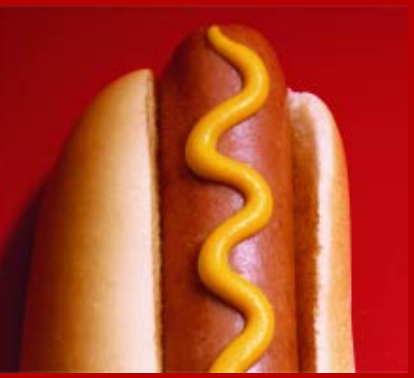
Assessing the Health Affects of Bioactive Foods Component: Session 5

Overview of Systems Biology: Sources of Phenotypic Variation

Raymond L. Rodriguez, Director
UC Davis Center of Excellence in Nutritional Genomics

March 24-25, 2005



VYTORIN™
(ezetimibe/simvastatin) tablets

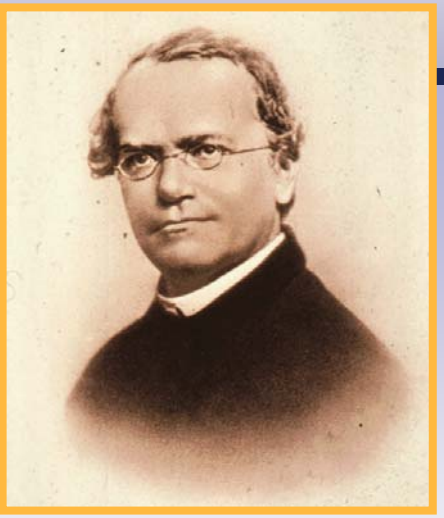
There are 2 sources of cholesterol:
food and family.

You bring 2 things to the dinner table —
Your appetite and your genotype.

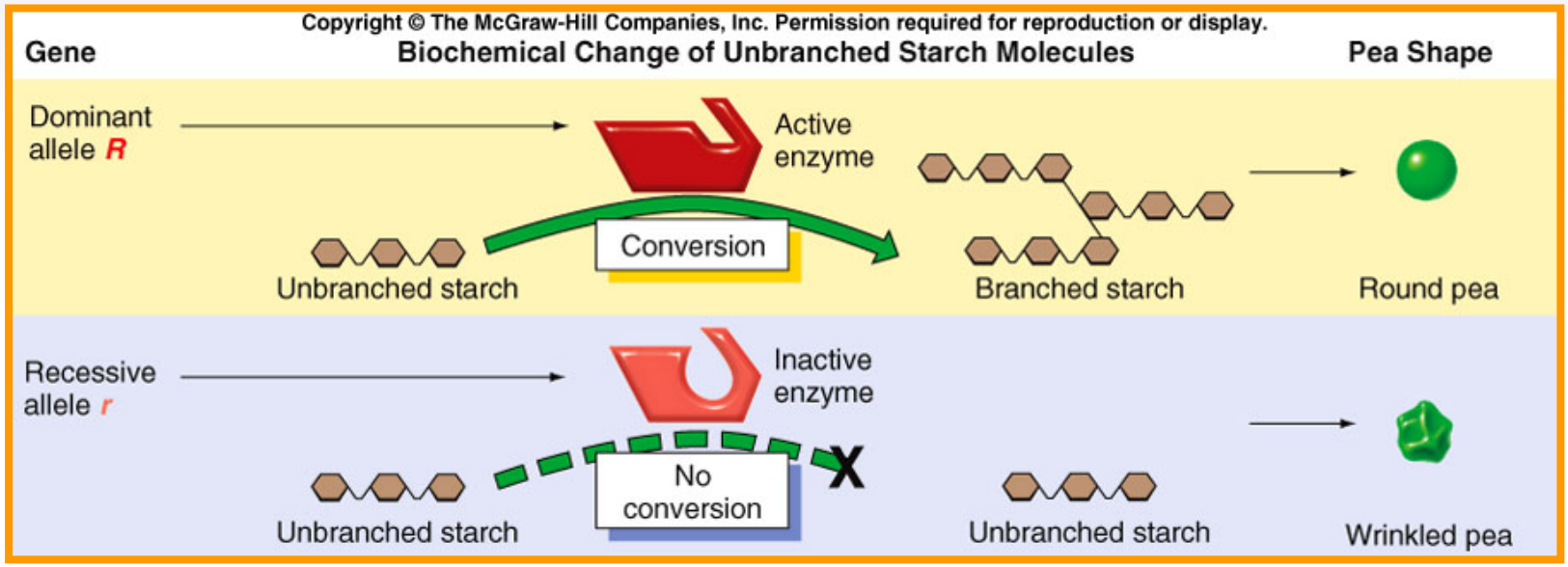
The source of phenotypic variation?

The source of phenotypic variation is common genetic variation, modified and modulated through epigenetic, environmental, sociocultural and lifestyle filters.

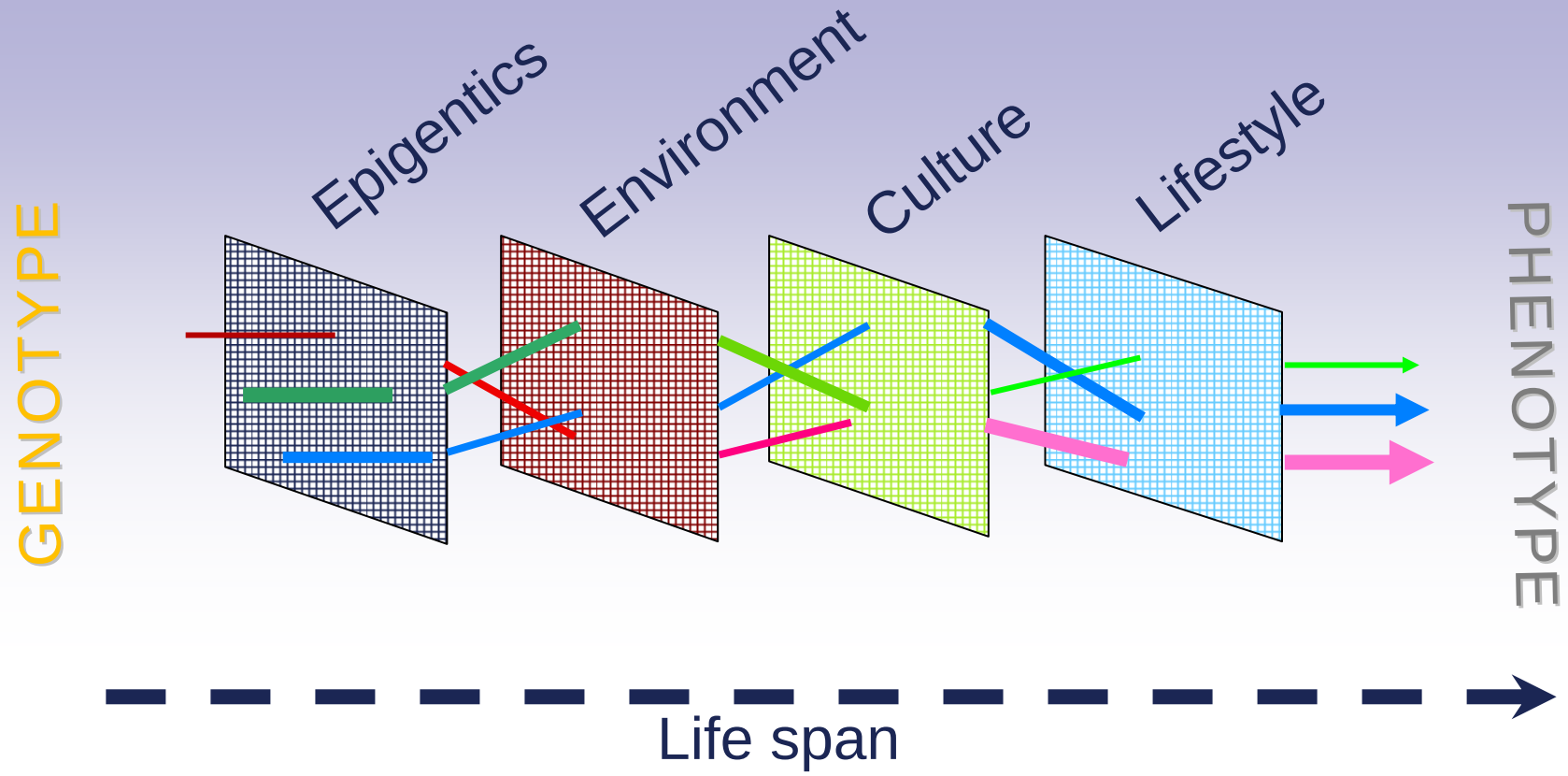
Linking genotype to phenotype



- 140 years after Mendel described the first heritable phenotype (round -*R* verses wrinkled- *r*) researchers isolated the genetic determinant, “starch branching enzyme 1” (SBE1). The *rr* genotype results in the accumulation of sucrose in early seed development which causes these seeds to wrinkle when they mature.

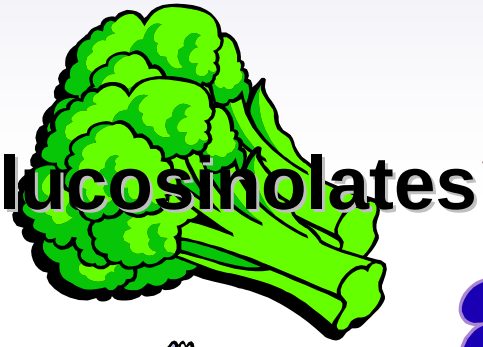


Modifying and potentiating filters of genetic variation



It is unlikely that a single gene, SNP, mutation, biomarker or risk factor will have positive predictive value for chronic disease and certain types of cancer.

Diet is a key componet of our environment



Courtesy of Clare Hasler

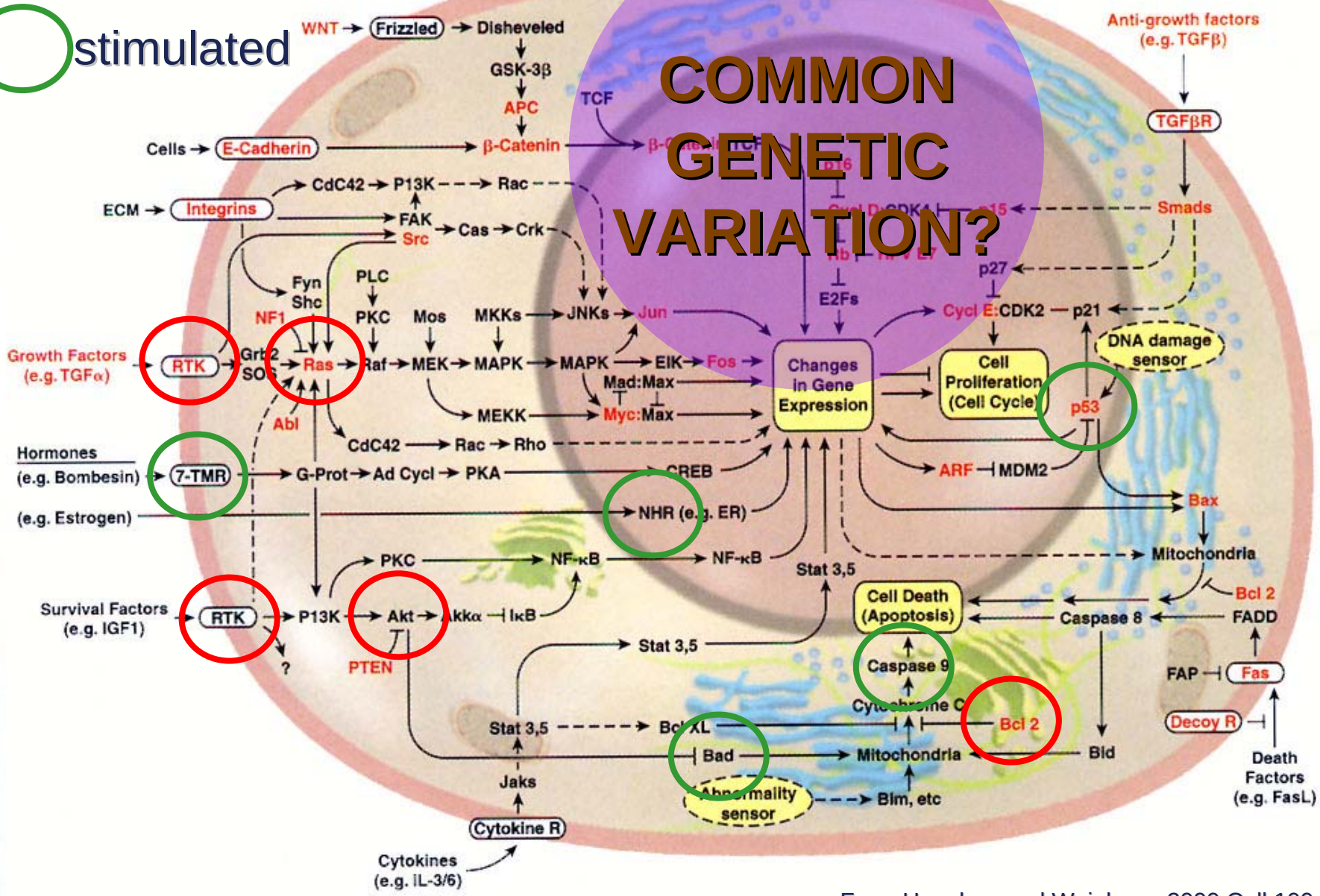
Soy — a model functional food

DIETARY INPUT	PROCESS	OUTCOME
Nutritious foods and food supplements with health promoting bioactive properties	Molecular mechanism(s) for bioactivity	More effective dietary Interventions to optimize health and reduce disease risk
Isoflavones (genistein) →	**Binds hERβ receptor to affect estrogen-dependent gene expression** →	**Mitigate post-menopausal symptoms, reduce cancer risk**
Proteins (lunasin) →	**Induced chemopreventive gene expression** →	**Reduce cancer risk**
Oils (n-3;n6) →	**Binds GPR40 (7-TMR)** →	**Amplify glucose induced insulin secretion**

repressed

stimulated

COMMON GENETIC VARIATION?



From Hanahan and Weinberg, 2000 Cell 100:50-57

What next?

Individualized nutrition and genome-based dietary recommendations

Roche Holding's AmpliChip CYP2D6

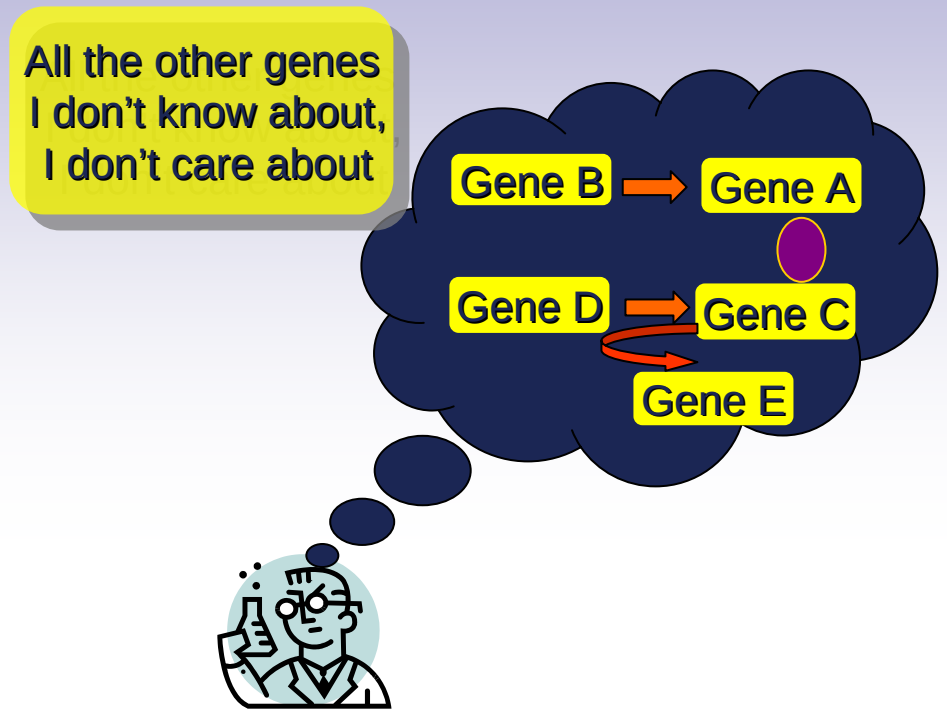
NitorMed's BilDil

CYP2C8 Test for granulocytopenia

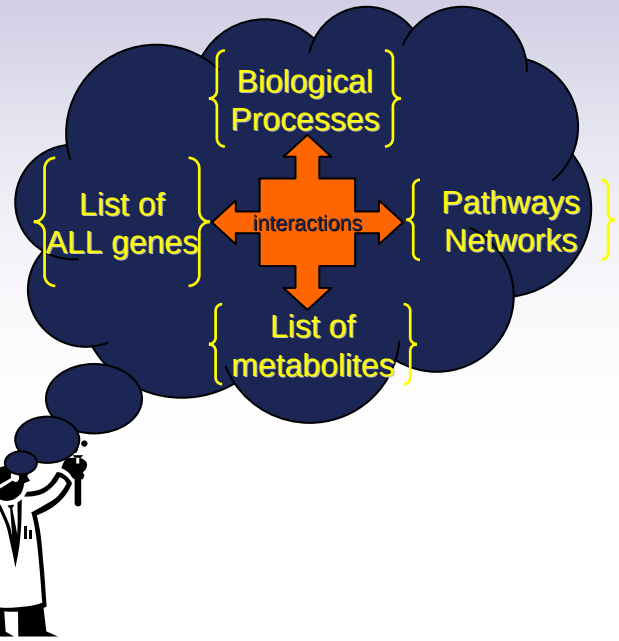
What this entails?

- A multidisciplinary approach to studying diet x gene interactions.
- Technology for low-cost, high throughput SNP analysis, sequencing and gene expression profiling.
- Access to datasets for large, diverse human populations the include dietary and medical histories, genotype and gene expression data and metabolomic profiles on various bodily fluids.
- Access to information from studies on model animal systems.
- Bioinformatic tools and theories for dimensionality reduction and visualization of large, complex datasets.
- Use of “best practices” for the obtaining, storing, and handling confidential information involving human subjects.
- A “systems biology” approach to investigating the relationship between nutrition and disease.

The need for systems biology

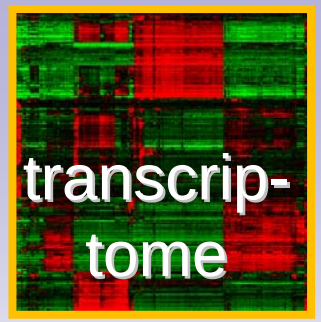


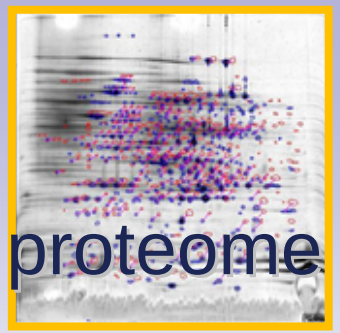
1990

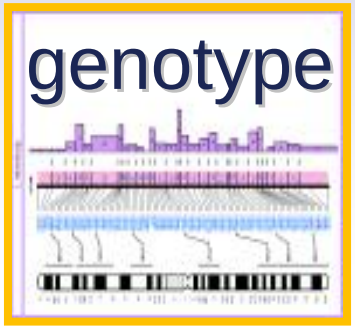


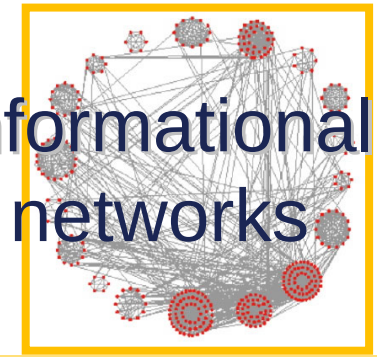
2005

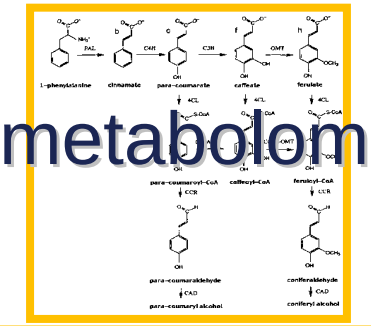
Systems biology







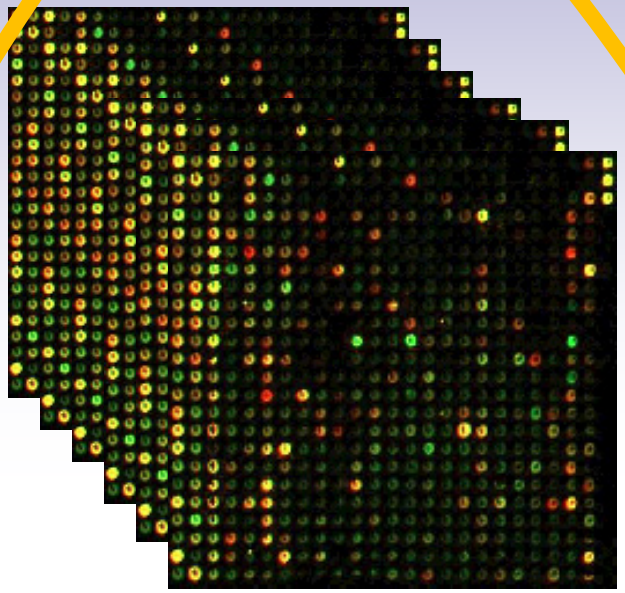




The need for systems biology: the case for dimensionality reduction

Caloric Restriction *v.s.* Control Diet

High Dimensionality



- **Informatics**
- **Expression profile**
- **Biochemical pathway**
- **Inflammation**
- **Oncogene-induced pathway**

Experiments are designed with the assumption that only a few parameters change from sample to sample

Tens of thousands of genes are tested on tens and hundreds of samples

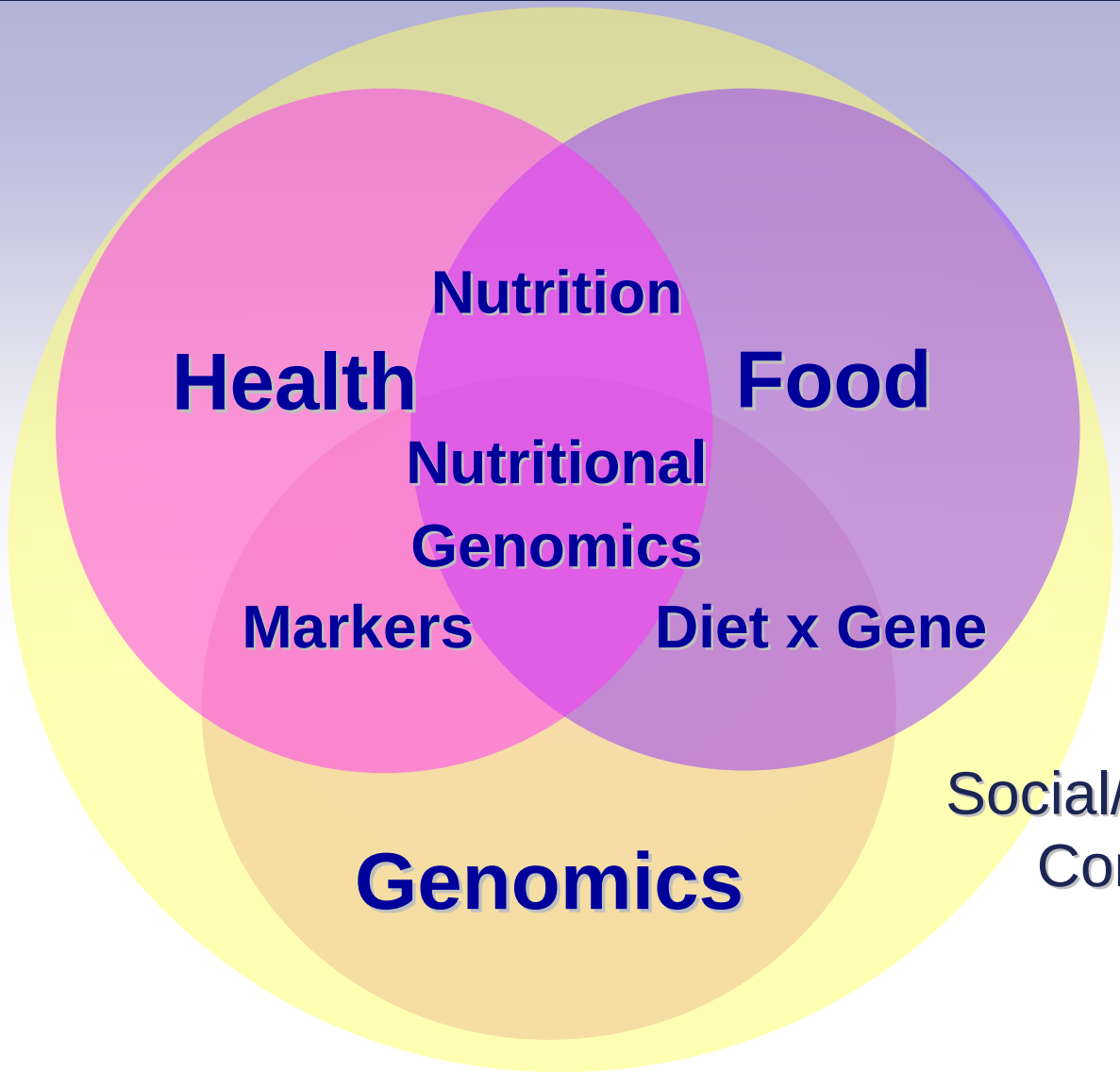
The datasets may reduced back to a few embedded dimensions responsible for observed changes

Systems Biology and Health

Systems biology involves the representation and analysis of an intact biological system. Like many of the technological developments over the past 20 years, such as genomics, proteomics, combinatorial chemistry, and bioinformatics, there is high hope that systems biology will help move molecular research closer to the practice of medicine. Science traditionally has taken a reductionist approach that evolves to focus on the integration of data from these new technologies, but will this be enough to effect the transition from data to information, to knowledge to biomedical application?

Michael N. Liebman Ph.D. U. Penn

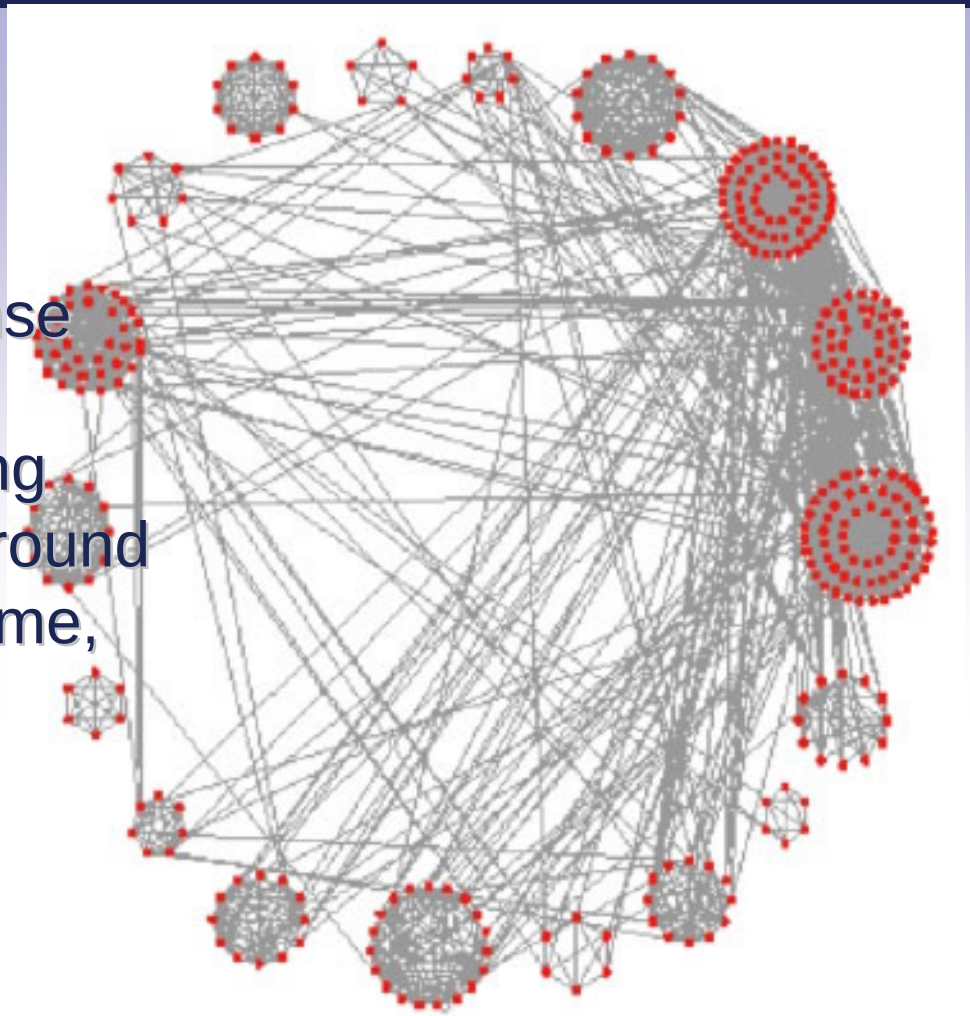
Nutritional genomics is the study of the molecular interactions between nutritional stimuli and the genome, and how these interactions promote health or cause disease in human populations.



Social/Cultural Context

Sources of nutrigenomic complexity

- Variety of foods
- Seasonal variations in food selection and content
- Food fads and public response to news, studies and ads
- Food preparation and cooking
- Cultural and religious background
- Socio-economic status, income, geographic environment
- Access to health care
- Age and health status
- Exercise, life-style
- Genetic background
- Complexity of disease

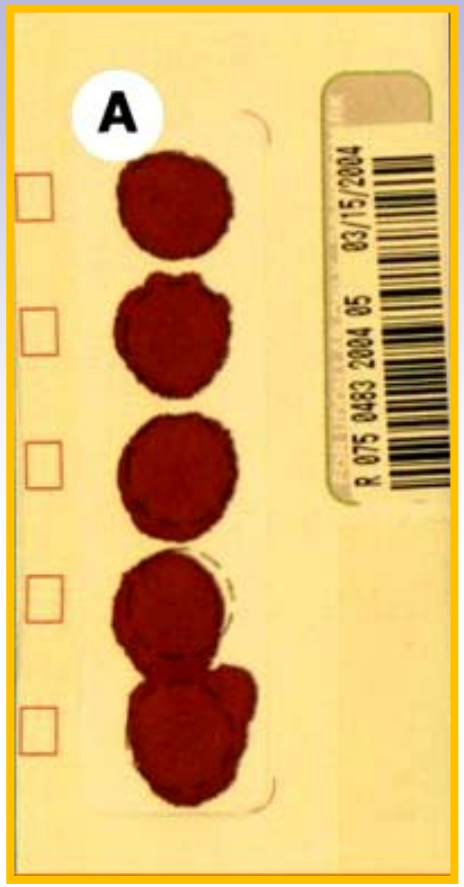


Common genetic variation: The source of phenotypic variation

Nutritional genomics seeks to link diet and disease risk through common genetic variation in human populations

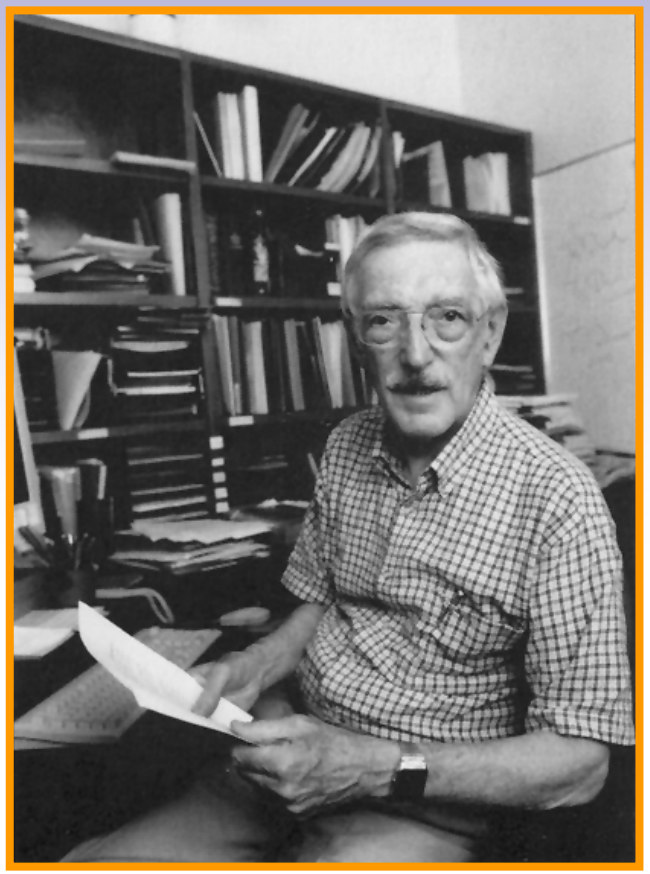
The case for nutritional genomics.
Newborn Testing.

Since 1962, millions of infants have been screened for IBEMs



- 188 “genetic diseases” (inborn errors of metabolism — IBEM) have been identified.
- Last year, 7 million US newborns were screened for from 4 to 16 IBEMs.
- 3000 infants were diagnosed with serious disorders
- Every state screens for PKU, galactosemia
- Dietary intervention is the preferred treatment for PKU and galactosemia.

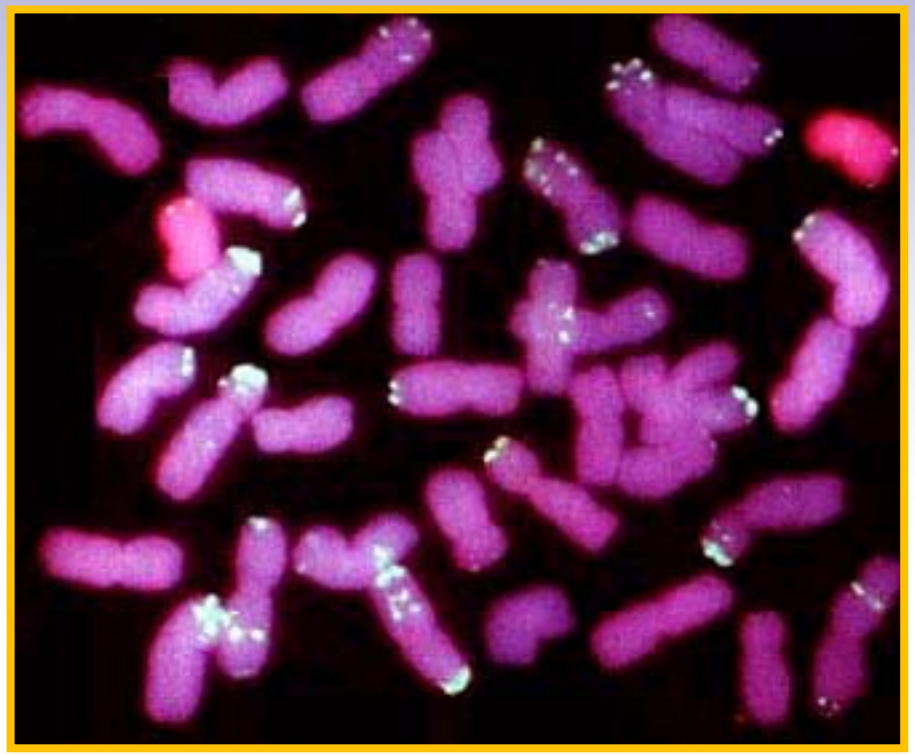
The case for nutritional genomics. What the experts are say.



Allele 1	Allele 2
G-C	G-C
C-G	C-G
A-T	A-T
A-T	A-T
T-A	T-A
T-A	T-A
A-T	A-T
G-C	C-G
G-G	G-G
C-G	C-G
C-G	C-G
T-A	T-A
A-T	A-T
A-T	A-T
C-G	C-G

Prof. Bruce N. Ames, CHORI Director, Pilot Projects Core

"Single nucleotide poly-morphisms provide a powerful tool for invest-igating the role of nutrition in human health and disease and …can contribute to the definition of optimal diets."



http://snp.cshl.org;

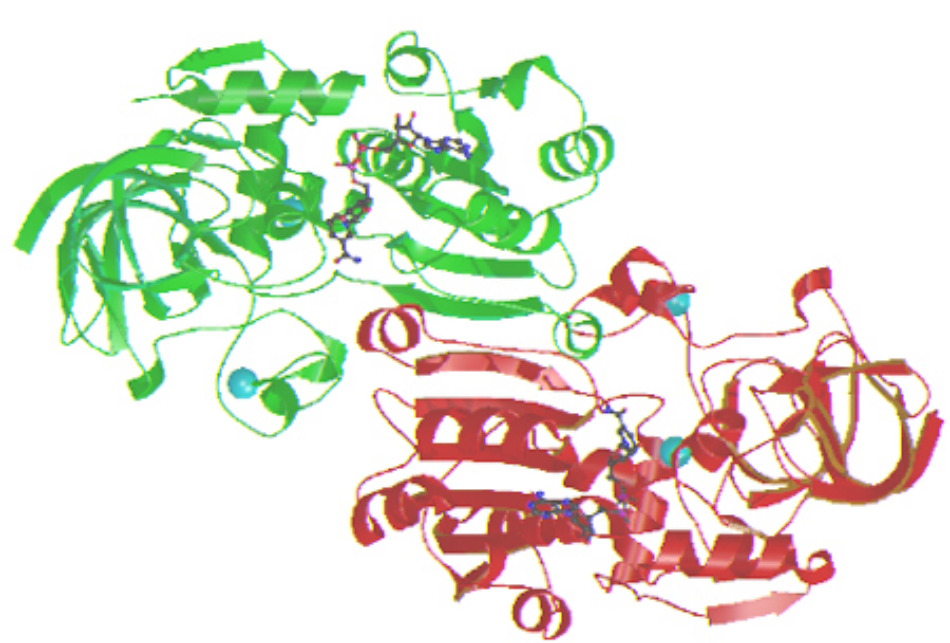
http://snp.ims.u-tokyo.ac.jp

- Human genome consists of 3 billion base pairs
- Humans are 99.9% identical at the DNA level
- 0.1% difference represents ~6 million SNPs
- 150,000 to 300,000 are coding SNPs (cSNPs
- 1/3 of cSNPs in the enzyme-encoding gene > K_m of the enzyme.

Coding SNPs and the K_m Concept*

SNPs that increase the K_m reduce the enzyme's affinity for its substrate or cofactors, thus reducing its reaction rate.

"About 50 human genetic disease are the result of defective enzymes that can be remedied or ameliorated by administering high doses of the vitamin component of the corresponding coenzyme."



http://phillips.mbb.ki.se/frames/structures/ADH2.html

*** Ames et al, *Am. J. Clin. Nutr.* 75, 616 – 658 (2002)**

Potential Vitamin Responsive SNPs

Enzyme	Cofactor	Δ bp	Δ aa	Freq(%)	K_m *
MTHFR	FAD	677C→T	222A→V	~15	↓
ALDH	NAD	-	487E→K	~50 †	150 fold ↓
GPDH	NADP	131C→G	44A→G	11	5 fold ↓ ‡

* Increased K_m for cofactor = decreased affinity
† Asian heterozygote + homozygote
‡ Rural southern India, may be aided by increased intake
http://www.kmmutants.org/

Example of SNP-Based Adverse Diet/Gene Interaction

Nature Genetics

letter

Identification of a variant associated with adult-type hypolactasia

Nabil Sabri Enattah[1], Timo Sahi[2], Erkki Savilahti[3], Joseph D. Terwilliger[4], Leena Peltonen[1,5]* & Irma Järvelä[1,6]

Published online: 14 January 2002, DOI: 10.1038/ng826

Adult-type hypolactasia, also known as lactase non-persistence (lactose intolerance), is a common autosomal recessive condition resulting from the physiological decline in activity of the lactase-phlorizin hydrolase (LPH) in intestinal cells after weaning. LPH hydrolyzes lactose into glucose and galactose. Sequence analyses of the coding and promoter regions of *LCT*, the gene encoding LPH, has revealed no DNA variations correlating with lactase non-persistence[1,2]. An associated haplotype spanning *LCT*, as well as a distinct difference in the transcript levels of 'non-persistence' and 'persistence' alleles in heterozygotes, suggest that a *cis*-acting element contributes to the lactase non-persistence phenotype[3,4]. Using linkage disequilibrium (LD) and haplotype analysis of nine extended Finnish families, we restricted the locus to a 47-kb interval on 2q21. Sequence analysis of the complete region and subsequent association analyses revealed that a DNA variant, C/T_{-13910}, roughly 14 kb upstream from the *LCT* locus, completely associates with biochemically verified lactase non-persistence in Finnish families and a sample set of 236 individuals from four different populations. A second variant, G/A_{-22018}, 8 kb telomeric to C/T_{-13910}, is also associated with the trait in 229 of 236 cases. Prevalence of the C/T_{-13910} variant in 1,047 DNA samples is consistent with the reported prevalence of adult-type hypolactasia in four different populations. That the variant (C/T_{-13910}) occurs in distantly related populations indicates that it is very old.

The frequency of lactose intolerance varies with age, race and ethnicity

N. European

Indian children

Afr American children

Indian adults

Mex American - adult

Cretans

Cypriots

N. American Jews

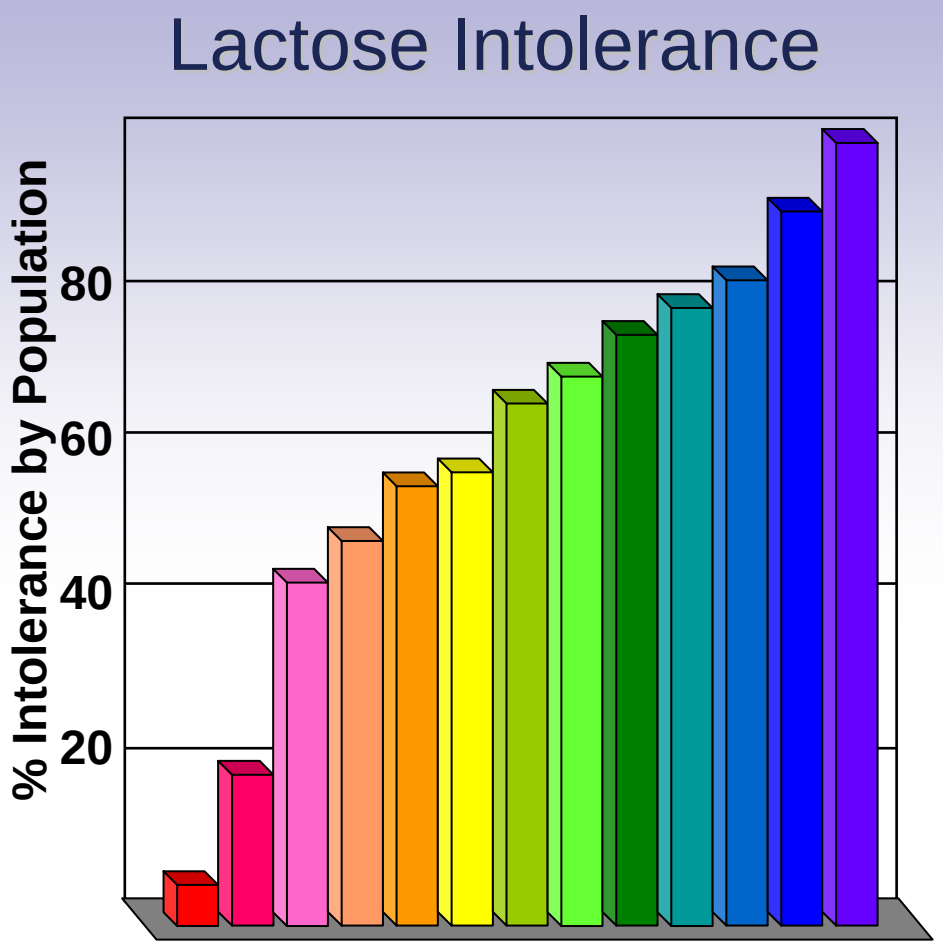
Mexicans - rural

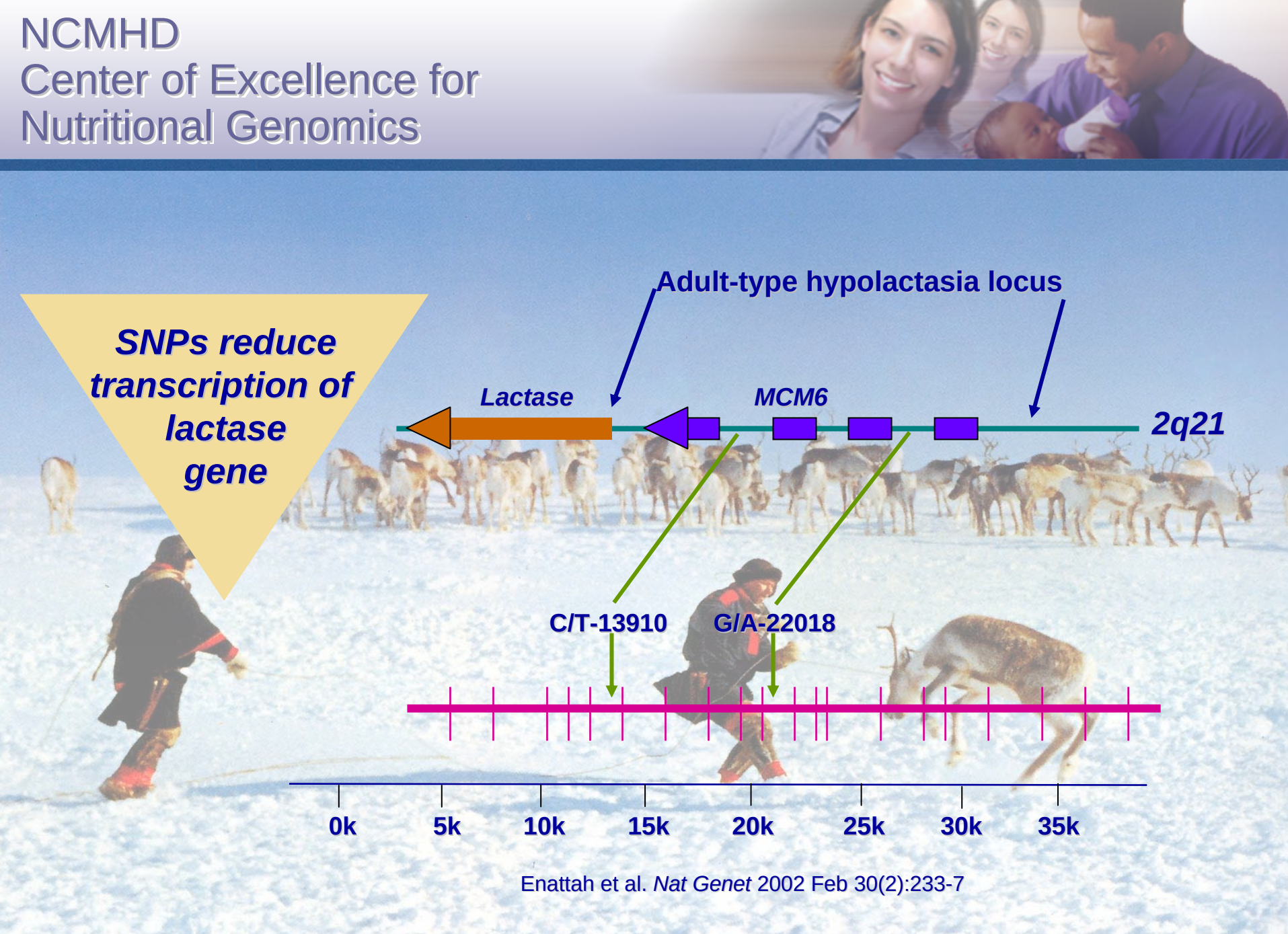
African American - adult

Alaskan Native

Asian Americans

SE Asians

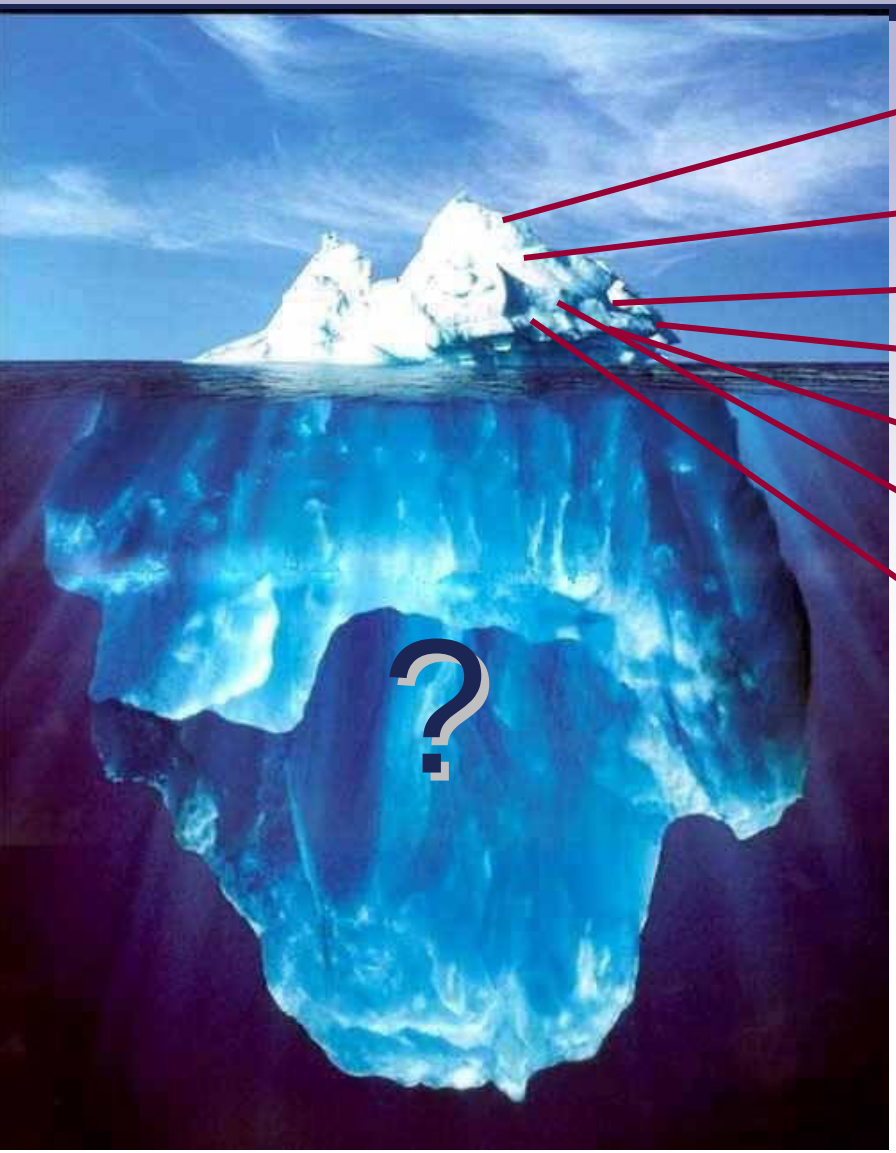




Enattah et al. *Nat Genet* 2002 Feb 30(2):233-7

- If common genetic variants (e.g., SNPs) in genes encoding enzymes (or their promoters), can affect reactions rates in metabolic pathways, then these genetic variation in human populations may explain differences in the way we respond to, and benefit from, our nutritional environment.

NCMHD
Center of Excellence for Nutritional Genomics



Lactose intolerance

Alcohol intolerance

Galactosemia

MTHFR

GPDH

NAT2

PKU

Adverse diet/genome interactions due to well known mutations and common genetic variants are just the tip of the iceberg.

- What are some of the other SNPs that may be keeping us from deriving full benefit from our nutrition?
- What genetic variants are we carrying in our genome, that over time, and in response to the foods we eat, will increase our risk of disease?
- What adjustments can we make in our diets now that will compensate for the diet-related genetic variants so that we can achieve and enjoy optimal health earlier and maintain it longer?