



Epigenetics for Disease Resistance

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The study of heritable phenotype changes that do not involve alterations in the DNA sequences called as epigenetics. Epigenetics most often involves changes that affect gene activity and expression, but the term can also be used to describe any heritable phenotypic change. These epigenetic changes may last through cell divisions for the duration of the cell's life, and may also last for multiple generations, even though they do not involve changes in the underlying DNA sequence of the organism. Epigenetic modifications are defined as stable and heritable alterations in gene expression and cellular function without changes to the original DNA sequence. C.H. Waddington (1942) first used the term epigenetics to depict a phenomenon that genetics could not explain, the knowledge in this field has soared and evolved into a branch of science with well-understood molecular mechanisms.

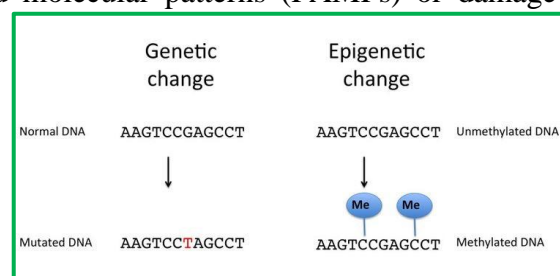
Molecular mechanisms of epigenetics

1. DNA methylation
2. Histone modifications
 - Acetylation
 - Methylation
 - Phosphorylation
3. RNA mediated interference

How does epigenetics work? (See Figure)

Epigenetics and disease resistance

Because of global impact of diseases, developing disease-resistant crop varieties is essential to secure and enhance crop production in sustainable agriculture (Zhou *et al.*, 2020). To this end, it is vital to decipher the molecular mechanism underlying the plant host-pathogen interactions. Recognition of pathogen-associated molecular patterns (PAMPs) or damage-associated molecular patterns (DAMPs) by plant pattern recognition receptors (PRRs) activates the pattern-triggered immunity (PTI), whereas detection of pathogen-secreted effectors by plant resistance (R) proteins initiates the effector-triggered immunity (ETI). Increasing evidence revealed that epigenetic processes such as DNA



methylation, histone post-translational modifications, chromatin assembly and remodeling govern this defense-related transcriptional reprogramming and play key roles in the regulation of crop disease resistance against a wide range of phytopathogens, including viruses, bacteria, fungi, oomycetes, nematodes and herbivorous insects

Case studies

Atighi et al. (2020) investigated the role of DNA methylation in the interaction between host plants and parasitic nematodes. They demonstrated that DNA hypomethylation is associated with reduced susceptibility in rice towards root-parasitic nematodes and is likely to be part of the basal pattern-triggered immunity response in plants.

Erdmann and Picard (2020) studied RdDM pathway in plants that regulates a number of processes by establishing and reinforcing specific DNA methylation patterns, which can lead to transgenerational epigenetic effects on gene expression and phenotype.

Koulagi et al. (2020) attempted to engineer resistance against *Meloidogyne incognita* and ToLCV by stacking dsRNA constructs of the Integrase gene of *M. incognita* and AC4 genes of ToLCV, using co-transformation protocol in tomato and provided evidence for generating resistance through RNAi against multiple biotic stress.

Conclusion

Epigenetic processes such as DNA methylation, histone post-translational modifications, chromatin assembly and remodeling are highly interconnected and manipulate plant transcriptional reprogramming in biotic and abiotic stress responses. DNA methylation marks can be trans generationally inherited and suitable for epi-breeding in all crops. However, information about histone post-translational modifications is likely to be erased during meiosis and only relevant to epi-breeding in clonally propagated crops. Epigenomic variations such as DMRs related to disease resistance traits could be employed as **molecular epigenomic markers to assist the evaluation and selection processes**.

In addition, epigenetic modeling could be used to predict the effect of epigenetic variations on crop disease resistance and provide instruction for epigenetic engineering in crop resistance breeding. With the development of epigenetic methodology and theory on crop-pathogen interactions, exploiting epigenetic variations would provide new avenues for crop disease resistance improvement in the future.

References

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