

Techniques for Rapid Identification of Plant Pathogens

Manikandan Muthu*

Department of Biotechnology, Saveetha School of Engineering, Saveetha Institute of Medical and Technical Sciences, Tamil Nadu, India.

*Corresponding author: Manikandan Muthu, Department of Biotechnology, Saveetha School of Engineering, Saveetha Institute of Medical and Technical Sciences, Tamil Nadu, India, E-mail: danmanikanmuthu.sse@saveetha.com

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Description

Plant pathogens are important yield-limiting factors that significantly reduce crop productivity worldwide, posing serious threats to food security, the world's most pressing agricultural issue. Chemical treatment is still the most effective method for reducing plant disease incidence, but repeated application can make pathogens less susceptible. Overspray can also harm the soil microbiota and pollute the environment. As a result, effective diagnostic methods for rapidly identifying plant pathogens in the early stages of infection become essential for ensuring agricultural sustainability and food security. In order to achieve this objective, numerous molecular methods have been developed for the rapid detection of plant pathogens. However, they are generally unsuitable for in-situ analysis, take a long time to complete, are expensive, and require skilled operators. Any of the nanotechnology tools for diagnosing plant pathogens, such as micro needle patches, nano pore sequencing, nano barcoding, nano biosensors, quantum dots, equipment for nano diagnostic kits, metal nanoparticles, miRNA-based nano diagnosis and array-based nano sensors, can be used to protect plants. In light of their potential to facilitate high-throughput analysis and enhance plant pathogen identification sensitivity, accuracy and speed. The use of nanotechnology for faster, cheaper and more accurate diagnosis of plant pathogens is the focus of this review.

Interactions among Various Types of Noncoding RNAs

Plant pathogens harm crops and put global food security in jeopardy. Using crosstalk between various signaling pathways, plants have constructed intricate defense networks against pathogens. Non-coding RNAs and protein-coding genes are important regulators of signaling pathways that confer immunity on plants. The term transcriptional noise was first used to describe the discovery of ncRNAs in plant transcriptomes. The significance of non-coding RNAs has been emphasized by recent reviews. However, additional research is required to comprehend interactions among various types of noncoding RNAs. The aim of this review is to investigate how pathogenic diseases in various plant species interact with long, small, and circular RNAs. Plant ncRNAs, their biological functions, and their significance in utilizing the most recent molecular-based crop

protection technologies could all be discovered through advances in genomics and bioinformatics. In a co evolutionary arms race with their pathogens, plants rapidly diversify and specialize genes involved in virulence and resistance. Molecular decoys, trans-kingdom RNA interference, two-speed genomes, and receptor networks are just a few of the significant advances in plant-pathogen interactions that resulted from the expansion of the functional landscape of genes. This is typical of the evolutionary process known as genetic co-option, in which existing genes are used to perform new biological functions. Cis-regulatory variation, Horizontal Gene Transfer (HGT), mutations that alter molecular promiscuity, rewiring of gene networks and protein complexes, and co-option all play a role in interactions between plants and pathogens. The functional and predictive biology of interactions between plants and pathogens relies heavily on our comprehension of these molecular mechanisms. Sulfurs biochemical adaptability allows it to play a variety of roles in interactions between plants and pathogens. This review highlights new evidence that plants can limit the availability of S during immune responses and evaluates the current understanding of the mechanisms by which pathogens acquire S from their plant hosts. We talk about the discovery of S-related host disease-susceptibility genes that can be changed genetically to make new crops resistant. Last but not least, we provide a synopsis of the issues that need to be addressed in the future as well as a research plan that makes use of systems biology methods to gain a comprehensive comprehension of the various roles that this crucial component plays in the resistance and susceptibility of plants to disease.

Manure Fertilization Affects Endophytic Pathogens

Through the food chain, pathogens can colonize the endosphere of plants and spread to humans. However, we still don't know enough about how agricultural practices like fertilization affect endophytic microbial communities and human pathogens. We used a high-throughput qPCR array and 16 S rRNA gene amplicon sequencing in this microcosm experiment to find out how manure fertilization affects the microbiomes of soils and plants and how this affects endophytic pathogens. According to our findings, manure fertilization had a significant impact on soil microbiomes but less so on endophytic microbial communities. The plant endosphere depends on soil

for bacterial communities and human pathogens. Manure fertilization increased the number of pathogens in the soil and endosphere. An integrated comprehension of how manure fertilization affects endophytic pathogens is provided by these findings. Predators are frequently used by biological control programs to reduce the number of vectors in agro ecosystems in order to control pathogens carried by vectors. In the meantime, the preference of the vector for host status—healthy or infected—determines the disease's spread. However, the controlled affectivity of predators in pathogen transmission is not altered by vector preferences. So, we looked at plant-vector-pathogen models to see how different predation rates and vector preferences for host status affected pathogen transmission in plants. Predators' effects on vector abundance and pathogen transmission in both a non-spatial and a spatially structured meta population model were the focus of our discussion. Predators can control the spread of vector-borne pathogens, as we demonstrated, by reducing the abundance of vectors and preventing the prevalence of pathogens. On the other hand, vector preference significantly influences the controlled affectivity of predators. Additionally, pathogen prevalence oscillation amplitude can be increased by predation in both

plants and vectors; indicating that the presence of a predator may enhance the pathogen dynamics-related effects of environmental stochasticity. In conclusion, our findings add to the prediction made by theoretical disease models that a predator can be a natural enemy for pathogen control and that interactions between predators and vector preferences play a unique role in the spread of vector-borne pathogens. All life on Earth, as well as interactions between plants and pathogens, are based on genetic polymorphisms. The report of phenotypic variation in resistance properties and the identification of underlying major genes were the initial goals of studies on plant-pathogen interaction. The study of plant-pathogen interactions is currently shifting its focus away from families of single dominant genes involved in gene-for-gene interactions and toward an understanding of the plant immune system in relation to a much more intricate signaling network and quantitative resistance. Genome analyses and studies on wild pathosystems progressed simultaneously, revealing enormous variation in natural plant populations. Studies on genetic diversity and the evolution of plant-pathogen interactions must now be placed in the appropriate molecular biological and evolutionary context.