UNIVERSIDAD INTERAMERICANA DE PUERTO RICO

Recinto Metropolitano

Laboratorio Biología 1103-Destrezas I. Sección 72755

Dr. José E. Martínez Ruiz MS; PhD

Conference on Plant Epigenetics

Noor Hasan (M00623858)

 Fecha de conferencia: 23 de marzo de 2023

Fecha entrega de ensayo: 28 de marzo de 2023

The conference held on March 23, 2023, with guest speaker Dr. Mary Gehring was on plant epigenetics, which is a phenomenon where the phenotype does not match the genotype. This happens when DNA is modified by DNA methylation (5-methylcytosine), which is a process in which a methyl group is added to cytosine in the 5’ carbon. Methylation impacts how the DNA is read by the cell, which then produces mutations. DNA methylation can be found in animals, plants, and fungal genomes. It is typically associated with gene silencing, seen in the example of tomato fruit ripening, which has a wild-type copy of the gene called CNR (colorless non-ripening). When the CNR gene is methylated, this causes it to be silenced and for the tomato to not ripen and stay yellow. On the other hand, in the non-methylated CNR gene, the tomato successfully ripens and become red. DNA methylation is heritable, when a gene contains methylation, it will be inherited by the offspring during DNA replication. Dr. Gehring presented the Arabidopsis plant as a model system for epigenetic research due to several factors, such as its short life cycle, how it easily reproduces, has an ability to mutate, edit, and add genes, is easy to grow, has a small genome, and has natural variation.

Transposable elements (TEs) are what make up large fractions of genomes and are highly methylated. TEs can rapidly increase in copy number if not suppressed and can move around the genome. TEs are silenced by the host through DNA methylation and are promoted through DNA demethylation. Where there are TEs, there will be more DNA methylation (mCG, mCHG, mCHH). In Arabidopsis, a major DNA demethylase gene is ROS1 (REPRESSOR OF SILENCING1). ROS1 is enhanced by DNA methylation and suppressed by DNA demethylation. The ROS1 gene works as an epigenetic rheostat, as it adjusts the level of demethylation as a result of methylation alterations and gives stability to the genome. Disrupting the rheostat can cause phenotypic instability that is heritable across generations. In the 817 bp region of ROS1, there is a methylation-sensitive silencer sequence. Methylation of the silencer lessens its repressive ability on ROS1, and loss of methylation in the silencer leads to stronger repression of ROS1.

ROS1 is one of four DNA demethylases, which are DME (DEMETER), ROS1 (REPRESSOR OF SILENCING), DML2 (DEMETER-LIKE2), DML3 (DEMETER-LIKE3). These make up the DEMETER (DME) family of 5-methylcytosine DNA glycosylases. These are all found in plants. In Dr. Gehring’s experiment, a plant was created that lacked all four DNA demethylases (drdd). In wild-type plants DNA demethylation promotes FLC (FLOWERING LOCUS C) expression, which delays flowering. The absence of the DNA demethylases in the drdd plants caused early flowering, due to a decrease in FLC expression.

These findings presented by Dr. Gehring provide a detailed insight in the process of DNA methylation and demethylation as well as the different factors that relate to it, such as TEs and epigenetic rheostat. In plants specifically, methylation explains processes such as flowering and leaf shape. In general, DNA methylation is necessary for basic development, and can also explain mutated development such as diseases like cancer. DNA methylation is a biological process that, when better understood, can aid in many scientific advancements. DNA methylation is a occurrence that happens not only in plants, but humans as well, and can explain certain processes in diseases like cancer.