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Analyzing ML/DL Techniques for Detection of Yellow Leaf Curling and Mosaic Virus: A Systematic Literature Review

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Abstract: Plants play a critical role in securing global food supplies and maintaining economic stability, serving as the primary source of sustenance for both human and animal populations. Given that a substantial portion of the world's inhabitants relies on agriculture and related sectors, the impact of plant diseases cannot be overstated. Leaf diseases, in particular, pose obstacles that impede the ideal growth of plants. The timely identification of these diseases becomes paramount in order to employ interventions and minimize losses in crop yield and overall plant well-being. Such actions are essential in averting potential ecological disruptions. In the recent years, due to technological advancements machine and deep learning techniques have been increasingly used for the detection and classification of plant diseases. This study focuses on systematic literature review of various machine and deep learning techniques for the detection of Yellow Leaf Curling and Mosaic Virus of the Geminiviridae Family. The article for the review were extracted from IEEE Xplore, SCOPUS and Science Direct between 2019 to 2023. The study focused on parameters such as (1) Objective of the article (2) Data Sources and Preprocessing (3) Feature Selection or Representation (4). Model Architectures (5) Strengths and (6) Limitations. This paper suggests possible solutions of dataset creation and disease detection through hyperspectral imaging (HSI) and generative AI based on their combined capabilities.

Keywords*: yellow leaf curl virus, mosaic virus, machine learning, deep learning, Hyperspectral Imaging, Generative AI*

1. Introduction

The Geminiviridae family comprises plant viruses distinguished by their geminate icosahedral virions housing the viral genome. With a preference for plant hosts, these viruses elicit a spectrum of symptoms, encompassing mild manifestations to severe debilitations [1], [2] Taxonomic classification of Geminiviridae allocates them into four distinct genera, characterized by genomic and biological differentiators: Begomovirus, Mastrevirus, Curtovirus, and Topocuvirus. Significantly, Geminiviridae's pertinence to agriculture surfaces through its involvement in maladies impacting economically vital crops [3] Among these, the begomoviruses, chiefly disseminated by whitefly vectors, hold salience [4], [5]

1.1 **Impact on Agriculture**

Geminiviridae's relevance to agriculture is underscored by its implication in pathogenic conditions affecting crops of economic importance. A paramount subset within the Geminiviridae family is the begomoviruses, renowned for their role in this context. Their transmission via whitefly vectors enhances their prevalence [6]. Begomoviruses exhibit a wide array of pathogenic effects on crops such as peppers, tomatoes, beans, and cotton, typified by leaf curling, stunted growth, mosaic patterns, and yellowing [5]

In the 1979 growing season, a significant leaf spot disease affected cucumber (Cucumis sativus L.) crops cultivated in plastic greenhouses along the coastal area between Koutsouras and Goudouras in the Sitia Area, Lasithi, Crete, Greece. This issue was first documented by Yamashita in 1979. Subsequently, this disease spread to most cucumber-growing regions in Crete, resulting in substantial agricultural losses. In a parallel scenario, the Cucurbit Genetics Cooperative (1989) reported a similar problem in Spain. Starting from 1982, a yellowing disease began to severely impact muskmelon (Cucumis melo L.) cultivation within polythene greenhouses located on the southeast coast of Spain. Over time, this disease significantly diminished the profitability of muskmelon production in the region by reducing both fruit quantity and average fruit size.

The symptoms of the affected plants manifested in two distinct ways: one characterized by small yellow spots on the leaves and the other by an intense yellow discoloration near the leaf stalk's base. In both cases, the disease progressed from older leaves to younger ones. Interestingly, a close association was observed between the presence of the greenhouse white-fly Trialeurodes vaporariorum and the appearance of these symptoms, suggesting a potential link between the disease affecting muskmelon and previously reported cases. Notably,

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despite the absence of isolated virus particles, all these studies attributed the yellowing disease to the cucumber yellows virus (CuYV). This causal agent was consistently identified in various reports[6]

Diseases can be discerned through visual examination by observing symptoms that appear on various parts of plants, including leaves, leaflets, roots, and stems. Since some diseases exhibit similar characteristics, identifying them solely through optical observation is not a straightforward process. However, the integration of technology within greenhouses, such as the utilization of sensors, image processing, and deep learning, has greatly facilitated the detection and quantification of diseases in plants. This technological approach enables the early detection of diseases, preventing them from causing widespread damage throughout the entire greenhouse. It has been established that early detection and diagnosis of plant diseases are highly beneficial in maintaining the health of plants within the greenhouse [7].

1.1.1 **Yellow Leaf Curling**

Yellow leaf curling, an emblematic symptom, is extensively induced by numerous begomoviruses, particularly within the Begomovirus genus of Geminiviridae. This symptomatology is an outcome of intricate tripartite interactions involving the virus, host plant, and environmental determinants [8]. Molecular and physiological underpinnings of yellow leaf curling encompass multifaceted processes including viral replication, plant hormone perturbation, gene expression modulation, stress response induction, cellular distortion, vascular system disruption, phloem dynamics, and dampened plant defence mechanisms [9], [10] It is imperative to recognize the variability in the mechanistic landscape of yellow leaf curling across diverse begomovirus-host interactions ([11], [12]. The interplay of factors such as virus strain, host plant species, co-pathogens, and environmental conditions accentuates the nuanced expression and severity of this symptom [13] Notably, the interface between the virus and its insect vector crucially governs viral transmission and proliferation within plant populations [14].

1.1.2 **Yellow Leaf Mosaic**

Yellow leaf mosaic, another prevalent symptom evoked by begomoviruses, particularly those within the Begomovirus genus, is hallmarked by mosaic patterns of light and dark green on leaves, often accompanied by localized yellowing [15] The genesis of yellow leaf mosaic symptomatology entails a convoluted interplay between the virus, host plant, and ambient milieu. The underlying processes encompass viral replication, cellular dynamics, disruption of chloroplast functionality, vascular transport perturbations, hormonal imbalances, stress responses, photosynthetic repercussions, RNA silencing abrogation, and genetic variability [16]. The intricate etiology of this symptom underscores the role of myriad factors including virus strain specificity, host plant divergence, ecological nuances, and interactions with co-infecting agents. The intricate interplay underscores the intricate nature of plant-virus relationships and the consequent symptomatology [17].

1.2 **Interactions Between Plants and Begomovirus Pathogenic Agents: Implications for Leaf Health and Plant Development on Yellow Leaf Curl and Yellow Leaf Mosaic**

1.2.1 **Plants and Global Food Security**

Plants, as the primary source of sustenance for human and animal populations, hold a pivotal role in ensuring global food security and economic stability. The dependence of a significant portion of the world's population on agriculture and related industries underscores the profound implications of plant diseases [18] Leaf diseases, in particular, present challenges that hinder optimal plant growth. Timely disease detection becomes crucial to implement interventions and mitigate losses in yield and plant health, thereby preventing potential ecological imbalances.

1.2.2 **Proactive Disease Management: Zucchini Yellow Mosaic Virus: Challenges and Impact**

In the pursuit of proactive disease management, research endeavours continually uncover novel reservoirs of resistance against prevailing ailments such as the zucchini yellow mosaic virus (ZYMV). Tracing back to 1982, a debilitating yellowing disease has plagued muskmelon (Cucumis melo L.) crops cultivated in polythene greenhouses along the southeastern Spanish coastline [19]. This affliction casts shadows on the economic viability of muskmelon cultivation, resulting in significant reductions in fruit yield per plant and average fruit weight [20] The disease symptoms manifest in two distinct patterns: one involving discrete yellow spots on leaves, and the other characterized by intense yellow discoloration at the base of leaf petioles. This progression encompasses the entire leaf, except the vascular veins, in a yellow blanket that signals disease propagation. The malady initiates in mature leaves and advances gradually toward younger foliage. The correlation between the presence of the greenhouse whitefly, Trialeurodes vaporariorum, and disease manifestation suggests a resemblance to similar afflictions documented in Japan, Holland, France, and Bulgaria [21].

1.2.3 **Unravelling Viral Interactions : Tomato Mosaic Virus: Impacts Beyond Tomatoes**

Further unravelling the complexities of plant-virus interactions, the Tomato Mosaic Virus (ToMV) emerges as a viral pathogen affecting not only the tomato genus but also extending its impact to other plants such as tobacco and nuts [22]. Characterized by symptomatic yellowing and curling of juvenile leaves, ToMV-induced stunting and reduced plant productivity are evident, leading to a 23% decrease in tomato fruit yield [23].

1.2. 4. **Viral Challenges and Economic Ramifications: Tomato Yellow Leaf Curl Virus and Beyond**

In the domain of viral diseases, the [14] (TYLCV) stands as a formidable challenge to tomato cultivation across tropical and subtropical regions worldwide, resulting in significant economic consequences in affected countries. attributed to virulent Begomovirus strains and propagated by whiteflies, with the potential to cause yield reductions of up to 100% . The global magnitude of this concern is evident in its annual impact on an estimated one million hectares of cultivated land. The unique characteristics of tomato curl virus include leaf curling coupled with interveinal yellowing centred around vascular veins [24] Similarly, yellow leaf curl disease inflicts notable losses on cucurbit plants in Thailand, recently attributed to the squash leaf curl China virus [25] Notably, cucumber plants exhibited severe yellow leaf disease symptoms in 1996, with disease transmission confirmed through grafting and whitefly-mediated inoculation. Despite ongoing investigations, only partial DNA fragments of begomoviruses have been identified from affected cucurbit species, including cucumber, muskmelon, cantaloupe, and wax gourd [26] This paper aims to elucidate the role of technology for early detection of Yellow Leaf Curling and Mosaic Virus of the Geminiviridae Family hence corrective measures can be taken to spread of the disease.

2. Machine Learning (ML) and Deep Learning (DL)

Machine Learning (ML) a subset of Artificial Intelligence serves as a comprehensive framework that incorporates a wide array of algorithms and techniques, spanning from supervised to unsupervised learning approaches. Prominent algorithms within this domain encompass linear regression, decision trees, and k-means clustering, among others. On the other hand, Deep Learning (DL) can be considered as a distinct subfield within the broader domain of Machine Learning (ML), characterised by its focus on neural networks with a minimum of three layers. Although these networks are less complex than the neural structures found in humans, they are highly skilled at identifying patterns from large collections of data [7].

Machine learning (ML) can effectively function with a moderate dataset. However, when confronted with complex problems, domain-specific expertise is often required for feature extraction and manipulation. While deep learning (DL) is widely recognised for its insatiable need for data, and its effectiveness is frequently dependent on the availability of abundant data. The strength of this system rests in its ability to autonomously extract features from unprocessed data.

When considering the computational aspects, it is observed that classical machine learning (ML) models are typically designed to be computationally efficient, allowing them to be deployed on standard computational infrastructure. Deep learning requires substantial computational resources, often requiring the use of dedicated hardware accelerators like GPUs [27]

In order to comprehend the dilemma surrounding interpretability, it is worth noting that numerous conventional machine learning models are highly regarded for their ability to provide insights into their decision-making processes. However, in the case of deep learning, particularly complex neural architectures, there are often difficulties in explicability, resulting in them being perceived as opaque entities [28]

With a focus on its application breadth, machine learning (ML) demonstrates versatility and is applicable in several fields, ranging from healthcare diagnostics to financial predictions. The primary areas where deep learning has received recognition are in the fields of image and speech recognition, natural language processing, and complex game playing strategies, as exemplified by DeepMind's AlphaGo [29]

The field of machine learning encompasses a wide range of algorithms that are used to simulate structural dynamics. These algorithms vary in complexity, ranging from simple linear models to more complicated structures such as gradient boosting techniques. Within the domain of deep learning, there is a prominent emphasis on neural structures. This emphasis has led to the emergence of several architectural models such as deep feedforward networks, convolutional neural networks (CNNs), recurrent neural networks (RNNs), and modern transformers [30]. The following sections explain some the widely used deep learning technologies.

2.1 Deep Learning Technologies

Deep learning adopts totally automatic learning process that makes it suitable for deep feature extraction. In the recent years, deep learning technologies have been used in HSI to extract spectral only features, spatial only features and spectral-spatial features [31] The commonly used deep learning networks include stacked auto-encoders (SAEs), deep belief networks (DBNs), convolutional neural networks (CNNs).

2.1.1 Stacked Auto-Encoder (SAE)

An Auto Encoder (AE) is a type of neural network designed to acquire non-linear features by utilizing a concealed layer during its training process (see Fig. 1). In the encoding step, AE network maps the input x $\in R^d$ to a compressed data y $\in R^h$. In the decoding step, the input data is reconstructed to z $\in R^d$ using the data compression. In mathematical terms, these encoding and decoding processes can be represented as follows:

$$y = f\left(W_y\, x + b_y\right) \tag{1}$$

$$z = f(W_z\, y + b_z) \tag{2}$$

Where, Wy and Wz represent the weights connecting the input to the hidden layer and the hidden layer to the output, while by and bz represent the biases of the hidden and output units. The function f(·) signifies the activation functions that introduce nonlinearity into the network. To train the Auto Encoder (AE) effectively, the objective is to estimate and optimize these parameters in a way that minimizes the error between the input (x) and the reconstructed output (z).

$$argmin_{W,b}[error(x,z)] \tag{3}$$

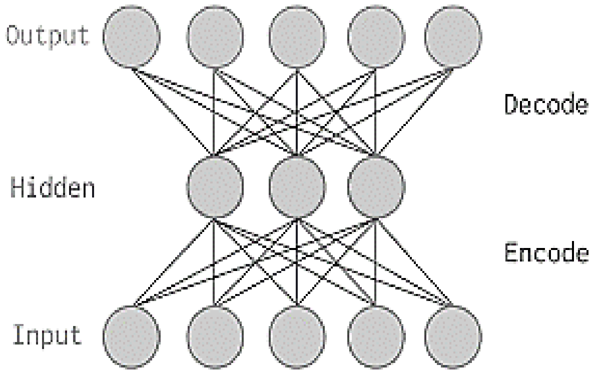

Fig. 1. Schematic illustration of AE

A Stacked Auto Encoder (AE) is formed by vertically stacking the input and hidden layers of individual AEs (Refer to Figure 2). This composite model is employed to produce intricate nonlinear features from the provided input dataset. Within this architecture, the encoded output of the first layer acts as the input for the second AE, and likewise, the encoded output of the second layer serves as the input for the third AE, and so forth. This iterative process proceeds in accordance with the depth of the Stacked Auto Encoder network [32].

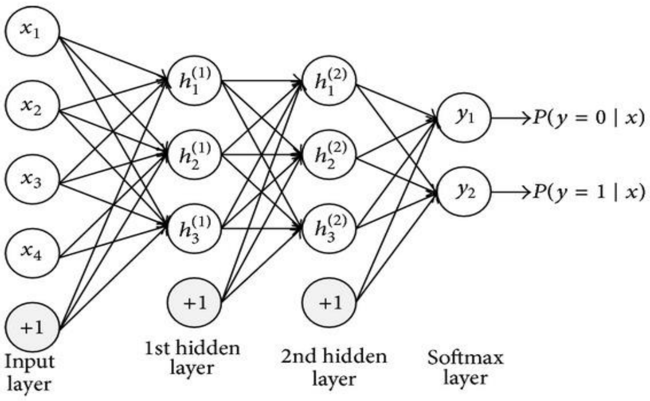

Fig. 2. SAE with two hidden layer and classifier

2.1.2 Deep Belief Networks (DBNs)

The main building block of DBN is a layer wise training model named Restricted Boltzmann machine (RBM)

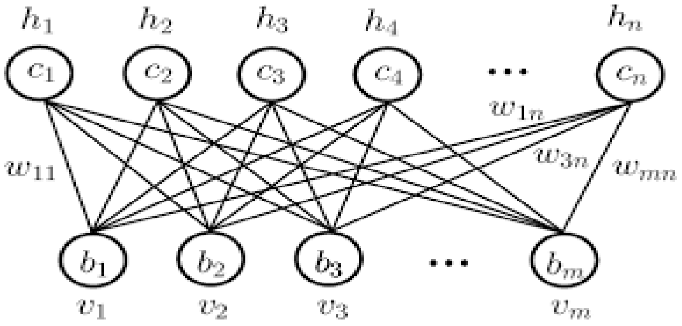

Fig. 3. Graphical description of Boltzmann machine (RBM)

The RBN model made up of two layer network having hidden units h= $\{0,1\}^n$ and visible units v=$\{0,1\}^m$ (See Fig. 3). The combined energy of these units is defined as:

$$E(v,h;\theta) = -\sum_{i=1}^{m} b_i v_i - \sum_{j=1}^{n} c_j\, h_j - \sum_{i=1}^{m}\sum_{j=1}^{n} w_{ij} v_i h_j \tag{4}$$

$$= -b^T v - c^T h - v^T wh$$

Where θ= $\{b_i, c_j, w_{i,j}\}$. The weight between hidden unit *j* and visible unit *i* is defined by w_{ij} that is leant using the divergence. The bias of visible units is represented by b_i and bias of hidden units is represented by c_j. DBN is established by stacking RBM's one after another as shown in Fig. 4 [33] .

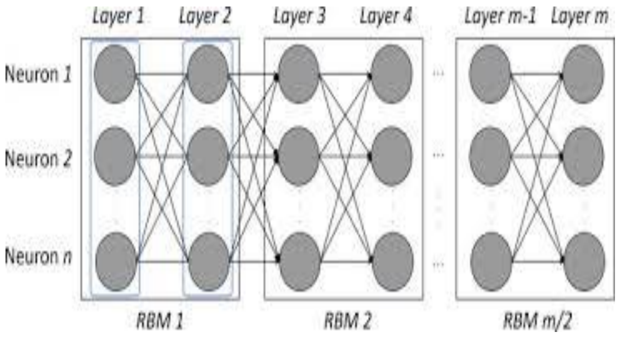

Fig. 4. Graphical description of Deep Belief Networks (DBNs)

2.1.3 Convolutional Neural Network (CNN)

CNN is modelled using convolution layers and pooling layers which are placed alternatively and having fully connected layers connected at the end of the network [34]. At each convolution layer, multiple feature maps are generated by convolving the input cube with multiple learnable filters [35] Suppose X is an input cube of size *mnd* where *m* are rows, *n* columns and *d* are bands. Spatial dimension is represented by *mn* and *d* represents the spectral dimension. Considering *k* filters at the convolution layer, j^th^ filter is represented by bias b_j and weight w_j. Suppose x_i is the i^th^ feature map of X, then j^th^ output of the convolution layer can be defined as:

$$y_j = \sum_{i=1}^{d} f(x_i * w_j + b_{j)}\ where\ j = 1,2,3, \dots .k \qquad (5)$$

In Eq. 5 f(.) is an activation function and * is the convolution operator. The pooling layers are used to reduce progressively the spatial size of the feature maps. The size of the feature maps is shrunk during pooling operation and extracted features becomes more abstract. The average pooling operation for a *pxp* window size neighbor denoted as S:

$$z = \frac{1}{F} \sum_{(i,j\in S)} x_{ij} \qquad (6)$$

Where x_{ij} is the activation value for the position (i,j) and F is the number of elements in S. Further, more deep and abstract features are extracted using fully connected layers by reshaping feature vectors in n-dimensional vectors. This layer is represented as:

$$Y' = \sum_{i=1}^{C} f(WX' + b) \qquad (5)$$

Where Y' refers to the output, W refers to the weight, X' refers to the input and b refers to the bias respectively.

2.2 Objective of the study

The systematic literature review has been conducted with the following objectives.

1. Compare the dataset being used in the research whether it is self-created or publicly available data set.
2. Type of plants of focus in the research for the identification yellow leaf curl or yellow mosaic virus.
3. Identify the methods used for feature selection and representation.
4. Various machine learning and deep learning techniques used in the research and major focus in these techniques by the research community.
5. Usage of hyperspectral imaging techniques for the identification of yellow leaf curl or yellow mosaic virus by the research community.

3. Methodology

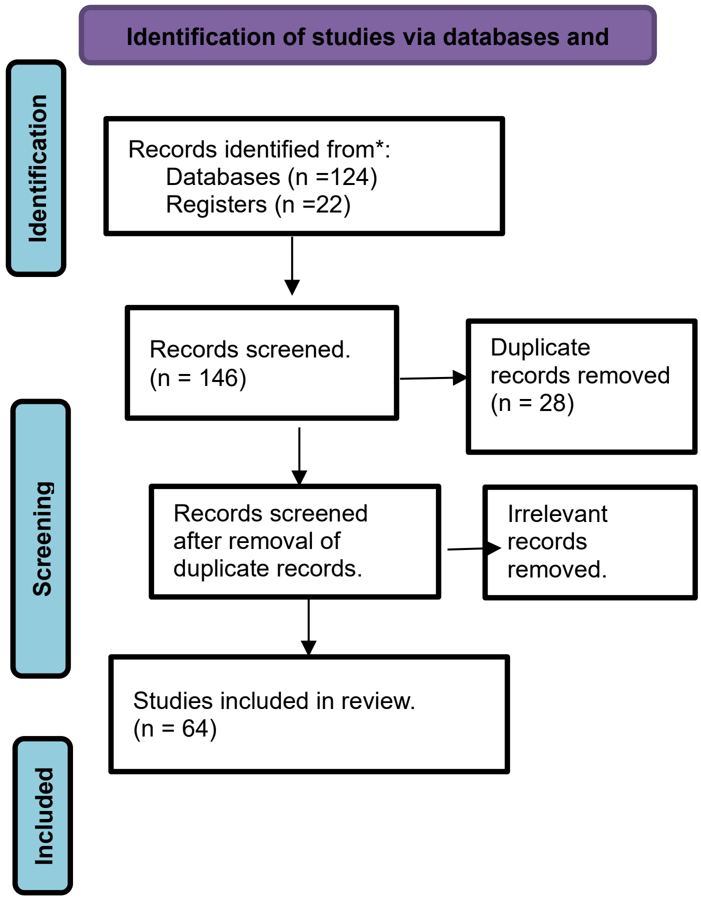

Fig. 5. Selection procedure of the study [36].

3.1 Methods

3.1.1 Characteristics of research

In this systematic literature review study in relation to yellow mosaic virus and yellow leaf curl virus, the articles were extracted for the years 2019 to 2023. Only the articles published in English language were considered for the study. All these articles are either published as part of conference proceedings or as part of journal publication.

The systematic literature review was carried out according to PRISMA statement guidelines. The articles were extracted from three popular citation databases namely IEEE explore, Scopus and Science direct.

The literature search consisted of two sets of searches with three terms. The first set of literature search included the terms “yellow mosaic virus”, “machine learning” and “deep learning”. The second set of literature search included the terms “yellow curl virus”, “machine learning”, and “deep learning”. As each database has its own set of rules for search the queries were formed keeping in mind the main search terms. The search query used in Scopus database was TITLE-ABS-KEY ((yellow AND virus) AND (plants OR leaf OR leaves) AND (machine AND learning OR deep AND learning)). Similarly, the search query used in IEEE was "All Metadata":"yellow leaf curl virus") AND ("All Metadata":machine learning OR "All Metadata":deep learning). Finally, the search query used in science direct was (yellow leaf curl virus) AND (plants OR leaf OR leaves) AND (machine AND learning OR deep AND learning) as well as (yellow mosaic virus) AND (plants OR leaf OR leaves) AND (machine AND learning OR deep AND learning)

3.1.2 Inclusion and Exclusion Criteria

The systematic literature review considered the following inclusion and exclusion criteria.

- Only the articles published between 2019 and 2023 were included.
- Only the research articles published in scientific peer-reviewed journals and conference proceedings were included.
- Only the studies that proposed and implemented machine learning and/or deep learning models to identify yellow mosaic are yellow curl virus were included.
- Only the researchers reported in English were included.
- The studies that focused on yellow curl or yellow mosaic virus without any implementation through machine learning or deep learning methods to detect the virus were excluded.
- The research articles that focused only on the disease without any machine learning or deep learning approaches were excluded.
- Review studies, abstracts, commentaries, book chapters, or editorials were excluded.

3.1.3 Study Selection

The screening of the articles by experts was done by reading the article type, title, and abstracts. Two experts with domain knowledge reviewed all articles independently. The articles excluded by the experts were compared and deliberated by looking at the entire text of the article. The final decision to exclude the articles was taken with consensus of the research team.

3.1.4 Data collection process

The data from the articles considered for systematic literature review was extracted based on six parameters. These parameters include (1) Objective of the article (2) Data Sources and Preprocessing (3) Feature Selection or Representation (4). Model Architectures (5) Strengths and (6) Limitations. Fig 1 provides PRISMA flow chart followed in this study. A total of 146 articles were obtained from query searches in Scopus, IEEE explore and science direct that included both journal articles and conference proceedings. The publications extracted for systematic literature review are from 2019 to 2023. Among the 146 articles, 28 articles found to be duplicates as they were retrieved from different databases. The duplicates were removed, and the remaining 118 articles were reviewed by the domain experts. Among the 118 articles, 64 found to be Irrelevant to the study based on the exclusion criteria. The final 64 articles are considered for the current study. Among the 64 articles, 57 focus on identification of yellow curl virus. and the remaining 7 articles focus on identification of yellow mosaic virus. Table 1 provides summary of articles selected for the study based on the chosen characteristics for yellow mosaic virus and yellow curl virus.

Fig 6 provides different datasets used by the researchers for the identification of yellow leaf curl virus and yellow mosaic virus in different leaves of the plants which includes tomato, rice, apple, citrus, soybean, pepper, chilli, and tobacco.

Table 1. Summary of articles

Paper Identification	***Approach***	***Strengths***	***Limitations***
[37]	Res-Net+U-Net	Reduce associated labor costs, increase accuracy and precision and enable larger automated scouting operations, reducing sample size bias.	Introduced potential biases, Intra-class lighting and camera settings created correlated features extraneous to disease symptoms.
[38]	Different ML models fusion with MLP	outperformed the state-of-the-art Deep learning model and demonstrated versatility across various conditions	complexity of the training, the lack of available data, and the use of poor hardware on the farm
[39]	RANSAC for curve fitting, logistic regression, multilayer perceptron model, and support vector machine	enhance the expected outcome, covers a comprehensive range of plants, and provides high accuracy in its results.	potential degradation in sensitivity due to the dataset imbalance problem
[40]	Multi-headed DenseNet-based architecture	distinguish various plant diseases with different characteristics using image fusion and has a high success rate with low standard deviation	multiple infections on one crop
[41]	Convolutional Neural Networks (CNN)	high accuracy, efficiency in terms of storage requirements, compared to pre-trained models.	Developments can be made to add this technology to a surveillance system to further automate the process.
[42]	IML-TYLCVs	successfully combined machine learning with molecular virology, web server provides a user-friendly interface	cannot be evaluated in real time, using genome sequences for predictions showed bias
[43], [44]	CNN and transfer learning (TL)-	data augmentation to enhance model performance, user-friendly platforms like web and Android applications.	misdiagnosis by farmers, the detrimental effects of wrong treatments
[45]	Pre-trained CNN models	use of numerous pre-trained CNN models and a comprehensive dataset	limitation of the number of synthetic dataset images, the mix ratio can only reach a maximum of 70%
[46]	self-supervised Contrastive learning method (CLA)	align labeled and unlabeled data in the fine-tuning stage, generating more general visual representations and improving domain adaptation ability.	rely heavily on large-scale labeled data, and the unlabeled data used can be messy
[47]	Convolutional Swin Transformer (CST) based on	high detection accuracy and outstanding robustness, even in images with significant noise	lose global information from images due to the convolutional kernel size

	the Swin Transformer		
[48]	Deep Convolutional Neural Network (CNN)	DCNN model enhances performance accuracy, reduces response time, and has the potential to work with incomplete or fuzzy background images.	current use of sigmoid function is limited due to vanishing gradient
[49]	Multi-Input Multi-Task Neural Network, combining CNN features	Multi-Input Multi-Task Neural Network model increases efficiency, yields faster learning for similar detection tasks, and provides superior results compared to single-task experiments	High computational resources are necessary
[50]	Deep learning-based semantic segmentation with classification capabilities	helps in recognizing new species holding diseases, decreases the bias, building of a more generalized model for disease classification.	Model cannot work well for plant diseases with low segmentation score.
[51]	PLS-based parallel fusion method, PLS projection method	improve recognition accuracy and reduce computational time	Irrelevant feature information added during the fusion step
[52]	Dense convolutional neural network	efficiently classify various types of plant leaves with high accuracy and real-time performance	small dataset of plant images and classification done on limited number of diseases
[7]	Automated intelligent system Fast.ai	high accuracy, development of a Web application	The model is tested for plants in controlled environment
[53]	Random Forest, SVM, Naive Bayes, KNN	high classification accuracies, eliminating the need for trained experts.	Naive Bayes, showed relatively low accuracy for some pathogens.
[31]	CNN	high training accuracy and better detection rates	model trained with only the PlantVillage dataset performed poorly in detecting bacterial spot and healthy leaves in real-world conditions
[54]	Simplified CNN model and novel method of augmentation	high accuracy, ability to perform well on different datasets.	computationally heavy and possibly an overkill for scenarios with fewer classes, such as plant diseases.
[55]	CNN	practical implementation on a low-cost device.	lack of public datasets and the cost of equipment
[56]	CNN, VGG16, VGG19, ResNet50	automatic feature extraction, saving researchers from labor-intensive tasks and errors, and demonstrates high accuracy	might benefit for a larger dataset
[57]	Deep learning algorithms as and	high training and testing accuracies	asymptomatic leaves with still low virus contents, biochemical

	support vector machine (SVM)		features have not yet been impaired, and pigments have not yet been degraded
[58]	HSI+SVM	offers valuable insights into leaf physiological properties and potential monitoring of virus spread	Difficulty in detecting the virus in infected plants due to phloem limitation and the irregular distribution of virions
[59]	Enhanced radial basis function neural network (ERBFNN)	efficiently segments disease-affected areas with high accuracy and better performance	focus is only on tomato leaf diseases and not on other parts of the plant
[60]	Fast WDBlock based GAN (FWDGAN)	FWDGAN produces higher-quality images improving efficiency and accuracy	produce poor image quality and consume excessive computing resources.
[61]	CNN	high precision by automatically extracting features, and higher image dimensions resulted in higher accuracy	domain of computer vision in plant disease recognition is still underdeveloped
[62]	CNN	classify diseases with high precision by automatically extracting features from the dataset,	field of automated plant disease recognition remains underdeveloped
[63]	Deep CNN model	achieves higher accuracy than traditional machine learning methods.	need to work on a larger database to get better results
[64]	Asymptotic Non-Local Means algorithm (ANLM) Multi-channel Automatic Orientation Recurrent Attention Network (M−AORANet)	effectively reduce noise while retaining detailed features	image noise can interfere with the network, leading to incorrect feature extraction and classification.
[66]	CNNs—ADM (Anomaly Detection Model), DIM (Disease Identification Model), and LPDM (Leaf mold/Powdery Mildew Distinguishing Model)	timely identification of tomato leaf disease, simple suggestions for treatment and prevention, provides automatic responses and is always available	incompatibility with the version of the user’s device operating system
[1]	CNNs	capable of extracting meaningful features automatically for classification	network exceeds 10 layers, the accuracy goes down due to insufficient data

[67]	Spectral methods with Machine Learning (KNN+RF+SVM)	effective stress detection	decrease in accuracy when applied at larger scales due to ambiguity of characteristic bands
[68]	Inception Convolutional Vision Transformer (ICVT) with f soft split token embedding	ICVT network successfully models both local spatial information and high-level information	rely heavily on the quality of feature extraction and are prone to interference leading to lower recognition accuracy.
[69]	Radiometic features + ANOVA+ Gradient Boosting	proposed method is effective and applicable for tomato leaf disease detection and classification	relies solely on the Plant Village dataset for its disease images
[66]	data augmentation method using MMDGAN, and B-ARNet model	superior image quality	previous methods still have room for improvement, implying that even the proposed method might not be perfect
[70]	CNN ,VGG16, InceptionV3, GoogleNet BN7	specialized tasks reduces the impact of overfitting for deeper Inception-based models, shows better generalization to new data	lack of diversity in the Plant Village dataset, which limits the effectiveness
[71]	CNN as the embedding module, clustering is performed on the embeddings to create the class prototypes.	Lightweight model, requires minimal resources, and maintains high detection accuracy	deep learning methods have limitations for mobile applications due to their resource requirements.
[22]	CNN models	significant improvement in model performance	exhibit a drop in performance when tested with independent data
[72]	different configurations of neural networks	high classification accuracy,	misclassification errors can occur
[73]	deep Convolutional Neural Network (DCNN) mode	high accuracy, no signs of overfitting,	hardware limitations
[74]	EfficientNet deep learning architecture	highest accuracy and precision rates	need for efficient models with fewer parameters that train faster without compromising performance.
[75]	PDICNet model using ResNet-50 for feature extraction, MRDOA for optimal feature selection, and	high accuracy and F1-score	High computational resources are necessary

	DLCNN for classification		
[76]	Trilinear Convolutional Neural Networks (T-CNN) model	higher versatility and generalization in identifying crop diseases	perform less effectively in real-world environments due to complex backgrounds
[23]	Kapur-based thresholding technique	high accuracy of the proposed method	poor representation of disease symptoms, image background and capturing conditions; limited variations in disease symptoms
[54]	Convolution Neural Network (CNN) model	requires only 1.5 MB of storage space compared to about 100 MB needed by pre-trained models	less than perfect accuracy, and there is an imbalance in the number of images per class in the dataset.
[77]	Convolutional neural networks (CNNs)	high accuracy, uses a well-regarded architecture (VGG16) for its foundation	The number of tomato leaf images in each category is not balanced.
[78]	MFFN, combined with ResNet50 and an Adaptive Attention Mechanism	minimizes perception loss,	Some diseases exhibit similar features which can lead to model miss-classifications.
[79]	Conditional Generative Adversarial Network (C-GAN)	high accuracy	do not have diverse images
[80]	Deep batch-normalized eLu Alex Net(DbneAlexnet) trained with Gradient Jaya-Golden search optimization (GJ-GSO)	unified segmentation and classification,	Alterations in the structure of various models can affect recognition variability
[81]	TomFusioNet framework	high accuracy, reduces mobile computation waste, efficiently removes background clutter utilized within a smartphone app, all without requiring any human intervention	suffer from overfitting, gradient vanishing, low accuracy in real-time applications, high false-positive rates, and a lack of a deployable end-to-end framework for practical farmer use
[82]	CNN, data augmentation, channel orthogonal constraint	design of data augmentation and discriminative feature learning is effective	Study needs be done on multiple leaves in one image, multiple diseases in one plant leaf, and covariate shift between training data domain and test data domain
[83]	CNN	The model achieved the highest performance	Pre-trained models such as Inception V3 and ResNet-based

			CNN models can be used for much deeper feature extraction
[84]	Artificial neural networks	Ability to detect TYLCV symptoms early as 42days after transplanting.	The model was test for single type of disease
[85]	AR-GAN, utilizes Activation Reconstruction Loss (ARL) improve the performance of a CNN classifier	visually compelling synthetic images,	coping with small datasets, limited annotated samples, and class imbalance in machine learning
[86]	Deep Convolutional Neural Network (DCNN)	high accuracy and outperforming similar approaches	Deep learning system with drone technology and IoT is required for real-time detection.
[87]	CNN	better chance of maintaining healthy crops	lack of suitable research material, high degree of brightness and contrast background hindrances
[88]	Contour feature techniques, combined with adaptive thresholding.	Data pre-processing, including noise removal and image resizing ; Multiple deep learning models; Model evaluation precision, recall, and F1 score.	Pre-processed images were 1 pixel, does not work well with complex images. Only few REgion of Interest were captured. Inefficient contour and cropping feature
[89]	Transfer learning; data augmentation techniques	Transfer learning to fine-tune pre-existing models; data augmentation to prevent overfitting	focus on increasing the dataset size
[90]	Gradient Boosting Machine a machine learning algorithm.	Reduced Influence of Complex Background; Handling Leaf Deformations and Occlusions; Accurate Severity Estimation	Infected tea leaves are often damaged, deformed, and occluded; Insufficient Number of Disease Image Samples
[29]	Optimized pre-processing techniques for detecting PYLCV-infected chilli plants using FTIR	only technique that produced a 100% accuracy. This optimal performance was further confirmed by principal component analysis clustering	Tested only on machine learning models
[82]	CNN+SVM	Provides a new direction for early SMV detection based on hyperspectral images.	potential limitation in the dataset size
[59]	CNN, K-Means, SVM	Deep learning models are effective in sugarcane disease identification	Experimental results are not provided
[68]	SV preprocessing method with the 3SV-CTRI 1	3SV and the performance of specific spectral indices and machine learning algorithms	Availability of the public dataset images with specialized camera

	spectral index, combined with machine learning (SVM)	collectively contribute to the overall performance.	

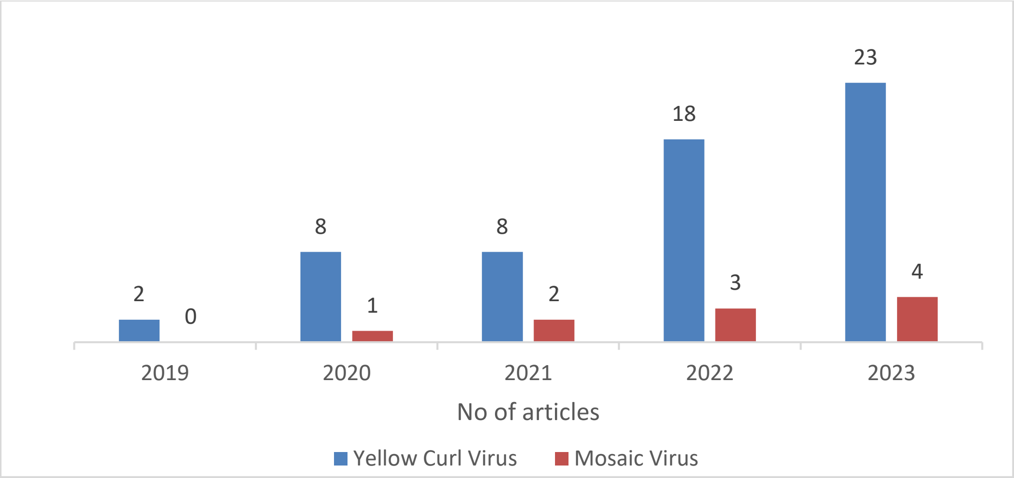

Fig. 6. The number of publications between 2019 and 2023 (n = 64)

3.1. 5 Comparative Characteristics

While analysing the relevant features for detecting Yellow Curl Virus, various crucial aspects are examined. The initial utilisation of diverse data sources, including field images and public databases, highlights the importance of implementing rigorous preprocessing methods such as normalisation, denoising, enhancement, transformation, and augmentation. These steps are necessary to ensure that the data is prepared for analysis. Feature selection strategies, ranging from manual curation to automatic extraction, are compared to the direct use of raw data input for deep learning (DL) models, in terms of their individual benefits and limitations. The usefulness of ML techniques such as Support Vector Machines (SVM), Random Forest, Naïve Bayes, and DL models such as Convolutional Neural Network (CNN) and other variation of CNN's as well transfer learning models are assessed for disease detection. Each model offers distinct methods for feature extraction and classification. Performance assessment is based on a set of measures that include classification accuracy, sensitivity, specificity, F1-score, and area under the receiver operating characteristic (ROC) curve, kappa coefficient among others. These metrics provide valuable information about the effectiveness of the model. Additionally, this study examines how the amount of the training data, and the imbalance of classes affect the performance of the model, emphasising the need to fix these concerns. Furthermore, it considers computing resources, such as hardware specifications and software frameworks, that impact the scalability and efficiency of the model.

3.1. 5.1 Data Sources and Pre-processing

The data sources and preprocessing methods across different datasets highlights a wide range of sources and techniques used in plant disease detection research. The Plant Village dataset is notable for its extensive compilation of images depicting both infected and healthy leaves. The Plant Village dataset has been majorly used by the researchers which encompasses a range of illnesses, including mosaic, curl virus, and leaf mould in tomato leaves. Only two papers used images captured by Unmanned Aerial Systems (UAS) and ASD FieldSpec which allows for a multi-modal approach to analysis. In addition to Plant Village, other datasets such as the Cucumber Plant Diseases Dataset, Citrus leaves disease, NGBVI dataset, iBean leaf image dataset, Augmented leaf, disease, PlantDoc, Apple dataset and Banana leaf disease, Apple leaves Dataset and Rice plant dataset have been used in the research. Preprocessing techniques used in the research include normalisation[75], noise removal [59] scaling [58] anisotropic filtering [91], cropping [71] spectral separation [67], Savitzky-Golay 1st derivative [29]), resizing and image enhancement is mainly used in deep learning models.

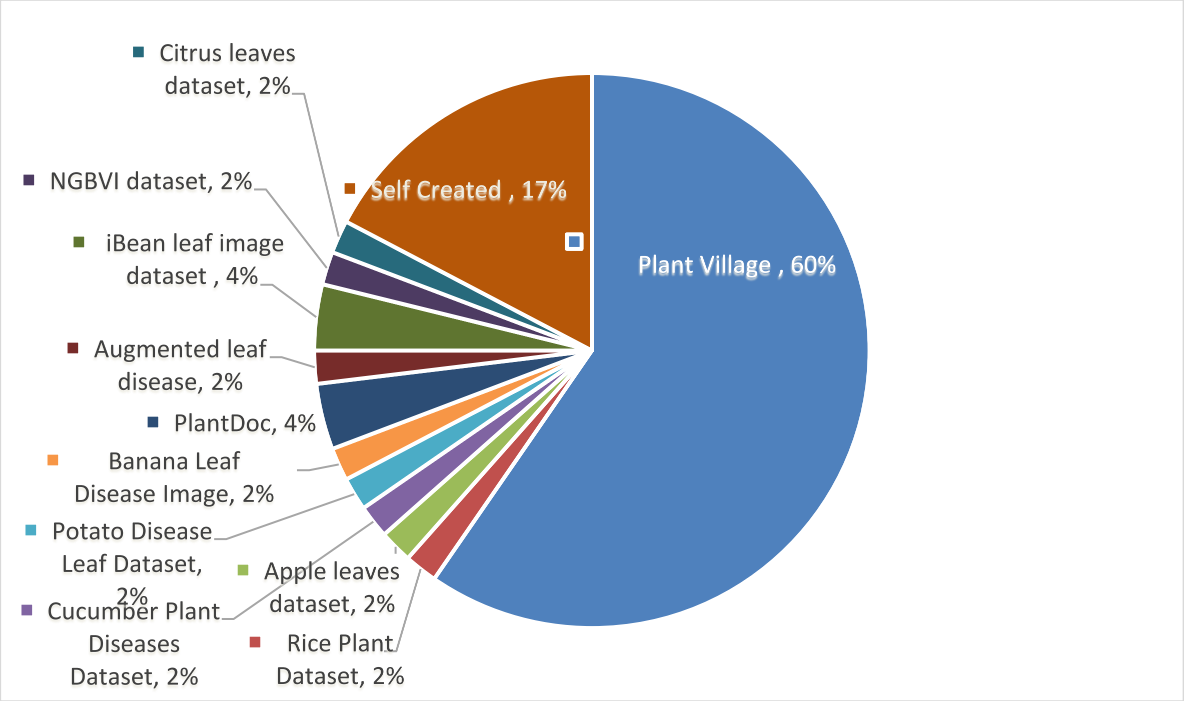

Fig 7. Source dataset used in the research between 2019 and 2023 (n = 64)

Referring to Fig 7, it is estimated that majority (60%) of the research is based on Plant Village dataset which is a large publicly available database that contains 54303 healthy and unhealthy leaf images divided into 38 categories by species and disease. The self-created dataset (17%) second highest database used in the research wherein samples for training and testing is captured by the researchers under controlled environments.

3.1. 5.2 Feature Selection or Representation

Feature selection or representation plays a pivotal role in the domain of plant disease detection and classification, offering a fundamental mechanism to extract discriminative information from plant images. By selecting or representing relevant features, such as texture, color, shape, and deep learning-based representations, researchers can effectively capture the distinctive characteristics of various plant diseases. This process not only reduces the dimensionality of the feature space but also enhances the interpretability and generalization capability of disease detection models. [75] utilized the modified Red Deer optimization algorithm (MRDOA) to acquire optimized and salient features, demonstrating its superiority over optimization algorithms like Genetic Algorithm (GA), Moving Average (MA), and Particle Swarm Optimization (PSO). The study employed by [92] on spectral index wavelength (SIW), threshold method, and variance inflation factor (TVIF) as feature selection methods, reveal the effectiveness of SIW in selecting appropriate features. Recursive feature elimination (RFE) was applied by [84] employing a greedy search to identify the best-performing feature set. In a separate study, [5] utilized partial least squares (PLS) regression to select features from a deep feature set. They observed that while the selection of optimal features may overlook redundant information, it may also omit some primary features which emphasizes the importance of exploring feature selection methods with minimal error rates. Furthermore, in deep learning models like Convolutional Neural Networks (CNNs), the convolutional layers consist of filters that autonomously learn to capture local patterns, edges, and textures, thereby inherently selecting salient features directly from the input. In transfer learning, pre-trained models that have been trained on large-scale datasets (e.g., ImageNet) are utilized as feature extractors for new tasks or domains with limited data. Specifically, the learned representations from the earlier layers of these models capture generic features such as edges, textures, and shapes, which are often transferable across different visual recognition tasks. These representations can then be fine-tuned or used as fixed feature extractors, depending on the size and diversity of the target dataset and the complexity of the new task.

3.1. 5.3 Model Architectures

The comparative examination of model architectures used for detecting Yellow Curl Virus (YCV) and Mosaic Virus (MV) demonstrates a wide range of techniques, including both machine learning (ML) models and deep learning (DL) models. Machine learning models such as random forests, support vector machines (SVM), logistic regression, and k-nearest neighbours (KNN) are capable of effectively detecting YCV and MV. They achieve this by utilising handcrafted features and fusion approaches with multi-layer perceptron (MLP) networks, resulting in enhanced performance. Convolutional neural networks

(CNNs) are the most prevalent deep learning architecture being used in the research. They automatically extract hierarchical features from raw data, resulting in extremely accurate detection of YCV. Pre-trained models such as AlexNet, ResNet, U-Net, DenseNet, Inception, and EfficientNet are examples of models that demonstrate the efficacy of Convolutional Neural Networks (CNNs) in extracting distinctive features for YCV detection. In addition, CNN performance is being improved by utilising techniques like as transfer learning, contrastive learning, and self-supervised learning. These methods leverage pre-trained models or domain adaption procedures. Hybrid models that integrate convolutional neural networks (CNNs) with other deep learning architectures or machine learning models demonstrate the collaboration between diverse approaches to enhance the accuracy of YCV identification. Moreover, the utilisation of advanced techniques such as spectral methods in conjunction with machine learning algorithms integrated with deep learning classification models exemplify the ongoing pursuit for more precise and economical solutions in YCV detection.

It is evident from Fig 8 is that Convolution Neural Network (CNN), a popular deep learning model has been used majorly (41%) for the identification of the disease. Many of the approaches include machine learning techniques while few other research has combined both machine learning and deep learning techniques. There is a clear shift to usage of deep learning techniques due to their ability learn deep features for accurate identification and classification.

3.1.5.4 Training Data Size and Imbalance

The analysis of image datasets in the context of model performance and generalisation for plant disease detection research shows a significant range of variability in dataset sizes. The impact of imbalance in data set size in overall performance of the model was reported by [39], [85] and [54] .Generally small sample numbers can lead to overfitting, a situation where the model memorises the training data instead of being able to generalise effectively to new, unknown data. Moreover, datasets that have uneven class distributions, such as those with a smaller number of samples for specific diseases or plant species, might worsen these difficulties, resulting in biassed predictions by the model. The amount of the training dataset significantly influences the effectiveness of models for plant disease detection. Increased dataset size and diversity typically enhance model performance and generalisation. Methods such as data augmentation, resampling techniques, and the creation of streamlined models with reduced parameters are recommended to alleviate the impact of class imbalance and enhance model effectiveness. Furthermore, the implementation of standardised methods for collecting and annotating datasets among research groups might increase the availability of top-quality datasets, hence improving the efficiency of models used for detecting plant diseases.

3.1.5.5 Computational Resources

The computer resources needed for training and inference in plant disease detection depends on dataset sizes and model complexities. The presence of many datasets, including the Plant Village dataset and other datasets specialised to plants, which vary in size from tens of thousands to several hundreds of thousands of images, highlights the necessity for a strong computational infrastructure capable of efficiently managing large-scale data processing. The presence of spectrum data, hyperspectral measurements, and reflectance spectroscopy data increases the computational complexity due to the high-dimensional characteristics of this data and the requirement for specialised processing techniques.

Furthermore, the computing needs may be affected by the intricacy of the utilised models, such as deep learning architectures like CNNs and hybrid models. Models that have greater parameter sets and deeper architectures typically require additional computational resources, like high- performance GPUs or TPUs, to effectively train and provide predictions. In addtion, the selection of software frameworks such as TensorFlow or PyTorch might impact the effectiveness and expandability of model training and deployment.

Discussion and Recommendations

Hyperspectral Imaging (HSI) is gaining importance in the recent years due to its ability to combine the power of digital imaging and spectroscopy which makes it capable to identify and distinguish materials even with minute differences. Hyperspectral Imaging (HSI) also known as Imaging Spectroscopy is the method of acquiring the light intensities that are emitted from various environmental objects.

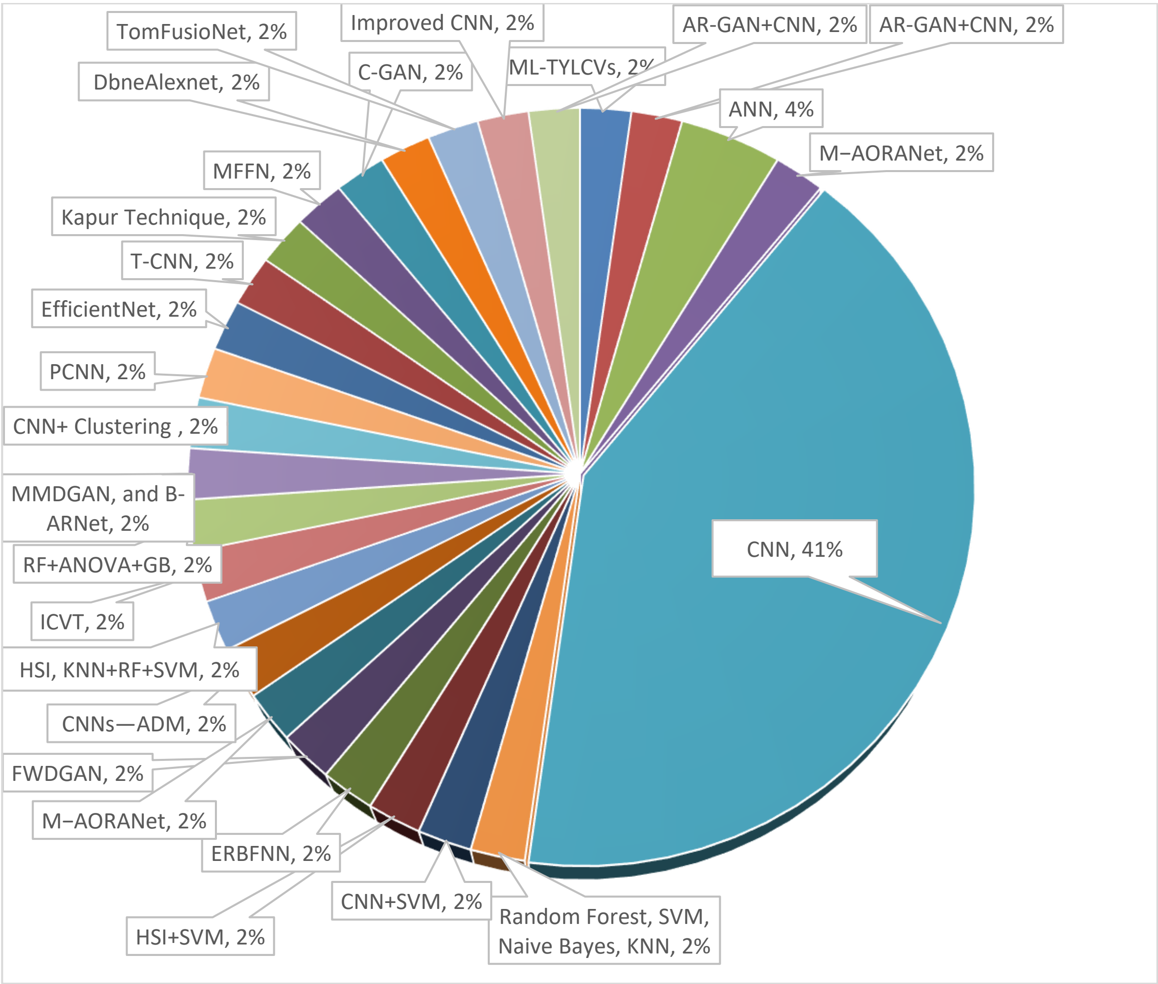

Fig 8. Approaches used to identify the disease between 2019 and 2023 (n = 64)

The light reflected from different objects vary in terms of energy and wavelength. Hyperspectral image details are collected in cubic structure (see Fig. 9) which includes spatial and spectral information (X, Y and Z axis). There are currently no good databases available that contains healthy and unhealthy leaf images of categories by species and disease. Spectroscopy analyses the electromagnetic spectrum of sunlight that is absorbed, scattered or reflected by global surface-level objects (Sea or Land). The image spectrometers help to recognize the unique spectral features for each spatial resolution element of various surface-level objects based on the light intensity. The spectrum provides the signature that is caused by variation in reflectance or emittance of an object at each wavelength. HSI measures the reflected solar signal in the electromagnetic spectrum from the visible (390 to 700 nm) to the infrared (700nm to 1mm) with very narrow bandwidth up to 5 or/and 10 µm. Among the datasets that are publicly available Plant Village dataset is widely used in the research for the identifications of yellow leaf curl virus and yellow mosaic virus. Plant Village consists of RGB images of plant leaves and backgrounds. There is a need to build a hyperspectral imaging-based database for the benefit of research community. Currently there are many portable hyperspectral cameras such as BlackMobile from HAIP

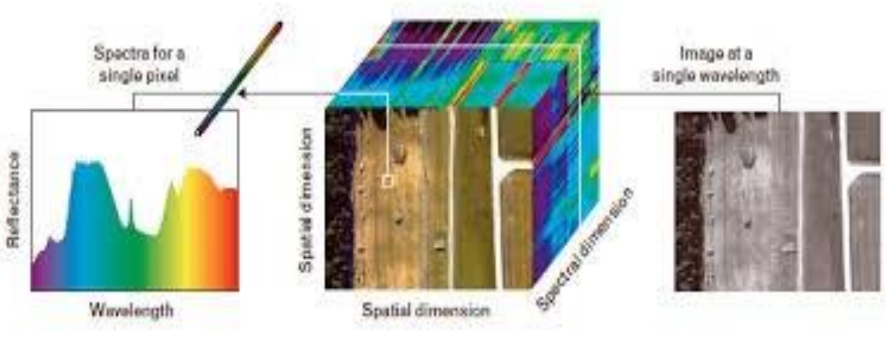

Fig. 9. Basic data cube structure of HSI

solutions [93] and SpecimIq from Konica Minolta company available that makes it possible to capture the images.

In the recent years research has focused much on yellow leaf curl detection and yellow mosaic virus detection in plant leaves of tomato, rice, apple, citrus, soybean, pepper, chilli, and tobacco. Melons contribute good percentage to a nation's economy. However, there is not much research done in melon plants specially musk melon. In 2023, first report has been released on muskmelon (Cucumis melo) being infected by Cucurbit aphid-borne yellows virus infecting in India [94].

Survey of research limitations shows the lack of inadequate and availability of images however with the advent of generative AI more samples can be generated using on the base samples. Generative AI (GenAI) is capable of producing a wide range of data, including images, videos, music, text, and 3D models. It accomplishes this by identifying patterns in already collected data and exploiting those patterns to create novel and distinctive outputs. generative models for diffusion have also been created to allow for more precise control over the image generating process and the production of high-quality images [101]. The study of image generation has seen a rise in the use of Generative Adversarial Networks (GANs). Generator and discriminator are the two components that make up GANs. The discriminator assesses whether the input comes from the real data space or not, while the generator tries to learn the distribution of genuine samples to generate new data.

Deep leaning techniques surpass machine learning techniques to achieving disease detection accuracy which is because deep learning techniques can learn deep features. However, deep learning techniques require large about of input dataset which can be addressed through hyperspectral imaging and generative AI through following ways.

Enhanced Image Processing: Hyperspectral image quality can be raised by applying generative AI models, like Variational Autoencoders (VAEs) or Generative Adversarial Networks (GANs). For example, GANs can create high-resolution hyperspectral images from low-resolution ones, which facilitates the identification of minute spectral deviations linked to illnesses or environmental factors [60]

Data Augmentation: It is possible to create synthetic hyperspectral data using generative AI. In order to enhance the dataset and provide machine learning models with a wider and more varied set of instances to train on, this synthetic data can be mixed with real hyperspectral data. This could potentially improve the models' performance in tasks involving the identification or categorization of diseases [95]

Anomaly Detection: Generative AI models can be trained to recognize the typical spectra or patterns of healthy plants or environments. When used for real-time monitoring, any departure from the patterns that have been learned might be reported as abnormal. This is beneficial for the early identification of illnesses or changes in the environment. [96]

Hyperspectral Data Reconstruction: Hyperspectral data can be reconstructed from a small range of spectral bands using generative models. This can save cost and time on data collection while still yielding useful spectrum information [97]

Image Fusion: Hyperspectral data can be fused with other forms of images, such as RGB or thermal images, by combining hyperspectral imaging with generative AI. This fusion can offer a more thorough perspective of an object or scene, which is helpful for several purposes [98].

Data Denoising: Hyperspectral images can benefit from the use of generative models to reduce noise and artifacts, enhancing the data quality for analysis and interpretation. [99].

Targeted Data Generation: Generative models can be trained to produce hyperspectral images with specific features. This might be helpful for training or research purposes when recreating various settings or scenarios[100].

The combination of hyperspectral imaging and generative AI holds significant promise for advancing various fields, including agriculture by improving data quality, analysis capabilities, and the efficiency of data collection and processing.

4. Conclusion

The pivotal role of plants in ensuring global food security and economic stability cannot be overstated, given their status as the primary source of sustenance for human and animal populations worldwide. Plant diseases, especially those affecting leaves, pose significant challenges that hinder optimal plant growth, underscoring the importance of timely disease detection and intervention. Addressing these issues is not only crucial for preserving crop yields and plant health but also for preventing potential ecological imbalances.

In recent years, the integration of machine and deep learning techniques has emerged as a promising approach for the detection and classification of plant diseases. This systematic literature review has focused on the detection of the Yellow Leaf Curling and Mosaic Virus of the Geminiviridae Family, analyzing articles from reputable sources like IEEE Xplore, SCOPUS, and Science Direct published between 2019 and 2023.

One notable suggestion arising from this study is the potential for dataset creation and disease detection using hyperspectral imaging (HSI). HSI combines the capabilities of digital imaging and spectroscopy, offering a promising avenue for enhancing disease detection accuracy and efficiency. Embracing such innovative technologies and interdisciplinary approaches will undoubtedly play a crucial role in safeguarding our agricultural systems, ensuring food security, and sustaining economic stability in the face of evolving plant diseases and ecological challenges.

Author contributions

Jacintha Menezes: Conceptualization, Literature Review, Writing - Original Draft, Writing - Review& Editing

Nadeesha Hemachandra: Literature Review, Writing - Original Draft, Writing - Review& Editing

Conflict of Interest

The authors declare that they have no conflicts of interest.

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