

# Optimizing Patient Care

## Identifying and Bypassing Genetic Polymorphisms

Presenter:  
Benjamin Lynch, ND

Orthomolecular Medicine Today  
Vancouver BC, Canada  
April 25 - 27, 2014

*“Clinicians will be central to helping consumer-patients use genomic information to make health decisions.” – NEJM*



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I am President and CEO of SeekingHealth.com, SeekingHealth.org and founder of MTHFR.Net

## How are these linked?

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- Orange skin and beta carotene
- Low RBC folate yet high serum folate
- Anger from cheese
- Symptoms improve during pregnancy
- Methylfolate and Itchiness/Rash
- Depression and Chronic Disease
- Elevated serotonin in autism
- Preeclampsia and nitric oxide

# Genetic and Epigenetic Contributions to Human Nutrition and Health: Managing Genome–Diet Interactions

PATRICK J. STOVER, PhD; MARIE A. CAUDILL, PhD, RD

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## ABSTRACT

The Institute of Medicine recently convened a workshop to review the state of the various domains of nutritional genomics research and policy and to provide guidance for further development and translation of this knowledge into nutrition practice and policy. Nutritional genomics holds the promise to revolutionize both clinical and public health nutrition practice and facilitate the establishment of (a) genome-informed nutrient and food-based dietary guidelines for disease prevention and healthful aging, (b) individualized medical nutrition therapy for disease management, and (c) better targeted public health nutrition interventions (including micronutrient fortification and supplementation) that maximize benefit and minimize adverse outcomes within genetically diverse human populations. As the field of nutritional genomics matures, which will include filling fundamental gaps in knowledge of nutrient–genome interactions in health and disease and demonstrating the potential benefits of customizing nutrition prescriptions based on genetics, registered dietitians will be faced with the opportunity of making genetically driven dietary recommendations aimed at improving human health.

*J Am Diet Assoc.* 2008;108:1480-1487.

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*P. J. Stover is a professor and director, and M. A. Caudill is an associate professor, Division of Nutritional Sciences, Cornell University, Ithaca, NY.*

*Address correspondence to: Patrick J. Stover, PhD, Cornell University, Division of Nutritional Sciences, Ithaca, NY 14853. E-mail: vis13@cornell.edu*

Public health nutrition continues to be challenged by increasing expectations from the food supply on one hand, and fundamental gaps in nutrition knowledge on the other, which can constrain the development and implementation of nutrition and food policy (1). Current demands on the food supply are no longer limited to ensuring general safety and preventing micronutrient deficiencies. Increasingly, there is interest in engineering medicinal qualities into the food supply to enable diets that promote health and “nurture” a sense of well-being that transcends the mere absence of disease by improving biological functions and even increasing lifespans.

Unquestionably, nutrition is one of the primary environmental exposures that determines health. Common human chronic diseases, including type 2 diabetes, metabolic syndrome, cardiovascular and neurological disease, and many cancers are initiated and/or accelerated by nutrient/food exposures. However, it is also recognized that chronic diseases are complex in their etiology and include a substantial genetic component; individuals respond differently to foods and even individual nutrients. Investigation in this new field of nutrition research, often referred to as *nutritional genomics*, focuses on deciphering the biological mechanisms that underlie both the acute and persistent genome-nutrient interactions that influence health.

Nutritional genomics, while centered on the biology of individuals, distinguishes itself from other “omics” fields by its unique focus on disease prevention and healthy aging through the manipulation of gene–diet interactions. Nutritional genomics promises to revolutionize both clinical and public health nutrition practice and facilitate the establishment of (a) genome-informed nutrient and food-based dietary guidelines for disease prevention and healthful aging, (b) individualized medical nutrition therapy for disease management, and (c) better

Why?



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# Treat the Patient. Not the SNPs

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## Key Points about SNPs and Clinical Use

- Most SNPs not clinically relevant
- Optimizing pregnancy
- Increases compliance
- Fantastic for disease prevention
- Ability to optimize patient's wellness
- Identify possible nutrient deficiencies
- Identify predispositions and risks
- Contributing cause towards patient signs/symptoms
- Ability to create a long-term plan
- Forces a need to understand the normal function and interactions.
- Identify reasons why patient responds poorly/favorably to treatment.

# The first step to a healthy pregnancy

Babies with genetic disease are often born to healthy parents.  
The Counsyl Test gives you insight to a healthy future.

[Get Started](#)[Learn More](#)

## RESULTS

Gene Name / Variation	Mutation Not Present	Mutation(s) Present	Call	
SHMT / C1420T		+/-	Hetero	Minus "-" represents no mutation
AHCY / 1	-/-		A	Plus "+" represents a mutation
AHCY / 2	-/-		T	"-/-" indicates there is no mutation
AHCY / 19	-/-		A	"+/-" indicates there is one mutation
MTHFR / C677T	-/-		C	"++" indicates there is a double mutation
MTHFR / A1298C	-/-		A	
MTHFR / 3	-/-		C	
MTR / A2756G		+/-	Hetero	
MTRR / A66G		+/-	Hetero	
MTRR / H595Y	-/-		C	
MTRR / K350A	-/-		A	
MTRR / R415T	-/-		C	
MTRR / S257T	-/-		T	
MTRR / 11		+/-	Hetero	
BHMT / 1	-/-		A	
BHMT / 2		+/-	Hetero	
BHMT / 4		+/+	C	
BHMT / 8		+/+	T	
CBS / C699T	-/-		C	
CBS / A360A	-/-		C	
CBS / N212N	-/-		C	
COMT / V158M		+/+	A	
COMT / H62H		+/+	T	
COMT / 61	-/-		G	
SUOX / S370S	-/-		CG	
VDR / Taq1	-/-		C	
VDR / Fok1	-/-		C	
MAO A / R297R	-/-		G	
NOS / D298E	-/-		G	
ACAT / 1-02		+/-	Hetero	



Do you recommend this product?

I Have homozygous mutation in COMT V158M, COMT H62H, VDR Taq, MAO-A R297R and CBS C699T.

I have heterozygous mutations MTRR A66G, MTRR K350A, BHMT-02, and BHMT-08.

Please help I want to buy the right supplements. I am 29 year old mom with 3 babies, I need al the energy and mood and every thing and beyond help.

## Methylation Profile; plasma

PRIMARY & INTERMEDIATE METABOLITES										
	RESULT/UNIT		REFERENCE INTERVAL		PERCENTILE					
					2.5 <sup>th</sup>	16 <sup>th</sup>	50 <sup>th</sup>	84 <sup>th</sup>	97.5 <sup>th</sup>	
Methionine	2.0	μmol/dL	1.6 -	3.6						
Cysteine	50	μmol/dL	20 -	38						
S-adenosylmethionine (SAM)	205	nmol/L	86 -	145						
S-adenosylhomocysteine (SAH)	46.1	nmol/L	10 -	22						
					68 <sup>th</sup>		95 <sup>th</sup>			
Homocysteine	20.6	μmol/L	<	11						
Cystathionine	0.30	μmol/dL	<	0.05						

METHYLATION INDEX					
	RESULT	REFERENCE INTERVAL		PERCENTILE	
				68 <sup>th</sup>	95 <sup>th</sup>
SAM : SAH	4.5	>	4		

## Testing Levels of Various Folate Forms

### AMINOACIDS IN PLASMA

Glutathione (oxidised)	<b>0.51</b>	µmol/L	0.16 - 0.50
Glutathione (reduced)	<b>3.2</b>	µmol/L	3.8 - 5.5

### DERIVATES

S-Adenosylmethionine (RBC)	<b>213</b>	µmol/dl	221 - 256
S-Adenosylhomocysteine (RBC)	<b>52.0</b>	µmol/dl	38.0 - 49.0

### FOLIC ACID DERIVATES

5-CH <sub>3</sub> -THF	<b>8.8</b>	nmol/l	8.4 - 72.6
10-Formyl-THF	<b>3.7</b>	nmol/l	1.5 - 8.2
5-Formyl-THF	<b>1.60</b>	nmol/l	1.20 - 11.70
THF	<b>0.52</b>	nmol/l	0.60 - 6.80
Folic Acid	<b>9.2</b>	nmol/l	8.9 - 24.6
Folinic Acid (WB)	<b>7.1</b>	nmol/l	9.0 - 35.5
Active folate (RBC)	<b>359</b>	nmol/l	400 - 1500

### NUCLEOSIDE

Adenosine	<b>23.6</b>	10 <sup>-8</sup> M	16.8 - 21.4
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AMINOACIDS IN PLASMA

Nitrotyrosine

Glutathione (oxidised)

Glutathione (reduced)

MISCELLANEOUS

Ammonia (plasma)

NO (Nitric oxide)

Derivates

S-Adenosylmethionine (RBC)

S-Adenosylhomocysteine (RBC)

FOLIC ACID DERIVATES

5-CH3-THF

10-Formyl-THF

5-Formyl-THF

THF

Folic Acid

Folinic Acid (WB)

Folic Acid, active (RBC) *mislabeled*

BIOLOGICAL AMINES

CATACHOLAMINES IN PLATELETS

Histamine (whole blood)

NUCLEOSIDE

Adenosine

28.7	µg/l	1.1 - 6.8
0.51	µmol/L	0.16 - 0.50
3.0	µmol/L	3.8 - 5.5
50	µmol/L	8 - 40
88.5	ng/mL	18.0 - 35.0
225	µmol/dl	221 - 256
52.8	µmol/dl	38.0 - 49.0
6.9	nmol/l	8.4 - 72.6
2.9	nmol/l	1.5 - 8.2
3.80	nmol/l	1.20 - 11.70
0.53	nmol/l	0.60 - 6.80
14.0	nmol/l	8.9 - 24.6
15.3	nmol/l	9.0 - 35.5
326	nmol/l	400 - 1500
	-	
29.4	µg/l	10.0 - 65.0
24.8	10 <sup>-8</sup> M	16.8 - 21.4

## Genetics: Nuclear DNA

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### Nuclear DNA (nDNA)

- Paternal and Maternal Sets
- Histones = Protection
- Repair mechanisms

### Folate

- DHFR
- MTHFD
- MTHFR
- SHMT
- FOLR
- TYMS
- SLC19A1

### B12

- TCN2 and TCN3
- MMAB (aka cblB)

### Methionine Cycle

- MTR/MTRR
- MAT1
- AHCY
- CBS

### Methyltransferases

- COMT
- PEMT
- BHMT
- GAMT
- HNMT
- GNMT
- PNMT

### Glutathione

- GSTM1
- GCS
- GPX1
- GR

### Detoxification

- Cyt P450's
- SULT
- NAT

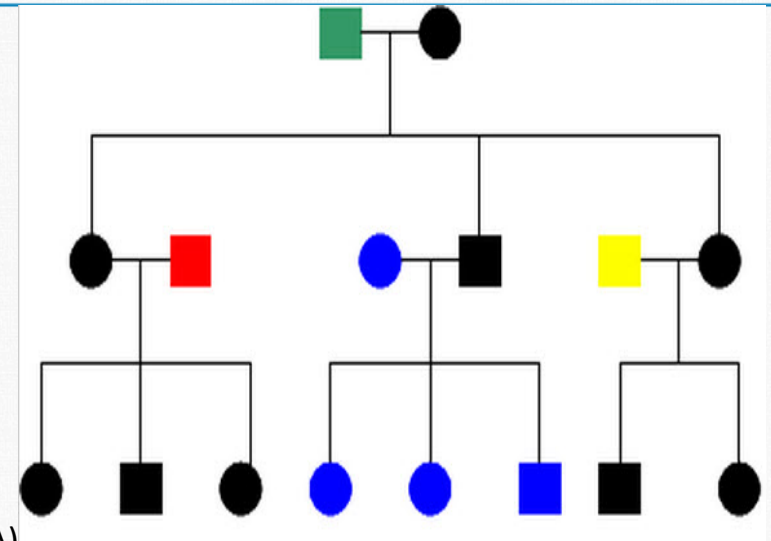
### Additional:

- APOE
- BCMO1
- FUT2
- GAD
- MAOA
- PON1
- SOD2
- DAO
- G6PD
- NOS1, 2 and 3

## Genetics: Mitochondria

### Mitochondrial DNA (mtDNA)

- Inherited only from Maternal side (family hx Important)
- Majority of ATP produced in mitochondria
- Require importing nDNA gene products to function
- SNPS/mutations in mtDNA may be pathological
  - Cancer
  - Diabetes
  - Cardiovascular Diseases
  - Neurodegenerative Diseases
  - Aging
  - Degenerative Diseases
- Lack of Histones = high rate of mtDNA mutagenesis (10x nDNA)
- Mitochondrial Transcription Factor A (TFAM) = Protective coating and regulation
- mtDNA copy number  $\uparrow$  cell survival and function



### Mitochondrial

- SOD
- CAT
- NDUF
- ATP
- COX

<http://cshperspectives.cshlp.org/content/5/5/a012641.full.pdf> and  
<http://www.nature.com/scitable/topicpage/mtdna-and-mitochondrial-diseases-903> and  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3753274/pdf/pone.0074513.pdf>

(c) 2014: Benjamin Lynch, ND

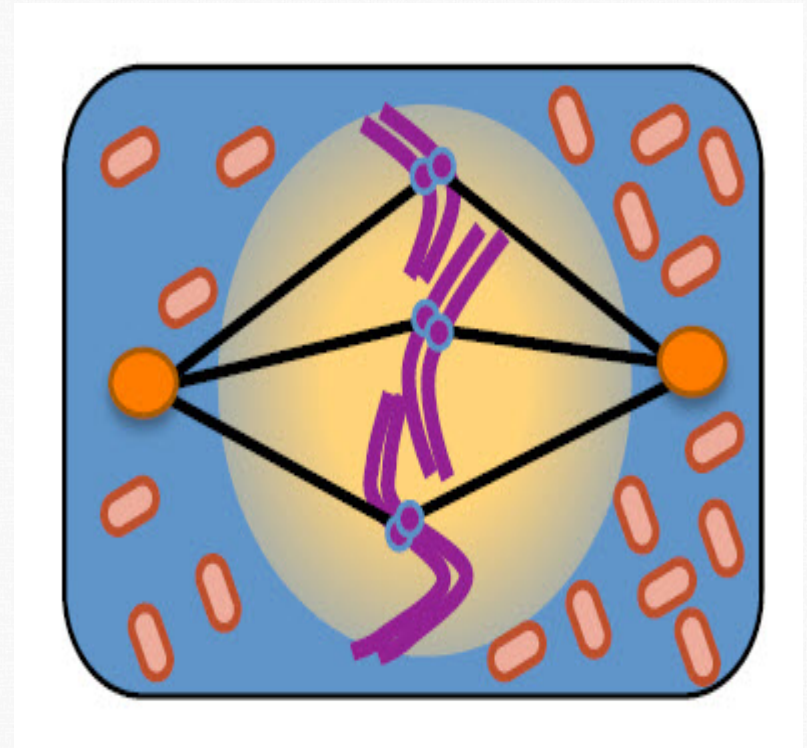
## Genetics: Mitochondria

### Mitochondrial DNA (mtDNA)

- Sperm – 700 molecules of mitochondria
- Oocytes – 200,000 molecules of mitochondria

### Cell Division and Mitochondria:

- Mitochondria 'float' in cytoplasm
- Lack of Spindles
- Randomized



Acton B et al. Mol. Hum. Reprod. 2004;10:23---32 European Society of Human Reproduction and Embryology

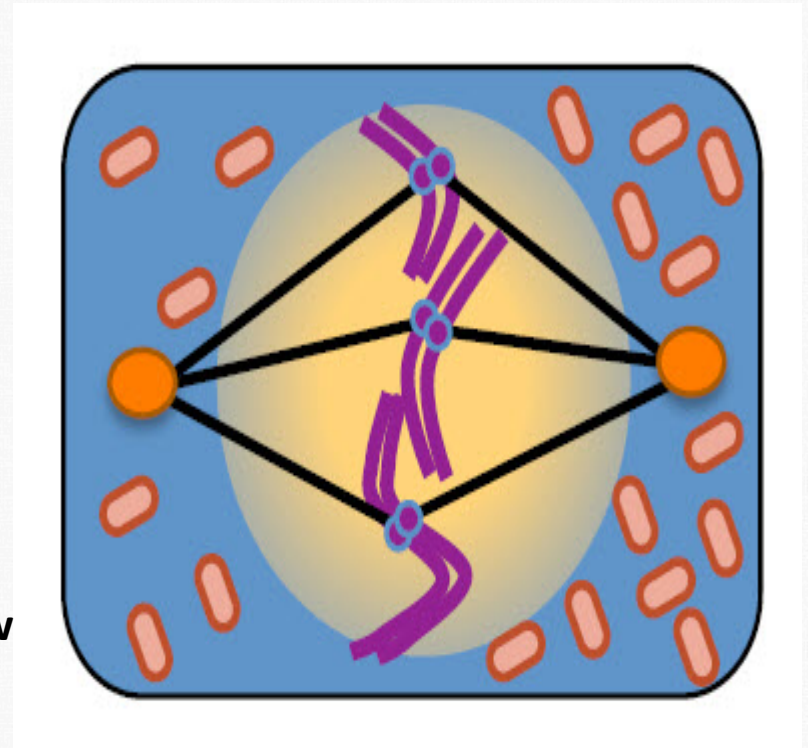
## Cell Division and Replication of 'Sick' Cells?

### Stimulate DNA Bases and $\uparrow$ Cell Proliferation

- “New” cells created:
  - $\downarrow$  Glutathione
  - Oxidized cell membrane
  - $\downarrow$  Potassium
  - $\uparrow$  ROS
  - $\uparrow$  Cell death

Flare of Patient Symptoms with addition of Folate / B12.

**Necessitates Treatment Flow**





# Epigenetics

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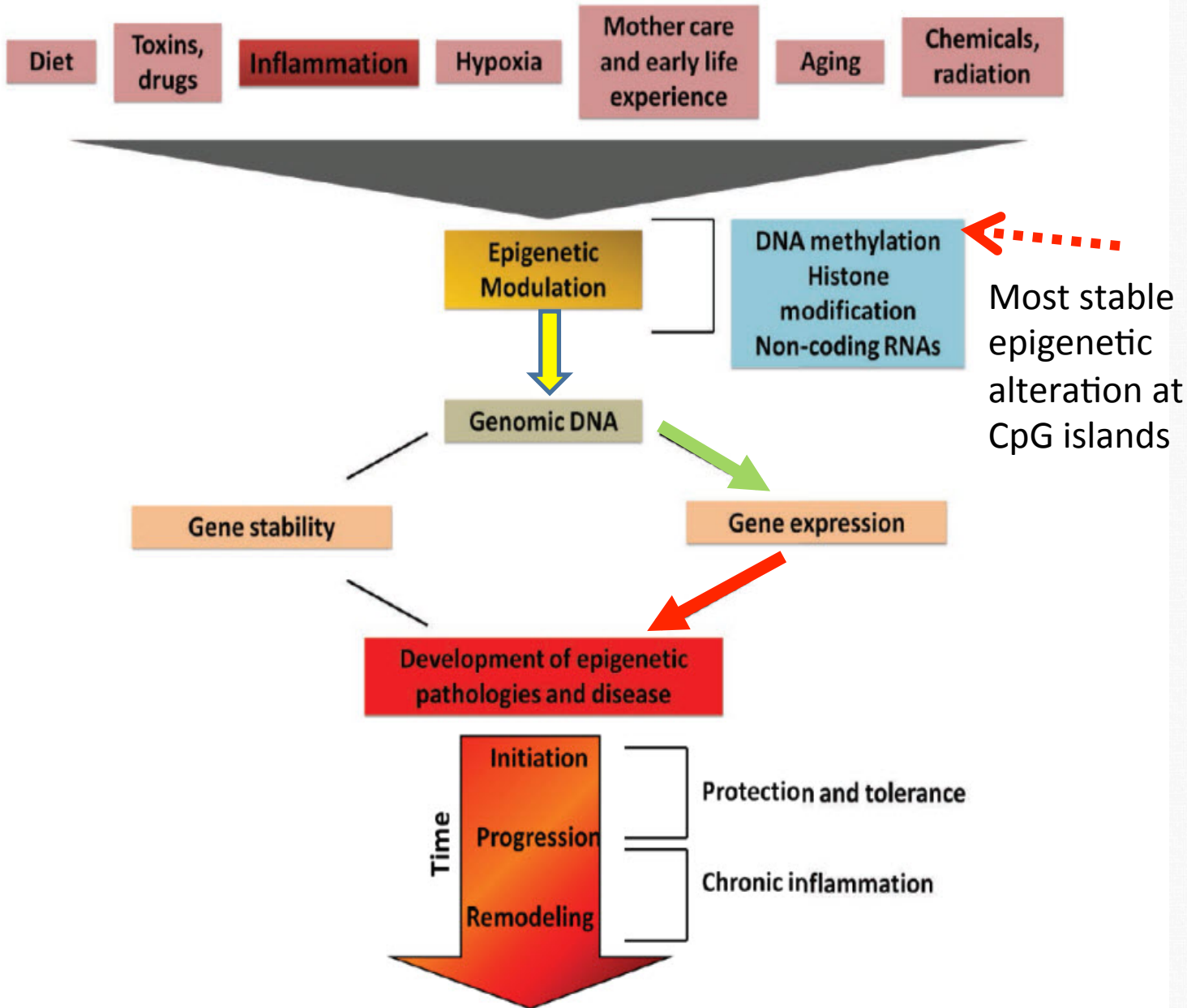
- “As an organism grows and develops, carefully orchestrated chemical reactions activate and deactivate parts of the genome at strategic times and in specific locations.

Epigenetics is the study of these chemical reactions and the factors that influence them.”

- “Epigenetic changes are environmentally responsive mechanisms that can modify gene expression independently of the genetic code.”

<http://learn.genetics.utah.edu/content/epigenetics/> and Epigenetics and the developmental origins of inflammatory bowel diseases.



# Environmental Factors Affecting the Epigenome



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## Epigenetic Example: Inflammatory Bowel Disorders

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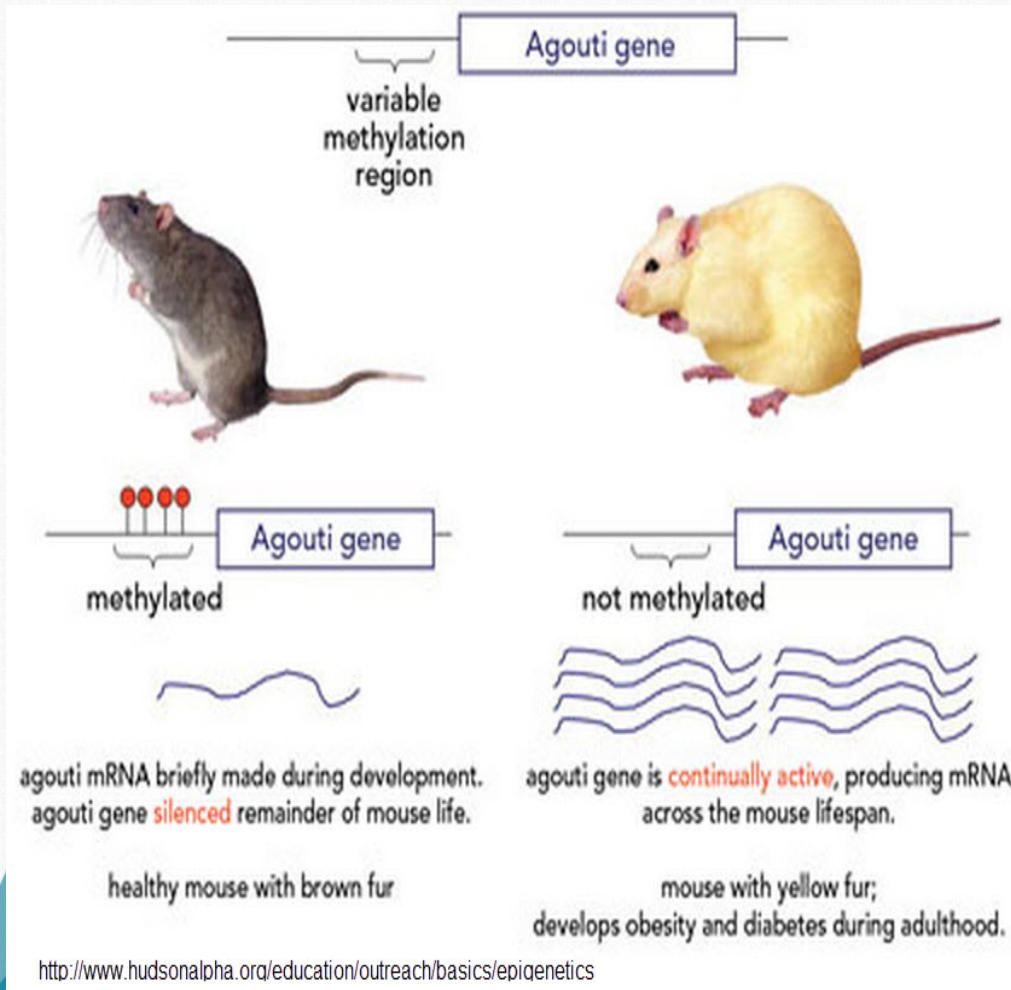
-  High monozygotic twin discordant rates in Crohn disease and UC.  
70+ loci associated with CD. 40+ for UC = epigenetic control.
-  High monozygotic twin concordant rates in Celiac disease.  
*Single* HLA locus linked to 40% of heritability = genetic control

### Epigenetic Control in Crohn's Disease and UC

Source: Epigenetics and the developmental origins of inflammatory bowel diseases.

# Epigenetics in Action

## a) Lab Setting



## b) Environment



# Epigenetics 1<sup>st</sup>

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## Key 'Big Picture' Disturbances

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- Environment
- Lifestyle
- Diet
- Pathogens
- Heavy Metals
- Xenobiotics
- Oxidative Stress
- Nutrient Deficiencies
- Nutrient Excess
- SNPs


### **System-Wide Dysfunction**

# MTHFR: Why now?

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## Folic Acid → GMH

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 MTHFR increasing in the population.

- Folic acid fortification
  - ↑ Full-Term Pregnancies
  - ↑ Folate SNPs
  - ↑ Methylation SNPs
  - ↑ Inferior SNPs
  - ↑ Metabolic Issues

↑ **Susceptibility to Environmental Exposures**

**Natural *De*Selection:**  
Survival of the 'Unfittest'



# Folic Acid Fortification, Increase in MTHFR and Rise in Autism?

by [Dr Lynch](#) on May 11, 2012 in [MTHFR and Pregnancy](#)

If we sit back and evaluate the dates when folic acid fortification began and the fast rise of autism – do they correlate?

“In Spain, the prevalence of the MTHFR 677TT genotype has reportedly approximately doubled in the population since the introduction in 1982 of folic acid supplements for women in early pregnancy”...

“Folic acid fortification and supplement use might be “a genetic time bomb.” The first premise of this dramatic claim, that folic acid use increases the proportion of children born with the T allele of MTHFR, is as yet poorly documented and is clearly in urgent need of further study.

Studies of the MTHFR genotype frequencies in children before and after fortification should be carried out in countries planning fortification of food with folic acid. Thus, saving fetuses that have a genetic constitution that favors abortion or nonsurvival could lead to children being born with genotypes that favor increased disease during life”[1]

Folic acid fortification started heavily in 1992.[2]

Autism began to quickly rise in 1993.

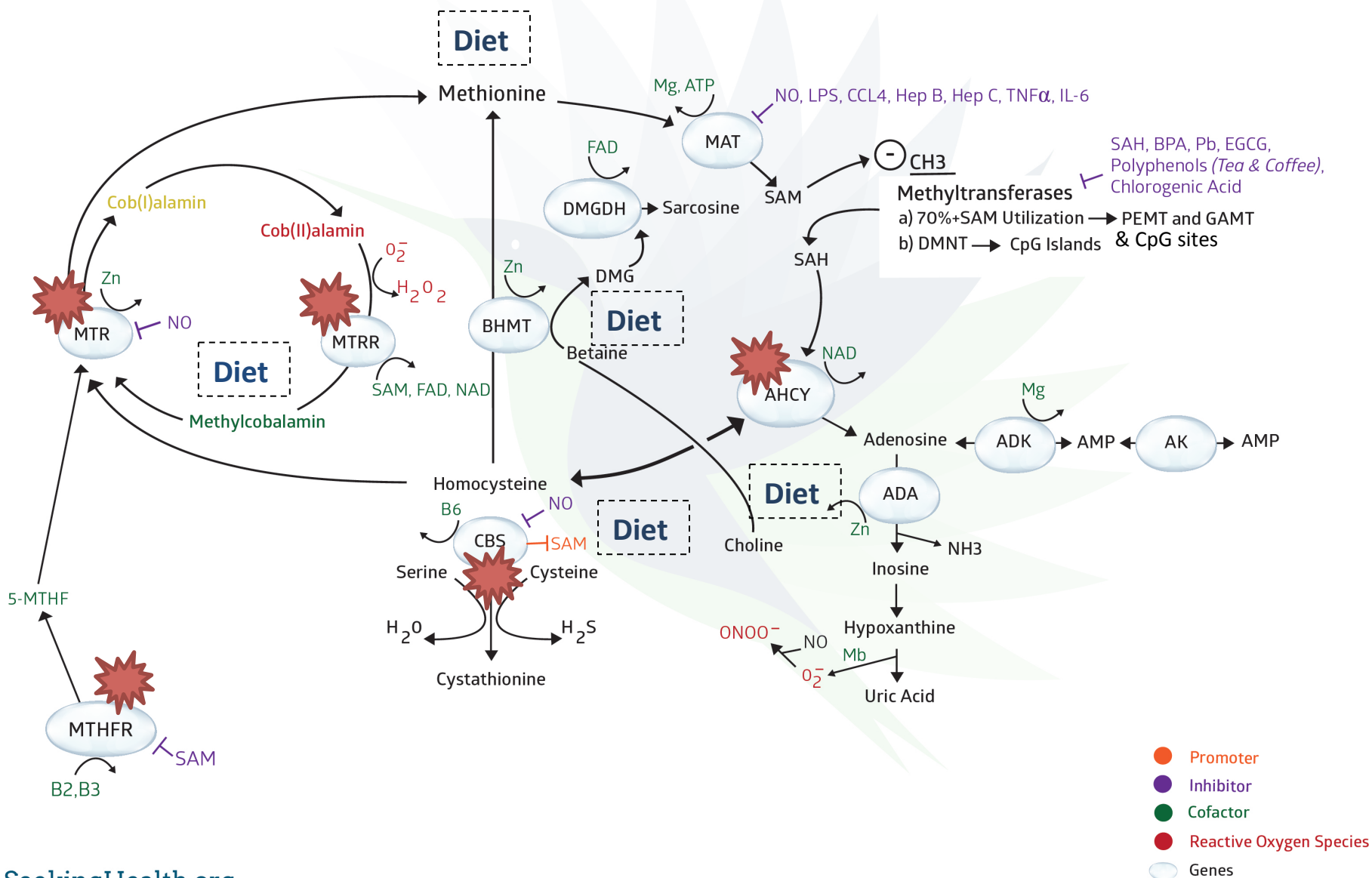
“In the early 1990s, autism diagnoses began to soar. In the 10 years between 1993 and 2003, the number of American schoolchildren with autism diagnoses increased by over 800%. In 2006, the CDC noted a slight decrease in the number of new cases diagnosed.[3]

Autism began to rise at the same time folic acid fortification began.

(c) 2014: Benjamin Lynch, ND  
Is the rise of autism due to an increased survival rate of babies with MTHFR defects?

# Methylation

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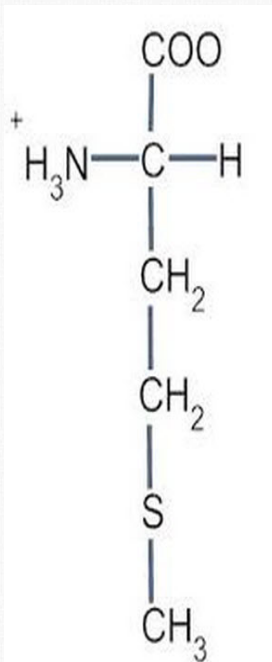


# Homocysteine

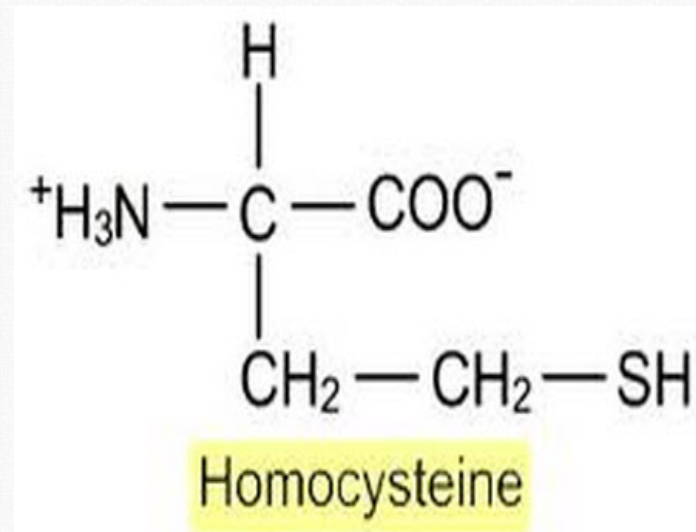
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# Homocysteine

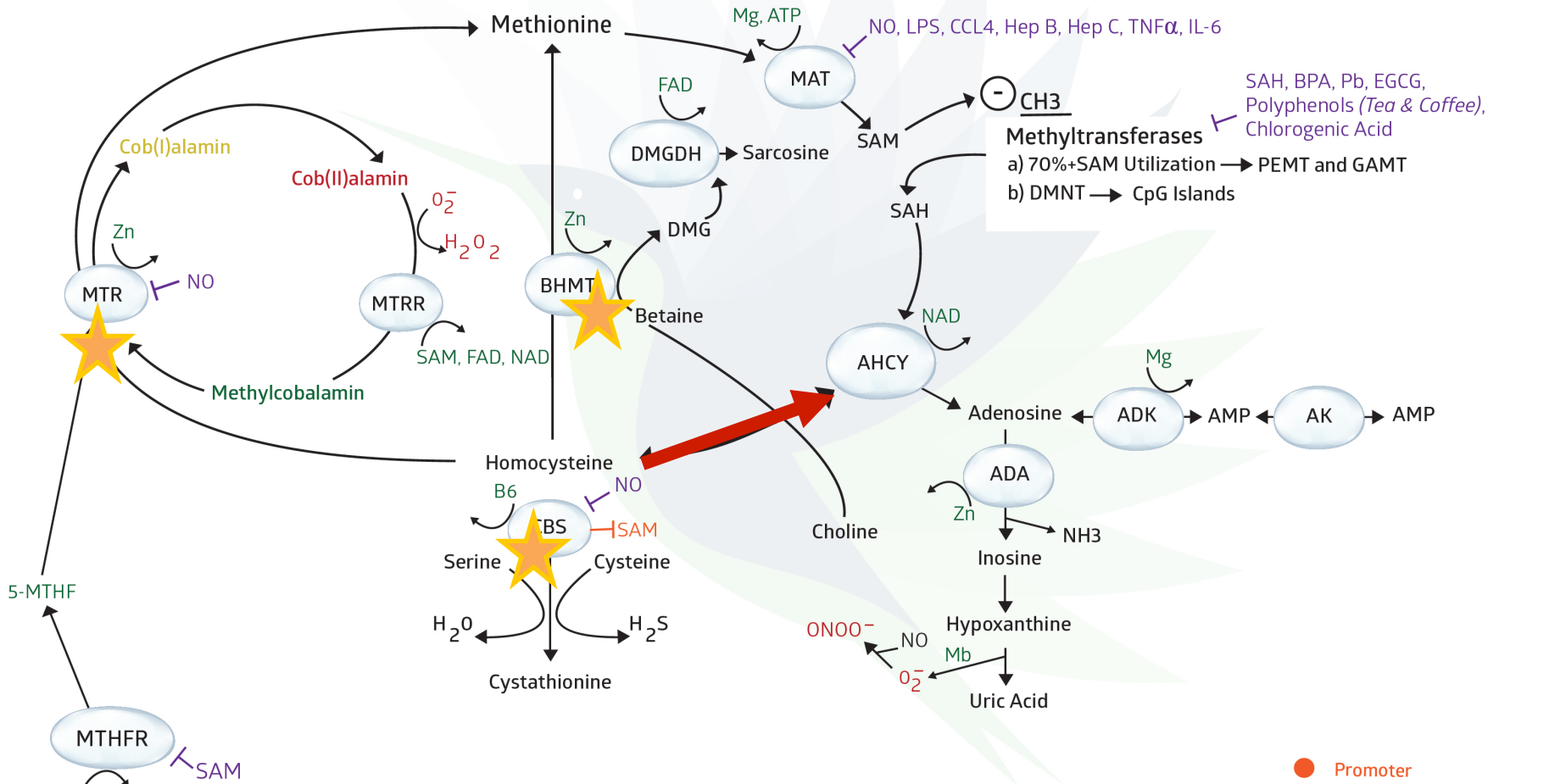
- Methionine = Methyl-Homocysteine
- Breakdown product of SAM → SAH via AHCY



Methionine



### Homocysteine Metabolism (Routes)



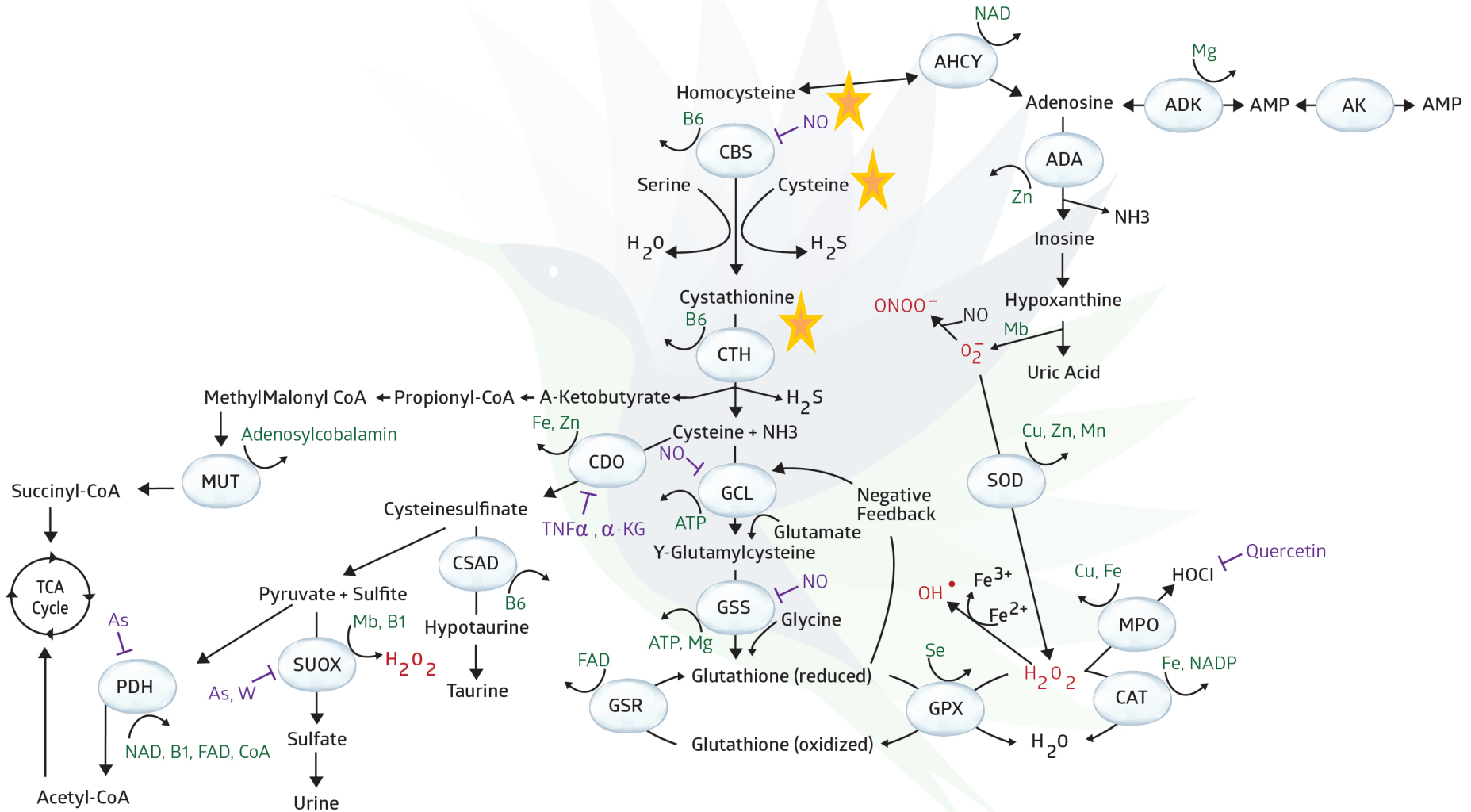
**Low homocysteine (< 6) is an important finding**

- Promoter
- Inhibitor
- Cofactor
- Reactive Oxygen Species
- Genes





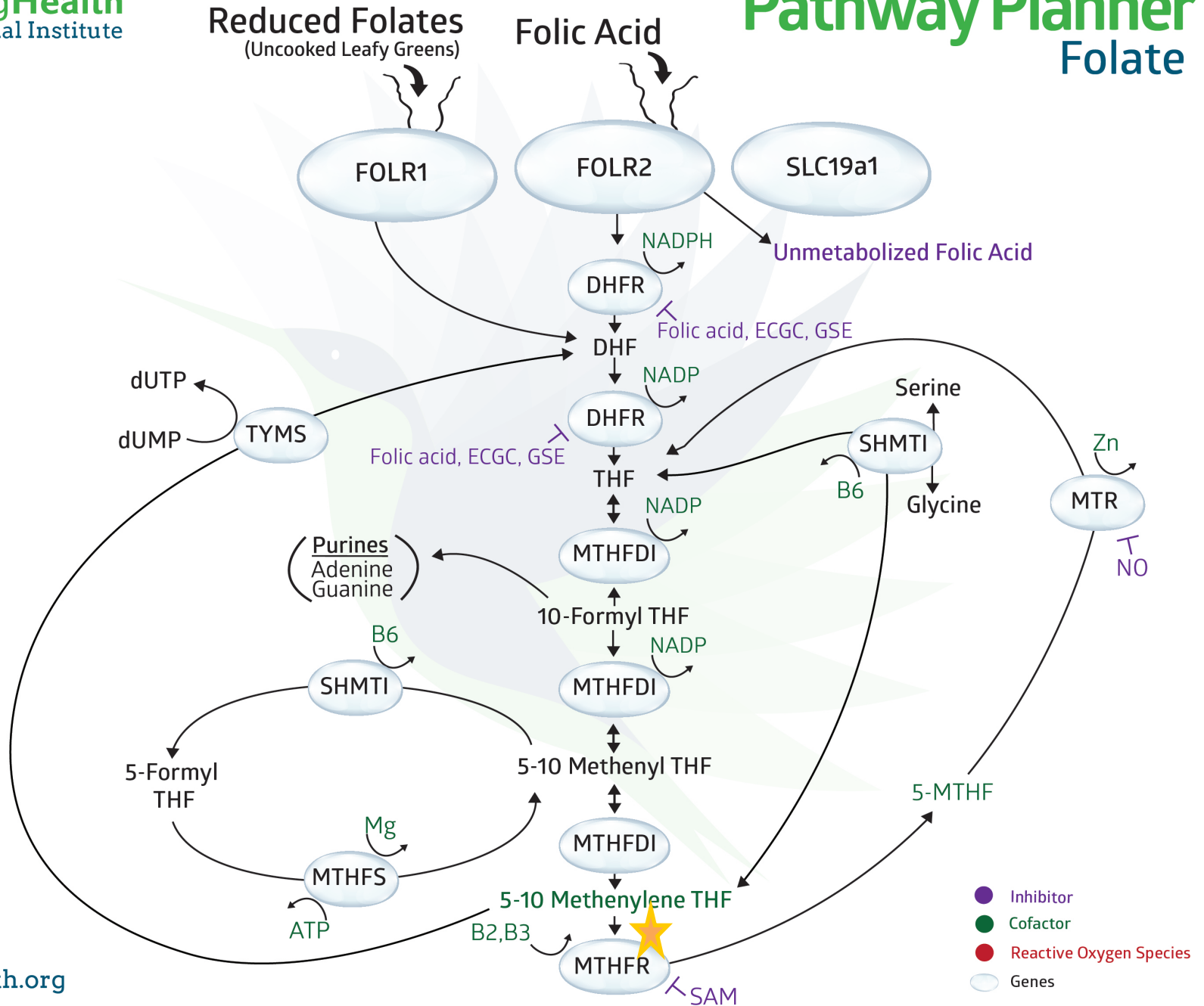




- Inhibitor
- Cofactor
- Reactive Oxygen Species
- Genes

# Folate Cycle

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Gene	Variant	rsID & (orientation)	Risk Allele	Issue
SLC19A1	80A>G	Rs1051266 (-)	G	↑ Serum folate levels (↓ RBC Folate)
MTHFD1	1958G>A	Rs2236225 (-)	C	↓ Stability and Activity
MTHFR	C677T	Rs1801133 (-)	T	↓ One carbon metabolism
MTHFR	A1298C	Rs1801131 (-)	C	↓ One carbon metabolism (with 677)

Showing raw data for SNP **Rs1051266**, which is on chromosome 21.

**21**  
48m bases  
450 genes

Jump to a gene:  Go a SNP:  Go

or a chromosome:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

« Return to your whole genome.

Gene	Position	SNP	Versions	Genotypes															
SLC19A1	46957794	<b>rs1051266</b>	C or T	<table border="0"> <tr><td>CC</td><td>GG</td><td>Benjamin Lynch</td></tr> <tr><td>CT</td><td>GA</td><td>MATHEW LYNCH</td></tr> <tr><td>CT</td><td>GA</td><td>NADIA LYNCH</td></tr> <tr><td>CT</td><td>GA</td><td>TASMAN LYNCH</td></tr> <tr><td>CT</td><td></td><td>THEODOR LYNCH</td></tr> </table>	CC	GG	Benjamin Lynch	CT	GA	MATHEW LYNCH	CT	GA	NADIA LYNCH	CT	GA	TASMAN LYNCH	CT		THEODOR LYNCH
CC	GG	Benjamin Lynch																	
CT	GA	MATHEW LYNCH																	
CT	GA	NADIA LYNCH																	
CT	GA	TASMAN LYNCH																	
CT		THEODOR LYNCH																	

Reference Links:

- [Entrez Gene](#)
- [Google Scholar \(Gene\)](#)
- [dbSNP Lookup](#)
- [Google Scholar \(SNP\)](#)

dbSNP Orientation: Minus

Orientation (+) = do nothing

Orientation (-) = Flip the Base

A → T    G → C  
T → A    C → G

AMINOACIDS IN PLASMA

Nitrotyrosine

Glutathione (oxidised)

Glutathione (reduced)

MISCELLANEOUS

Ammonia (plasma)

NO (Nitric oxide)

Derivates

S-Adenosylmethionine (RBC)

S-Adenosylhomocysteine (RBC)

FOLIC ACID DERIVATES

5-CH3-THF

10-Formyl-THF

5-Formyl-THF

THF

Folic Acid

Folinic Acid (WB)

Folic Acid, active (RBC) *mislabeled*

BIOLOGICAL AMINES

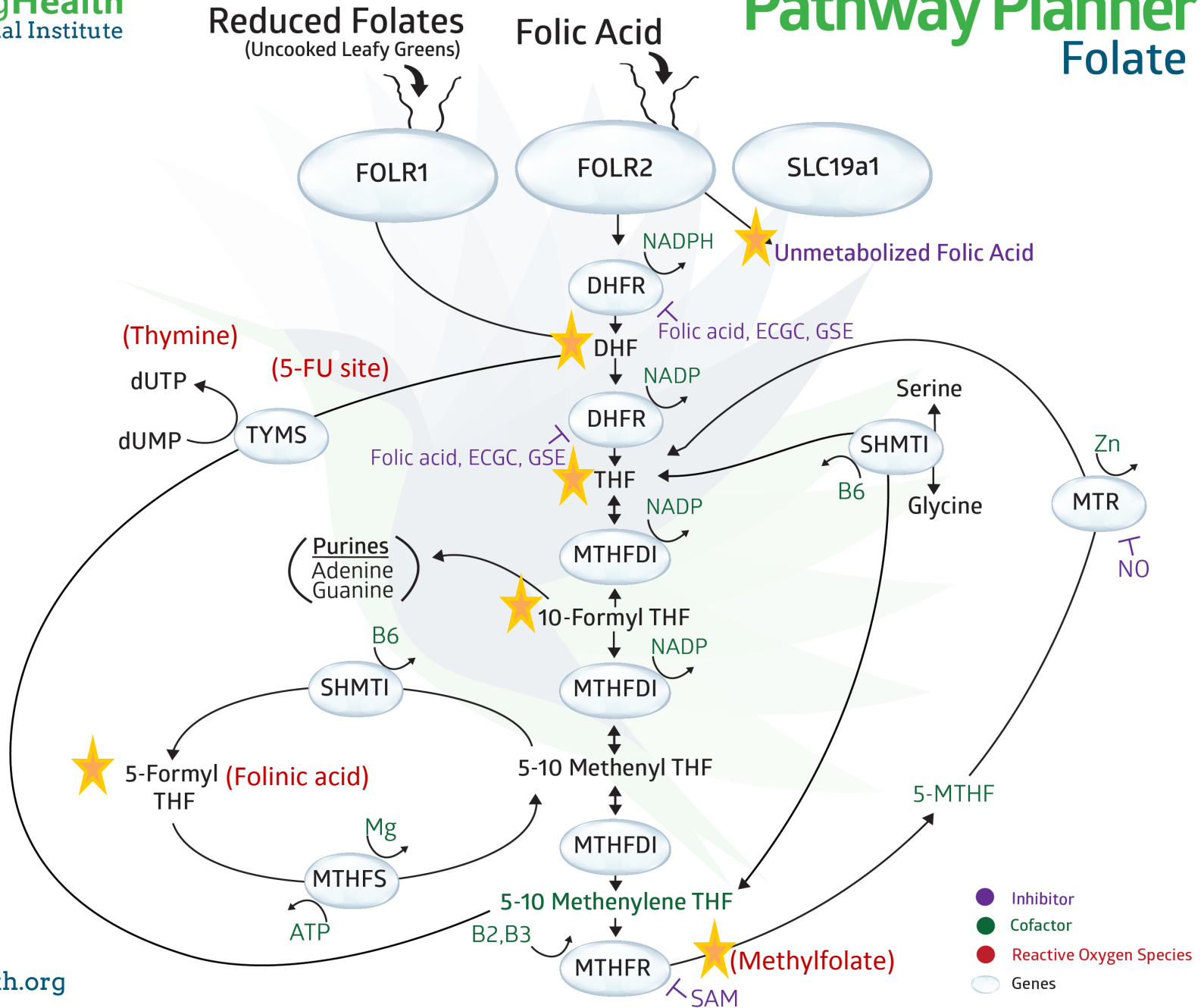
CATACHOLAMINES IN PLATELETS

Histamine (whole blood)

NUCLEOSIDE

Adenosine

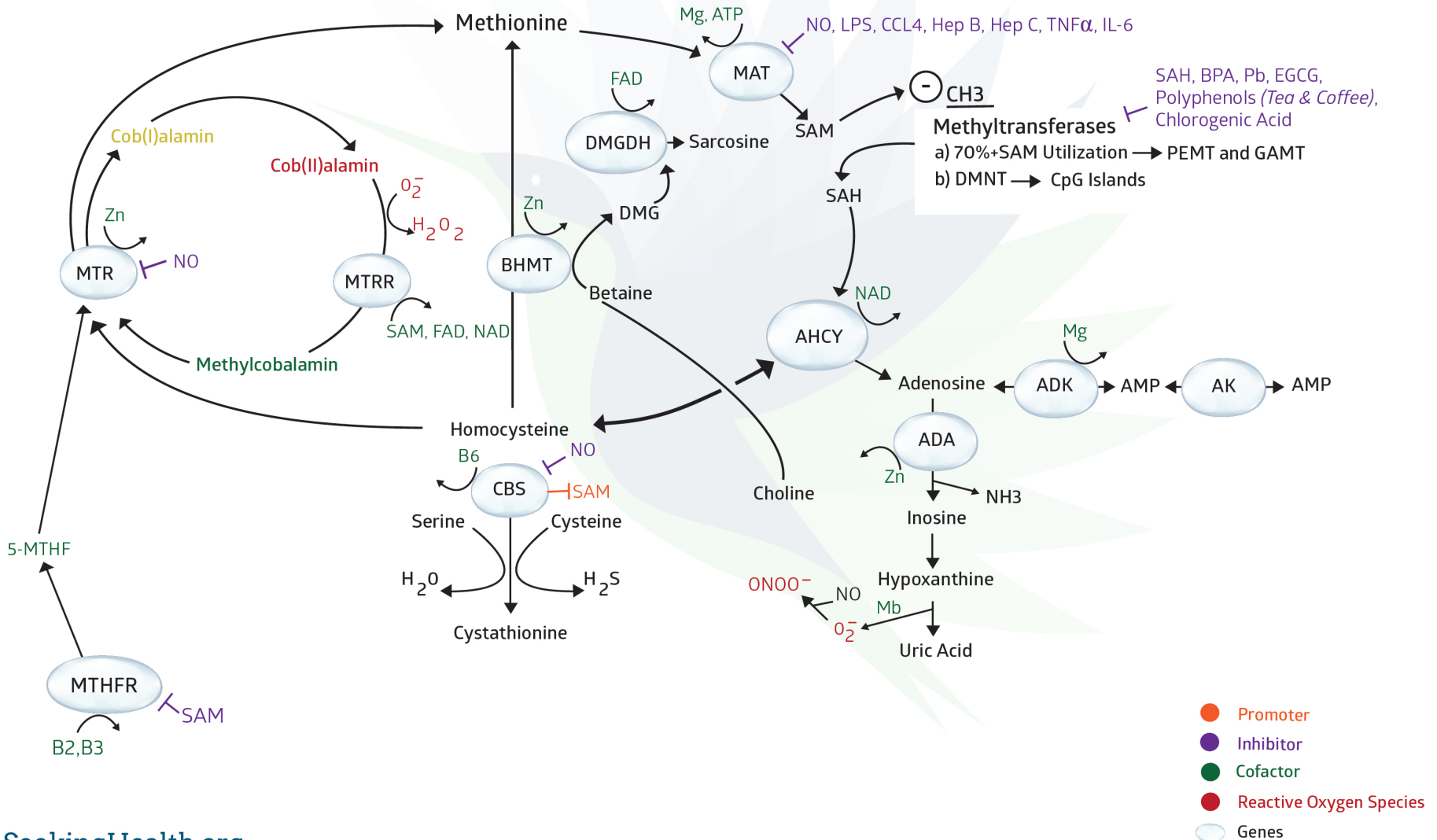
28.7	µg/l	1.1 - 6.8
0.51	µmol/L	0.16 - 0.50
3.0	µmol/L	3.8 - 5.5
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6.9	nmol/l	8.4 - 72.6
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326	nmol/l	400 - 1500
	-	
29.4	µg/l	10.0 - 65.0
24.8	10 <sup>-8</sup> M	16.8 - 21.4



# Methionine Cycle

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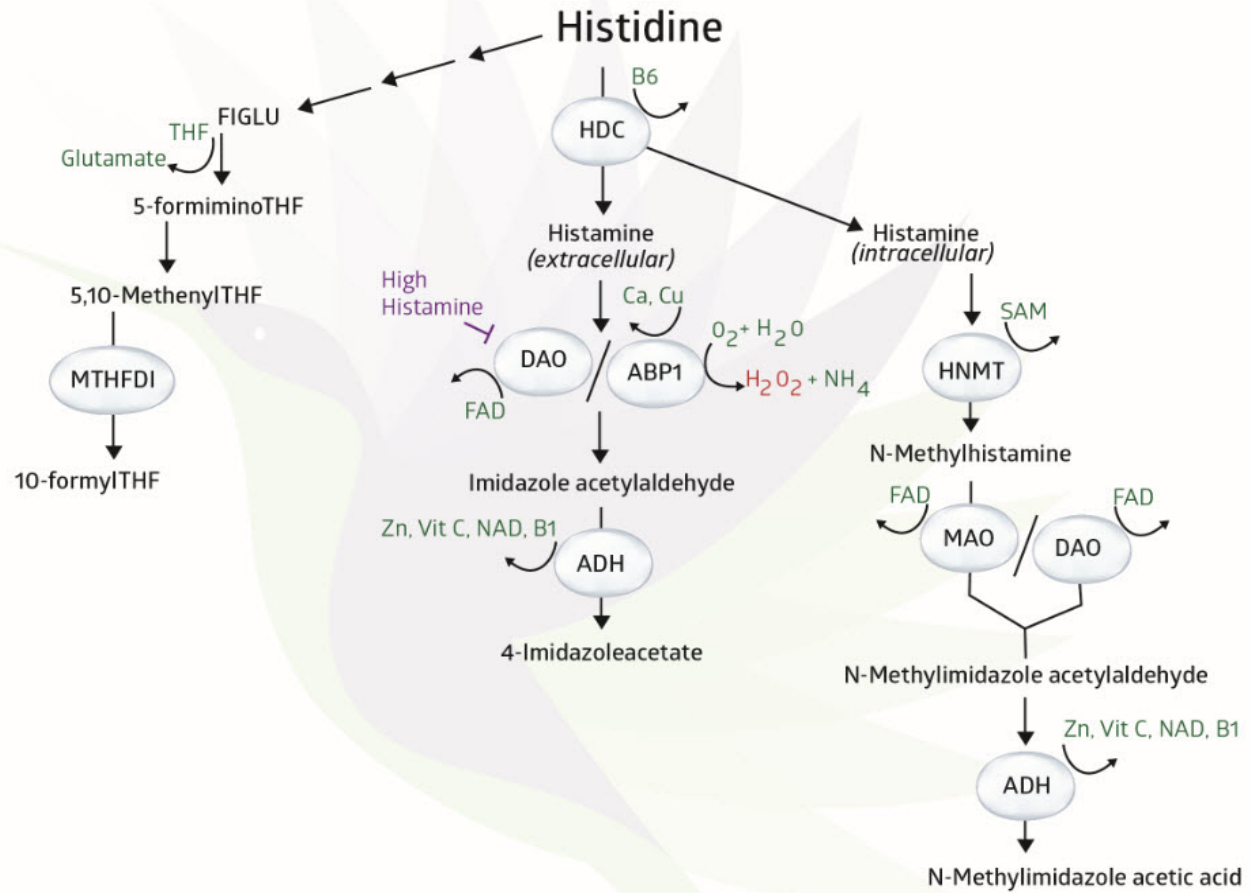


# Histamine

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# Pathway Planner

## Histamine



- Inhibitor
- Cofactor
- Reactive Oxygen Species
- Genes

Gene	Support	Function	Issue
MTHFR	B2	Provides substrate for MTR/MTRR	↓ MTHF = ↓ MTR/ MTRR
MTR (methionine synthase)	B12 / Zinc	Transfers CH <sub>3</sub> - from MethylB12 → to Hcy = cob(I)alamin + methionine. Then, remethylates the cob(III)alamin with MTHF.	↓ THF, ↑ Hcy, ↓ SAM, ↑ ROS
MTRR (methionine synthase reductase)	B2 (FAD)	Remethylates the cob(I)alamin with MTHF. 2 [methionine synthase]-cob(II)alamin + NADPH + 2 SAM = 2 [methionine synthase]-methylcob(III)alamin + 2 SAH + NADP(+)	↑ reduced Cb(I), ↓ MTR, ↑ Hcy, ↓ SAM, ↑ ROS
MAT1A	Magnesium, Cobalt, K	Catalyzes the formation of SAM from methionine and ATP	↓ SAM, ↑ Hcy
AHCY	NAD	catalyzes reversible hydrolysis of SAH (AdoHcy) to adenosine (Ado)	↑ SAH, ↑ Adenosine → ↑ uric acid. ↑ <sup>44</sup> MethylT inhibition

Gene	Variant	rsID & (orientation)	Risk Allele	Issue
MTR	A2756 G	Rs1805087 (+)	G	↑ MTR function
MTRR	A66G	Rs1801394 (+)	G	↑ Oxidation of B12
CBS	833T>C	Rs5742905 (-)	C	↓ Homocysteine

<http://www.genecards.org>

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Effects of methionine synthase and methylenetetrahydrofolate reductase gene polymorphisms on markers of one-carbon metabolism

## SAM Deficiency via MATI/III Inhibitors

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### Oxidative Stress

- NO
- TNF $\alpha$
- IL-6

Causes vicious cycle

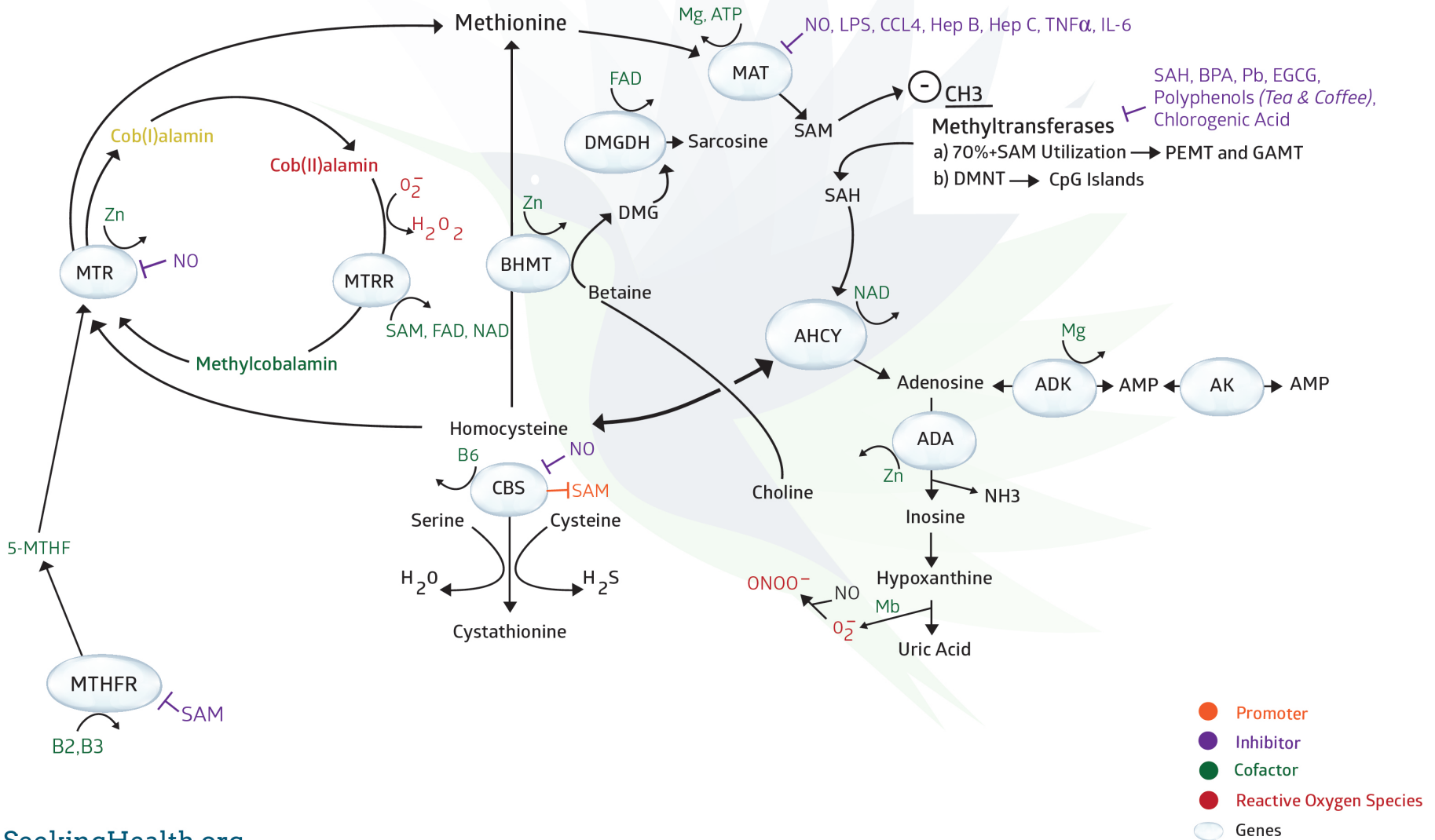
↓ SAM → ↓ CBS activity → ↓ Glutathione

**Methionine intake may NOT ↑ SAM**

<http://emergency.doctorsonly.co.il/wp-content/uploads/2011/03/SAMe-therapy-in-liver-disease-J-HEP-11.12.pdf>

# Choline Cycle

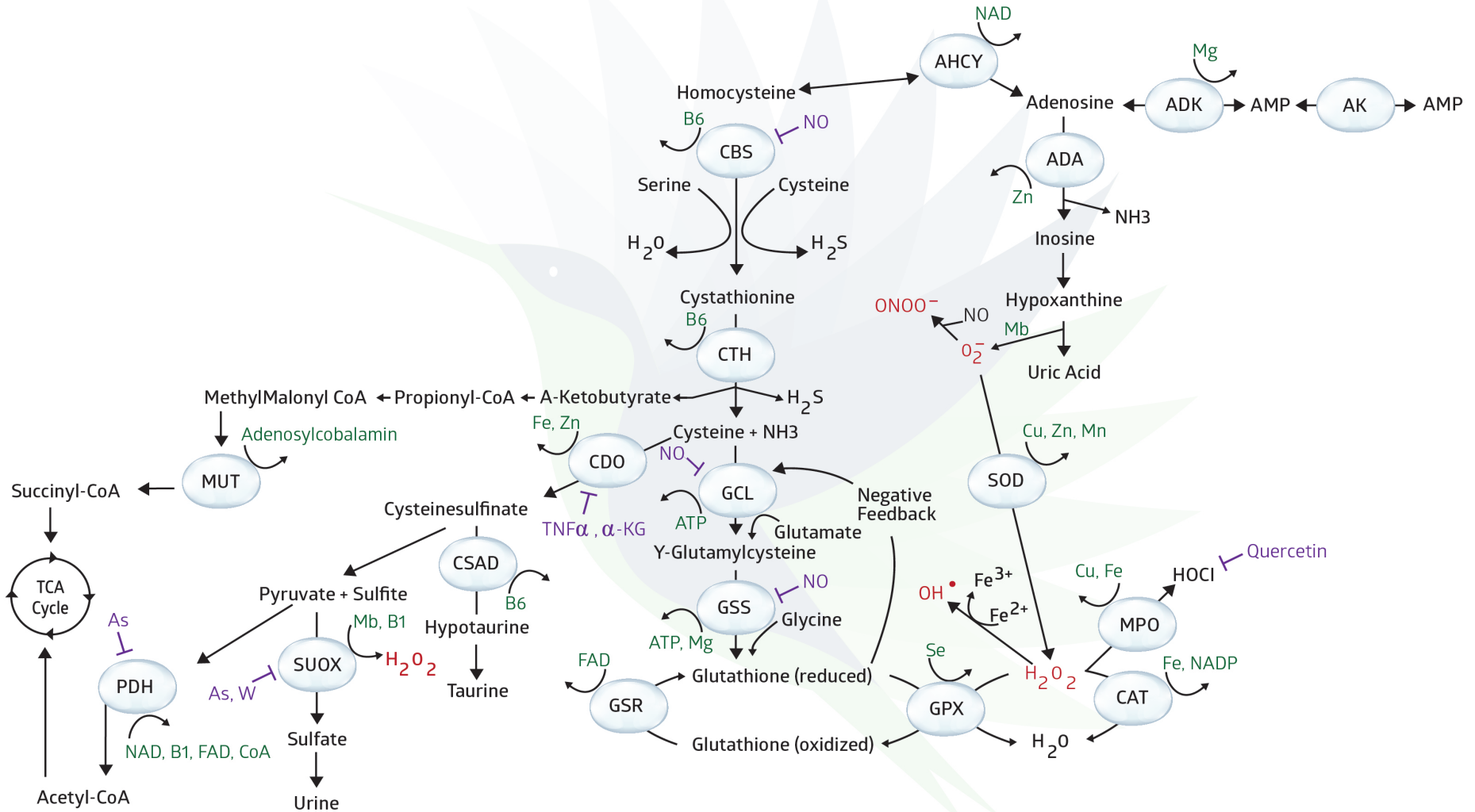
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# Transsulfuration Cycle

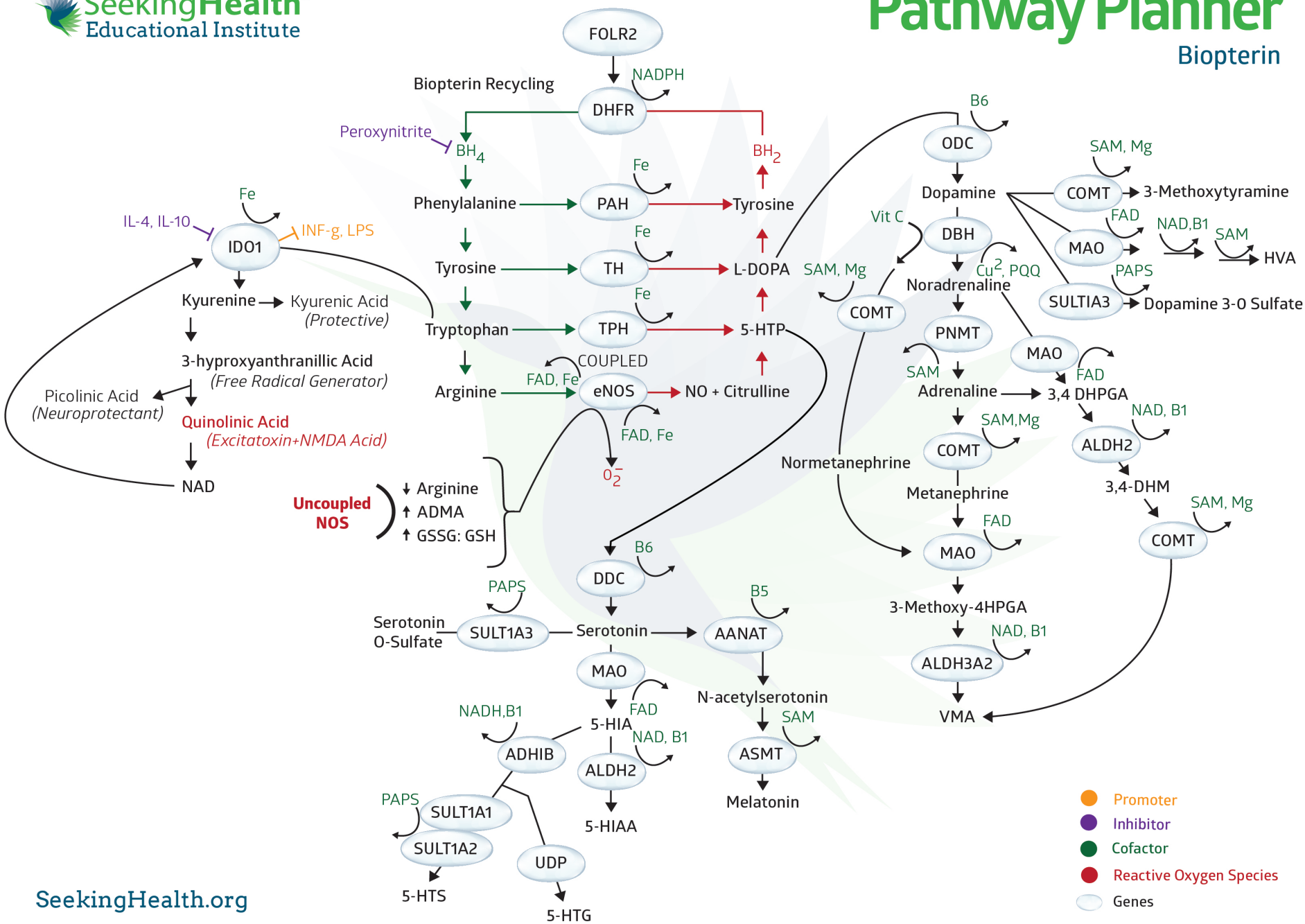
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- Inhibitor
- Cofactor
- Reactive Oxygen Species
- Genes

# Neurotransmission

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**Uncoupled NOS**

- ↓ Arginine
- ↑ ADMA
- ↑ GSSG: GSH

- Promoter
- Inhibitor
- Cofactor
- Reactive Oxygen Species
- Genes

## Neurotransmission: More than SNPs

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- Diet
- Lifestyle
- PAPS (Sulfonation)
- IDO (Kyurenine – Tryptophan)
- Th1/Th2 (Cytokines)
- Methylation (SAM)
- Cofactors
- Substrate
- Infections
- Heavy Metals

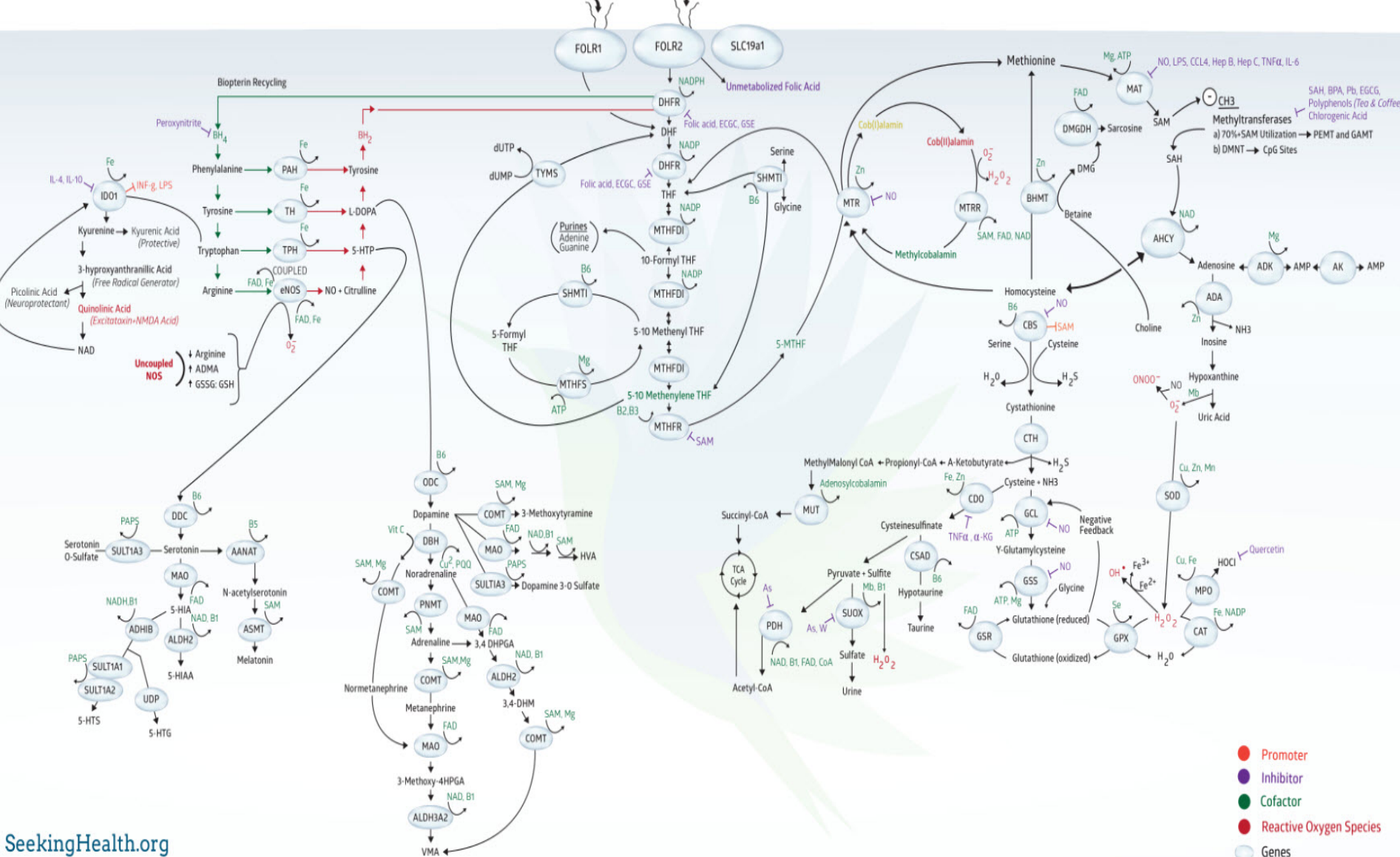
### **SNPs**

- COMT
- MAOA
- GAD1
- GAD2
- HNMT
- PNMT
- MAOB

Gene	Cofactor	Function	Variant	Issue
COMT	SAM, Mg	Catalyzes catecholamine and catechol hormones	rs4680, rs769224, rs4633	Downregulation ↑ Catechols/ Catecholamines
MAOA	B2 (FAD)	Catalyzes deamination of amines (dopa, serotonin, epi/norepi)	rs6323 and rs10548363	Downregulation ↑ amines
GAD1 and 2	Mg, B6	Glutamate → GABA	many	Downregulation ↓ GABA, ↑ Glutamate



## Reduced Folates (Uncooked Leafy Greens) Folic Acid



## Stay Informed

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### Great ways to stay informed:

- Newsletter Available at [www.MTHFR.net](http://www.MTHFR.net)
- Facebook: <https://www.facebook.com/drbenjaminlynch>
- October 2013 Nutrigenomics Conference [www.SeekingHealth.org](http://www.SeekingHealth.org)
- March 2014 Nutrigenomics Conference – [www.SeekingHealth.org](http://www.SeekingHealth.org)

**Thank You**