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Opinion Article

Usage of Non-Mammalian Models in Epigenetic Research

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DESCRIPTION

In the beyond couple of many years, legacy has been portrayed as the exchange of aggregates from precursors to their relatives through a selective transmission of genotype that is DNA succession variety. Recent advances in molecular research have demonstrated that "epigenetics" variations in addition to genetic variation play a role in the transmission of phenotypes. The term "the long-term or stable regulation of gene expression and function induced by environmental factors without a change in the chromosome or DNA sequence" has been used to describe epigenetics in modern terms. This definition was developed in 2008 at a cold spring harbor meeting. Mechanisms that enable the stable transmission of parental environment-induced phenotypic traits to a subsequent generation or generations without modifying the DNA sequence are referred to as "epigenetic inheritance" in this context.

In a variety of organisms, numerous mechanisms for epigenetic modifications have been described, and new mechanisms are likely to be discovered. Histone lysine tail modification, post-translational modification of genes regulated by non-coding/small RNA (ncRNA/sRNA), and chromatin remodelling through cytosine methylation in CpG dinucleotides (often referred to as DNA methylation) are important mechanisms underlying epigenetic modifications. Individually or collectively, these processes and their components play a crucial role in turning on or off gene expression, thereby facilitating or inhibiting the production of particular proteins. The possibility of DNA methylation plays a significant role in biological processes. Since then, researchers have paid a lot of attention to DNA methylation, which is still the most widely studied epigenetic mark because of its transgenerational stability. A few studies have reported DNA methylation's potential as a heritable epigenetic mark. DNA methylation can take place anywhere in the genome, including in the open reading frame and promoter regions. A methyl (CH_3) group from S-Adenosyl-L-Methionine (SAM) is attached to the fifth carbon atom of cytosine or the sixth nitrogen atom of adenine when DNA methyl transferase is present. By altering the way DNA coils around histones and making it more likely for transcription factors to bind to the DNA, this biochemical modification has the potential to reorganize chromatin. The likelihood of gene expression is determined by the position of DNA methylation in relation to the gene (exon, transcriptional start site, or promoter). For instance, DNA methylation at the 5th end of the gene was linked to gene silencing, while gene body methylation has multiple functions that include controlling transcriptional elongation, controlling alternative splicing, and suppressing intragenic promoter activity. DNA methylation machinery is somewhat conserved across organisms, despite its variability. However, extrinsic environmental cues can directly alter the absolute levels and patterns of DNA methylation, which can be significantly different across species and between tissues and developmental stages in an organism. For instance, the nematode worm caenorhabditis elegans' DNA cytosine methylation level can be zero percent, while the fruit fly *Drosophila melanogaster* or the aquatic invertebrate *Artemia's* methylation level ranges from 0.1 to 0.4 percent.

CONCLUSION

All three orthologous DNMTs are present in the genomes of *Apis mellifera* and *Nasonia vitripennis*, as well as CpG methylation in several genes, with a global DNA methylation level of approximately 1.5% of total cytosine. DNA methylation, on the other hand, is relatively higher in vertebrates. In mammalian substantial tissues, the genomic DNA is hypermethylated at 70%-80% of all CpG locales across the genome. DNA methylation may play different roles in different organisms, as suggested by the species-specific differences in methylation levels.

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