

Discovering the role of *Maize Unstable factor for orange1 (Ufo1)*, a novel epigenetic regulator, in histone modification on *pericarp color1 (p1)* gene

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Abstract:

Epigenetics has been proven to be an essential regulator of gene expression at the transcription level. The study of epigenetic gene regulation has blossomed in recent years from prokaryotes to eukaryotes. However, mechanisms of epigenetic gene regulation, including DNA methylation, chromatin modification, and small RNA interaction remain elusive. In maize, although the epigenetic phenomena have been seen in paramutation, genomic imprinting, transposon elements, and transgene silencing, detailed regulatory mechanisms still need to be clarified. In this proposal, we are focusing on a novel epigenetic regulator in maize, *Unstable factor for orange1 (Ufo1)*, which is a dominant mutation, and capable of disrupting the silencing status of the maize Myb transcription factor encoded by *pericarp color1 (p1)*. *Ufo1*-induced gene expression is associated with loss of DNA methylation on *p1* gene. Also, DNA methylation and histone modification usually interplay each other and regulate the gene expression collectively. In this proposal, we are interested to study how *p1* gene is regulated by *Ufo1* through histone modifications. This will allow us to study role of chromatin in the generation of several alleles of a single locus. Through this study, we will also be able to further understand the role of gene specific modifiers in epigenetic regulation in the plant genomes.