



Role of Epigenetics in Plant Disease Development and Disease Defense

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Abstract

Epigenetics, the study of heritable changes in gene expression that do not involve alterations to the underlying DNA sequence, has emerged as a critical player in the regulation of plant disease development and disease defense. Plant-pathogen interactions trigger a cascade of epigenetic modifications that influence gene expression and ultimately determine the outcome of the interaction. These modifications include changes in DNA methylation, histone modifications, and small RNA-mediated gene silencing. Several studies have shown that changes in DNA methylation patterns can lead to alterations in gene expression that either promote or suppress disease development in plants. Similarly, histone modifications, such as acetylation and methylation, have been shown to regulate the expression of genes involved in disease resistance. Moreover, small RNAs play a key role in plant defense against pathogens, either by inducing silencing of pathogen genes or by activating plant defense responses. Understanding the complex interactions between epigenetic modifications and disease resistance is essential for developing novel strategies to control plant diseases. The application of epigenetic modification technology to enhance plant resistance against pathogens could offer a sustainable and environmentally friendly approach to crop protection. Overall, the role of epigenetics in plant disease development and disease defense is an exciting area of research with enormous potential for future advances in plant pathology and crop protection.

Introduction

Plants are constantly exposed to various pathogenic microorganisms such as bacteria, fungi, viruses, and nematodes, which can cause significant damage to crops and reduce yield. Plants have evolved complex defense mechanisms to protect themselves from pathogens, including physical barriers, chemical defense, and immune responses. Recent research has revealed that epigenetic mechanisms also play a crucial role in plant-pathogen interactions, providing an additional layer of defense against invading pathogens (Qian-Hao Zhu et al., 2016; Law & Jacobsen, 2010; Lamke & Baurle, 2017). Since the word "epigenetics" first appeared in literature about a century ago, researchers are trying to untangle the clues that suggested gene function could be affected by factors other than merely sequence variations (Jablonka and Lamb, 2002). In its literal sense, the term "epigenetic" implies "in addition to alterations in genetic sequence." The term now refers to any procedure that modifies gene activity without altering DNA sequence and leads to modifications that can be passed on to daughter cells (Deans & Maggert, 2015). Epigenetics is the study of heritable variations in the functions of gene without any alteration in its sequence. Because of its significance in biological systems, epigenetics is regarded as revolutionary science. The process of cellular differentiation is the

key illustration of epigenetic modification in eukaryotic biology (Reik, 2007). By activating certain genes while blocking the expression of others, the zygote divides and creates all the different cell types that make up an organism during morphogenesis. C.H. Waddington first used the term "epigenetics" in 1942 to refer to the study of epigenesis (Waddington, 1942). He felt that cell fates were defined in development (canalization), much like how a marble rolls down to the point of lowest local elevation. He used the term "epigenetic landscape" to describe biological development. Some of the classical examples of epigenetic mechanisms were Agouti mouse model, wild type toadflax, epimutant peloric flowers, and formation of queen bee in queen cups. Epigenetic pathways also play a significant role in plant-pathogen interactions. Several studies have demonstrated that the pathogen infection can alter the DNA methylation patterns of plants, altering gene expression and the way the plant reacts to infection.

Mechanisms of epigenetics

1. DNA methylation: Several eukaryotic organisms, including plants, have the ability to methylate cytosine nucleotides in nuclear DNA at any position in the sequence, including CG, CHG, and CHH (H represents A, C, or T) (Suzuki & Bird, 2008). Methyl Transferase 1 (MET1), Chromomethyltransferase-3 (CMT3), and Domain Rearranged Methyltransferase (DRM1/DRM2) are the enzymes involved in DNA methylation. Transposon silencing, genome imprinting, and X-chromosome inactivation were few examples of DNA methylation

2. Histone modification: Modification of histone protein leads to change in the chromatin structure, making the gene accessible or inaccessible for transcription (Bannister & Kouzarides, 2011). It can occur due to methylation, acetylation, phosphorylation, sumoylation and ubiquitination.

3. RNA directed DNA methylation (RdDM): It is one of the three pathways for gene silencing that occurs in all eukaryotic genomes. In this process, the double-stranded RNA (dsRNA) produced by RNA-dependent RNA polymerase 2 (RDR2) were first converted into short interfering RNAs (siRNAs) of 24 nts by Dicer like 3 (DCL3) proteins, followed by methylation of 3' ends by hua enhancer 1 (HEN1) and incorporation into argonaute 4 (AGO4) (Storz, 2002). A scaffold RNA produced by RNA polymerase V (Pol V) having complementary sequence with the AGO4-bound siRNAs were base paired which further recruits domain rearranged methyltransferase 2 (DRM2) and catalyses *de novo* methylation of DNA.

Methods to investigate epigenetic modification

Various approaches are being used to comprehend how epigenetics works. Mass spectrometry, methylation Specific PCR, methylated DNA immunoprecipitation (MeDIP), restriction landmark genotyping, ChIP on Chip Assays, whole genome bisulfate sequencing, HPCE Assay, etc. are some of the methods used to study epigenetic modifications.

1. Bisulfite sequencing: The process of treating DNA with bisulfite to identify its methylation pattern is referred to as bisulfite sequencing (also known as bisulphite sequencing). When DNA is treated with bisulfite, all the cytosine residues were converted to uracil while the 5-methylcytosines were unaffected leaving only the methylated cytosines in the DNA after the bisulfate treatment. In light of the fact that the methylation state of each individual cytosine residue is affected by the bisulfite treatment, a DNA segment's methylation status can be determined at the single-nucleotide resolution (Susan et al., 1994).

2. Methylated DNA immunoprecipitation (MeDIP): Methylated DNA immunoprecipitation, often known as MeDIP or mDIP, is a molecular biology technique used to enrich for methylated DNA sequences on a large scale (chromosome- or genome-wide) using an antibody produced against 5-methylcytosine (5mC) (Weber et al., 2005).

Role of epigenetics in plant-pathogen interaction

Plants have developed inducible defense mechanisms to combat microbial infections, including pathogen-associated molecular pattern-triggered immunity (PTI) and pathogen-derived effectors-triggered immunity (ETI), in addition to structural barriers and constitutive secondary metabolites (Jones and Dangl, 2006; Keller *et al.*, 2016). The ability of the plant to significantly alter its gene expression in response to pathogen infection is essential for the activation and efficacy of PTI and ETI. The significance of epigenetic alterations such as DNA methylation, chromatin modifications, and remodeling, in the transcriptional control of defense-related genes is rapidly emerging as one of the mechanisms underlying this crucial transcriptional reprogramming. Pathogens employ epigenetic pathways to compromise the plant host defenses, much like plants do. In order to survive in a changing environment, hosts and pathogens have developed an unmatched amount of epigenetic processes.

How pathogen induced epigenetic modification in host plant?

Certain genetic loci have been altered directly or indirectly as a result of pathogen pressure. An epigenetic change may become a stable (epi) genetic feature of tolerance or resistance after receiving enough stress. Many signals, including short RNAs, are activated by infection with a suitable pathogen (*r*). From the infection site (leaf), the signal (smRNAs) diffuses systemically to non-infected tissues, including those that produce gametes. In the specified loci, such as R-gene and R-gene-like loci, the signal causes a loss or gain of DNA methylation and such epimutations could be stably transmitted to immediate progeny. Hypomethylation can increase the frequency of homologous recombination, while hypermethylation can increase the frequency of C/T mutations (Alvarez *et al.*, 2010; Yadav & Chattopadhyay, 2011). Panigrahi *et al.*, 2021). The possibility of epialleles and alleles conferring novel avirulence gene recognition specificities will increase as a result of the selection of individuals from a population of variations of epimutations and mutations. This will enable future incompatible interactions and resistance to the same pathogen.

How host plant induced epigenetic modification in pathogen?

Organisms that are pathogenic and invasive exhibit a remarkable ability to adapt in the face of challenges posed by their hosts and the environment. Recent research has shown that plant pathogens rely on epigenetic processes to accomplish this. One noteworthy phenomenon is the variation in effector genes caused by epigenetic changes, which allows pathogens to evade the host's immune system. Additionally, epigenetic modifications can induce reprogramming and diversification of transcriptional patterns by activating transposable elements. The control of gene expression through epigenetic mechanisms offers a versatile way to generate adaptable and heritable phenotypic diversity across successive generations in pathogen population (Kasuga & Gijzen, 2013; Rodríguez-Negrete *et al.*, 2013; Studt *et al.* 2013; Baidyaroy *et al.* 2001; Siersleben *et al.* 2014).

Conclusion

In conclusion, epigenetic mechanisms are important in the interactions between plants and pathogens. Plant immunological responses to harmful microbes are regulated by DNA methylation, histone changes, and RNA-based processes. The creation of novel control methods for plant diseases, such as the use of epigenetic modifiers to boost plant defence or the creation of pathogen-specific RNAi-based crop protection techniques could result from a better understanding of the function of epigenetics in plant-pathogen interactions. Epigenetic mechanisms play an important role in plant-pathogen interactions. In plants, the activation and effectiveness of PTI and ETI rely on different epigenetic modifications for successful reprogramming of its gene expression upon recognition of pathogen infection. Like plants, an epigenetic mechanism also works in pathogen to counteract the plant defense and to promote

virulence during infection. So, the hosts and pathogens have evolved an unparalleled level of epigenetic process to persist in variable environment. Nonetheless, a greater understanding of how epigenetic mechanisms contribute to plant defense and how pathogens may counteract this response for their own benefit could open new possibilities for novel crop protection strategies.

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