

# Plants display 'molecular amnesia'

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(PhysOrg.com) -- Plant researchers from McGill University and the University of California, Berkeley, have announced a major breakthrough in a developmental process called epigenetics. They have demonstrated for the first time the reversal of what is called epigenetic silencing in plants.

The findings are important to develop a better understanding of gene regulation in the continuing quest to breed enhanced crops that produce higher yields, are more resistant to disease and can better tolerate environmental stress – all keys to helping improve the world's food supply. But perhaps even more important, the discovery may lead to new insights into how epigenetic processes work in the human body, which could assist in developing new ways of modifying our genetic makeup to help us avoid such diseases as cancer.

Although nearly every cell in our body is genetically identical, the researchers explained, each cell type expresses a distinct set of genes. Changes to the proteins around which DNA is wound are called "epigenetic" modifications, because they alter patterns of this gene expression without changing the actual DNA sequence. However, like changes in DNA sequence, epigenetic modifications can be passed on from parent cell to daughter cell, ensuring each cell line has the proper characteristics consistently over many generations.

This process must be repeated each generation, and there is good evidence in animals that, during early development, there is a wave of epigenetic reprogramming that effectively "resets" this system. Some

genes, it seems, must be more actively reset than others. And genes that do the same thing in every cell, regardless of tissue type, may not have to be reset at all.

One kind of gene is quite distinct from all of the others, because it is nearly always epigenetically inactivated. These are the genes carried by transposons, or "jumping genes." Transposons are mutagens, genes that can modify their host cell in different ways, and lead to a predisposition to cancer, for example.

The researchers' experiments with corn – technically known as "maize" – suggest the propensity to maintain epigenetic states can vary depending on the position of the transposons within the genome.

Many organisms, from worms to humans to plants, have learned to tame transposons by epigenetically "silencing" them: if they can't express their genes they can't jump. If they can't jump for long enough, their DNA sequence slowly accumulates errors, and they become molecular fossils. Most transposons in most organisms are silenced in this way, but some remain quite active.

In previous studies from the laboratory of two of the article's authors, UC Berkeley professors Damon Lisch and Michael Freeling, with the support of the National Science Foundation at UC Berkeley, epigenetic silencing was triggered in maize. Once triggered, the maize plant "remembers," and keeps the transposon "silenced" generation after generation, even after the trigger is lost.

"However, we have found that at some positions in the genome, this is not the case. At these positions, although the trigger works fine, and the transposon is silenced, once the trigger is lost, the transposon reawakens," said Jaswinder Singh, a professor in the Plant Sciences Department at McGill University, and lead author of the new article. The

study, "A Position Effect on the Heritability of Epigenetic Silencing," was published in October in the journal *PLoS Genetics*.

This "molecular amnesia" has never before been documented in plants and no one has seen it associated with a particular position in the genome of any species before. These data suggest the epigenetic landscape of plant genomes may be more subtle and interesting than previously thought, with the ability to remember epigenetic silencing varying depending on position.

"This may relate to the degree to which a given gene or group of genes must be reprogrammed each generation," Singh said. "We can now use transposons to probe for variations in the epigenetic landscape of the maize genome. It may turn out that forgetting can be as important as remembering. Our findings suggest that erasure of heritable information may be an important component of epigenetic machinery."

Provided by McGill University

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