Epigenetics: Useful Tool in Plant's Gene Regulation

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The field of epigenetics encompasses the study of heritable changes in gene expression that occur without alterations to the DNA sequence itself [Jablonka et al. 2002]. Epigenetics emerged as a field of research in the mid-20th century and has since grown significantly. The term "epigenetics" was first introduced by developmental biologist Conrad Waddington in 1942 to describe the interactions between genes and their environment during the development of an organism. Waddington used the concept of an "epigenetic landscape" to depict how different environmental factors can influence gene expression and development [Waddington et al. 2014, Deichmann et al. 2016].

Epigenetic mechanisms gained further attention in the 1970s with the discovery of DNA methylation. Scientists found that the addition or removal of methyl groups from the DNA molecule can lead to changes in gene expression patterns without altering the underlying DNA sequence [Riggs et al. 1975] [Holliday et al. 1975]. This discovery sparked interest in understanding how environmental signals and developmental cues can influence gene activity through epigenetic modifications. Over the years, advancements in molecular biology techniques, such as high-throughput sequencing and genome-wide profiling, have allowed researchers to explore epigenetic modifications on a larger scale. They have uncovered complex mechanisms involving DNA methylation, histone modifications, and non-coding RNAs that can regulate gene expression and contribute to various biological processes. It has contributed significantly to our understanding of how environmental factors, such as nutrition, stress, toxins and drought, can impact gene expression and potentially influence disease susceptibility [Iwasaki et al. 2014]. By studying the epigenetic regulation of gene expression, researchers aim to unravel the mechanisms that govern development, precisely reprogram the plant's transcriptome and create a balance among various important agronomic traits.

Types of Epigenetic Regulations

The three primary epigenetic regulations are histone modification, DNA methylation, non-coding RNA and. These techniques influence gene transcription, which in turn affects gene expression, rather than altering the DNA sequence [Gayon et al. 2016].

Histone modification

Most frequently, the amino acids on the histone tails acetvlated, methylated, are or phosphorylated to modify histones [Felsenfeld et al. 2014]. The strength of the connections between histones and DNA can change depending on the kind of alteration, changing how chromatin is structured. For instance, acetylation reduces the interaction of the histone tail with the DNA's negatively charged phosphate groups by removing the positive charge from the histone [Rothbart et al. 2014]. The chromatin opens up and is more readily accessible for gene transcription when the contact between the positive and negative charges is reduced.

Several posttranslational changes of histones include acetylation, methylation, phosphorylation, ubiquitination, and sumoylation. Various environmental influences have been shown to cause dynamic epigenetic changes, a crucial signal-induced transcription mechanism [Jiang et al. 2020].

DNA Methylation

One of the most explored epigenetic processes is DNA methylation [Ashapkin et al. 2020]. In plants, a class of enzymes known as DNA methyltransferases links a methyl group (-CH3) to cytosine in symmetric, CG and CHG; and asymmetric, CHH, contexts (where H is any nucleotide except G) [Maeji et al. 2018].

Noncoding RNA

According to size, regulatory RNA may be broadly categorised into two groups [Ponting et al. 2009]: long non-coding RNAs (lncRNAs) and short chain non-coding RNAs (siRNAs, miRNAs, and piRNA. Non-encoding RNAs have been implicated in



epigenetic alteration in recent years, and several studies have demonstrated that they may affect gene and chromosomal expression to govern cell development [Amaral et al. 2008].

Roles of Epigenetics in Plants

Epigenetics plays a crucial role in how plants respond and adapt to environmental stressors. Environmental stressors such as drought, extreme temperatures, salinity, and pathogen attacks can have a detrimental effect on plant growth and survival. However, plants have evolved various mechanisms to cope with these stresses, and epigenetics is one of them.

Epigenetic Regulation in Plant Growth and Development

Throughout their lives, plants can develop new organs, which allows them to sustain growth while modifying their rate for flexibility to respond to environmental changes. In addition to chromosomal variety, epigenomics also contributes to the maintenance of plants' flexible and growth developmental patterns [Ahn et al. 2017]. Recent work has shown the important role of epigenetic mechanisms in the regulation of plant growth and reproduction, including DNA methylation, histone variations and modifications, nucleosome positioning, and small [Feng et al. 2010]. These genetic and epigenomic factors that direct cell modification fates from vegetative to reproductive phase transitions regulate plant growth and development stages [Barozai et al. 2018]. The widespread 5-methyl cytosine methylation observed in the genomes of higher plants serves the crucial role of protection against the activation and movement of transposable elements expression of certain and control developmental genes. Numerous additional eukaryotic creatures still exhibit DNA methylation, despite distinct differences in the methylation enzyme systems and roles [Zhang et al. 2010].

Epigenetic Memory and Transgenerational Inheritance

Transgenerational inheritance, explain that it refers to the transmission of epigenetic marks from one generation to the next. Research findings that suggest certain epigenetic modifications can be inherited and potentially influence the traits or behaviors of subsequent generations. The following generation of stressed plants could continue to reflect differences in the epigenetic control of gene expression brought on by exposure to environmental stress [Molinier et al. 2006]. These effects may even be transmitted to at least two seed generations in some cases [Cong et al. 2019].

Stress adaptation occurs when a plant experiences stress repeatedly and becomes better equipped to handle future stresses [Rahavi et al. 2011]. This idea has been expanded to encompass a variety of features of how plant stress memories are created, where the changed condition of the plant's stress response is passed on through mitosis or meiosis [Mirouze et al. 2011; Murgia et al. 2015]. The genetic mechanisms behind stress memory in plants as well as its potential consequences on agricultural yields, particularly in severe conditions, are of major interest. Increased genome methylation is linked to genome integrity and stress tolerance, according to a previous study on Arabidopsis thaliana and Scots pine (Pinus silestris) growing close to the Chernobyl reactor [Kovalchuk et al. 2003].

DNA methylation and histone modification have changed as a result of several stressors, demonstrating their significance in a universal function in stress memory. Noncoding RNAs with variable expression are one of the other possible stress memory mechanisms. Small noncoding RNA, dicerlike proteins 2 and 3 (DCL2 and DCL3), have been demonstrated to have a significant role in the formation of transgenerational stress memory in the presence of several stressors [Migicovsky et al. 2013].

Phenotypic plasticity

Under stress, DNA sequence differences are frequently linked to plant phenotypic variety. It has recently been demonstrated that epigenetic changes can influence phenotypes individually or collectively by regulating gene expression in response to stress (e.g., DDT, heavy metals, salt stress). Natural populations may act differently when their environmental conditions are altered. The stress response mechanisms in one plant may not be the



same as those in another [Bruce et al. 2007]. Environmental factors continuously shape postembryonic plant development, resulting in a high level of phenotypic plasticity. Although plants cannot escape their surroundings, they adapt to the changing and unfavorable growth conditions. The control of gene expression patterns and epigenetic regulation work together to promote metastable changes in gene activity. All these factors help the plants to cope to the unpredictable environments [Pikaard et al. 2014].

Environmental factors such as heat and dryness, can cause DNA's coding, promoter, or transposon regions to become hypo- or hypermethylated. Mechanisms of DNA methylation in the maize inbred line during heat stress During the seedling stage, B73 identified 325 differentially methylated genes.

Conclusion

Recent research findings have demonstrated that new stable phenotypes can be generated through epigenetic modifications in a few generations, contributing to the stability and survival of the plants in their natural habitat, even though the preexisting genetic variation in the populations can explain a portion of the plants' adaptation. Epigenetic regulation can result in dynamic alterations, such as the plant hypersensitivity reaction (HR), alterations in the chromatin structure, and an impact on the plant phenotype, all of which help native plants adapt to stress. Therefore, understanding how epigenetic factors contribute to phenotypic plasticity and heritable variation is crucial to comprehending how naturally occurring populations may adapt to changing environmental conditions, particularly in global climate change.

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