# Genome Imprinting in Plants: Mechanisms, Functions and Agricultural Significance

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## INTRODUCTION

Genome is the complete set of genetic material in an organism. However, gene activity is regulated not only by DNA sequence but also by multiple regulatory mechanisms. One such important mechanism is genome imprinting where, gene expression depends on whether the gene comes from the mother or the father. In normal Mendelian inheritance, both parental genes contribute equally. However, in genome imprinting, only one allele is expressed while the other is silenced. This is called monoallelic expression.

In plants, genome imprinting primarily occurs in the endosperm, a tissue formed after fertilization that plays a crucial role in supplying nutrients to the developing embryo. With advancements in molecular biology and sequencing technologies imprinting has been recognized as an important factor influencing seed size, nutrient allocation and overall crop productivity (Rita and Kohler, 2020). Studies in major crops such as maize, rice and the model plant Arabidopsis thaliana have clearly demonstrated its role in regulating seed development. In modern agriculture where, challenges like climate change and food security are becoming more significant, a better understanding of genome imprinting offers promising opportunities for improving crop yield, quality and resilience.

## PRINCIPLES OF GENOME IMPRINTING

Genome imprinting is an epigenetic process, which means it controls gene expression without changing the DNA sequence. The core principle is that only one parental allele is selectively silenced depending on its origin. For example, If the maternal allele is imprinted, it is silenced and only the paternal allele is expressed. Similarly, if the paternal allele is imprinted, only the maternal allele remains active. This parent-specific expression is controlled by epigenetic marks such as DNA methylation and histone modifications. Importantly, imprinting represents an exception to Mendel's laws as gene expression is not determined solely by dominance or recessivenes but by parental origin.

## THEORIES EXPLAINING GENOME IMPRINTING

The most widely accepted explanation for the evolution of genome imprinting is the parental conflict hypothesis, also known as the kinship theory. This theory suggests that maternal and paternal genes have different evolutionary interests. Paternal genes tend to promote greater extraction of nutrients from the mother to enhance offspring growth and survival. In contrast, maternal genes aim to distribute resources evenly among all offspring to maximize overall reproductive success. This conflict leads to selective activation or silencing of certain genes.

In plants, this theory is supported by observations that increased paternal genome contribution often results in larger seeds, while increased maternal contribution leads to smaller seeds. Such findings highlight the role of imprinting in balancing growth and resource allocation (Fang and Settles, 2015).

## MECHANISMS OF GENOME IMPRINTING (Kohler and Weinhofer, 2010)

### DNA Methylation

DNA methylation involves the addition of methyl groups to cytosine bases which serves as a primary silencing mechanism. Differentially methylated regions (DMRs) between maternal and paternal alleles act as imprinting control regions that regulate nearby gene expression. In plants, active DNA demethylation mediated by enzymes such as DEMETER (DME) plays a crucial role in activating maternal alleles in the central cell prior to fertilization.

### Histone Modifications

Histones are proteins around which DNA is wrapped. Chemical modifications, such as methylation of histone H3 at lysine 27 (H3K27me3), alter chromatin structure and regulate gene accessibility, thereby controlling gene expression.

### Small RNA-Mediated Regulation

Small interfering RNAs (siRNAs) play a role in guiding DNA methylation and demethylation processes reinforcing allele-specific silencing. These RNA-directed DNA methylation (RdDM) pathways are particularly important in regions associated with transposable elements, suggesting a link between genome defense mechanisms and the evolution of imprinting.

## METHODS USED TO STUDY GENOME IMPRINTING

### Next-Generation Sequencing (NGS)

NGS is a powerful technology that allows genome-wide identification of imprinted genes by analyzing allele-specific expression patterns. This is done by sequencing RNA (RNA-seq) from tissues like the endosperm and comparing small genetic differences such as SNPs between the two parents. These differences act as markers to trace the origin of each transcript. By analyzing this data researchers can determine which genes are expressed only from one parent and are therefore imprinted. Thus, NGS considered as large-scale, high-resolution identification method of imprinted genes in plants (Bing *et al.*, 2025).

### Bisulfite Sequencing

This method is used to study DNA methylation patterns at single-base resolution. When DNA is treated with sodium bisulfite, it converts unmethylated cytosines into uracil while, remaining methylated cytosines unchanged. By sequencing this DNA, differentially methylated regions (DMRs) between parental alleles can be determined.

### RNA Sequencing (RNA-seq)

RNA-seq enables the detection of transcripts derived from maternal or paternal alleles providing insights into gene expression dynamics. *i.e.*, When two genetically different plant lines were crossed which have SNPs. Differences in RNA sequencing identify whether the transcript came from the mother or father.

### CRISPR-Based Epigenome Editing

This is an advanced and emerging method. Unlike normal CRISPR (which edits DNA), this technique modifies epigenetic marks without changing the DNA sequence offering new possibilities for functional studies and crop improvement. Enzymes like methyltransferases or demethylases are used as CRISPR tools.

- Add methylation → silence a gene
- Remove methylation → activate a gene

## FUNCTIONS OF GENOME IMPRINTING IN PLANTS

(Rodrigues and Zilberman, 2015)

### Regulation of Endosperm Development

The endosperm is a critical tissue that supports embryo growth. Imprinted genes regulate cell division and differentiation in the endosperm.

### Control of Nutrient Allocation

Imprinting ensures proper transfer of nutrients from the mother plant to the developing seed, influencing seed size and quality.

- Paternal genes → promote nutrient uptake
- Maternal genes → restrict excessive nutrient use

This balance is essential for seed viability.

### Growth Regulation

Some imprinted genes act as growth promoters, while others act as growth inhibitors, maintaining a balance in seed development. For example, regulation of seed size and growth depends on:

- Increased paternal expression → larger seeds
- Increased maternal expression → smaller seeds

### Parental Conflict and Evolutionary Regulation

Imprinting reflects the evolutionary conflict between maternal and paternal genomes over resource allocation. This ensures:

- Efficient use of maternal resources
- Survival of offspring

This aligns with the parental conflict hypothesis.

### Regulation of Gene Expression During Early Development

Imprinted genes control early developmental processes, especially during early stages of seed formation. They act as regulators that switch genes ON or OFF depending on parental origin.

### Protection Against Transposable Elements

Some studies suggest imprinting evolved as a defense mechanism against transposable elements. Epigenetic silencing helps maintain genome stability.

## EXAMPLES OF GENOME IMPRINTING IN CROPS

### Maize (Zea mays)

One of the earliest and most classical examples is the R locus in maize, which controls anthocyanin pigmentation in kernels. This gene shows a clear parent-of-origin effect, where the allele inherited from the female parent is fully expressed, producing uniformly colored kernels, whereas the same allele inherited from the male parent shows reduced or mottled expression due to partial silencing. Another important example in maize is the mee1 gene, which exhibits imprinting in both the endosperm and early embryo. In this case, the maternal allele becomes demethylated and active after fertilization, while the paternal allele remains relatively methylated and less expressed, indicating epigenetic regulation.

### Arabidopsis thaliana

Several imprinted genes such as MEDEA (MEA), FIS2, and FIE have been identified, which are essential for proper endosperm development and are regulated through DNA methylation and histone modifications. Additionally, the gene PHERES1 is another example that is controlled by Polycomb group proteins and shows parent-specific expression during early seed development.

Genome imprinting in cereals like, rice and wheat mainly occurs in the endosperm, where it regulates seed development, grain filling, and nutrient allocation. In rice, several imprinted genes influence seed size and yield, while in wheat similar mechanisms are believed to control grain quality and storage product accumulation (Rita and Kohler, 2020).

## ADVANTAGES OF GENOME IMPRINTING

- Improved seed development and viability

- Efficient nutrient utilization
- Regulation of optimal seed size
- Contribution to hybrid vigor (heterosis)
- Potential for targeted crop improvement through epigenetic breeding

## CONSEQUENCES AND CHALLENGES

→ **Sensitivity to imbalance:** Disruption of parental genome balance can lead to defective seed development

→ **Epigenetic instability:** Environmental factors may influence epigenetic marks

→ **Limited persistence:** Imprinting is often transient and not maintained in adult plants

→ **Complex regulation:** Interactions between multiple epigenetic mechanisms make it difficult to manipulate

## AGRICULTURAL SIGNIFICANCE

→ **Crop Yield Improvement:** Manipulating imprinted genes can enhance seed size and productivity

→ **Hybrid Seed Production:** Imprinting plays a role in heterosis and hybrid performance

→ **Nutritional Quality:** Better regulation of nutrient allocation improves seed composition

→ **Climate Resilience:** Epigenetic modifications may help crops adapt to environmental stress

## CONCLUSION

Genome imprinting is a unique epigenetic mechanism that introduces parent-of-origin-specific gene expression and challenging classical genetic principles. In plants, it plays a vital role in seed development, nutrient allocation, and growth regulation particularly in the endosperm. With advances in molecular technologies, our understanding of imprinting has expanded significantly revealing its potential in crop improvement and agricultural innovation. By integrating genome imprinting into breeding strategies enable the development of crop varieties with improved yield and quality for supporting global food security.

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