Strategic Living For Epigenetics

THE FUNCTIONAL LONGEVITY PROGRAM

The Science of Epigenetics

Hormones and Neurotransmitter

Lifestyle

Demo

Foods

More Lifestyle

Breathing Exercise

Definition

Epigenetics refers to the study of changes in gene expression or cellular phenotype that do not involve alterations to the underlying DNA sequence.

Essentially, epigenetic changes are like "marks" on the genome that regulate how, when, and to what extent genes are expressed without changing the genetic code itself.

These changes can be influenced by various environmental factors, such as diet, stress, toxins, and lifestyle, which can turn genes on or off or adjust their activity levels.

Unlike mutations, epigenetic modifications are often reversible and can sometimes be passed on to future generations.

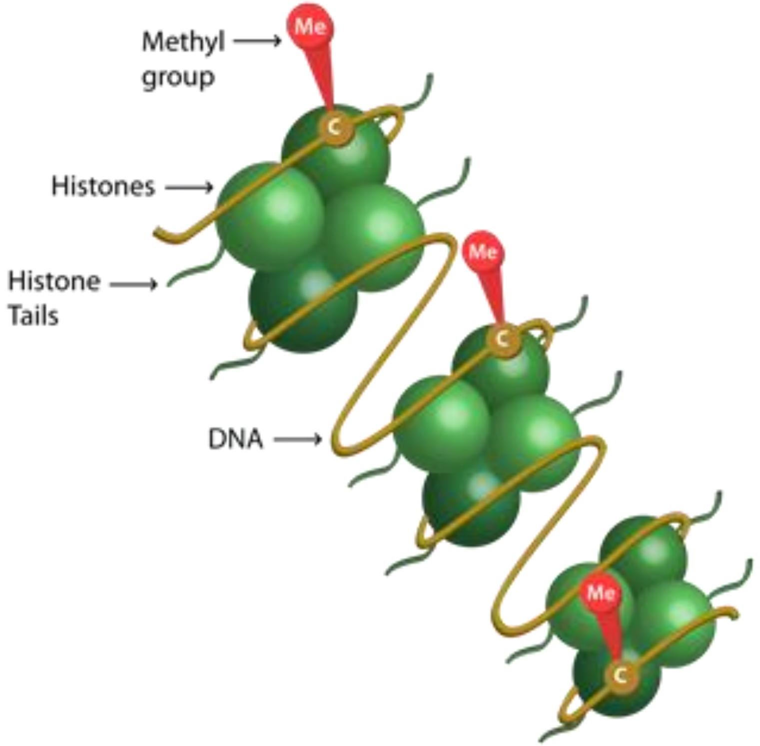
Mechanisms

DNA Methylation

This is adding a methyl group (CH_3) to the DNA molecule, usually at cytosine bases adjacent to guanine bases (CpG sites).

DNA methylation typically suppresses gene expression by preventing the binding of transcription factors or by recruiting proteins that compact the DNA, making it less accessible.

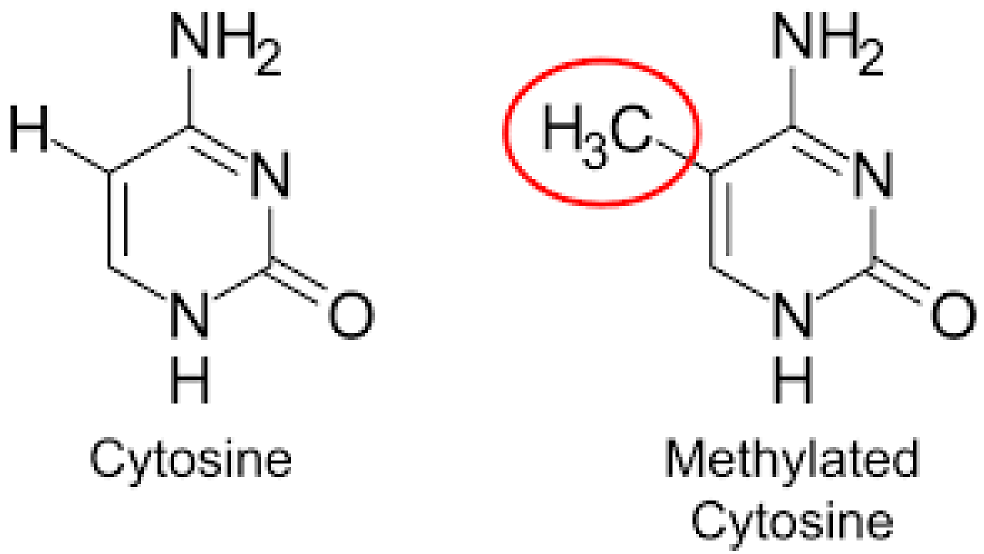
Methylation patterns can change in response to environmental factors, and they are often involved in processes like aging and the development of diseases such as cancer.



Helpful methylation turns off harmful genes (like viruses or cancer promoters) and supports normal development.

Harmful methylation can silence protective genes (like tumor suppressors) or disrupt normal cell function.

Healthy methylation is supported by nutrients like folate, B12, B6, choline, and zinc, while it can be disrupted by poor diet, alcohol, stress, toxins, and inflammation.



Histones

DNA is wrapped around histone proteins, forming a structure called chromatin.

Histones can undergo various chemical modifications, such as acetylation, methylation, phosphorylation, and ubiquitination.

These modifications influence how tightly or loosely DNA is wrapped around histones, thereby regulating gene accessibility.

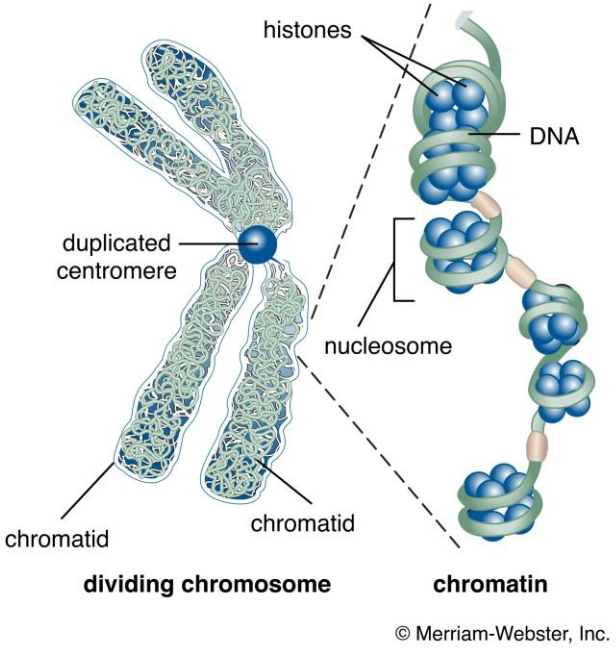
For example, acetylation of histones usually leads to a relaxed chromatin structure, allowing gene transcription, while deacetylation leads to tighter wrapping, reducing gene expression.

Acetylation (Adding Acetyl Groups): Think of this as putting "sticky notes" on specific pages of the book.

These sticky notes make the pages easier to open and read.

When the sticky notes (acetyl groups) are added to the pages (histones), it becomes easier for the "librarian" (the cell's machinery) to access and read the instructions on those pages (genes).

This means that the information in the book (genes) can be read and used more often.



Example in the Body:

When you exercise, your body may add these "sticky notes" to genes that produce energy or build muscle proteins.

This makes it easier for your cells to read these genes, helping your body to adapt and become stronger.

Deacetylation (Removing Acetyl Groups): Now, imagine someone starts removing the sticky notes, making the pages harder to open.

The book is still there, but it's more challenging for the librarian to get to certain sections. When the sticky notes are removed, the pages (genes) are tightly closed and not read as often, reducing activity.

Example in the Body: In response to stress, your body might remove the sticky notes from genes involved in inflammation control. This can reduce the production of proteins that help manage inflammation, potentially leading to prolonged inflammation and stress responses.

Histone Deacetylases (HDACs)

HDACs are like workers in the library who go around and remove the sticky notes from the book’s pages. When HDACs remove these sticky notes (acetyl groups) from the histones (the proteins around which DNA is wrapped), the DNA becomes more tightly coiled, making it harder for the cell's machinery to access and read the genes. This leads to reduced expression or activity of those genes.

Example in the Body

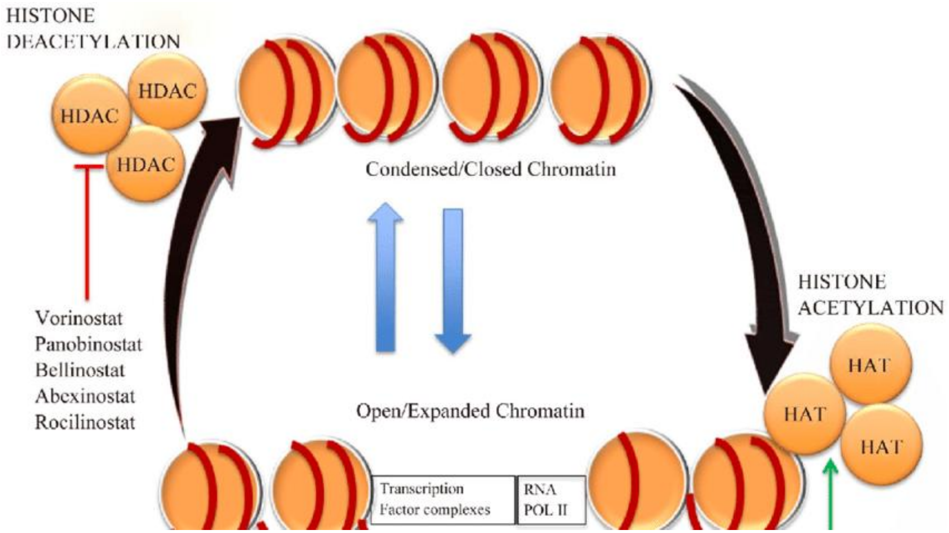
Imagine you are experiencing chronic stress. Your body might release signals that activate HDACs to remove the acetyl groups from genes that help manage inflammation. Those genes become less active with fewer sticky notes (acetyl groups), which may result in the body not producing enough anti-inflammatory proteins, potentially leading to prolonged inflammation.

Similarly, HDACs can be activated or influenced by various factors, such as:

Diet: Certain nutrients or lack thereof can influence HDAC activity.

Environmental Factors: Toxins or pollutants might increase HDAC activity, affecting gene expression.

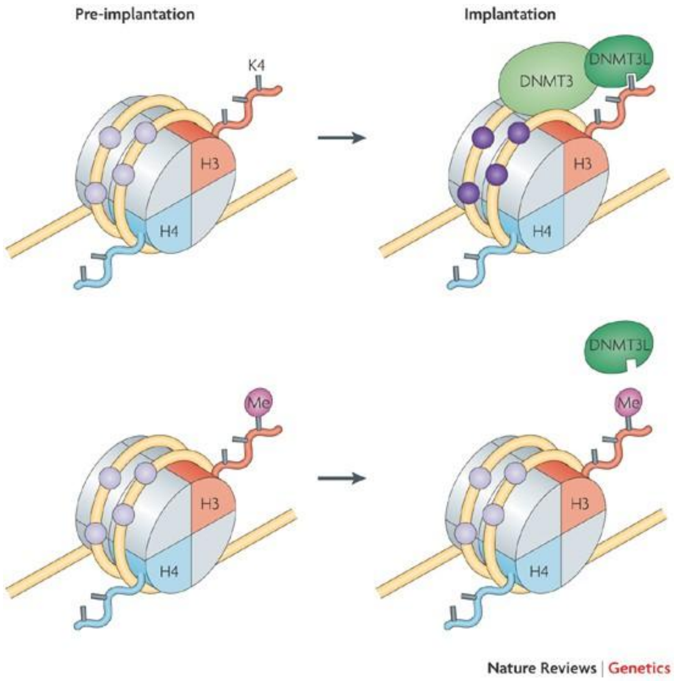
Medications: Some drugs are designed to inhibit HDACs to help treat conditions like cancer, where reducing HDAC activity can make it easier to activate tumor-suppressing genes.



Modifying Histone Methylation: Polyphenols, like curcumin in turmeric, can change the way methyl groups attach to histones, which can turn off harmful genes (like those promoting cancer) and activate helpful ones.

Providing Antioxidant Protection: Polyphenols protect histones and DNA from oxidative damage, helping maintain healthy gene expression patterns.

Overall, polyphenols help regulate gene expression in ways that support health by modifying histones and protecting them from damage.



More Polyphenols Specifics

Increasing Histone Acetylation: Polyphenols, such as those in green tea (EGCG) and red grapes (resveratrol), add acetyl groups to histones, relaxing DNA structure and making genes more accessible, which can help activate protective genes.

Inhibiting Histone Deacetylases (HDACs): Some polyphenols, like quercetin in apples and sulforaphane in broccoli, block enzymes that remove acetyl groups from histones, keeping DNA open and allowing beneficial genes to be more active.

To help prevent excessive HDAC activity, include a variety of plant-based foods in your diet, such as cruciferous vegetables (like broccoli and kale), berries, and soy products, which contain compounds that can inhibit HDACs.

Incorporate foods rich in antioxidants and anti-inflammatory agents, like green tea, turmeric, garlic, and nuts, to support healthy gene expression.

Omega-3 fatty acids from fatty fish, flaxseeds, and walnuts also protect against inflammation and chronic disease.

A balanced diet emphasizing these whole, unprocessed foods can promote overall health and reduce the risk of conditions linked to HDAC activity.

Non-coding RNAs

(ncRNAs), such as microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), do not code for proteins but play crucial roles in regulating gene expression at the transcriptional and post-transcriptional levels.

MicroRNAs can bind to messenger RNA (mRNA) molecules, leading to their degradation or preventing their translation into proteins.

Long non-coding RNAs can interact with DNA, RNA, or proteins to influence chromatin structure and gene expression patterns.

These mechanisms work together in complex networks to control gene activity in response to internal and external environmental signals, helping to adapt and respond to various conditions while maintaining overall genomic stability.

When non-coding RNAs do not regulate genes properly, it can disrupt critical processes in the body, contributing to various diseases.

ie:

If certain microRNAs that usually help control cell growth are not functioning correctly, they might fail to suppress the activity of genes that promote uncontrolled cell division, potentially leading to the development of cancer.

Additionally, imbalances in specific non-coding RNAs have been linked to neurodegenerative diseases like Alzheimer's, where abnormal levels of ncRNAs may affect the expression of genes involved in neuron survival and function.

To keep non-coding RNAs balanced, focus on a diet rich in antioxidants (like berries and green tea) and anti-inflammatory foods (such as fatty fish, turmeric, and olive oil) to protect against cellular stress and inflammation.

Include fiber-rich foods like whole grains and vegetables to support a healthy gut microbiome, which can positively influence ncRNA regulation.

Limit intake of processed foods and sugars to reduce inflammation and oxidative stress, which can disrupt ncRNA function.

Incorporate regular physical activity to promote healthy gene expression and manage stress through techniques like mindfulness and yoga to prevent imbalances in ncRNA levels.

Ensure adequate sleep to maintain proper gene regulation and avoid environmental toxins that could damage ncRNAs.

Together, these diet and lifestyle choices help support the healthy functioning of ncRNAs, contributing to overall wellness and disease prevention.

Lifestyle

The Role Of Exercise

Exercise influences epigenetic markers, which are changes that affect gene activity without altering DNA. Regular physical activity can modify these markers, particularly in genes related to metabolism and inflammation, leading to health benefits.

DNA Methylation Changes: Exercise can reduce DNA methylation in genes involved in metabolism, enhancing the body’s ability to use fats and sugars efficiently and lowering the risk of obesity and diabetes.

Histone Modifications: Exercise increases histone acetylation, relaxes DNA, and promotes the expression of genes that reduce inflammation and support muscle growth and recovery.

Reduced Inflammatory Gene Activity: Physical activity can decrease the expression of genes that cause inflammation, helping protect against diseases like heart disease, arthritis, and cancer.

Role of Sleep & Stress

Stress management and adequate sleep can significantly impact epigenetic regulation, affecting overall health.

Stress Management: Chronic stress can cause harmful epigenetic changes that activate inflammation-related genes and suppress protective genes.

Techniques like meditation and mindfulness can reduce these changes, lower stress-related health risks, and enhance the expression of genes that support mental health.

FKBP5 Gene: This gene plays a crucial role in controlling how the body responds to cortisol. Normally, FKBP5 helps regulate cortisol levels, ensuring that the body can return to a balanced state after a stressful event.

Stress Impact:

Chronic Stress: Prolonged exposure to stress can lead to changes in the methylation patterns of the FKBP5 gene. Specifically, chronic stress can reduce methylation in certain regions of this gene, leading to its overexpression.

Result: The body's response to cortisol becomes dysregulated when FKBP5 is overexpressed due to reduced methylation. This can result in an exaggerated stress response, where cortisol levels remain elevated for longer periods, increasing the risk of anxiety, depression, and other stress-related disorders.

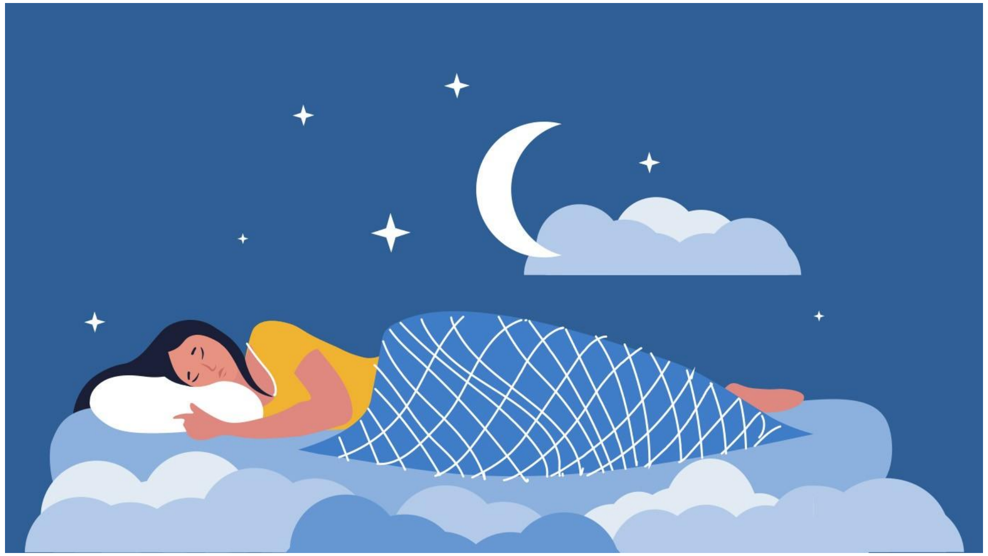
Nutrients like folate (found in leafy greens and legumes), vitamins B12 (in meat, fish, and dairy) and B6 (in poultry, fish, and potatoes), choline (in eggs and soybeans), and methionine (in meat, fish, and nuts) support methylation, helping regulate the FKBP5 gene.

These nutrients help maintain proper gene methylation patterns, balancing the body's stress response and reducing the risk of stress-related disorders.

Role of Sleep

Adequate Sleep: Proper sleep maintains circadian rhythms that regulate genes involved in metabolism, immunity, and cellular repair. Lack of sleep can disrupt these rhythms, increasing inflammation and the risk of diseases.

Managing stress and getting enough sleep help maintain healthy gene expression, reduce inflammation, and support overall well-being.



Why Epigenetics Is Not Simple

Understanding how diet, epigenetic changes, and health interact is challenging for several reasons:

It's hard to separate the effects of genes you inherit from those of epigenetic changes, which are influenced by diet and other environmental factors.

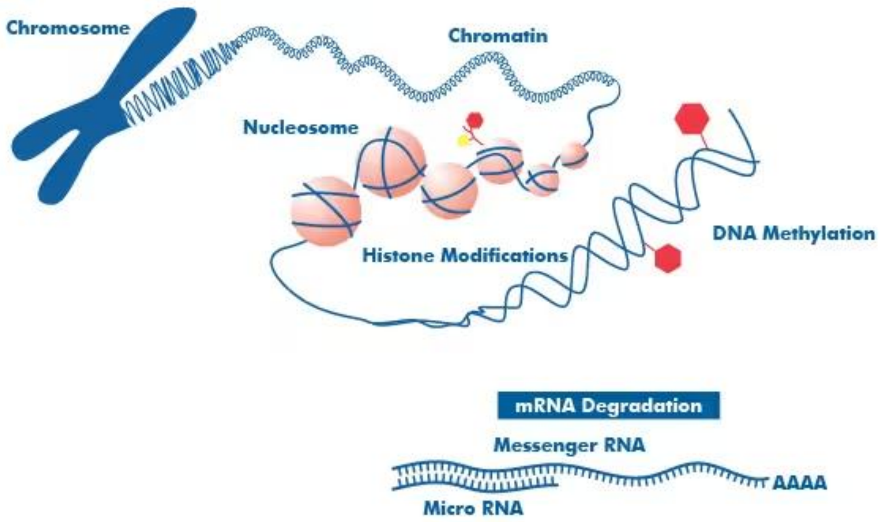
People respond differently to the same foods due to their unique genetic and epigenetic makeup, making it difficult to find universal patterns.

Diet is complex, containing many nutrients that can have mixed or opposing effects on gene regulation, so isolating the impact of one nutrient is tough.

Epigenetic changes can be temporary and reversible, influenced by many factors, so knowing if they have long-term health effects is challenging.

Long-term studies are needed to understand these effects, which are expensive, time-consuming, and hard to control.

Bringing together data from many scientific fields is complicated and requires advanced tools and collaboration to understand the full picture.



Diet can lead to epigenetic changes that impact an individual’s health and their descendants, potentially increasing or decreasing the risk of certain diseases across multiple generations.

For example, when a parent consumes a diet high in certain nutrients, like folate or antioxidants, or low in calories, it can cause changes in DNA methylation or histone modifications, which regulate gene activity without altering the DNA sequence.

If these changes occur in the reproductive cells (sperm or eggs), they can be passed down to their children. This could lead to an increased or decreased risk of conditions like obesity, diabetes, and cardiovascular diseases, depending on which genes are affected.

Similarly, a mother’s diet during pregnancy can directly influence the developing fetus’s epigenome.

For instance, inadequate nutrition or excess sugar and fat intake can alter the gene expression in the child's metabolic regulation, immune function, and brain development.

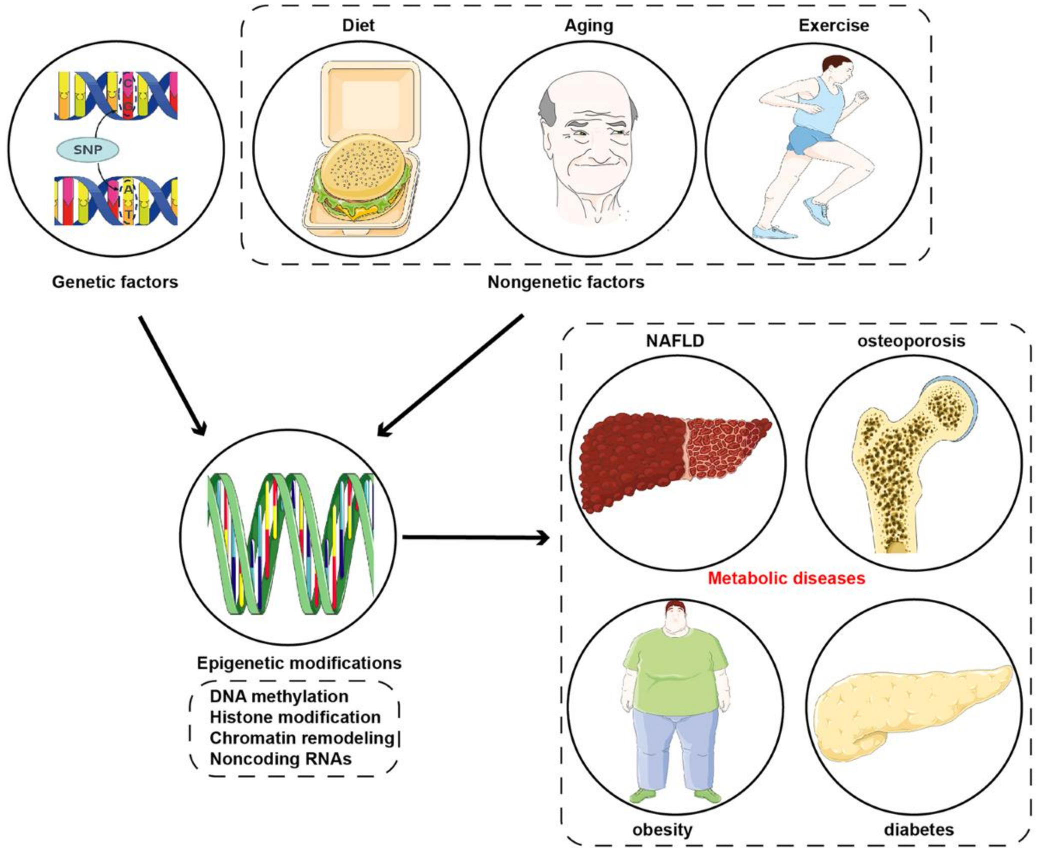
These changes can affect the child's long-term health, potentially leading to issues like insulin resistance, heart disease, or cognitive impairments later in life.

These epigenetic modifications can sometimes persist into the next generation. If a mother experiences nutritional deficiencies or excesses during pregnancy, her child's germ cells (which will become her grandchildren) can also be epigenetically modified.

This means that a poor diet in one generation can lead to health problems in multiple future generations due to inherited gene expression patterns.

Overall, the diet of one generation can set the stage for health outcomes in children, grandchildren, and beyond,

This shows how vital nutritional choices are not only for individual well-being but also for the long-term health of future generations.

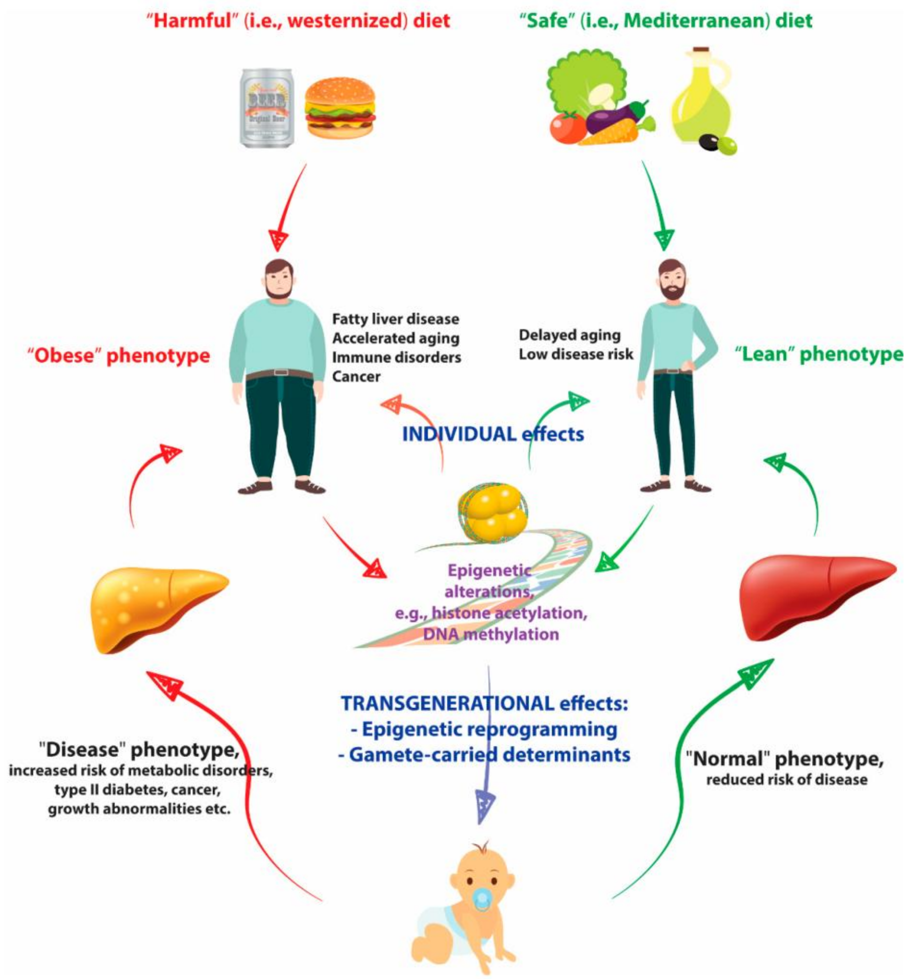


When working with clients with a genetic predisposition to a health condition, you want to use this information to encourage them to make changes.

But this info also needs to be considered when preventing degenerative diseases.

Or further degeneration — we don't know how much DNA has been influenced or changed by any client.

But focusing on how to influence epigenetics will help.



Example

Excessive alcohol use can alter epigenetic markers, leading to DNA methylation changes, histone modifications, and altered non-coding RNA expression that contribute to liver dysfunction, inflammation, and fibrosis.

Strategic epigenetic interventions can support liver repair and regeneration by influencing gene expression, reducing oxidative stress, and restoring metabolic balance.

Key Epigenetic Strategies for Liver Repair

Enhancing DNA Methylation & Detox Pathways

Glutathione Boosting: NAC, glycine, and selenium help restore glutathione, a key antioxidant that influences DNA methylation and detoxification.

Methyl Donors: Choline, betaine, and folate support proper DNA methylation patterns in liver cells

Histone Modification

Alcohol ↑ HDAC activity → Silences detox genes.

Butyrate, resveratrol (HDAC inhibitors) reactivate liver genes.

Disrupts histone methylation linked to → Inflammation & fibrosis.

SAMe, polyphenols restore methylation balance.

Non-Coding RNA Support:

miR-34a & miR-155 ↑ → Drive inflammation & fibrosis.

Curcumin, omega-3s reduce harmful microRNA activity.

LncRNAs (HOTAIR, MALAT1) → Promote liver damage.

Green tea (EGCG) modulates lncRNAs for repair.

Hormones & Neurotransmitters

It’s not just the food

Chronic stress and poor metabolic health can lead to excess DNA methylation, silencing beneficial genes.

Balanced hormones and neurotransmitters help maintain proper gene activation and silencing.

DNA Methylation

Cortisol (Stress Hormone): Chronic stress increases DNA methylation of genes related to neuroplasticity, metabolism, and immune function, potentially silencing beneficial genes and increasing disease risk.

Estrogen: Regulates DNA methylation in reproductive tissues, influencing the expression of tumor-suppressor and metabolic genes.

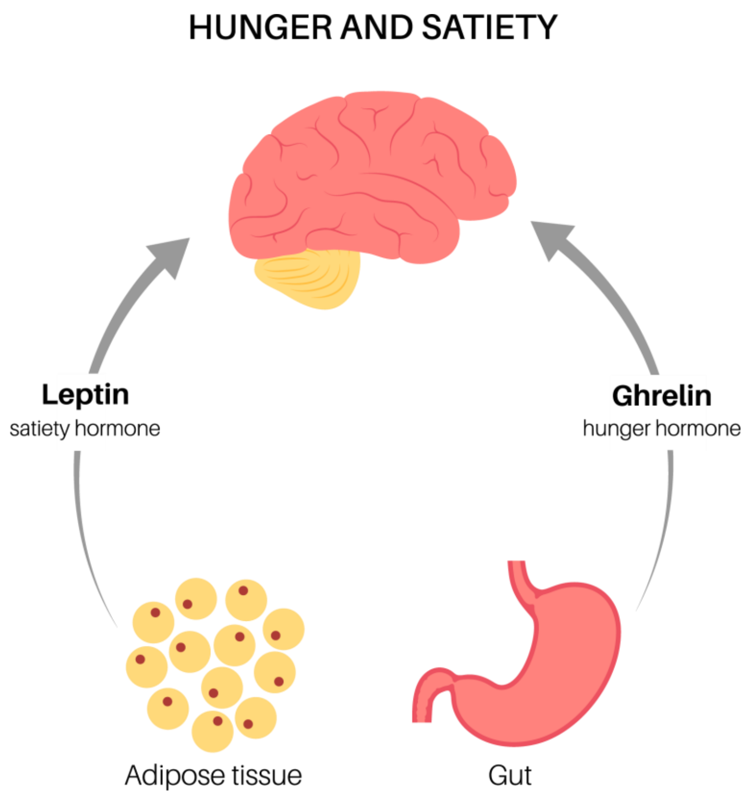
Testosterone: Impacts DNA methylation patterns that control muscle growth, reproduction, and behavior.

Thyroid Hormones (T3, T4): Influence DNA methylation of genes responsible for metabolism, energy production, and brain function.

Insulin: Regulates DNA methylation in genes controlling glucose metabolism, influencing the risk of diabetes and metabolic disorders.

Leptin (Satiety Hormone): Alters DNA methylation in genes that regulate appetite, fat storage, and energy balance, linking obesity with epigenetic changes.

Ghrelin – overproduction leads to low DNA methylation



Dopamine: Excess dopamine can lead to hypermethylation of reward-system genes, increasing susceptibility to addiction and impaired motivation.

Serotonin: Plays a role in neuronal DNA methylation, influencing mood regulation, depression, and neurodevelopmental disorders.

Glutamate: Regulates synaptic plasticity and is linked to DNA methylation changes in neurodegenerative diseases like Alzheimer's.

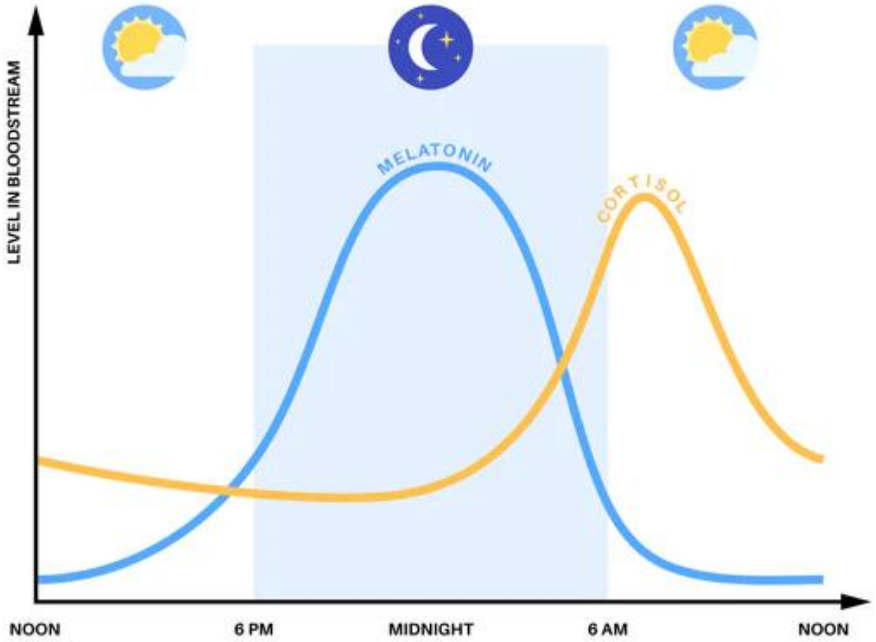
GABA (γ-aminobutyric acid): Helps balance DNA methylation, preventing excessive neuronal excitability and reducing anxiety disorders.

Histone Modification

Hormones:

Estrogen, cortisol, and melatonin influence histone modifications, affecting reproductive health, stress adaptation, and inflammation control.

Neurotransmitters like serotonin and dopamine regulate histone modifications, impacting mood, learning, and addiction pathways.



Estrogen & Progesterone: Influence histone acetylation in breast and uterine cells, regulating reproductive gene expression and cancer risk.

Cortisol: Alters histone methylation patterns that affect genes related to stress resilience, immune response, and brain function.

Insulin-like Growth Factor (IGF-1): Modifies histones to regulate genes controlling cell growth, tissue repair, and longevity.

Melatonin: Promotes histone acetylation, increasing the expression of antioxidant and anti-inflammatory genes that protect against aging and disease.

Testosterone: Affects histone acetylation in muscle cells, activating genes that promote muscle growth and regeneration.

Neurotransmitters:

Serotonin: Modulates histone acetylation, influencing genes that regulate mood, stress response, and cognitive function.

Dopamine: Affects histone deacetylation, which plays a role in motivation, reward-seeking behavior, and addiction pathways.

Norepinephrine: Regulates histone phosphorylation, impacting stress-related gene expression and brain function.

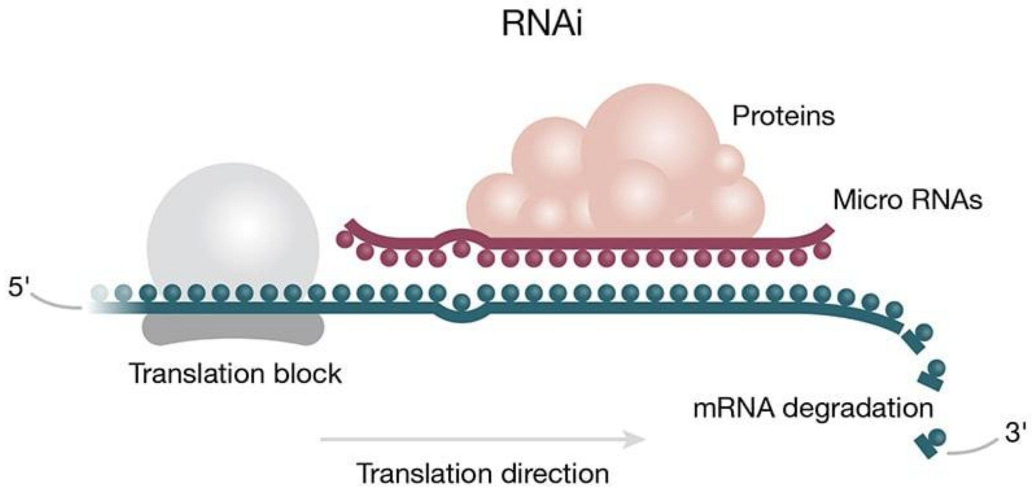
GABA: Plays a role in histone modifications that support brain plasticity, learning, and relaxation.

ncRNA

Non-coding RNAs (microRNAs, long non-coding RNAs, etc.) regulate gene expression after transcription, controlling cell signaling, metabolism, and inflammation.

Cortisol, estrogen, and insulin regulate ncRNA expression, impacting inflammation, metabolism, and reproductive health.

Serotonin and dopamine modulate ncRNA pathways, influencing mood, memory, and stress resilience.



Cortisol: Regulates microRNAs involved in immune response, inflammation, and metabolic adaptation to stress.

Insulin: Modifies ncRNA expression to control genes affecting glucose metabolism, insulin resistance, and fat storage.

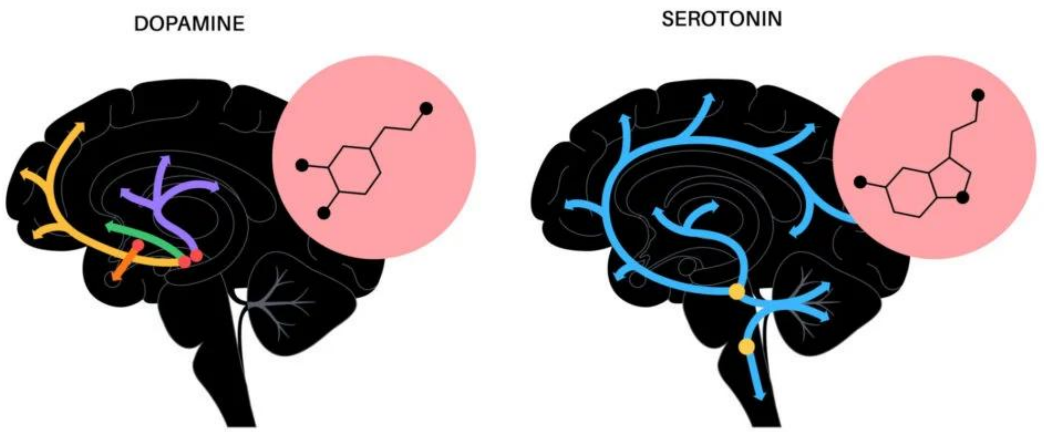
Estrogen: Alters ncRNA expression in genes related to breast cancer, cardiovascular health, and inflammation control.

Growth Hormone (GH): Regulates microRNAs controlling muscle growth, repair, and tissue regeneration.

Serotonin: Influences microRNAs involved in neuroplasticity, mood regulation, and cognitive function.

Dopamine: Modulates microRNAs that regulate genes related to reward-seeking behavior, motivation, and addiction.

GABA: Affects microRNAs controlling neuronal excitability, relaxation, and stress response.



Fermented Beverage

Beets: Supports DNA methylation with betaine and promotes gut microbiota for non-coding RNA regulation.

Radish: Supports DNA methylation, histone modification, and non-coding RNA regulation through its folate, glucosinolates, and antioxidant compounds.

Red Onion, White Onion, or Shallots: Provide quercetin, which influences DNA methylation and detox-related non-coding RNA expression.

Non-chlorinate Water: Provides a clean base for fermentation. Spring water is best.

Himalayan Sea Salt: Controls microbial balance and encourages beneficial fermentation.

Sauerkraut Brine or Whey: Provides probiotics that influence histone modification and non-coding RNA activity via gut-brain interactions.

Mustard Seeds: Contain sulforaphane, which modulates histone modification and detox-related non-coding RNA expression.

Fresh Ginger: Contains gingerol, which regulates non-coding RNA expression related to inflammation and oxidative stress.

Turmeric: Curcumin affects histone modification and non-coding RNA activity.

Black Pepper: Enhances the absorption of turmeric and other nutrients.

Garlic: Supports DNA methylation, histone modification, and non-coding RNA through sulfur compounds that influence gene expression and inflammation.

Fresh Lemon Juice: Contains flavonoids that regulate non-coding RNA expression and support histone modification.

Pomegranate Juice: Supports histone modification through ellagic acid and urolithins, regulating gene expression and inflammation.

A Closer Look At Food

Blueberries – Brain-Boosting Epigenetics

The Science:

Rich in anthocyanins, blueberries influence DNA methylation and histone modification.

They activate genes for brain growth and suppress those linked to inflammation.

The Takeaway:

Daily blueberries may boost memory and protect against cognitive decline.

Broccoli – Cancer-Fighting Power

The Science:

Sulforaphane in broccoli reactivates tumor-suppressor genes via DNA methylation.

Especially effective for breast and prostate cancer.

The Takeaway:

Cruciferous veggies help your genes defend against cancer.

Dark Chocolate – Mood Gene Modulator

The Science:

Polyphenols in dark chocolate influence non-coding RNAs linked to serotonin and dopamine.

The Takeaway:

A square of 70%+ dark chocolate can help balance mood-regulating genes.

Turmeric – Anti-Inflammatory Gene Switch

The Science:

Curcumin modifies histones and blocks HDACs, turning on anti-inflammatory genes.

The Takeaway:

Add turmeric + black pepper to fight inflammation at the genetic level.

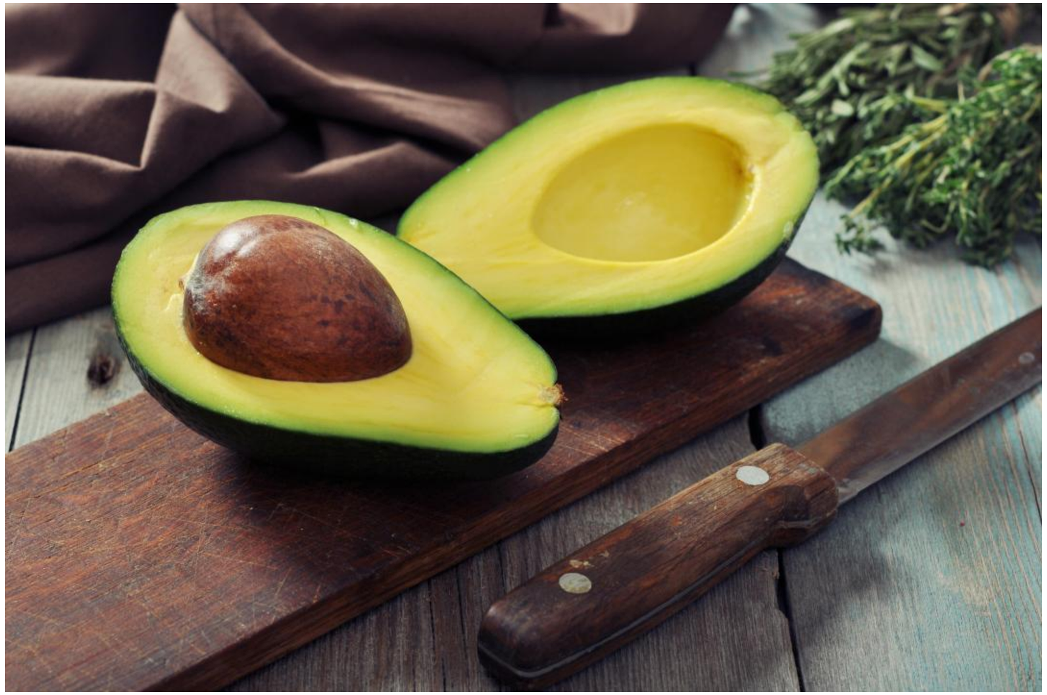
Avocados – Longevity in a Fruit

The Science:

Healthy fats in avocados activate FOXO3, the "longevity gene."

The Takeaway:

Eating avocados may support longer, healthier lives via gene regulation.



Green Tea

The Science:

EGCG in green tea blocks HDACs and reactivates tumor-suppressor genes.

The Takeaway:

Daily green tea may help prevent cancer through gene modulation.

Epigenetic Messages

Every bite sends instructions to your DNA.

Some foods turn on protective genes—others do the opposite.

Ultra-process foods turn off protective genes

White sugar brings nothing to table – it doesn’t protect

Therefore, why consume it

Lifestyle & Epigenetics

Deep Breathing – Epigenetic Stress Relief

Why it works: Activates the parasympathetic nervous system, reducing stress-induced DNA methylation.

Practice: Inhale 4 sec → Hold 4 sec → Exhale 6–8 sec.

Alternate Nostril Breathing – Inflammation Control

Why it works: Regulates non-coding RNAs that reduce oxidative stress and inflammation.

Practice: Inhale left → Exhale right → Inhale right → Exhale left. Repeat x5.

HIIT – Boosts Metabolism Genes

High-Intensity Interval Training alternates short bursts of intense exercise with brief recovery periods

Why it works: Alters DNA methylation in energy and muscle genes.

Practice: 20 sec high-intensity → 10 sec rest → Repeat x2.

Yoga/Tai Chi – Longevity Gene Activation

Why it works: Affects histone acetylation, supporting neuroprotection and circadian rhythms.

Practice: Flowing movements (e.g., Sun Salutations or Qi Gong) with breath.

Humming – Vagus Nerve & Inflammation

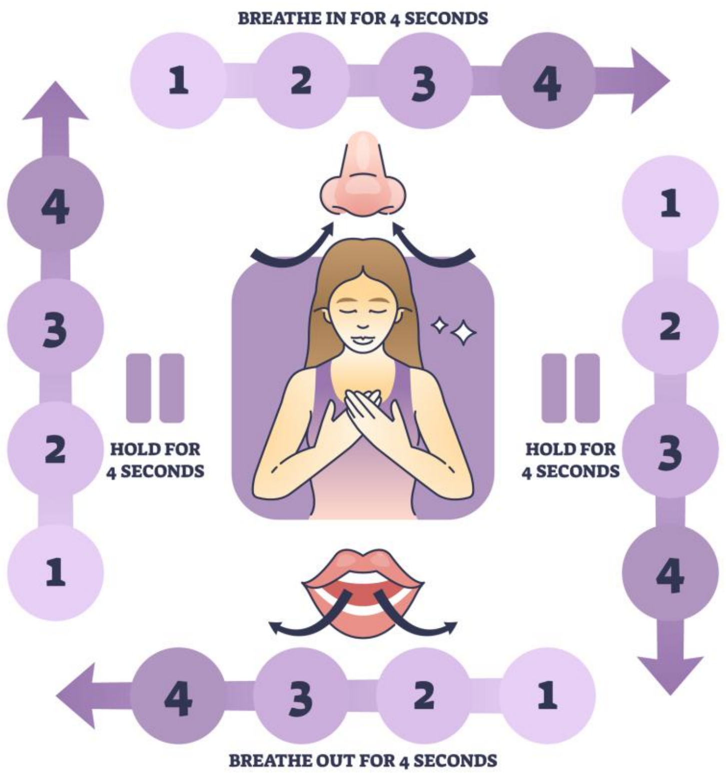
Why it works: Activates the vagus nerve, modulating inflammatory gene expression.

Practice: Hum deeply on exhale for 5–10 sec.

Box Breathing – Cognitive & Gene Support

Why it works: Supports genes like BDNF and FOXP3 linked to brain function and immune balance.

Practice: Inhale 4 → Hold 4 → Exhale 4 → Hold 4. Repeat.



Wim Hof Method – Mitochondria & Immunity

Breathwork, cold exposure, mindset training for physical and mental resilience.

Why it works: Boosts histone acetylation and mitochondrial gene expression.

Practice: 30 deep breaths → Breath hold → Deep inhale/hold 15 sec.

Repeat x2–3.

Cold Exposure – Stress & Metabolism Genes

Why it works: Modifies genes related to thermogenesis and stress resilience.

Practice: Hands in ice water for 10–20 sec + slow nasal breathing.

Chanting – Calm Through Gene Expression

Why it works: Influences microRNAs tied to neural repair and anti-inflammatory effects.

Practice: Chant “OM” or repeat a calming phrase (e.g., “I am present”).

Nature Time – Anti-Inflammatory Methylation

Why it works: Forest bathing or grounding adjusts methylation of inflammation-related genes.

Practice: Spend time barefoot in nature or visualize being in a forest.

Walking Meditation – Aging & Gene Health

Why it works: Affects histone markers linked to longevity.

Practice: Walk slowly, sync breath (inhale 4 steps, exhale 6).

Laughter – Mood & Immunity Genes

Why it works: Laughter alters gene expression related to inflammation and emotional resilience.

Practice: Laugh (real or fake) for at least 30 seconds.

Joy & Laughter

Laughter and joyful experiences trigger a cascade of feel-good chemicals—

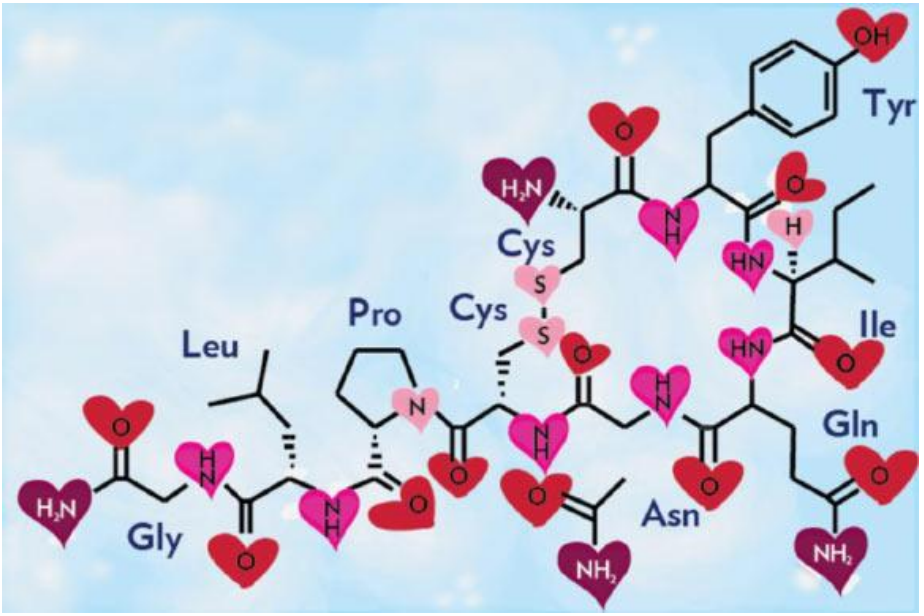
And these also influence your genes through DNA methylation, histone modification, and non-coding RNA.

Oxytocin – The Bonding Hormone

Epigenetic Impact: Reduces methylation of OXTR (oxytocin receptor gene), enhancing emotional connection and trust.

Histone acetylation in brain areas linked to empathy and regulation.

Joy Link: Laughter, touch, and eye contact release oxytocin →, boost social bonding, and calm stress genes.

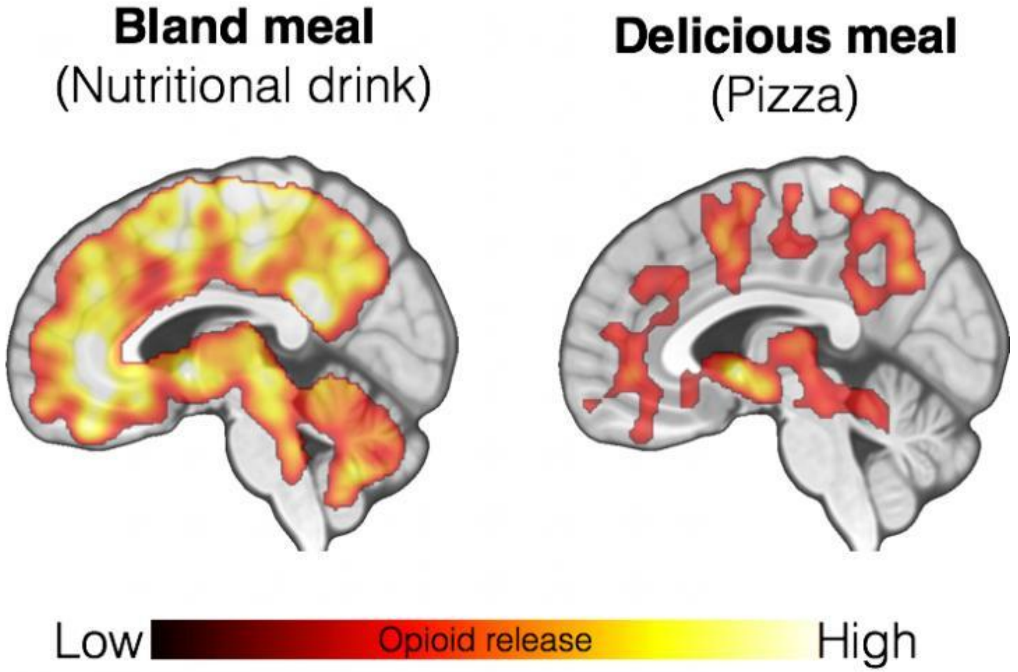


Endorphins – Natural Painkillers & Mood Lifters

Epigenetic Impact: Influence methylation of OPRM1 (opioid receptor gene), modulating emotional resilience and reward pathways.

Histone acetylation improves mood-related gene expression.

Joy Link: Laughter and movement trigger endorphins → reduce inflammation and support stress recovery.

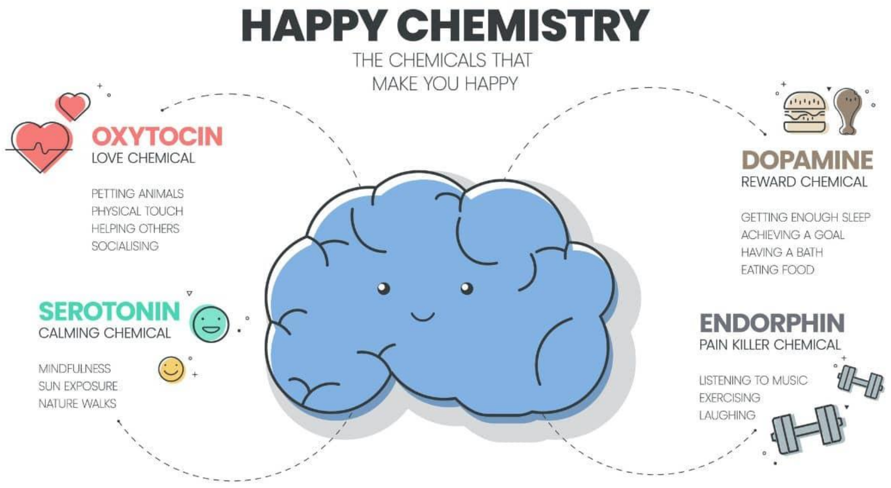


Dopamine – Motivation & Reward

Epigenetic Impact: Alters methylation and microRNAs related to pleasure, focus, and addiction resilience.

Promotes histone modifications tied to memory and learning.

Joy Link: Humor, play, and anticipation release dopamine → supports positive behavioral reinforcement and gene expression for resilience.



Serotonin – Mood Stabilizer

Epigenetic Impact: Methylation changes in serotonin transporter gene (SLC6A4) are linked to depression risk.

Serotonin pathways are shaped by microRNAs affecting emotional processing.

Joy Link: Laughter and connection elevate serotonin → promotes gene expression for calm and well-being.

Cortisol – Stress Hormone

Epigenetic Impact: Chronic cortisol elevates methylation of genes involved in inflammation and emotional regulation.

Joy Link: Laughter lowers cortisol, helping restore healthy epigenetic patterns.

Laughter Is a Genetic Reprogramming Tool

Activates neurotransmitters & hormones that positively affect gene expression

Supports emotional resilience, reduces inflammation, enhances immunity

Works through DNA methylation, histone changes, and non-coding RNA regulation