

# Discover

SCIENCE FOR THE CURIOUS

## Grandma's Experiences Leave a Mark on Your Genes

Your ancestors' lousy childhoods or excellent adventures might change your personality, bequeathing anxiety or resilience by altering the epigenetic expressions of genes in the brain.

By [Dan Hurley](#) | Tuesday, June 11, 2013



Alison Mackey/DISCOVER

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Darwin and Freud walk into a bar. Two alcoholic mice — a mother and her son — sit on two bar stools, lapping gin from two thimbles.

The mother mouse looks up and says, “Hey, geniuses, tell me how my son got into this sorry state.”

“Bad inheritance,” says Darwin.

“Bad mothering,” says Freud.

For over a hundred years, those two views — nature or nurture, biology or psychology — offered opposing explanations for how behaviors develop and persist, not only within a single individual but across generations.

And then, in 1992, two young scientists following in Freud’s and Darwin’s footsteps actually did walk into a bar. And by the time they walked out, a few beers later, they had begun to forge a revolutionary new synthesis of how life experiences could directly affect your genes — and not only your own life experiences, but those of your mother’s, grandmother’s and beyond.

The bar was in Madrid, where the Cajal Institute, Spain’s oldest academic center for the study of neurobiology, was holding an international meeting. Moshe Szyf, a molecular biologist and geneticist at McGill University in Montreal, had never studied psychology or neurology, but he had been talked into attending by a colleague who thought his work might have some application. Likewise, Michael Meaney, a McGill neurobiologist, had been talked into attending by the same colleague, who thought Meaney’s research into animal models of maternal neglect might benefit from Szyf’s perspective.



Michael Meaney, neurobiologist.

“I can still visualize the place — it was a corner bar that specialized in pizza,” Meaney says. “Moshe, being kosher, was interested in kosher calories. Beer is kosher. Moshe can drink beer anywhere. And I’m Irish. So it was perfect.”

The two engaged in animated conversation about a hot new line of research in genetics. Since the 1970s, researchers had known that the tightly wound spools of DNA inside each cell’s nucleus require something extra to tell them exactly which genes to transcribe, whether for a heart cell, a liver cell or a brain cell.

One such extra element is the methyl group, a common structural component of organic molecules. The methyl group works like a placeholder in a cookbook, attaching to the DNA within each cell to select only those recipes — er, genes — necessary for that particular cell’s proteins. Because methyl groups are attached to the genes, residing beside but separate from the double-helix DNA code, the field was dubbed epigenetics, from the prefix *epi* (Greek for over, outer, above).

Originally these epigenetic changes were believed to occur only during fetal development. But pioneering studies showed that molecular bric-a-brac could be added to DNA in adulthood, setting off a cascade of cellular changes resulting in cancer. Sometimes methyl groups attached to DNA thanks to changes in diet; other times, exposure to certain chemicals appeared to be the cause. Szyf showed that correcting epigenetic changes with drugs could cure certain cancers in animals.

Geneticists were especially surprised to find that epigenetic change could be passed down from parent to child, one generation after the next. A study from Randy Jirtle of Duke University showed that when female mice are fed a diet rich in methyl groups, the fur pigment of subsequent offspring is permanently altered. Without any change to DNA at all, methyl groups could be added or subtracted, and the changes were inherited much like a mutation in a gene.



Moshe Szyf, molecular biologist and geneticist.

McGill University

Now, at the bar in Madrid, Szyf and Meaney considered a hypothesis as improbable as it was profound: If diet and chemicals can cause epigenetic changes, could certain experiences — child neglect, drug abuse or other severe stresses — also set off epigenetic changes to the DNA inside the neurons of a person's brain? That question turned out to be the basis of a new field, behavioral epigenetics, now so vibrant it has spawned dozens of studies and suggested profound new treatments to heal the brain.

According to the new insights of behavioral epigenetics, traumatic experiences in our past, or in our recent ancestors' past, leave molecular scars adhering to our DNA. Jews whose great-grandparents were chased from their Russian shtetls; Chinese whose grandparents lived through the ravages of the Cultural Revolution; young immigrants from Africa whose parents survived massacres; adults of every ethnicity who grew up with alcoholic or abusive parents — all carry with them more than just memories.

Like silt deposited on the cogs of a finely tuned machine after the seawater of a tsunami recedes, our experiences, and those of our forebears, are never gone, even if they have been forgotten. They become a part of us, a molecular residue holding fast to our genetic scaffolding. The DNA remains the same, but psychological and behavioral tendencies are inherited. You might have inherited not just your grandmother's knobby knees, but also her predisposition toward depression caused by the neglect she suffered as a newborn.

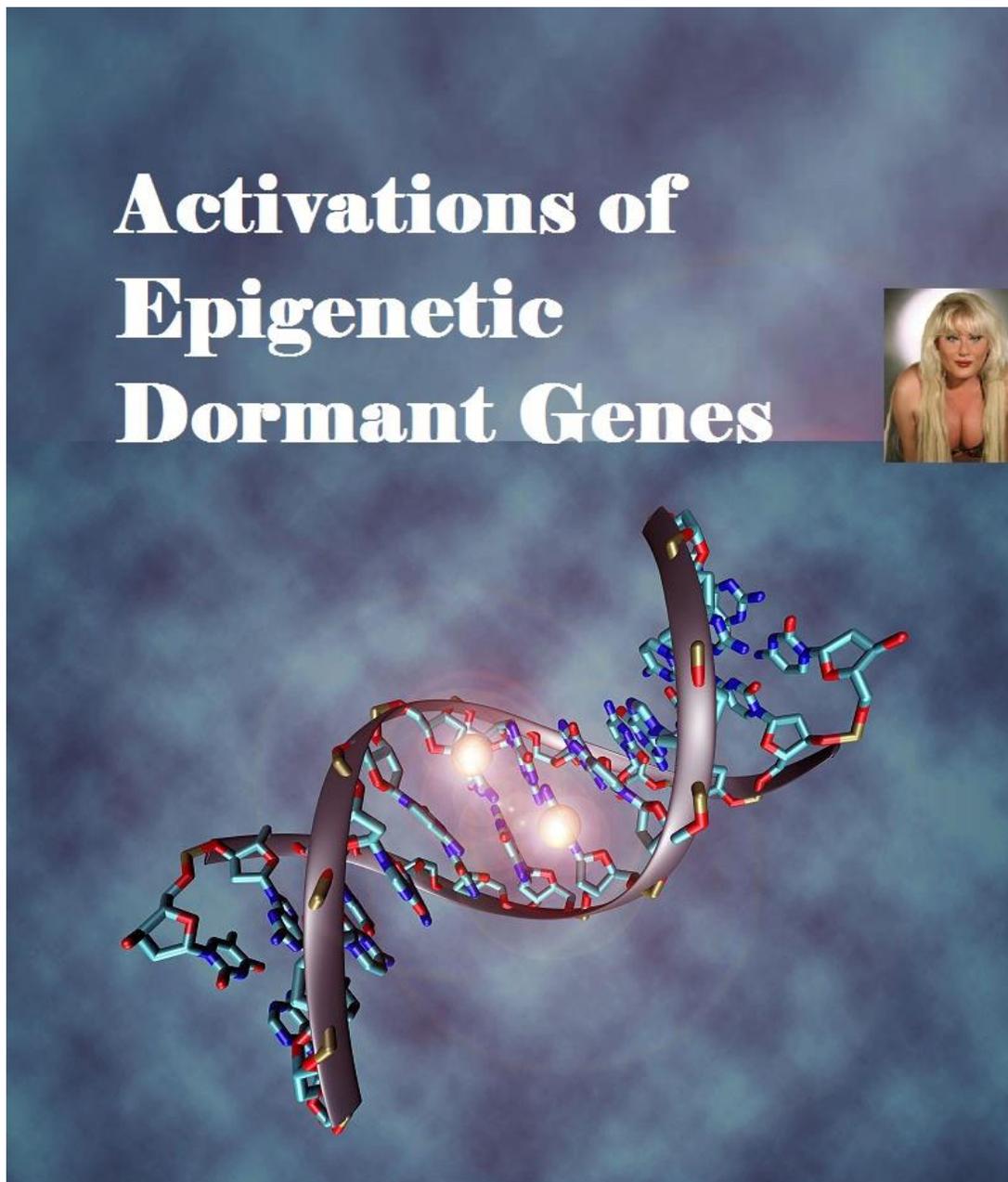
Or not. If your grandmother was adopted by nurturing parents, you might be enjoying the boost she received thanks to their love and support. The mechanisms of behavioral epigenetics underlie not only deficits and weaknesses but strengths and resiliencies, too. And for those unlucky enough to descend from miserable or withholding grandparents, emerging drug treatments could reset not just mood, but the epigenetic changes themselves.

Like grandmother's vintage dress, you could wear it or have it altered. The genome has long been known as the blueprint of life, but the epigenome is life's Etch A Sketch: Shake it hard enough, and you can wipe clean the family curse. [www.cybermagneticchair.com](http://www.cybermagneticchair.com)

[http://indavideo.hu/video/Turn\\_on\\_your\\_Genes\\_-\\_Epigenetics\\_part\\_1](http://indavideo.hu/video/Turn_on_your_Genes_-_Epigenetics_part_1)

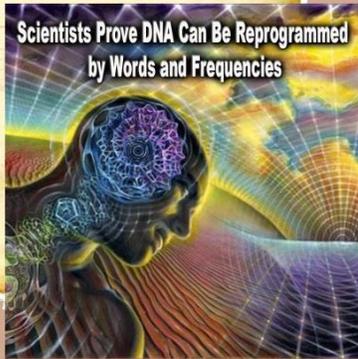
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<http://www.downloads.imune.net/medicalbooks/Activation%20of%20Epigenetic%20Dormant%20Genes%20with%20Cybermagnetics.pdf>



# Cybermagnetics Can Open Closed Epigenetic Genes

**THE FUTURE OF  
GENETICS IS  
CYBERMAGNETICS**



Two generations at once are exposed to the same environmental conditions (diet, toxins, hormones, etc.). An epigenetic changes has been documented in the mother and the progeny

Permanent Epigenetic Changes in the fetus

Epigenetics Research at Florida A&M University is supported by grants from the NIH, National Institute on Minority Health and Health Disparities. (8-12MD007582-28 and 1P20 MD006738-01)

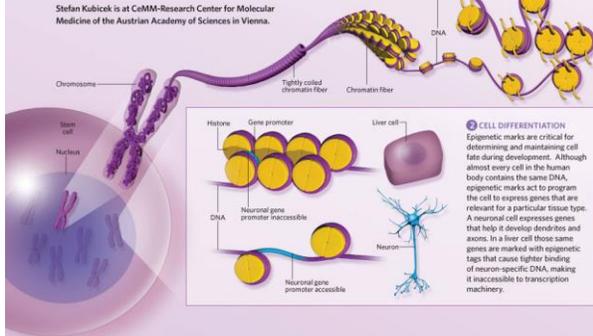
# EPIGENETICS: A PRIMER

There are many ways that epigenetic effects regulate the activation or repression of genes. Here are a few molecular tricks cells use to read off the right genetic program. By Stefan Kubick

What makes the ~200 cell types in our body remember their identity? What prevents them from becoming cancer cells? Why do we inherit some traits from our father, others from our mother? How do our experiences and environment influence our thinking? Why do plants bloom in spring but not in winter? These important and quite different questions are all addressed by the field of epigenetics, which studies heritable changes in a phenotype arising in the absence of alterations in the DNA sequence. The idea of transgenerational inheritance of acquired characteristics goes back to Lamarck in the early 19th century, but still only correlative evidence exists in humans. In contrast, many cellular epigenetic phenomena are now well understood on the molecular level. In humans, they include the parent-of-origin specific expression of genes (imprinting) and the shutting-down of almost all genes on one of the two X chromosomes in females (X-chromosome inactivation).

All these epigenetic phenomena are characterized by chemical modifications to DNA itself (DNA methylation) or to histones, the proteins around which DNA is wound. These modifications change during development as stem cells give rise to liver cells and neurons, but also in response to environmental signals—in plants, for example, during the cold of winter or in humans when immune cells are activated after an infection. One of the biggest controversies in the field is whether histone modifications are inherited through cell division (called the “histone code hypothesis”) or whether they only form transient indicators of transcriptional states (“signaling model”).

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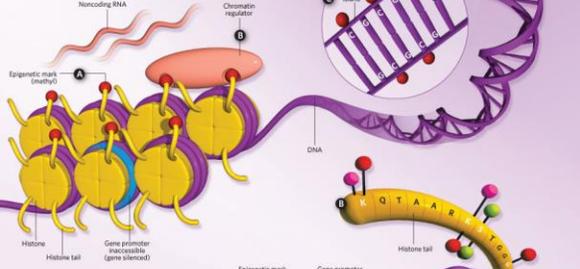
**OVERVIEW**  
Epigenetic events regulate the activities of genes without changing the DNA sequence. Different genes are expressed depending on the methyl-marks attached to DNA itself and by changes in the structure and/or composition of chromatin. The main components of chromatin are histones (in bundles of eight units) around which 146 base-pairs of DNA are wound like a thread around a spool, forming a structure called the nucleosome. There are various epigenetic mechanisms that can affect the nucleosome: chemical modification (via molecular additions to histone tails or DNA), a change in its positioning on DNA (via chromatin remodeling proteins), or a variation in histone subtypes.



**CELL DIFFERENTIATION**  
Epigenetic marks are critical for determining and maintaining cell fate during development. Although almost every cell in the human body contains the same DNA, epigenetic marks act to program the cell to express genes that are relevant for a particular tissue type. A neuronal cell expresses genes that help it develop dendrites and axons. In a liver cell those same genes are marked with epigenetic tags that cause tighter binding of neuron-specific DNA, making it inaccessible to transcription machinery.

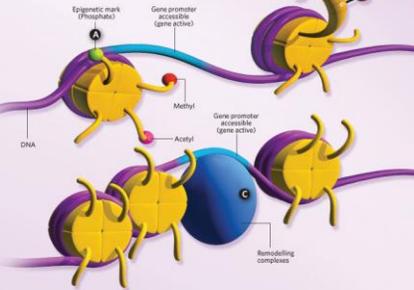
## 1 INACTIVATING MARKS

There are many epigenetic modifications that change whether or how much of a gene is transcribed into RNA. Epigenetic marks that inactivate genes include methylation at certain positions on histone tails. These chemical modifications are made by a number of histone-modifying enzymes and then recognized by other chromatin regulators. Evidence is beginning to emerge that different classes of noncoding RNAs (ncRNAs) regulate these processes. Many of the histone modifications that inactivate genes can be reversed by other epigenetic changes (see below). However, direct methylation of DNA causes a permanent and heritable change in gene expression. Methylation of the DNA often occurs at clusters or “islands” of cytosine (CpG islands) that commonly occur within gene promoters.



## 2 ACTIVATING MARKS

The heritability of DNA methylation, which often occurs in the early stages of development, allows cells to keep irrelevant genes silenced in successive generations of liver or skin cells. However, some genes—such as the plant genes that govern winter dormancy and springtime flowering—require recruited genes to be reactivated. Several modifications, including the acetylation, phosphorylation, as well as methylation of certain positions on a histone tail can cause DNA to unwind, releasing the genes that are otherwise inaccessible. These modifications occur mostly at specific positions on the accessible tails of the histones, and subsequently recruit additional activating proteins. Histone-remodeling complexes, which slide histones in one direction or another, can also make genes accessible to transcription.



# Cybermagnetics Unlocks the Dormant Epigenetic Genes