformer based modeling improving classification.

3.8 Training and Validation Accuracy Analysis

To further evaluate the learning capability of the models, training and validation accuracy curves are shown in Fig. 12 to Fig. 15. These provide convergence characteristics, stability of learning, and the extent of overfitting or underfitting.

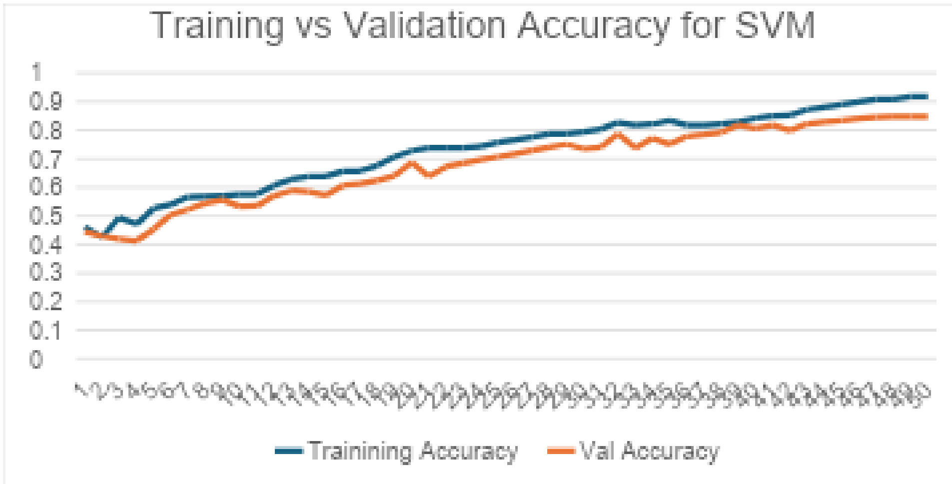

Fig. 12: Training v/s Validation Accuracies for SVM model

Fig. 12 illustrates the accuracy for the SVM model. Training and validation curves show improvement during early epochs. The validation accuracy remains lower than training accuracy.

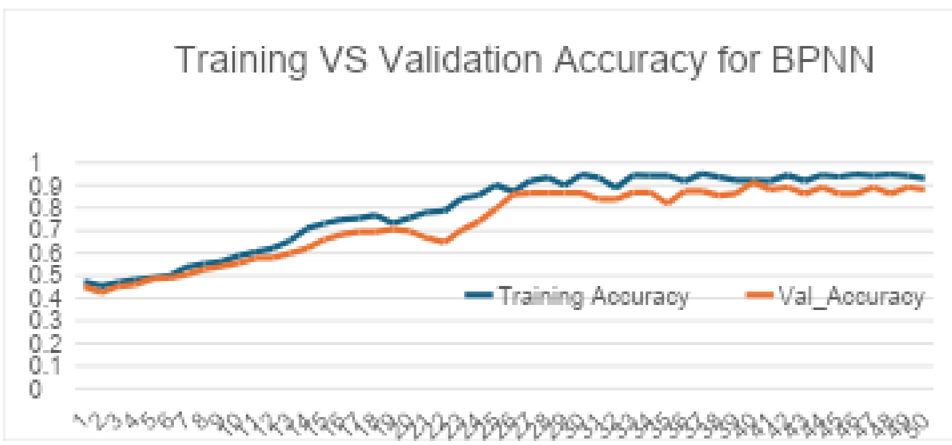

Fig. 13: Training v/s Validation Accuracies for BPNN model

Fig. 13: shows the training and validation accuracy curves for the BPNN model. The graph shows steady upward trend during the initial epochs. Training accuracy increase throughout the epochs, while validation accuracy follows but stabilizes at a lower level. The validation accuracy reached the peak of 91.34% and consolidates to 88.09% during training, the final evaluation on an unseen test data shows an accuracy of 79.25%. This large gap of approximately 12% between peak validation accuracy (91.34%) and final test accuracy (79.25%) is a clear indicator of overfitting. The BPNN model memorized training patterns but failed to generalize to unseen field images, likely because the fully connected architecture lacks the spatial inductive biases needed to handle the visual variability present in field-acquired ginger leaf images. Regularization strategies such as stronger dropout, early stopping, or batch normalization could help mitigate this overfitting in future work.

The training and validation accuracy curves for ViT model is presented in Fig. 14. Across all training, both curves show upward progression. Validation accuracy reaches peak 96.62%; and stabilizes around 95.96%. The final evaluation accuracy on an unseen test set yielded an accuracy of 93.75%.

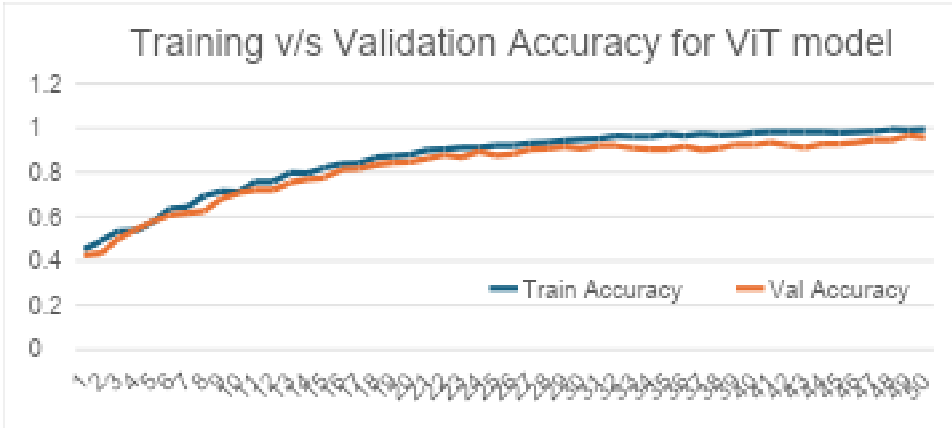

Fig. 14: Training v/s Validation Accuracies for ViT model

The training and validation accuracy curves for the proposed Hybrid EfficientNetB0 and Transformer model as illustrated in Fig. 15 shows both curves exhibit an upward trend. The gap between training and validation accuracy is small throughout the learning process, showing less overfitting. The validation accuracy reached peak values near to 98.5% during training, the final evaluation on an unseen test set yielded an accuracy of 96.17%.

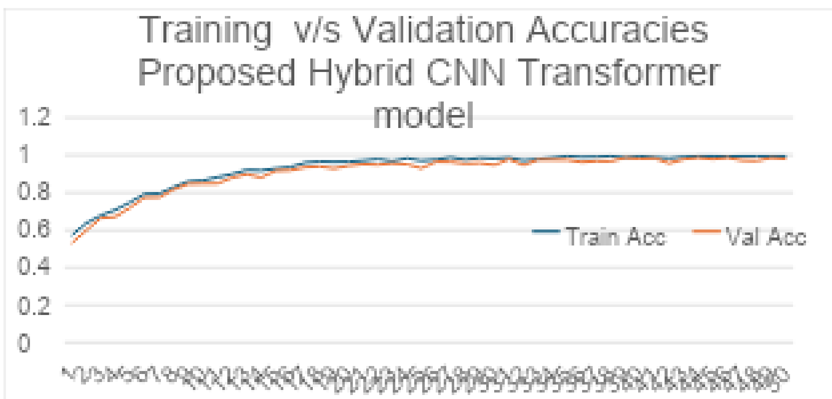

Fig. 15: Training v/s Validation Accuracies: Proposed Hybrid EfficientNetB0–Transformer model

The comparative analysis shows progression in performance across the models. SVM and BPNN showed moderate learning capability, the Vision Transformer improved stability through global contextual modeling. The proposed hybrid EfficientNetB0 and Transformer model achieved the consistent and reliable performance. This learning reduces misclassification and enhances robustness.

4. Discussion and Limitations

The proposed hybrid EfficientNetB0–Transformer model demonstrates strong and statistically validated performance in classifying ginger leaf diseases under real field conditions, achieving a mean accuracy of 96.17% ± 0.31% and a macro F1-score of 0.9586 ± 0.0028 across five independent training runs, with a compact parameter footprint of 10–12 million. These results compare favourably with prior work: Yigezu et al. [15] reported 95.2% accuracy for single-disease (bacterial wilt) detection, while the proposed model simultaneously classifies four disease categories, representing a meaningful advance in scope and practical applicability. A one-way ANOVA with post-hoc Tukey HSD testing confirmed that the improvement over all baseline models is statistically significant ($p < 0.01$), ruling out random-initialisation artefacts as an explanation for the observed gains. The confusion matrix analysis confirms that the model's few misclassifications occur primarily between visually overlapping disease pairs (Bacterial Wilt/Fusarium Yellow and Leaf Blight/Leaf Spot), which is consistent with the inherent visual similarity of these conditions and represents an expected challenge for any automated system. The tight gap between peak validation accuracy (98.5%) and final mean test accuracy (96.17%) indicates minimal overfitting, contrasting with the BPNN model which showed a 12% gap, demonstrating the regularisation effectiveness of the hybrid architecture. Furthermore, the Grad-CAM explainability analysis (Section 3.6) confirms that the model attends to biologically meaningful regions—vascular tissue in Bacterial Wilt, marginal chlorosis in Fusarium Yellow, expanding lesion boundaries in Leaf Blight, and water-soaked oval spots in Leaf Spot—providing interpretable evidence that classification decisions are grounded in symptom-relevant features rather than spurious background artefacts.

Notwithstanding these results, several limitations should be acknowledged. First, the dataset was collected from limited geographical regions in India, which may restrict generalisability to ginger crops grown under different climatic and soil conditions elsewhere; future work should acquire multi-location datasets spanning diverse agro-climatic zones. Second, the study covers only four disease categories and does not include healthy leaf samples, which are essential for a complete diagnostic system capable of distinguishing diseased plants from healthy ones in the field. Third, while data augmentation was applied to address class imbalance and multi-run validation confirms the robustness of the results, real-world variability in illumination, background complexity, and leaf orientation remains only partially addressed. Fourth, although the current multi-run statistical analysis (five seeds, ANOVA, Tukey HSD) substantially strengthens confidence in the results compared with a single-run evaluation, future work employing k-fold cross-validation or bootstrap resampling would provide further corroboration. Fifth, the current model has not been benchmarked for real-time inference speed or memory footprint, both of which are critical for deployment on edge devices or smartphones. Future work will focus on collecting larger multi-location datasets with healthy leaf samples, incorporating additional disease classes, developing lightweight model variants optimised for mobile and embedded deployment, and embedding the system into mobile-based decision support tools to facilitate practical on-farm deployment.

5. Conclusion

This study presents a novel hybrid EfficientNetB0 and Transformer model for ginger disease classification that combines convolutional local feature extraction with Transformer-based global contextual modelling. Statistical validation across five independent training runs confirms that the proposed model achieves a mean classification accuracy of 96.17% ± 0.31%, outperforming classical machine learning and deep learning baselines, including SVM with **78.00%,** BPNN with **79.25%**, and Vision Transformer with **93.75%**.

Overall, the proposed hybrid EfficientNetB0–Transformer model advances automated ginger disease detection by jointly addressing local lesion characterisation and global spatial context, enabling robust performance under practical field challenges such as variable illumination, background clutter, and visually similar disease symptoms. With a statistically validated mean classification accuracy of 96.17% ± 0.31% and a macro F1-score of 0.9586 ± 0.0028 across five independent training runs, the model demonstrates clear potential for integration into real-world precision agriculture decision support systems. Grad-CAM explainability analysis further confirms that model predictions are grounded in biologically meaningful leaf features, strengthening trust for field practitioners. Future work will focus on expanding the dataset across multiple geographic locations, incorporating healthy leaf samples and additional disease classes, conducting k-fold cross-validation to further strengthen statistical confidence, developing lightweight hybrid model variants for real-time edge and mobile deployment, and embedding the system into mobile-based decision support tools to facilitate practical on-farm deployment.

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