

## **IDENTIFICATION OF NATURAL OCCURRING EPIALLELES IN MAIZE INBRED LINES USING A WIDE-GENOME METHYLATION ANALYSIS**

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In the past, genetic variation among individuals was considered only as a result of alterations in the primary nucleotide sequences due to mutation or gene recombination. However, it is now known that epigenetic factors such as DNA methylation or histone modification can play a fundamental role in generating alternative states (epialleles) of gene expression among biological strains or individuals in a population. In maize plants, spontaneous epialleles have been identified at some loci as those which encode transcription factors that activate the biosynthesis of flavonoid pigments. For example, the *b1* locus can shift from a high expressed form (*B-I* epiallele) to a low-expressed form (*B'* epiallele). Importantly this transition correlates with both altered level of DNA methylation and differential chromatin structure within the regulatory region 100 kb upstream of the locus.

In order to gain further insight into rules governing both the establishment and the propagation of epialleles in maize, the maize genome for target regions showing methylation differences among individuals of the Mo17 inbred line was screened. The methylation state of approximately 1000 DNA sequences was investigated during different maize plant developmental stages using a methylation sensitive amplified polymorphism (MSAP) approach. While the majority of methylation profiles analyzed were faithfully maintained during plant development, individual to individual methylation differences were observed representing 2% of total DNA sequences analyzed. Newly formed epialleles were successfully transmitted meiotically, thereby mimicking traditional genetic mutations.

Evidence providing a possible explanation of alternative phenotypes observed, for example, in the progeny of long-term inbred lines, through the production at each plant life generation of novel epigenetic states, has been shown by our study.