Genomic Imprinting in Plants

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ABSTRACT

As per the standard Mendelian understanding of genetics, both the maternal and paternal genomes contribute equally to the offspring. However, there are few deviations to this mendelian idea including cytoplasmic inheritance, gene conversion, epistasis and many more. One such deviation is genome imprinting. A subset of parent-of-origin effects is caused by imprinted gene expression imprinted genes are expressed predominantly from either the maternal or paternal allele. This process is considered as epigenetic phenomenon because alleles that have identical or nearly identical sequences are expressed differently.

INTRODUCTION

Genomic imprinting is a parent-of-origin specific epigenetic phenomenon whereby some autosomal genes display differential expression depending on whether the allele was inherited via the female or male gamete. Because there is no change in the DNA sequence of the allele, but there is a change in the allele's expression state depending on whether it is transmitted via a female or male gamete, genomic imprinting is an epigenetic parent-of origin effect. Hence, there is some post meiotic "imprint" placed upon the allele during either female or male gametogenesis, which the maternally or paternally derived allele retains as a "memory" in post-fertilization tissues and which is responsible for the differential expression levels of the maternally inherited versus paternally inherited alleles at the imprinted locus. Genomic imprinting thereby represents one form of epigenetic inheritance where heritable changes in genome function can occur without a change in DNA sequence.

Imprinting is not widespread in eukaryotes. It is restricted to flowering plants, therian mammals, and some insects. This suggests that this epigenetic phenomenon is the result of convergent evolution, having evolved at least three independent times in the eukaryote tree of life. In both organism classes, imprinting occurs primarily in embryo-nourishing tissues.

TYPES OF IMPRINTING

Imprint can either activate or repress expression at particular loci and hence, they are referred as,

- Maternally Expressed Imprinted Genes (MEGs) - genes that are maternally expressed and paternally silent are referred to as MEGs.
- Paternally Expressed Imprinted Genes (PEGs) - genes that are paternally expressed and maternally silent are referred to as PEGs. Imprint can either activate or repress expression at particular loci.
- Binary imprinting – causes complete imprinting of a gene.
- Preferentially imprinting – causes partial/ incomplete imprinting of a gene.

IMPRINTING IN PLANTS

- In flowering plants, imprinted gene expression is almost entirely confined to a single tissue, endosperm.
- The endosperm is triploid and most angiosperm species are genetically identical to the embryo except for the addition of another maternal genome.

On double fertilization, two sperm cells are released from the pollen tube into the embryo sac, with one of them fertilizing the egg cell and the other one fertilizing the homodiploid central cell, resulting in the formation of a diploid embryo and a triploid endosperm, respectively. The endosperm is a functional analog of the mammalian placenta and serves to support and nurture the growing embryo. Vegetative nucleus helps pollen tube growth. (Batista and Köhler, 2020)

A HISTORICAL BACKGROUND ON EVOLUTION OF GENOMIC IMPRINTING

- HELEN CROUSE coined the term "imprinting" in 1960.
- Kernel-color phenotype in maize was the basis for the discovery of the first imprinted gene (1970) in any species by Dr. JERRY KERMICLE

Reciprocal crosses of maize (Zea mays) varieties differently colored kernels led to the discovery of 4 gene-specific imprinting. Kermicle demonstrated that full kernel pigmentation depends on maternal inheritance of R1 which regulates anthocyanin biosynthesis in the endosperm.

The first imprinted gene identified at the molecular level in plants was MEDEA (MEA, formerly FIS1) in Arabidopsis thaliana, which is an imprinted MEG essential to seed development. (Jiang and Köhler, 2012)

- The first mammalian imprinted gene Insulin like Growth Factor (Igf2) was discovered in mice (1991)

THEORIES ON THE ORIGIN OF IMPRINTING

1. Kinship hypothesis
2. Co-adaptation hypothesis

3. Host defense hypothesis

4. Dosage hypothesis

REGULATORY MECHANISMS OF IMPRINTING

- By DNA methylation
- Histone modification by PcG proteins (Kohler and Weinhofer-Molisch, 2010)

Dna Methylation

DNA methylation has been widely recognized as an important epigenetic mark distinguishing maternally and paternally inherited alleles in both mammals and plants. In plants, DNA methylation occurs in three different nucleotide sequence contexts: symmetric CG and CHG methylation as well as asymmetric CHH methylation (where H = C, T, or A)

Histone modification by PcG proteins

Differentially DNA-methylated regions are not restricted to the vicinity of MEGs, but have as well been identified in PEGs suggesting that other repressive mechanisms account for silencing of maternally inherited PEGs alleles. One major repressive mechanism involved in imprinted expression of a subset of genes relies on Polycomb group (PcG) proteins. PcG proteins are evolutionary conserved master regulators of cell identity that act in multimeric complexes repressing the transcription of target genes.

STRATEGIES TO SPECIFICALLY IDENTIFY IMPRINTED GENES

a) Finding genes with endosperm-specific expression patterns similar to those of other known imprinted genes

b) Identifying targets of imprinting regulators

c) Identifying genes misregulated in endosperm that has altered ratios of maternal and paternal genomes

d) Finding genes associated with differential DNA methylation between the embryo and endosperm

e) Assay the paternal and maternal origins of transcripts.

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