

DNA Methylation and Plant Breeding

Athanasios S. Tsaftaris and Alexios N. Polidoros

Department of Genetics and Plant Breeding

Aristotelian University of Thessaloniki

Thessaloniki 54006, Greece

- I. Introduction
 - II. DNA Methylation in Plants
 - A. Occurrence
 - B. Methods of Detection
 - C. Mechanisms of Maintenance, *De novo* Methylation, and Demethylation
 - D. DNA Methylation and Gene Action
 - E. Implications in Breeding
 - III. DNA Methylation, Genetic, and Epigenetic Variation
 - A. Genetic and Epigenetic Variation
 - B. The Extent of Variation in DNA Methylation and Its Inheritance
 - C. Variation of DNA Methylation as a Source of Heritable Epigenetic Phenotypic Variation
 - D. DNA Methylation and Somaclonal Variation
 - E. Implications in Breeding
 - F. DNA Methylation and Genetic Variation
 - IV. DNA Methylation, Heterosis, and F₁ Hybrid Breeding
 - A. Genome Function and Hybrid Vigor
 - B. Genome Methylation and Hybrid Vigor
 - C. Genome Function, DNA Methylation, and Performance of F₁ Hybrids
 - V. DNA Methylation and Transgene Inactivation in Transgenic Plants
 - A. Transcriptional Inactivation of Single Transgenes
 - B. Transgenes Inactivate the Transcription of Other Homologous Genes
 - 1. Transgene Inactivates Unidirectionally the Transcription of Its Allelic Gene
 - 2. Transgenes Inactivate Unidirectionally the Transcription of Non-allelic (Epistatic) Genes
 - C. Bidirectional Inactivation of Homologous Sequences Post-Transcriptionally
 - D. Avoiding Transgene Silencing
 - E. Implications in Breeding
 - VI. Conclusions and Future Prospects
- Literature Cited