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Robotics and AI-Assisted Disease Phenotyping in Bt Cotton Fields: Transforming Modern Plant Pathology

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ABSTRACT

The large-scale use of Bt cotton has greatly alleviated pressure from lepidopteran pests, but this development has inadvertently altered the pathosystem, elevating secondary or opportunistic pathogens as a significant source of losses. Traditional visual estimation techniques for disease assessment reliant on subjective scoring metrics remain costly and inefficient amid large-scale Bt cotton monocultures. In this review, we summarize recent innovations in autonomous ground and aerial robotics coupled with deep learning as a paradigm shift for disease phenotyping in Bt cotton. We discuss the latest advances in robotic technologies; artificial intelligence, including convolutional neural networks and vision transformers; and explainable AI tools for detecting sub-millimeter-level and multispectral plant diseases. In particular, we highlight challenges like disease mimicry in Bt plants and emerging pathosystems, such as Fusarium wilt and Alternaria leaf spots. We also propose a detect-analyze-respond robotic framework that integrates robotics, AI, and molecular techniques for next-generation plant pathology. Finally, we address key bottlenecks, including hardware robustness, generalizability of machine learning models across Bt varieties, and ethical concerns.

Keywords: Bt cotton, disease phenotyping, robotics, artificial intelligence, deep learning, plant pathology, high-throughput phenotyping

1. Introduction: The Bt Cotton Paradox

1.1. A Success Story with Unintended Consequences

Since Since its commercial introduction in the mid-1990s, Bt cotton, genetically modified with insecticidal proteins derived from the bacteria Bacillus thuringiensis, has revolutionized the world's cotton cultivation. The benefits of reduced use of insecticides, higher yields, and enhanced farmer income levels have been well-documented in China, India, the U.S., and Australia[1]. Nevertheless, the successes brought about by Bt technology have also led to unexpected changes in disease dynamics which were not foreseen by scientists and plant breeders. Prior to the advent of genetically-modified cotton varieties, damage caused by insects like

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Helicoverpa armigera and Pectinophora gossypiella was an important point of ingress for bacteria and fungi. One would imagine that fewer insect attacks should translate to less incidences of diseases. This is, unfortunately, not the case[2]. There is now a growing literature on changes in disease dynamics with respect to soil-borne vascular wilts like Fusarium oxysporum f. sp. vasinfectum and Verticillium dahliae, as well as the foliar pathogens Alternaria macrospora and Ramularia areola[3].

The reasons behind the change are many and varied. Canopy disturbance reduction modifies microclimate within fields, possibly increasing the prevalence of moisture-loving diseases. Root exudates may be altered as a result of transformation, leading to modifications in soil microbiology. There is even some evidence that Bt insertion itself can cause physiological shifts that make plants more vulnerable to vascular diseases[4]. Most importantly, however, because insect damage no longer exists to interfere with proper identification, the early signs of disease can be recognized provided the means are available. The difficulty, of course, is identifying the disease at appropriate scales in time and space, which becomes possible but also challenging when dealing with modern cotton farming[5].

1.2. Why Traditional Pathology Fails in Bt Cotton Fields

Bt cotton farms are typically big farms, ranging from over fifty hectares, with a high level of field uniformity and dense planting. Traditional scouting, which requires walking the transects, observing leaf and stem symptoms, and classifying the disease severity using a one-to-nine score system, faces four major shortcomings that have become increasingly untenable within the modern context of intensive agriculture [6], [7] . The first problem concerns subjectivity, since the inter-observer agreement of disease severities is often below sixty percent due to subtleties in symptom identification. The second problem relates to sample bias due to the inherent tendency of scouts to observe only edge rows and easily observable plants within a field, which overlooks the important variability existing in large fields in which foci of disease are common[8], [9]. The third limitation deals with time resolution, since traditional scouting done on weekly or even biweekly basis cannot effectively capture the dynamic nature of disease development in weather-

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friendly conditions. Finally, visual scoring throws away a great deal of information[10].

2. Fundamentals of Disease Phenotyping in the Bt Context

2.1. Key Diseases of Bt Cotton

However, the spectrum of disease in Bt cotton differs widely between geographical regions and environments, some pathogens have shown persistence across different production regions. The vascular discoloration, unilateral chlorosis of leaves, and eventual wilting leading to death is seen in fusarium wilt caused by Fusarium oxysporum f. sp. vasinfectum [11] . However, this disease has been particularly difficult to control in Bt cotton because some specific Bt lines make the plants more susceptible to the disease especially if nematodes are involved. Another difficult disease is verticillium wilt caused by Verticillium dahliae and is characterized by interveinal chlorosis, defoliation, and vascular streaking. This disease has increased in severity in Bt cotton because the constant planting in monoculture has built up the inoculum load [12] . Alternaria leaf spot causes large brown lesions with concentric rings on leaves, due to the reduced insect infestation in Bt cotton fields, the symptoms of early Alternaria infections are now being noticed. Bacterial blight, due to Xanthomonas citri pv. malvacearum, has made a comeback in varieties that only carry the Cry1Ac gene, showing up as angular water-soaked areas with bacterial ooze on both leaves and bolls [13] . The fungus Ramularia areola causes ramularia leaf spot, resulting in white, powdery lesions found mostly on lower leaves, where its development has been encouraged by the dense canopy typical of high-yielding Bt varieties. Lastly, there are the boll rots; complex diseases associated with Fusarium, Aspergillus, and Pantoea bacteria, leaving the bolls discolored and unopened[13].

2.2. Phenotypic Traits of Interest

In each of these diseases, phenotype characterization would require consideration of a broad range of traits going beyond just presence or absence of symptoms. Lesion characteristics such as lesion size and shape, lesion margin types like necrotic, chlorotic or water-soaked, as well as sporulation level, are necessary in order to determine the identity and stage of the disease[14]. Disease pattern characteristics

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like distance from the leaf margin, vein association, as well as differentiation between lower or upper leaf surface, are useful for discriminating between pathogens that have similar visual characteristics [15] . Temporal characteristic like lesion expansion rate and interval from initial infection to sporulation are key in determining disease progression and host resistance. Traits measured at the whole plant level include the Wilting Index, percentage defoliation and the extent of the vascular discoloration observed in cross-sections of the stems. Yield related traits such as number of retained bolls and cotton quality parameters like micronaire and strength are important[16].

2.3. Limitations of Traditional Visual Scales

The commonly applied one-to-nine scoring system, with one representing no symptoms and nine signifying the death of the plant, eliminates about ninety percent of the information that can be gleaned from the image of a leaf[17]. Two spots with the same area but different arrangement in the plant might represent very different types of resistance within the plant. Leaves that score equally on the same severity score might actually have vastly different levels of progression of the disease. The manual process of phenotype assessment, limited by the attention span of humans, can hardly do justice to this kind of information[18].

3. Robotic Systems for In-Field Data Acquisition

3.1. Ground Robots for Under-Canopy Phenotyping

The ground-based rovers yield high spatial resolution and have the distinct capability of capturing images of stems, petioles, and lower leaves, which are vital plant structures for detection of vascular wilts and disease progression from the lower parts of the canopy [19] . There have been numerous attempts to adapt platforms designed for different purposes for cotton plant phenotyping. Among them is the TerraSentia rover, created by EarthSense company for use in phenotyping of corn and soybean plants. This platform was adapted for cotton plants with the installation of new side cameras and multispectral sensors[20]. During experiments, these rovers were shown to be capable of identifying Fusarium wilt symptoms 8 days before the human scouts can identify them visually. Another example of such platform is the PhenoBot from the University of Arizona. It features an adjustable

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boom height and uses RGB and thermal cameras as well as LIDAR technology for measuring canopy structure [21] . This platform was capable of identifying Verticillium wilt 10 days earlier than a human scout. This was done using thermal imaging that shows higher temperature in the leaves due to vascular blockage, which makes transpiration impossible[22].

There are several advantages that ground rovers offer for Bt cotton phenotyping. First, rovers can work in dense canopies even during midday when microclimatic conditions are favorable for pathogens' development, but not prone to shadows that affect imaging from an aerial vehicle. Second, thermal imaging showed to be extremely useful in terms of identifying the vascular blockage before any visual wilting becomes apparent[22]. Nevertheless, there are disadvantages to using these technologies for phenotyping. They include rather low coverage speed which averages at 0.5 ha per hour for one robot; hence, it would take a few days for a large commercial field to complete surveys [23] . Moreover, environmental factors might have a negative effect on efficiency; specifically, rovers tend to get stuck because of mud, obstacles, and irrigation furrows. Finally, the batteries last no more than four-six hours due to canopy shade[24].

3.2. Aerial Systems for High-Throughput Canopy Surveillance

The aerial component of remote sensing, using mainly drones carrying multispectral and thermal cameras, allows rapid scanning of vast areas that complement the labor-intensive ground-based surveying method [25] . Common setups for aerial disease phenotyping by drones feature multispectral cameras with five to ten bands at blue, green, red, red edge, and near infrared wavelengths. Such bands allow calculation of vegetation indices, such as NDVI, NDRE, and PRI, which correspond to canopy condition and photosynthesis activity[26]. The thermal camera with wavelength in the range of eight to fourteen micrometers measures canopy temperature depression, an indicator of stomatal conductance that decreases in case of infection by vascular pathogens causing disruption of water flow through leaves [27] . Hyperspectral camera, with one hundred or more contiguous spectral bands, has not yet found wide application due to its high price and computational requirements but could provide spectral unmixing, thereby differentiating between disease and other stress factors

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like nitrogen deprivation and drought[28].

Multiple investigations have shown the efficacy of using drones for phenotyping cotton plants. In one instance, a drone equipped with a six-band multispectral camera was capable of mapping bacterial blight infections in Bt cotton with a success rate of eighty-seven percent [29] . In this example, the drone detected disease foci within the field that were not identified through traditional scouting methods. Another, more recent, but unpublished investigation conducted in Texas made use of thermal imaging in addition to RGB cameras and was able to predict the occurrence of Verticillium wilt eight days prior to ground observations with an AUC score of 0.91[30].

3.3. Hybrid Approaches: Drone-to-Rover Handoff

The best method in many cases would be using the hierarchy of both aerial and terrestrial systems together. With this method, the drone flies over the whole plantation, e.g., two hundred hectares within half an hour, and based on its observations with the help of a lightweight AI algorithm, detects the areas of concern with visible disease symptoms and sends the rover to conduct high-resolution imagery along with multispectral analysis [31] . The rover will also perform a biopsy in case of more advanced technology. In such a way, the efficiency of the first stage can be complemented with the precision of the second. According to the Cotton Research and Development Corporation, an unpublished proof-of-concept of using such technology in Australian cotton showed a successful decrease in time required to diagnose diseases after entering the field. Using manual scouting took up to three days while using drones and rovers took only four hours[32].

3.4. Gantry Systems and Cable-Suspended Robots

Automated gantries like the Field Scanalyzer by LemnaTec are ideal for research applications because they allow researchers to achieve controlled and repeatable imaging under either artificial or natural conditions. These gantry systems are not scalable to production environments, but they play an important part in generating ground truths used in training AI algorithms that will ultimately be implemented in autonomous machines. Cable-driven robots, where the robot moves through overhead cables, present an alternative between automated gantries and autonomous

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machines, and have been proven useful in cotton breeding research[33].

4. AI Pipelines for Disease Feature Extraction

4.1. Preprocessing Challenges and Solutions

The process of converting images obtained from robots into phenotyping information for disease phenotyping involves a series of steps to be taken using an artificial intelligence pipeline. The pipeline should take care of many issues in the area of preprocessing of data, detect and segment plants' organs and lesions, measure their features, and, in more sophisticated tasks, model the evolution of diseases over time [34] . There are preprocessing challenges associated with in-field images that are quite different from those associated with lab-based imaging techniques. Lighting variations in the form of cloud shadows and angle of the sun are among the most widespread challenges. Histogram equalization and color constancy approaches, such as the Gray World and White Patch approaches, are some of the approaches that could help in solving these issues[35]. Leaf motion as a result of winds leads to motion blur that might affect the identification of lesions on leaves and, hence, lead to poor classification results. In case fast shutter speeds cannot be achieved, DeblurGAN-v2 can be used to improve the clarity of the images. Shadows that could occur due to neighboring leaf objects or even the robot should be detected and appropriately either removed or taken into consideration while analyzing the results[36]. Shadow areas can be detected by applying intensity thresholds together with some morphological methods and subsequently inpainting them through use of adjacent pixel data. Scale variation is also a major problem, in which the same plant disease would look drastically different if observed from both 5cm and 50 cm away from the object[7].

4.2. Segmentation and Detection Architectures

Following the end of pre-processing, there should be execution of other AI techniques such as segmentation and detection. The common approach used in leaf and boll instance segmentation involves using Mask R-CNN with ResNet-50, resulting in an accuracy in the range of ninety-five percent when testing on CottonSeg version 1.0 consisting of fifteen thousand annotated cotton leaves [37] . As far as lesion detection goes for real-time applications, YOLOv8 is the current

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best model available, achieving a mean average precision of 0.92 while processing at forty-five frames per second on a Jetson Orin edge computing platform. YOLOv8 was tested on a data set of five thousand Alternaria lesions[38]. If pixel-level lesion segmentation is required rather than bounding box detection, then the commonly preferred network architecture is U-Net together with its different variations such as Attention U-Net and U-Net++. In the case of Fusarium wilt, which requires analysis of discolored stems for vascular discoloration, the most successful model has been a 3D U-Net, giving Dice similarity coefficient values above 0.88[39].

4.3. Quantitative Phenotyping Beyond Detection

The detection process itself, though, does not constitute proper phenotyping. The system needs to do quantitative measurements of the lesion parameters as well as those of plant organs. The conventional operations offered by computer vision libraries, in particular OpenCV, enable counting of lesions, total area and perimeter, and calculating some characteristic features of lesions' shape, such as circularity and solidity. When assessing disease severity, special attention should be paid to analysis in the color space[40]. The RGB image, for instance, can be transformed into the CIELAB model, thus allowing the calculation of chlorosis from the a axis – decreasing values of a indicate decreased levels of chlorophyll and progressing disease. If a particular pathogen produces any visible sporulation, like Ramularia areola, estimation of conidia density on lesions can be done using high-resolution density maps built using images acquired from lesions at fifty micrometers per pixel[41].

4.4. Time-Series Analysis for Disease Progression

Undoubtedly, the most advanced use of AI in disease phenotyping includes the application of time-series analysis to track the progression of disease. The development of cotton disease does not occur in a straight-line fashion. Instead, the disease progresses in a non-linear manner, which depends on various factors including the physiology of the host, the level of pathogen inoculum, and the environment[42]. LSTM networks and vision transformers with temporal attention mechanism have successfully been used to predict such disease progression patterns. One experiment involved giving a series of five canopy images from the same plant

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in ten days' interval [43] . Using these inputs, the vision transformer accurately predicted the severity of the disease on day fifteen with an average error rate of 0.6 on the one-to-nine rating scale, while humans predicted the outcome with an average error rate of 1.2. It is essential to note that temporal models are capable of distinguishing between tolerance and resistance in a plant. Tolerance refers to slow progression of the disease despite the high inoculum level of the pathogens while resistance refers to low multiplication of the pathogens despite time[44].

5. Bt-Specific Challenges and AI Countermeasures

5.1. Confounding Factors from Absence of Insect Damage

Though the basic principles of robotic phenotyping and the use of AI for the phenotyping of various crops remain the same, some particular challenges arise in the context of using these technologies in Bt cotton. Specifically, the lack of insect damage in Bt cotton plants may pose an obstacle for the development of appropriate algorithms, which were originally created by training on datasets including both Bt and non-Bt pictures [45] . Because insect bites are quite frequent in non-Bt crops, and because they can sometimes be confused with lesions caused by a fungal infection, there arises the possibility that the AI program will mistakenly identify the insect bite as a disease or even confuse some actual lesion caused by the fungi as insect damage due to the absence of the latter in Bt plants [46] . To deal with this problem, special training sets, which would contain different labels for insect bites, abiotic stress symptoms, pathogen-induced damage, and normal cells, should be compiled, with the help of domain adaptation methods, such as CORAL or DANN, for example[47].

5.2. Symptom Mimicry and Multi-Modal Disambiguation

Disease symptom mimicry creates an even greater hurdle in the task. There are several diseases that have identical symptoms to each other, but each would require different courses of treatment. Alternaria leaf spot creates round lesions on leaves, but they can be mistaken for glyphosate damage which causes interveinal chlorosis and necrosis [48] . Potassium deficiency in plants manifests itself in leaf margin burning and yellowing, and it may initially be taken for Verticillium wilt. Finally, drought creates symptoms of wilting and rolling of leaves, making it possible to

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confuse it with Fusarium wilt. Determining the cause of the symptoms is important as it determines whether the farmer needs to use fungicides, change his fertilization, adjust irrigation or do nothing at all [49] . Using multi-modal AI models that incorporate thermal and multispectral imaging into RGB data increases recognition accuracy significantly. In a recent ablation experiment, incorporating thermal and multispectral channels into AI models lowered the percentage of misdiagnosing glyphosate injury as Alternaria leaf spot from twenty-three to four percent[50]. The thermal channel is especially useful because fungal infections create heat signatures, as the lesions caused by pathogens are metabolically active, whereas there is no heat difference in areas affected by herbicides[51].

5.3. Data Scarcity and Few-Shot Learning for Novel Diseases

Limited availability of training data is another major challenge when dealing with novel or emerging diseases related to Bt. When an originally uncommon pathogen spreads rapidly into epidemic proportions in Bt cotton, like Ramularia areola has done in some cultivation zones, the number of available labeled examples is limited. Methods such as few-shot learning have been designed to tackle exactly this problem. In prototypical networks, a metric space is learned, where disease categories cluster; a disease can be identified from as little as five to ten examples based on how far it lies from class prototypes [52] . Synthesizing training data via Generative Adversarial Networks, such as StyleGAN, or diffusion models, such as Stable Diffusion fine-tuned on Bt cotton leaf images, could result in accurate simulation of lesions of uncommon diseases and therefore augment training data without any need for gathering more information in the field. Transfer learning across disease types, where a network pretrained on one hundred thousand images of generic plant diseases from the PlantVillage dataset was further fine-tuned on fifty examples of new Bt cotton disease, proved capable of classifying diseases with over eighty percent accuracy[53].

5.4. Explainable AI for Pathologist Acceptance

Explainability is not an abstract concept but a practical one, especially for plant pathologists who have spent years honing their ability to recognize diseases using visual cues. There are techniques in explainable AI that make it possible to see how

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models make their predictions. In gradient-weighted class activation mapping (Grad-CAM), a heatmap is applied to the input image with an indication of which parts (pixels) of the image contributed most to the predicted output [54] . This means that when using Grad-CAM in detecting Fusarium wilt, it is expected that the model should focus its decision on vascular bundles, meaning it picked up a relevant feature from the images. The SHapley Additive exPlanations (SHAP) provides insight into the contribution of the different input features to the prediction made[55]. This makes it possible to see if the model weights features appropriately. The model can then be challenged to use human-understandable concepts like chlorosis and sporulation density using Concept Activation Vectors (CAVs). If a CAV shows that the model is basing its decision on time of day or camera angle, then that model is rejected or revised[56].

6. From Phenotyping to Epidemiology: Spatiotemporal Modeling

6.1. Integrating Multi-Source Data for Disease Modeling

While the objective of disease phenotyping goes further than identifying disease status on single plants, epidemiological modeling becomes possible through integrating the robotic survey data with environmental, soil, and management data. Disease phenotyping with robotic survey data makes epidemiological modeling possible, something not achievable through human-based surveys. A comprehensive spatiotemporal disease model takes inputs from various data sets [57] . The robotic survey data provide spatial disease severity scores and lesion density data at a higher resolution, usually every 1 to 10 m. Climate data including temperature, relative humidity, and leaf wetting duration are important as these variables play a significant role in influencing infection and sporulation rate. Soil data including soil moisture content, soil texture, soil electrical conductivity, and quantification of soil pathogens through quantitative PCR are needed for modeling soil borne pathogens' development. Cultivar maps containing information on type of Bt and their planting dates are incorporated for considering differences in genetic resistance to diseases. All of these data will be stored in a geospatial database such as PostGIS[58].

6.2. Hotspot Detection and Anisotropic Spread Analysis

It is unlikely for disease to spread isotropically within cotton crops. For instance, the

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speed of disease spread within a field may be higher along the direction of the crop row than the cross direction due to factors such as the movement of the cultivating equipment, water flow within irrigation channels, and wind direction. An anisotropic disease spread can be quantified by using geostatistics with robotic measurements at a resolution of one meter. In a study conducted in Texas in 2022 for Verticillium wilt, the range along rows was forty-five meters, while the range across rows was only twelve meters, indicating a spread that is almost four times faster along rows than across them[16].

6.3. Early Warning Systems and Predictive Modeling

An early warning system stands out as the most useful implementation of spatiotemporal models of disease progression. The hybrid model, which uses the mechanistic SEIR model (Susceptible, Exposed, Infectious, and Removed classification for crops) combined with the Long Short-Term Memory neural network for weather prediction, can accurately forecast disease severity from seven to fourteen days in the future [59] . In the case of Alternaria disease outbreak in Gujarat, India, the hybrid model yielded an RMSE score of 0.9 on the one-to-nine severity scale, which was significantly better than the pure mechanistic model that yielded an RMSE of 1.7. The real-world usefulness of such a system would allow for targeted fungicide application, such as applying the fungicide only to the quadrant in which disease severity is forecasted to reach 4 within ten days[60].

6.4. Implications for Insect Resistance Management

A pertinent research question regarding Bt cotton crops concerns whether disease stress influences Bt toxin production. Early results indicate that serious infection with Fusarium wilt causes a reduction of up to 30% to 50% in Cry1Ac protein content within the infected vessels[4]. Should this observation be validated by more comprehensive research, it would mean that a detrimental feedback mechanism is at play, whereby disease stress lowers Bt production, thus enhancing insect survival and causing additional insect feeding. This, in turn, leads to increased plant stress and disease susceptibility. Such information can be gained using artificial intelligence (AI)-based phenotyping technologies[61].

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7. Case Studies from Field Deployments

7.1. Case Study 1: Gujarat, India – Alternaria macrospora Detection

In the state of Gujarat in India, for the 2025 Kharif season, a group of small-scale farmers cultivating one hundred twenty hectares of genetically modified Bt cotton that produces Cry1Ac and Cry2Ab toxins employed five affordable ground rovers built using the improved AgBot design. Each rover, valued at three thousand dollars, was fitted with RGB cameras and a Jetson Nano edge computing unit. Using a YOLOv8 classifier trained on a dataset of eight thousand labeled images of Alternaria macrospora spots, the system attained a mean average precision of 0.94 in validation. During the entire growing season, the rovers were able to inspect two percent of the total field surface daily, whereas traditional scouting could only survey 0.2 percent. Importantly, the AI system identified initial lesions caused by Alternaria with an average diameter of 1.2 mm, which went unnoticed by the scouts until the diameter exceeded five millimeters. Using the risk maps created by the AI system, fungicides were applied to only fifteen percent of the farm, compared to treating the whole one hundred twenty hectares with fungicide. This lowered the usage of fungicides by sixty-two percent, without compromising the yield. Initially hesitant about AI implementation, farmers gained confidence when during a trial run the rover identified a sentinel plant five days before any human recognition of symptoms was possible[32], [62], [63].

7.2. Case Study 2: Texas High Plains – Verticillium Wilt Mapping

An agribusiness firm farming two thousand hectares of continuous Bt cotton in the Texas High Plains carried out weekly multispectral drone flights over the crop with a MicaSense RedEdge-MX camera. A U-Net algorithm trained with twenty-five hundred manually segmented canopy pictures created per-pixel severity scores for Verticillium wilt. These scores were combined with the soil's electrical conductivity obtained during an electromagnetic induction survey. It was discovered that Verticillium wilt severity had a high correlation with the soil's electrical conductivity with an r-value of 0.81, showing that areas rich in clay soil with poor drainage were more susceptible to Verticillium infection. Consequently, variable-rate irrigation was used to minimize water supply to these high-electrical-conductivity

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regions, leading to a disease severity decline by twenty-three percent in the next planting cycle. Furthermore, the AI algorithm identified another previously unknown Verticillium outbreak pocket in a remote corner of the field not traversed in manual scouting due to the field's remoteness[62], [63], [64].

7.3. Case Study 3: Australia Real-Time Boll Rot Detection

At an eight hundred hectare Bt cotton farm in Namoi Valley of Australia, a robot designed from a cotton harvester was used. This robot had a hyperspectral imaging system with a wavelength range from four hundred to one thousand nanometers at five nanometer spectral resolution, along with a robotic arm having six degrees of freedom for taking tissue samples. A one-class support vector machine classifier trained using spectral data of healthy bolls could identify any abnormal bolls for further analysis. The system successfully diagnosed boll rot due to Pantoea agglomerans at a considerably earlier stage than manual inspection, and the false alarm rate was only five percent. LAMP assay results obtained from the robotically collected samples revealed that ninety-two percent of flagged bolls were affected by the pathogen. Thanks to this early warning, the grower was able to control the time of irrigation to decrease humidity of the bolls. Consequently, the boll rot yield loss decreased from about twelve percent to five percent in the next growing season[64], [65], [66].

8. Integration with Plant Pathology Workflows

8.1. AI as a Triage Tool for Molecular Validation

Successful implementation of robotics and AI-driven phenotyping does not render the plant pathologist obsolete but transforms and enhances his or her function. One of the most effective strategies is to use AI for prioritizing plants and fields for further analysis by humans and the genome. One example of an integrated approach could involve the following sequence of steps. First, a robot photographs ten thousand plants in the field. Next, an AI system identifies the five percent of plants that demonstrate the worst symptoms, or symptoms that deviate from the norm, as well as one percent that appear healthy [67] . The pathologist will inspect the highlighted plants using a tablet computer with the AI-created heatmaps and confidence measures displayed, collect tissue samples, and take note of anything that

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the AI might have overlooked. These tissue samples will then be run through PCR or LAMP to test for known pathogens. Molecular testing results will then be fed back to the machine learning model as new training data, further enhancing its accuracy. This approach effectively integrates the advantages of machine learning (high-throughput analysis) and molecular testing (diagnostic precision), recognizing the important fact that pathologist hours are a limited and valuable commodity[68].

8.2. Digital Specimen Libraries and Open Data Initiatives

One of the key barriers to adoption of the AI-based phenotyping solution is the availability of high-quality, open-source, pathologist-certified image data sets of Bt cotton pathogens. While the PlantVillage dataset represents one of the best sources of information on plant pathology in general, it does not contain many images of cotton plants and does not cover any specific issues related to Bt cotton. Therefore, an initiative similar to that launched by PlantVillage, but targeting the field of cotton plant pathogens, which might be referred to as the "Cotton Disease Image Repository," becomes absolutely necessary [69] . In order to develop such a repository, one needs images of each disease from several angles under various lighting conditions; pixel-level segmentation masks to train a machine learning model; full metadata containing Bt event type, plant growth stage, environmental factors, and validation of pathogens via PCR analysis; and version control to allow for releasing a new Bt event along with a new pathotype[10].

8.3. Mobile Apps versus Full Robotic Systems

For smallholder farmers in low-resource settings, the deployment of autonomously operating rovers cannot be made affordable. But mobile applications that leverage the phone camera and utilize a lightweight CNN like MobileNetV3 can help perform diagnostic work at a marginal cost that is nearly zero. In a 2024 experiment conducted in the Maharashtra region of India, there was a comparison among three methods: hiring an expert pathologist at forty dollars a plot for three hours, using a mobile application run by the farmer without any additional cost except for the smartphone for thirty minutes, and using a ground rover with AI at twelve dollars per plot for fifteen minutes[70]. The accuracy achieved with the expert pathologist was eighty-five percent, with the mobile application it was seventy-two percent,

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while with the rover it was ninety-four percent. The mobile application is no substitute for robotics but can act as a triaging tool for the smallholder to contact extension agents later[71].

9. Current Gaps and Future Directions

9.1. Hardware Limitations and Environmental Robustness

In spite of the outstanding progress achieved according to the results outlined above, there are significant shortcomings that need to be addressed in terms of hardware, software, ethics, and regulation. In terms of hardware, the issue with the life of a rover battery remains critical. Densely planted fields make rovers move at the speed of up to 0.5 m/s only. This leads to the possibility of covering only around fifty square meters per hour. Batteries with an exchange option are also possible but involve manual work [24] . Although solar energy helps to charge batteries efficiently, it adds to their weight and makes them less efficient. Environmental resistance is an additional problem that includes dust, humidity, and high temperatures that reduce the quality of both sensors and electrical components in general. IP67 protection is effective but increases the overall price and weight of the device. Hyperspectral cameras able to detect subtle signs of diseases are still too expensive – their costs exceed twenty thousand dollars[72].

9.2. AI Limitations and Model Generalization

Regarding the AI side of things, one of the unsolved problems is generalization among Bt events. A CNN trained using Cry1Ac cotton might not be able to generalize using Cry2Ab cotton due to the different canopy architecture, leaf morphology, and physiology. Domain adaptation would help, although data that is representative of the target domain needs to be obtained. Continual learning is another technique under development where a model can learn on its own while continuously being fed new data [73] . The danger in using this technique is how previous knowledge might be forgotten. Another vulnerability worth discussing is adversarial examples. Adversarial examples consist of deliberate perturbations of input data to cause misclassification in deep learning models with high confidence. This includes a sticker attached to a leaf, or a particular shadow pattern [74] . Adversarial examples have already been used against convolutional neural networks

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in laboratory conditions and have implications for malicious attacks in agriculture as well. Uncertainty quantification is a necessity for ensuring that AI systems can be used safely in practice. A standard CNN gives point estimates without any confidence intervals for predictions, making it difficult for the user to know when the model is simply guessing[75].

9.3. Ethical and Regulatory Considerations

The ethical and regulatory issues have received much less attention compared to the technical ones, yet they are just as important for responsible implementation. One of them concerns the question of data ownership. Who will own the high-resolution disease map of the farmer's field that the robot produced? The farmer who owns the land, the manufacturer of the robot, or the company that produces the Bt variety that is being tested? These legal aspects significantly lag behind the technological ones, which might slow down the implementation process [76] . Another issue is algorithmic bias For example, if the training datasets contain an excessive number of examples of certain Bt events, environments, or disease severities, then the accuracy of the machine learning algorithms might decrease dramatically for those cases that have not been covered [77] . The best way to detect such biases is to report the composition of the training datasets together with the corresponding performance metrics. Last, there is a risk of losing jobs for human agricultural scouts due to autonomous scouting, but it might create jobs in other areas, such as operating the drones and annotating the data used for training the models[78].

9.4. The Next Frontier: Robotic Micro-Sampling

What lies ahead extends beyond visualization to active intervention. Recent studies integrate AI-operated robotic arms with on-chip molecular diagnostics, creating autonomous closed-loop systems for identifying, diagnosing, and responding to disease. Typically, AI first detects lesions on plant leaves; a six-axis robotic arm then punches a 2-mm biopsy from the suspicious area and delivers it to an onboard LAMP chip for molecular pathogen detection and identification [79] . The entire process takes just 30 minutes, after which results and geotagged coordinates are transmitted wirelessly to enable targeted interventions by farm management systems. This concept was demonstrated in a Science Robotics study on

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Xanthomonas in tomatoes [80] . With its larger leaves and more intricate canopy structure, Bt cotton represents the logical next step.

10. Conclusions

The incorporation of robots and artificial intelligence in disease phenotyping has led to a revolutionary change in the application of plant pathology in Bt cotton. No longer bound by human limitations such as vision, endurance, and personal biases, the field is able to analyze disease severity in detail at the sub-millimeter scale across vast areas of several thousand hectares, monitor its evolution, and unravel the intricate relationships among Bt events, pathogen populations, and environmental conditions. Bt cotton has been an excellent test system for this revolution because of the way its insect resistance allows one to see what was invisible before. The principles learned from Bt cotton will be applicable to other genetically engineered crops like Bt corn and virus-resistant papaya, as well as conventional agriculture.

The way forward will require significant coordination between plant pathologists, robotics researchers, machine learning experts, agronomists, and social scientists. Although technical obstacles such as hardware resilience, model generalizability, uncertainty quantification, and susceptibility to adversarial attacks persist, they do not seem to be prohibitively difficult if sufficient research funding is directed toward them. The real difficulty may lie in convincing a risk-averse field of science that has used visual assessment methods for more than a hundred years to have faith in automated processes.

This review ends with an actionable recommendation from the fields of plant pathology and agricultural engineering. First, create openly accessible image databases for Bt cotton disease images, similar to the PlantVillage effort, but with metadata standards designed specifically for cotton. Second, invest in cross-disciplinary proof-of-concept research in cotton growing regions of India, China, the U.S., Australia, and Brazil to prove the effectiveness of robotics and AI for phenotyping in the field. Finally, set standards for ethical use of data and algorithms to prevent unfair bias or exploitation of farmers and data owners. The technology is there; the need is immediate. The revolution in plant pathology has already begun.

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