

Pharmacogenomics

薛佑玲

Institute of Biomedical Science
National Sun Yet-sen University
 ylshiue@mail.nsysu.edu.tw



國立中山大學

National Sun Yat-sen University

Importance of Genetics/Genomics to Medicine

- ✗ >12 million Americans with **genetic disorders (GD)**
- ✗ **80% of mortality rate (MR)** in America due to genetic component
- ✗ **2-3% background population risk** for a major birth defect (BD)
- ✗ **15% overall miscarriage risk** for any pregnancy
 - ✗ 25-50% first trimester miscarriage risk
 - ✗ 30-50% first trimester losses due to **chromosome anomalies**
- ✗ >30% pediatric hospital admissions due to GD

- ✗ **GD affect all major systems, any age, any race, male or female**



網址(D) <http://www.hcnp.med.harvard.edu/>

Google Neurodegeneration repair 新! 3 已擋截 選項 Center for Neurodegeneration repair



HARVARD CENTER FOR NEURODEGENERATION & REPAIR

VISITOR INFORMATION

- Neurodegenerative Disease
- The HCNR Solution
- Our Funding
- How You Can Help
- Request Info / Contact Us
- Press Room

DISEASE FILES

- Alzheimer's Disease
- ALS (Lou Gehrig's Disease)
- Huntington's Disease
- Multiple Sclerosis
- Parkinson's Disease

HCNR PROGRAMS

- Fellowship & Training Awards
- Optical Imaging Facility
- Magnetic Resonance Imaging Facility
- Center for Bioinformatics
- Advanced Tissue Resource Center
- Genetics Outreach Program
- Neurological Clinical Trials Service
- Laboratory for Drug Discovery in Neurodegeneration
- Cell-based Assays
- Regeneration & Repair Program
- International MS Genetics Consortium

MEMBERS' RESOURCES

- About the HCNR
- Contact / Directions
- HCNR Publications
- Join the HCNR
- Members' Directory
- Seminars & Conferences
- Open Positions

HCNR News Service:

HCNR News & Announcements:

Highlights - Public Presentation:
Alzheimer's Disease and the Aging Brain. Click [here](#) for highlights and videos of the Oct 17th HCNR Symposium.

EXTERNAL RESOURCES:

- Core Facilities
- Federal Funding
- Relevant Foundations

Search Engine:
[Google™](#) HCNR WWW

Breaking Neuroscience Research:

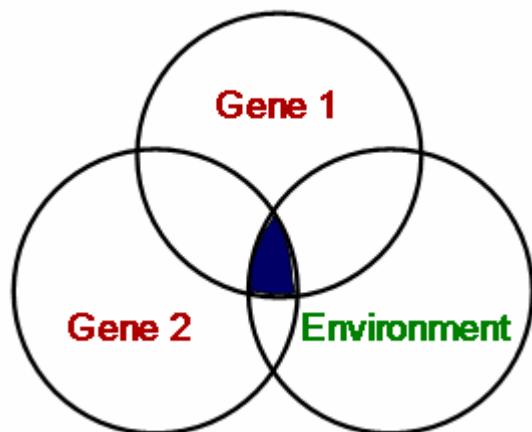
- [**Passive Aggressive—Must Antibody Therapy Start Early to Be Effective?**](#)
27 December 2005.
- [**Secretion of SOD1 Mutant Proteins Tied to ALS**](#)
23 December 2005.
- [**SfN: EPO—Not Just for Blood Cells Anymore, but Neurons, Too**](#)

Neuroscience in the Media:

- [**Female Hormone Key to Male Brain ...**](#)
Scientific American. 4 Jan 2006
- [**Reduced Brain Volume May Predict Dementia In Healthy Elderly People...**](#)
Science Daily. 4 Jan 2006

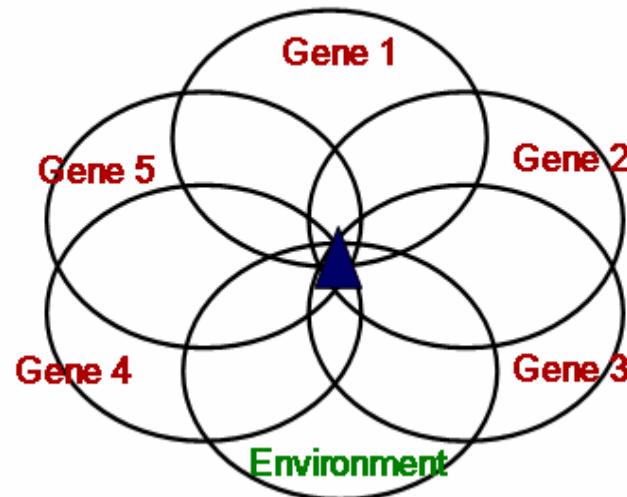


Complex Phenotypes - What can we Expect?



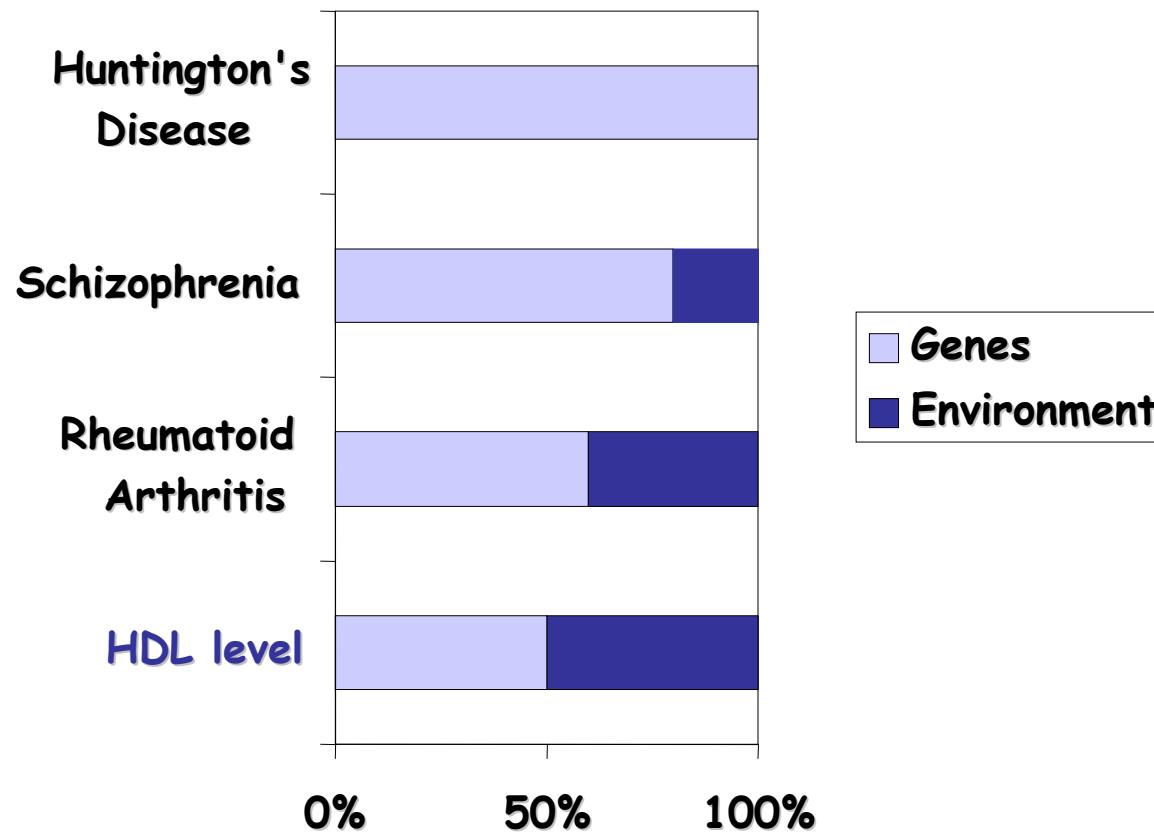
Few genes and environmental factors each contributing a large risk

- Intergenic: epistasis;
- Intragenic: dominant & polymorphisms

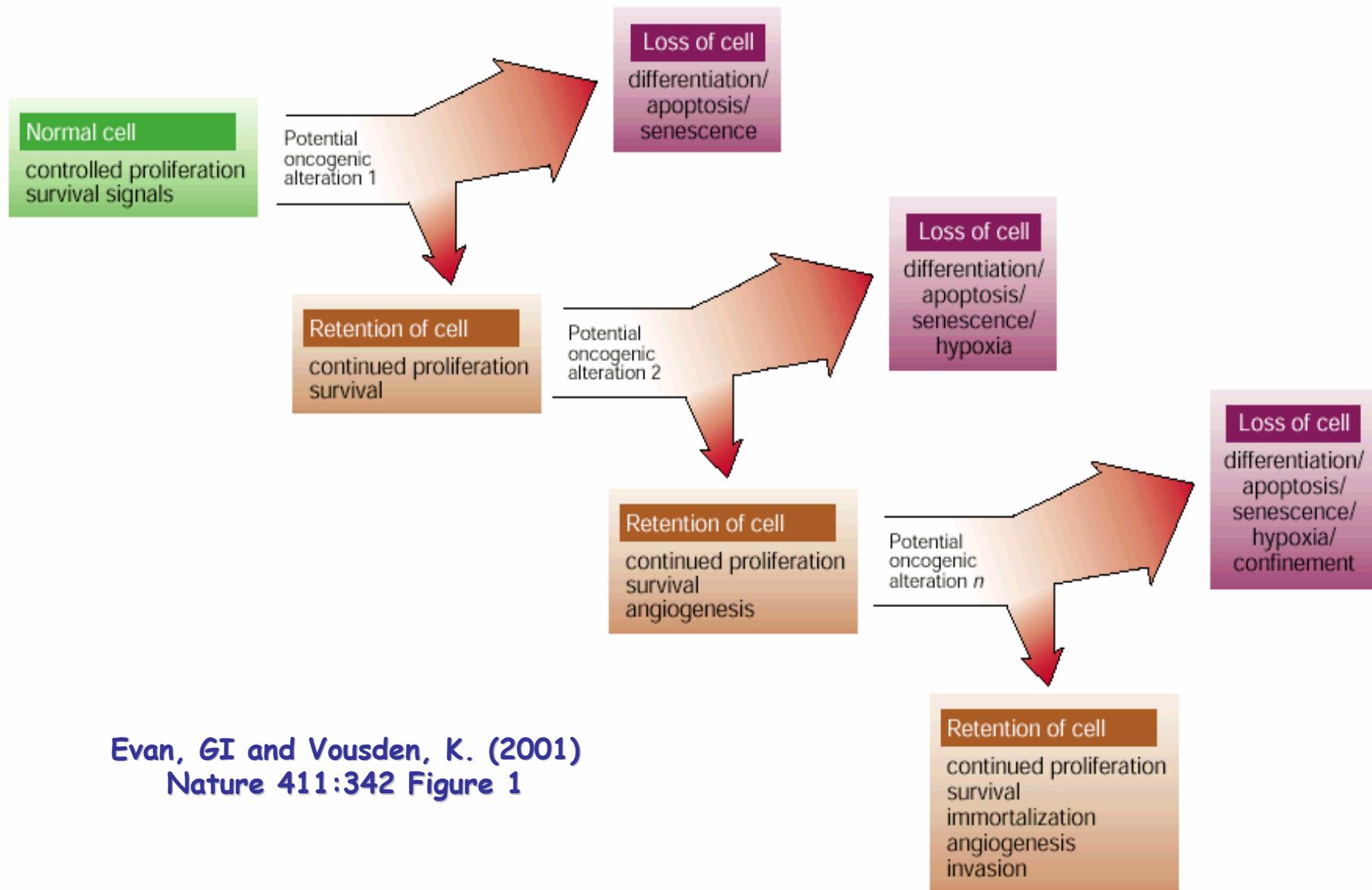


Many genes and environmental factors each contributing a small risk

Heritability: the Proportion of the Disease that is Due to the Genetic Factors



The Cancer Problem

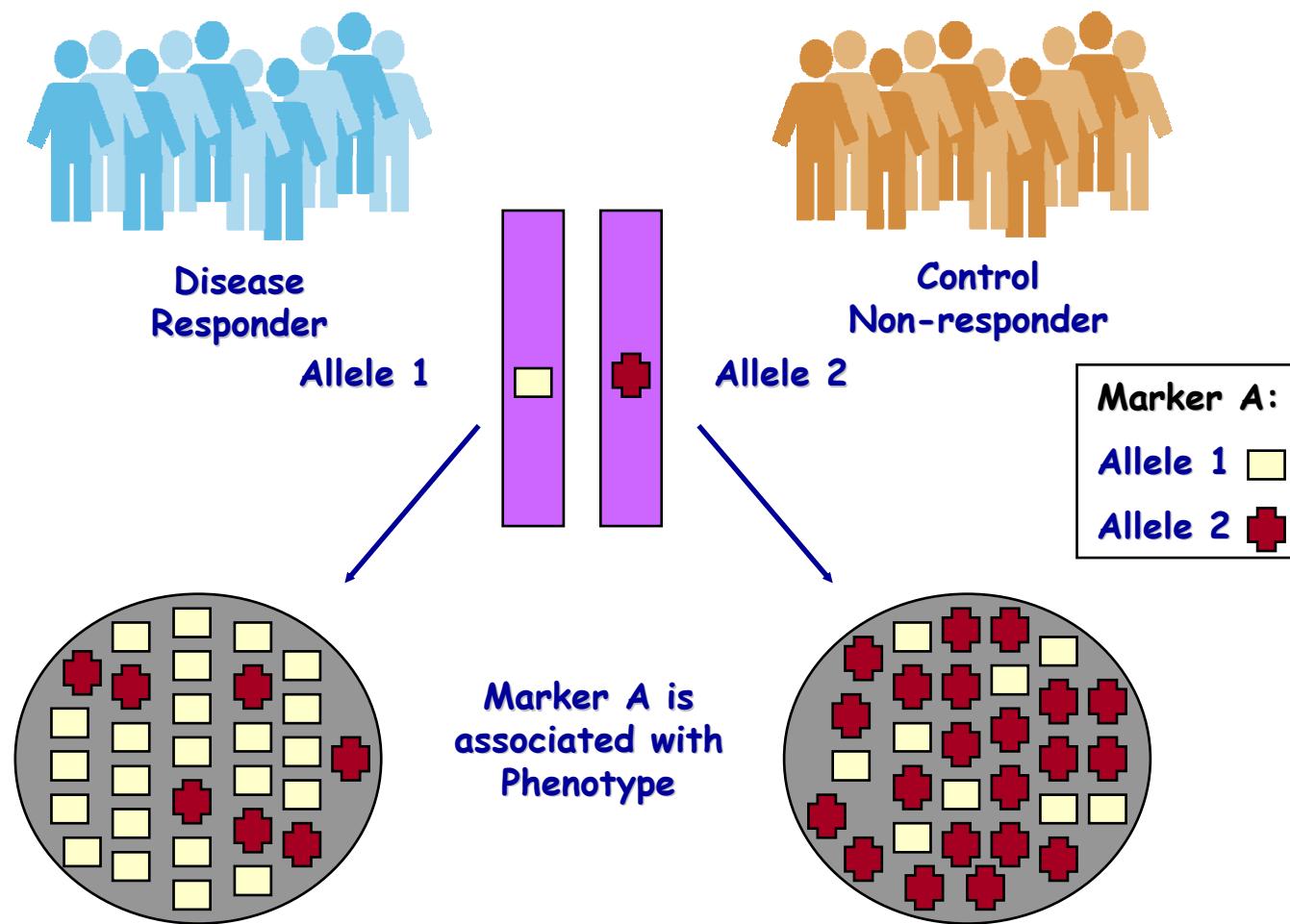


Evan, GI and Vousden, K. (2001)
Nature 411:342 Figure 1

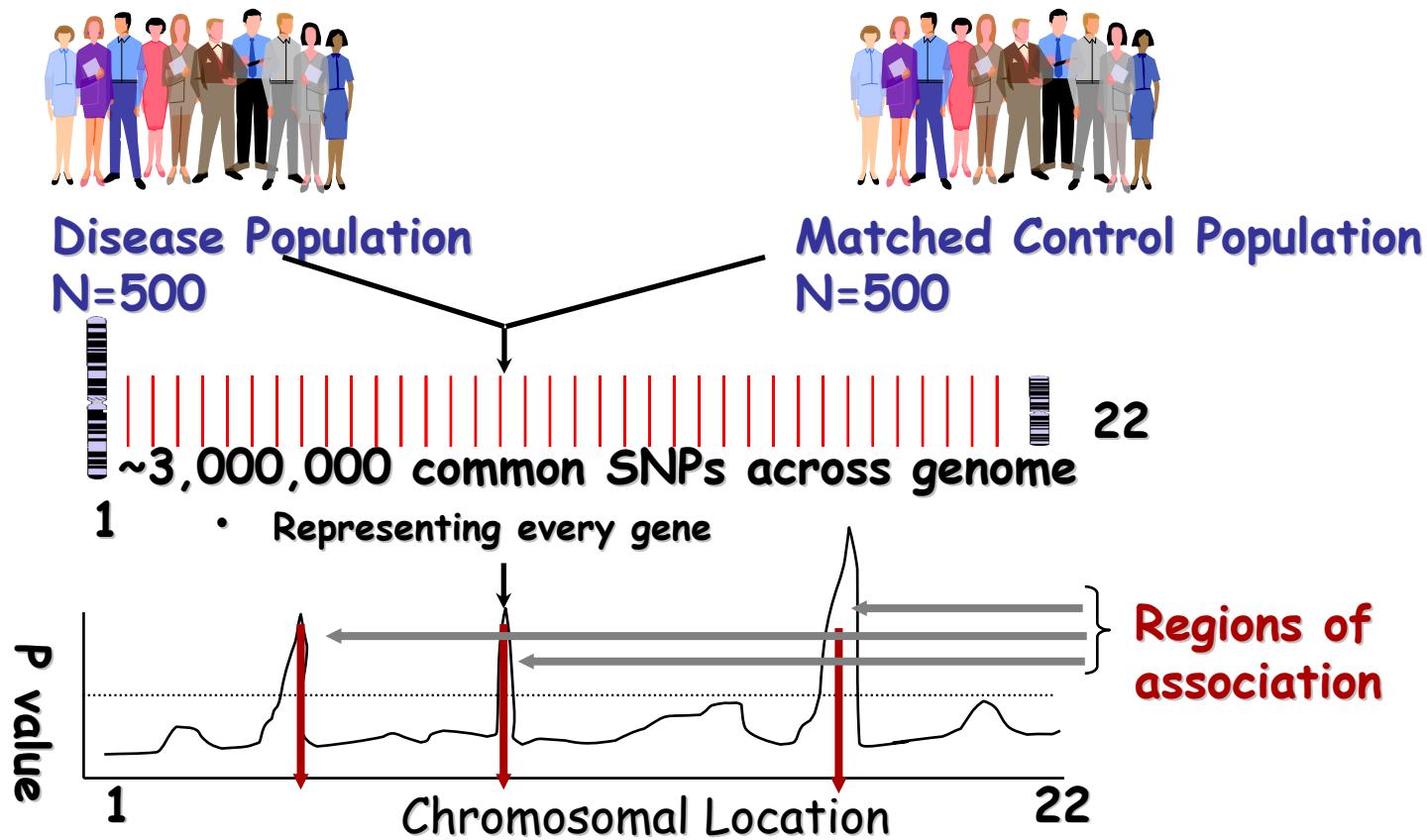
Mapping for Common Complex Diseases

Complexity	Solution
Reduced penetrance	Non-parametric study
Genetic heterogeneity	Multipoint linkage analysis; LD mapping; Genome-wide scan
Epistasis	Multipoint linkage analysis; LD mapping; Genome-wide scan
G × E interaction	Case only studies; Case-control study; Family-based design

Human Genetic Association Study Design



Whole Genome Association



Informatics to identify gene(s) mapped to associated SNP

Mutations & Polymorphisms

- ✗ Mutations become **polymorphisms** or “common alleles” when **frequency > 1% in a population** (arbitrary)
- ✗ **All** Single Nucleotide Polymorphisms (SNPs) (probably) exist in the human population
 - ✗ 3 billion × 4 (ACGT) at frequencies near 10^{-5}
- ✗ SNPs **linked** (associated) to a **phenotype** or **causative**

Haplotypes

- ✗ Representation of the DNA sequence of one chromosome (or smaller segments in *cis*)
- ✗ Indirect inference from pooled diploid data
- ✗ Direct observation from meiotic or mitotic segregation
 - ✗ Cloned or physically separated
 - ✗ Chromosomes or segments

Linkage & Association

- ✗ Family Triad
 - ✗ Parents & child (vs. case-control)
- ✗ Case-control studies of association in structured or admixed populations (Pritchard & Donnelly 2001)
 - ✗ Theor. Pop. Biol. Program STRAT
- ✗ Null hypothesis: allele frequencies in a candidate locus **do not** depend on phenotype (within subpopulations)

Searching for Disease Genes Almost Always Start with the DNA of Affected individuals

- ✖ Process at Decode Genetics Inc. (Example)
 1. Identify people with a particular disease
 2. Find affected people who are related in such a way that they are likely to share genes (pedigree)
 3. Extract the DNA of these individuals
 4. PCR amplify (robotically) SNPs along each person's chromosomes
 5. Look for clusters of SNPs among the DNA of patients from a single family
 6. Such clusters suggest → ?

Such Clusters Suggest a Gene Involved in the Disease is Located Nearby

- ✗ Big deal?
 - ✗ If this data is correct, the gene has now been linked to a particular chromosomal region
 - ✗ Presumably the gene will soon be found
- ✗ Where do you go next??
 - ✗ Gene annotation
 - ✗ Gene ontology, function, cellular localization, structure etc.
 - ✗ Identification of candidate drug targets

Defining Disease Phenotypes

- ✖ Some mechanisms underlying variation in clinical expression of disease traits
 - ✖ To choose a consistent phenotype for studies
- ✖ Phenotype definition & delineation
 - ✖ “Gene mapping” ⇒ “phenotype mapping”
 - ✖ Gaps between “phenotypes” & “genotypes”
 - ✖ Alleles cause phenotypes

Pharmacogenomics vs. Pharmacogenetics (definitions)

- ✗ Pharmacogenetics or Pharmacogenomics
 - ✗ Study of **the genetic basis** for differences in **drug response** or response to illness
- ✗ Pharmacogenetics
 - ✗ Effect of **variation in specific genes** and their protein products on **therapeutic response** - monogenic variation
- ✗ Pharmacogenomics
 - ✗ **Multigenic variation**, may also include environmental factors (Kalow 2001)

Reasons for Differences in Drug Response (1)

- ✗ **Genetic differences** in
 - ✗ Drug metabolism enzymes
 - ✗ Ability of drug to **bind** to target (drug target)
 - ✗ Amount of drug target produced
- ✗ **Different pathways** causing same disease
 - ✗ Genetic heterogeneity

Reasons for Differences in Drug Response (2)

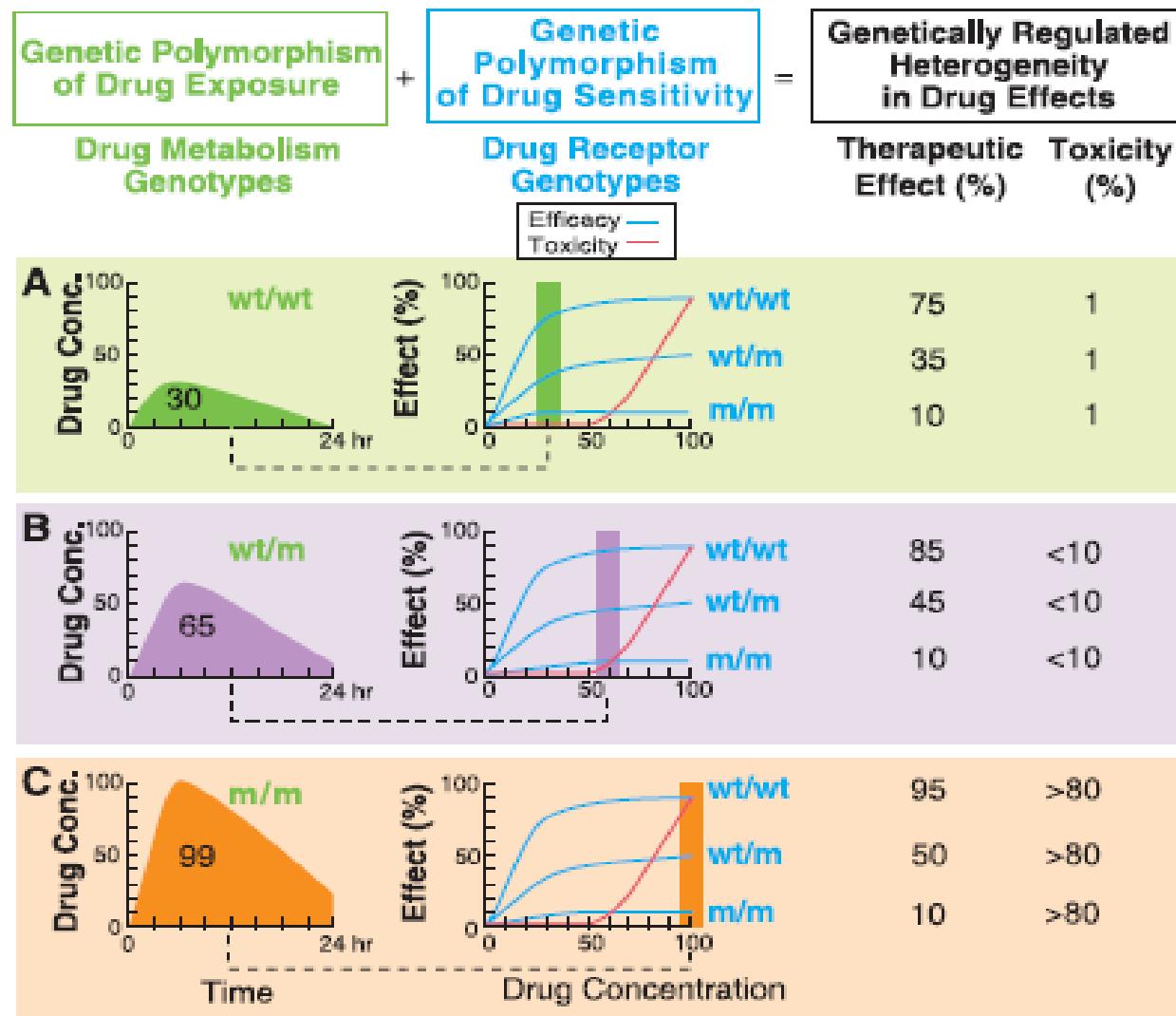
- ✗ **Genetic mutations**
 - ✗ Genome is **master program** for all cells
 - ✗ Proteome is **functional program** for a specific cell
- ✗ Genetic mutations cause **defects** in working proteins
 - ✗ Responsible for **much** of human disease

Reasons for Differences in Drug Response (3)

- ✗ Single nucleotide polymorphisms (SNPs)
 - ✗ One-unit changes in DNA sequence in at least 1% of the population
 - ✗ Major source of genetic variation
 - ✗ On average, any two people may vary by one nucleotide base in every thousand (2/1,000)
 - ✗ Millions of SNPs have been identified
 - ✗ “SNP chips” being developed to identify an individual’s SNP profile
 - ✗ SNP research may lead to hundreds of new drugs

Polygenic Determinants of Drug Effects

(Evans &
Relling,
1999;
Science
286, 487)



Consequences of Differences of Drug Metabolism (Wolf CR, Smith G, Smith RL, 2000)

- ✗ Extended effect from drug
- ✗ Adverse drug reaction/toxicity
- ✗ Inability to activate prodrug
- ✗ Increased dose needed for effect
- ✗ Alternative metabolic pathway
- ✗ Drug-drug interactions

Potential Benefits of Pharmacogenomics (1)

- × More powerful drugs
 - × Based on the proteins, enzymes, RNA molecules associated with genes and diseases
- × More effective, safer drugs from the beginning
 - × To reduce 100,000 deaths and 2 million hospitalizations in USA as the result of **adverse** drug response
- × More accurate doses
 - × Current method: **weight & age** ⇒ dosages based on **a person's genetics**
 - × How well the body processes the medicine & the time it takes to metabolize it
 - × www.ornl.gov/hgmis/medicine/pharma.html

Pharmacogenomics: Medicine and the New Genetics - Microsoft Internet Explorer

檔案(?) 編輯(E) 檢視(V) 我的最愛(A) 工具(I) 說明(H)

上一頁 → 搜尋 我的最愛 按鈕 檔案(?) 網址(?) 移至 連結 »

http://www.ncbi.nlm.nih.gov/sci/techresources/Human_Genome/medicine/pharma.shtml

Google 搜尋 新! PageRank 3 已擋截 檢查 選項

doegenomes.org Human Genome Project Information • Genomics:GTC • Microbial Genome Program • home

[skip navigation](#)

 Home Site Index News

About HGP Research Education Ethics Medicine Media

Gene Testing Gene Therapy Pharmaceuticals Genetic Counseling Diseases

Human Genome Project Information

Pharmacogenomics

Quick Links to questions and answers on this page:

- [Subject Index](#)
- [Send the url of this page to a friend](#)

Basic Information

- [FAQs](#)
- [Glossary](#)
- [Acronyms](#)
- [Links](#)
- [Genetics 101](#)
- [Publications](#)
- [Meetings Calendar](#)
- [Media Guide](#)

About the Project

- [What is it?](#)
- [Goals](#)
- [Progress](#)
- [History](#)
- [Ethical Issues](#)
- [Benefits](#)
- [Genetics 101](#)

Medicine & the New Genetics

- [Home](#)

What is pharmacogenomics?

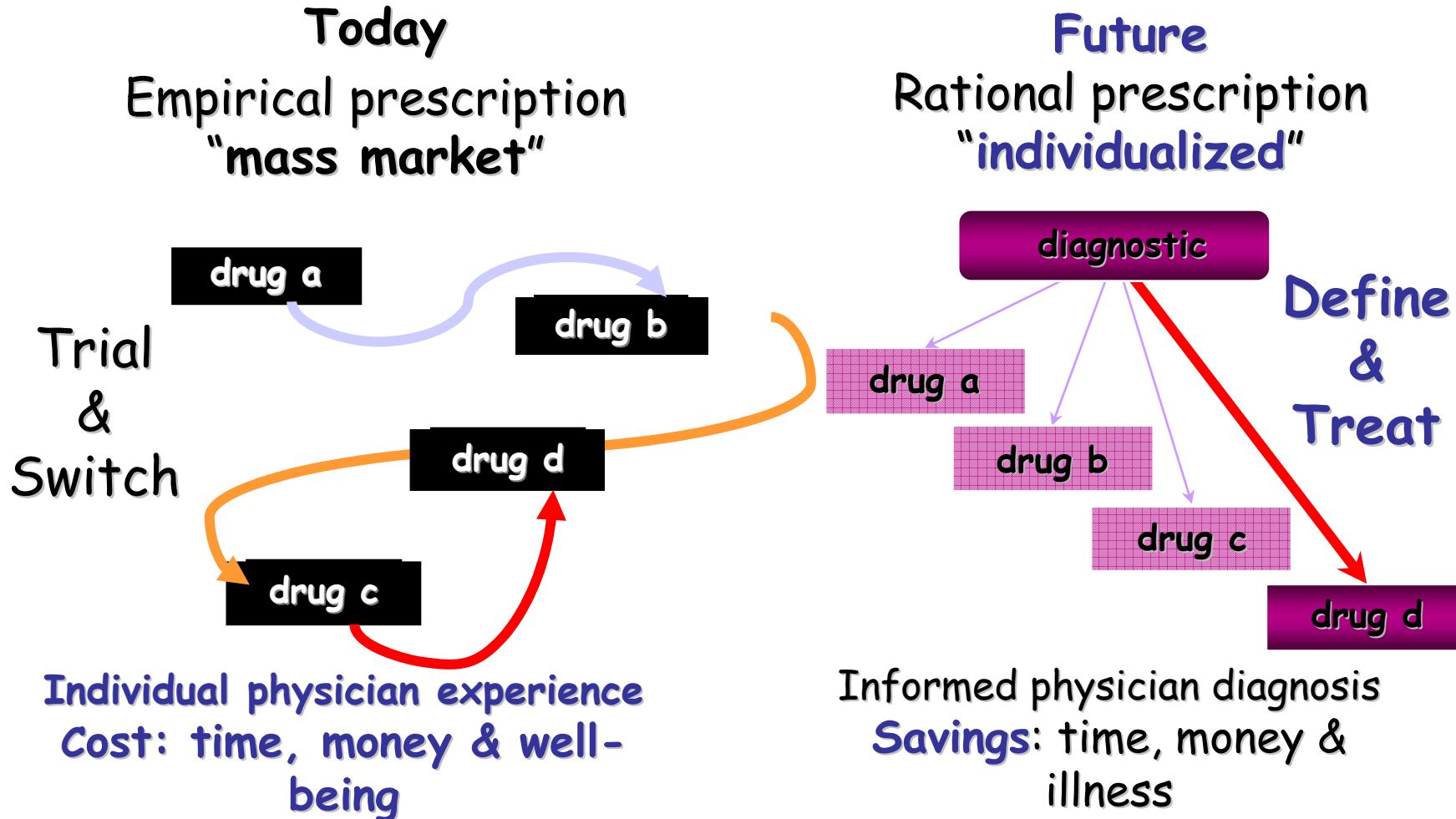
Pharmacogenomics is the study of how an individual's genetic inheritance affects the body's response to drugs. The term comes from the words pharmacology and genomics and is thus the intersection of pharmaceuticals and genetics.

Pharmacogenomics holds the promise that drugs might one day be tailor-made for individuals and adapted to each person's own genetic makeup. Environment, diet, age, lifestyle, and state of health all can influence a person's response to medicines, but understanding an individual's genetic makeup is thought to be the key to creating personalized drugs with greater efficacy and safety.

Pharmacogenomics combines traditional pharmaceutical sciences such as biochemistry with annotated knowledge of genes, proteins, and single nucleotide polymorphisms.

網際網路

Targeted Prescription of Medicines: Applied Pharmacogenomics



Potential Benefits of Pharmacogenomics (2)

- ✖ Screening for disease **in advance** & **prevention**
 - ✖ Knowing one's **genetic code** will allow a person to make adequate **lifestyle** & **environmental changes** at an early age ⇒ to avoid or lessen the severity of a genetic disease
 - ✖ Advance knowledge of a particular **disease susceptibility** will allow **careful monitoring**, & treatments can be introduced at the most appropriate stage to **maximize** their **therapy**

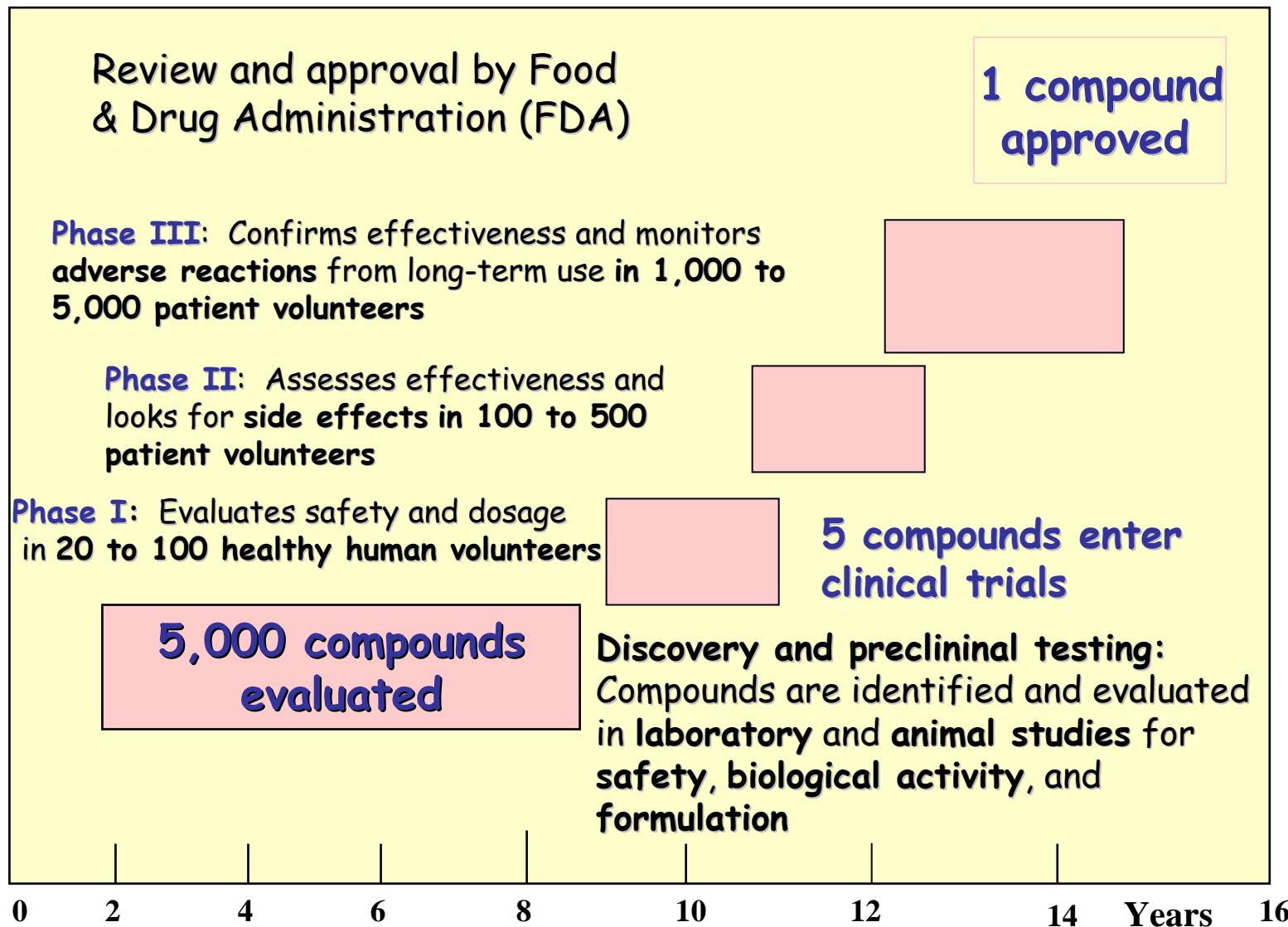
Potential Benefits of Pharmacogenomics (3)

- ✖ **Better vaccines**
 - ✖ Vaccines made of genetic materials, DNA or RNA
 - ✖ Promise all the benefits of existing vaccines
without all the risks
 - ✖ Activate the immune system, unable to cause infections
 - ✖ Inexpensive, stable, easy to **store** & capable of being engineered to carry **several strains of a pathogen at once**

Potential Benefits of Pharmacogenomics (4)

- ✖ Improved **drug discovery** and **approval process**
 - ✖ More easy to discover potential therapies using **genome targets**
 - ✖ Previously failed drug candidates may be **revived** as they are matched with **the niche population** they serve
 - ✖ The **drug approval process** should be facilitated as trials are **targeted for specific genetic population groups** ⇒ providing greater degrees of success

Bringing a New Drug to Market



Source: Tufts Center for the Study of Drug Development

Potential Benefits of Pharmacogenomics (5)

- * Lower overall health care costs

- * Decreases in the number of adverse drug reactions, the number of failed drug trials, the time it takes to get a drug approved, the length of time patients are on medication, the number of medications patients must take to find an effective therapy, the effects of a disease on the body (through early detection) & an increase in the range of possible drug targets will promote a net decrease in the cost of health care

Current Research Directions

- ✖ Identify new targets for new drugs
 - ✖ i.e., genes or their protein products that are associated with diseases
- ✖ Identify metabolic enzymes with genetic variations that alter response to current drugs
 - ✖ Wolf CR, Smith G, Smith RL, 2000

Pharmacist's Role in Pharmacogenomics

- ✖ Expanded role/additional responsibilities in
 - ✖ Drug selection and dose
 - ✖ Counseling on side effects and drug-drug interactions
 - ✖ Compounding - customized drugs, doses and dosage forms
- ✖ Strengthening of team approach to health care

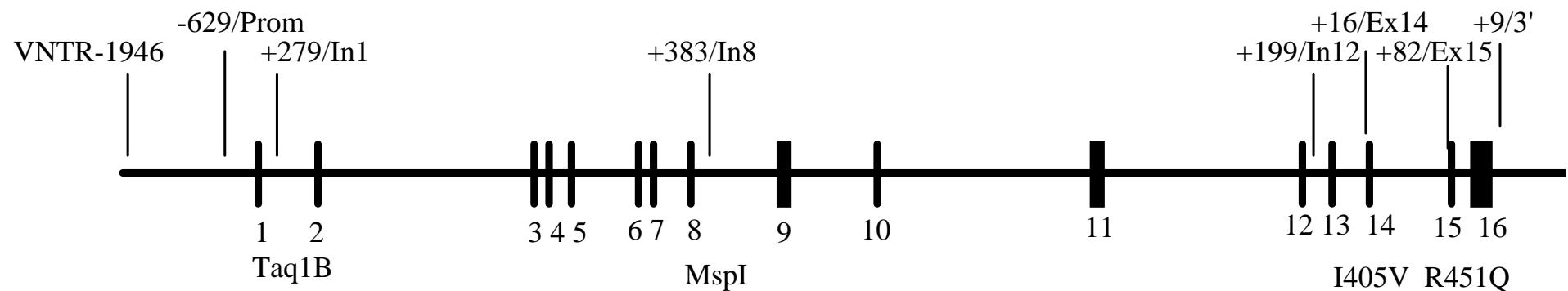
Example: Pharmacogenomics at Pfizer

- ✗ The study of **genome-derived data**, including human genetic variation, RNA and protein expression differences, **to predict drug response** in individual patients or groups of patients
 - ✗ Kitasato - Harvard Symposium (Oct. 2003)

Target Prioritization - Coronary Artery Disease

- ✗ High density lipoprotein (HDL) modulation
 - ✗ A significant market
- ✗ So many targets, but which is the best?
- ✗ Locus specific genetic association study
 - ✗ Candidate genes screened for polymorphism
 - ✗ Correlate genotypes with HDL levels
 - ✗ Increase CIR in the target
 - ✗ Consumption & injection room

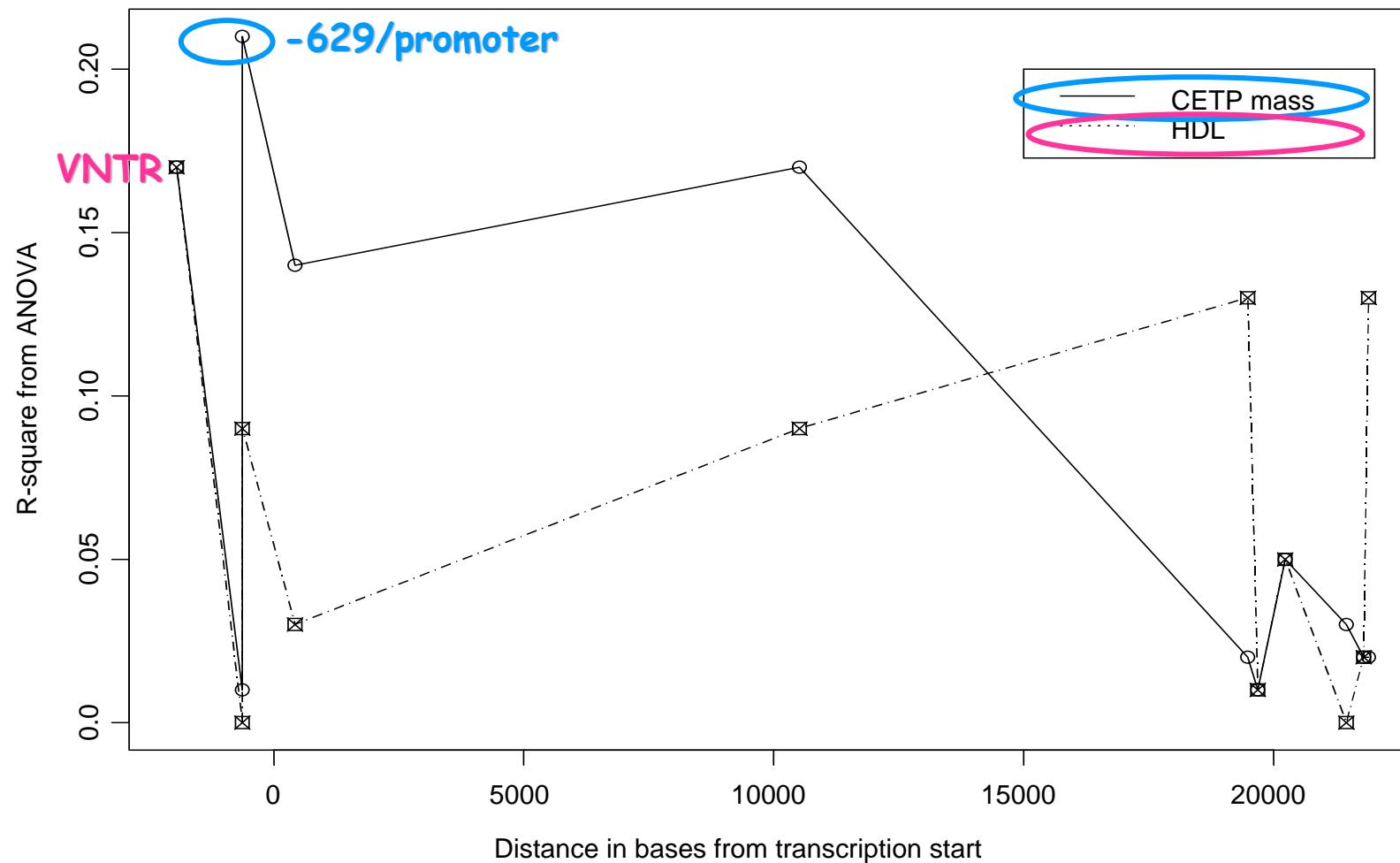
Cholesteryl Ester Transfer Protein (*CETP*)



- ✗ Spans 22 Kb on human chromosome 16
- ✗ Several **polymorphisms** identified
- ✗ Implicated in modulation of **HDL levels**
- ✗ SNPs genotyped in 110 healthy subjects

CETP Association Study (1)

Association of CETP markers and baseline phenotype



Clinical Study Population

- ✗ 54-week Phase IIIb open label assessment of the **safety** and efficacy of Atorvastatin (a-TOR-va-stat-in)
 - ✗ 3,916 patients randomised into **5 treatment groups**
- ✗ Subjects with **coronary heart disease (CHD)** and/or CHD risk factors
- ✗ 4 pretreatment visits, data on **blood pressure, lipids etc.** including HDL level

CETP Study (2)

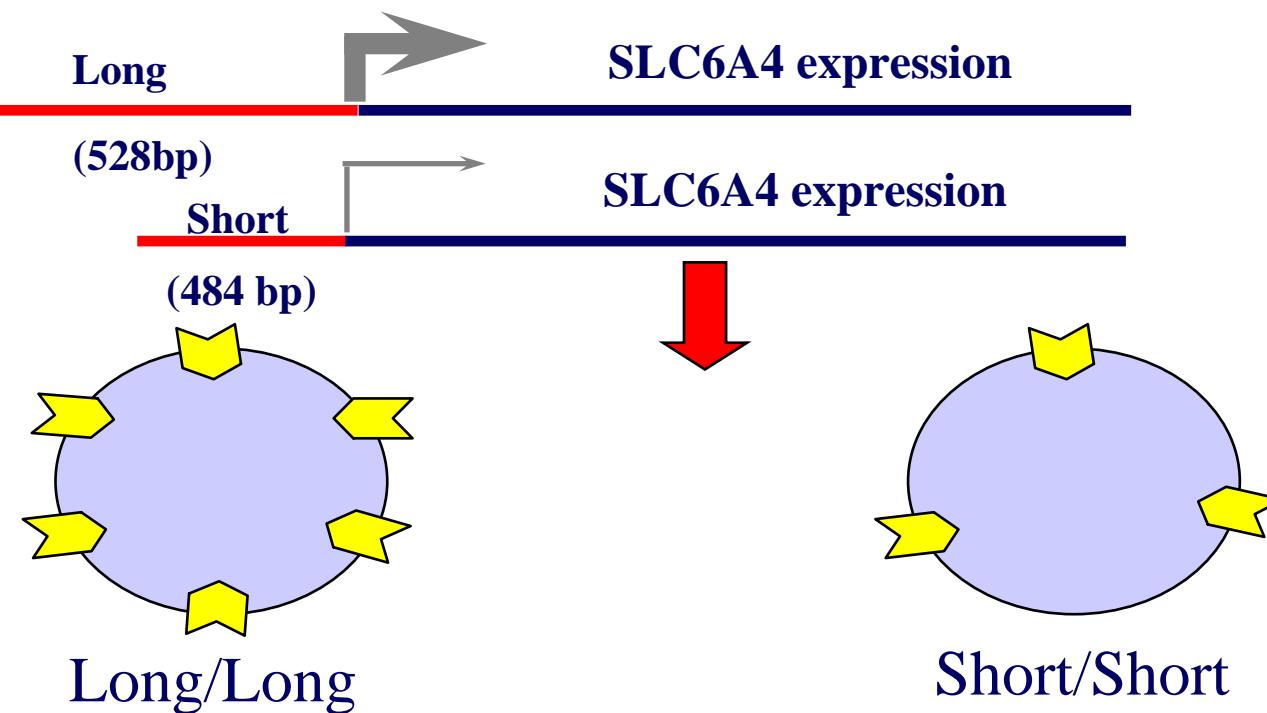
- ✗ Genetic variation in *CETP*
- ✗ Associated with **protective HDL levels**
- ✗ Increasing CIR for target
- ✗ Additional information obtained
 - ✗ Linkage disequilibrium
 - ✗ Ethnic diversity
- ✗ Studies in **larger populations** required

Selective Serotonin Reuptake Inhibitors

- ✗ Selective Serotonin Reuptake Inhibitors (**SSRIs**)
- ✗ Impacted on treatment of **depression**
- ✗ Improved tolerability and efficacy
 - ✗ **BUT** not all patients benefit
- ✗ The challenge for new compounds
 - ✗ Increased **efficacy**
 - ✗ Reduction in **adverse events**
 - ✗ Differentiation

Target Variation - *SLC6A4*

- ✗ Variation in promoter sequence
- ✗ 44-bp insertion/deletion (L and S alleles)





Molecular Psychiatry (1998) 3, 508-511
© 1998 Stockton Press All rights reserved 1360-4184/98 \$12.00

ORIGINAL RESEARCH ARTICLE

Polymorphism within the promoter of the serotonin transporter gene and antidepressant efficacy of fluvoxamine

E Smeraldi^{1,2}, R Zanardi¹, F Benedetti¹, D Di Bella^{1,2}, J Perez¹ and M Catalano^{1,2}

•Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (*SLC6A4*): 5HT transporter (*5HTT*)

Sertraline Targeting *SLC6A4*

- ✗ Sertraline
 - ✗ Zoloft (Pfizer), sertraline (HCl)
- ✗ Antidepressant effect
 - ✗ To inhibit the neuronal reuptake of serotonin
 - ✗ Very weak effects on norepinephrine & dopamine neuronal reuptake
 - ✗ At clinical doses, sertraline blocks the uptake of serotonin into human platelets
 - ✗ In receptor binding studies, sertraline has no significant affinity for adrenergic [alpha(1), alpha(2) and beta], cholinergic, GABA, dopaminergic, histaminergic, serotonergic (5-HT1A, 5-HT1B, 5-HT2) or benzodiazepine binding sites

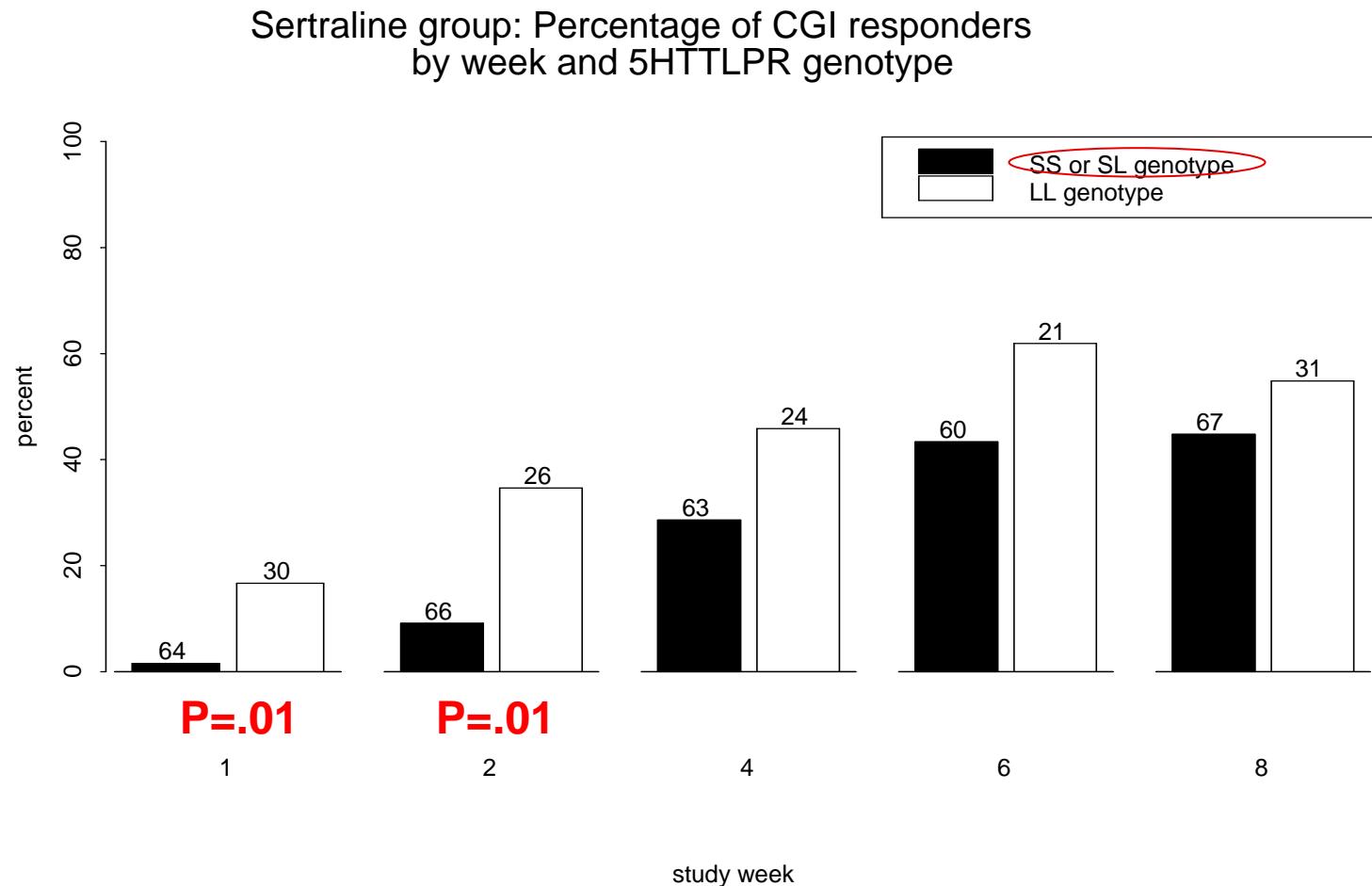
SLC6A4 & Sertraline Response

- ✗ Does genotype influence time to response? (Study R-0552)
 - ✗ 8 week, double-blind, placebo-controlled study of sertraline in elderly depressed outpatients with DSM-IV major depression
 - ✗ 66 sites within the US
 - ✗ Anonymized DNA samples collected to test for genotype effect on time-to-response to sertraline
 - ✗ 4-14 day washout period prior to randomization
 - ✗ Age > 60
 - ✗ HAM-D ≥ 18
 - ✗ HAM-D and CGI-I measures of response
 - ✗ Predominantly Caucasian (95%)

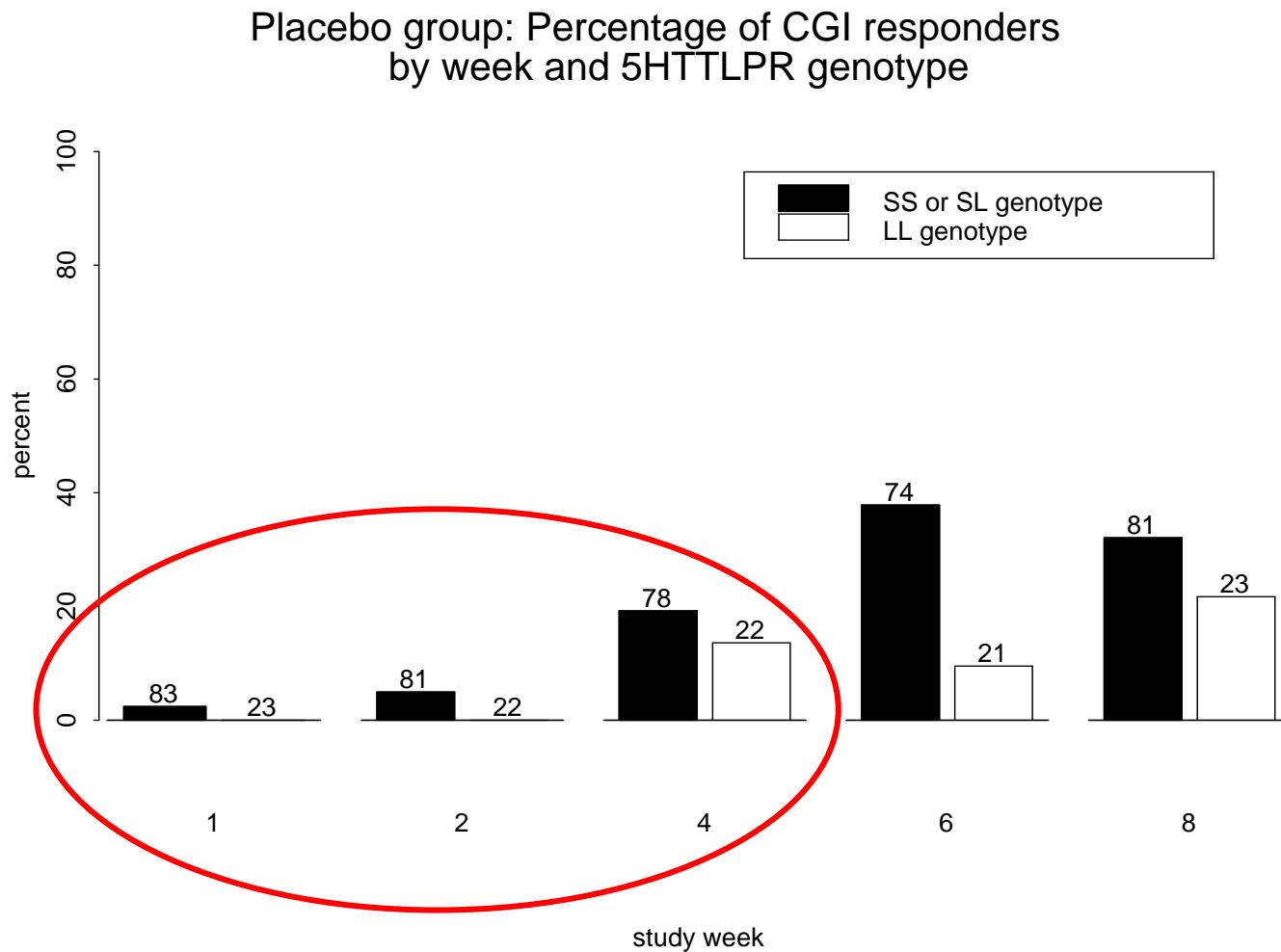
Case Control Evaluation

- ✗ Responders defined as
 - ✗ HAM-D
 - ✗ ≥ 50% reduction in HAM-D from baseline
 - ✗ CGI-I
 - ✗ Individual with a score of 1 or 2
- ✗ Response defined at each time point post-baseline and evaluated for a significant difference in response between the LL and SL/SS groups
 - ✗ Direct association testing a functional polymorphism for effect on response

L/L Genotypes Respond More Rapidly to Sertraline



Response Time to Placebo Not Significant



Pharmacogenomics I



- × Drug response variability
 - × Diseases
 - × Demographic Traits
 - × 人口統計學
 - × Age, race, gender
 - × General Health
 - × Nutritional status, organ function, *esp.* liver & kidney
 - × Drug Traits
 - × Concomitant treatments, interactions with drugs or food
- × Principles
 - × Genotypes
 - × Drug response
 - × Drug metabolism
 - × Disease subpopulation
 - × Diagnostic needs

Pharmacogenomics II - SNPs (1)



- × Single Nucleotide Polymorphisms (SNPs)
- × **Mutations** in genetic code
 - × Changes, deletions, insertions (nucleic acids)
 - × Protein profile changes
 - × Its **actions or reactions** to drugs change
 - × SNPs - over 1.42 million in human genome
 - × SNPs - in excess (DNA **coding regions**) about 60,000

Pharmacogenomics II - SNPs (2)



- ✗ Genetic change in enzymes, transporters, receptors, intracellular signal transduction proteins, cell cycle proteins
 - ✗ Alter the desired or adverse effects of drugs and biologics
- ✗ SNPs
 - ✗ 50 years ago
 - ✗ Changes in adverse events related drug metabolism

Pharmacogenomics II- SNPs (3)



- ✗ Acetylation variation with *isoniazid* 異菸鹼硫胼 (治肺病之藥) and *hydralazine* led to different neuropathies and lupus reactions, cutaneous or organ function, among patients receiving the same therapy
 - ✗ Slower acetylators
- ✗ Sulfonamides
 - ✗ Different hypersensitivity reactions between patients
 - ✗ Based on differences in metabolism

Pharmacogenomics II - SNPs (4)



- ✖ SNPs' effects
 - ✖ Early stop codons
 - ✖ Nucleotide repeats
 - ✖ Gene duplications
 - ✖ Exon skipping
 - ✖ Deletions of major amino acids
 - ✖ No transcripts
 - ✖ Genetic mutations in promoter SNPs, regulatory SNPs
 - ✖ More minor amino acid substitutions or deletions

Pharmacogenomics IV

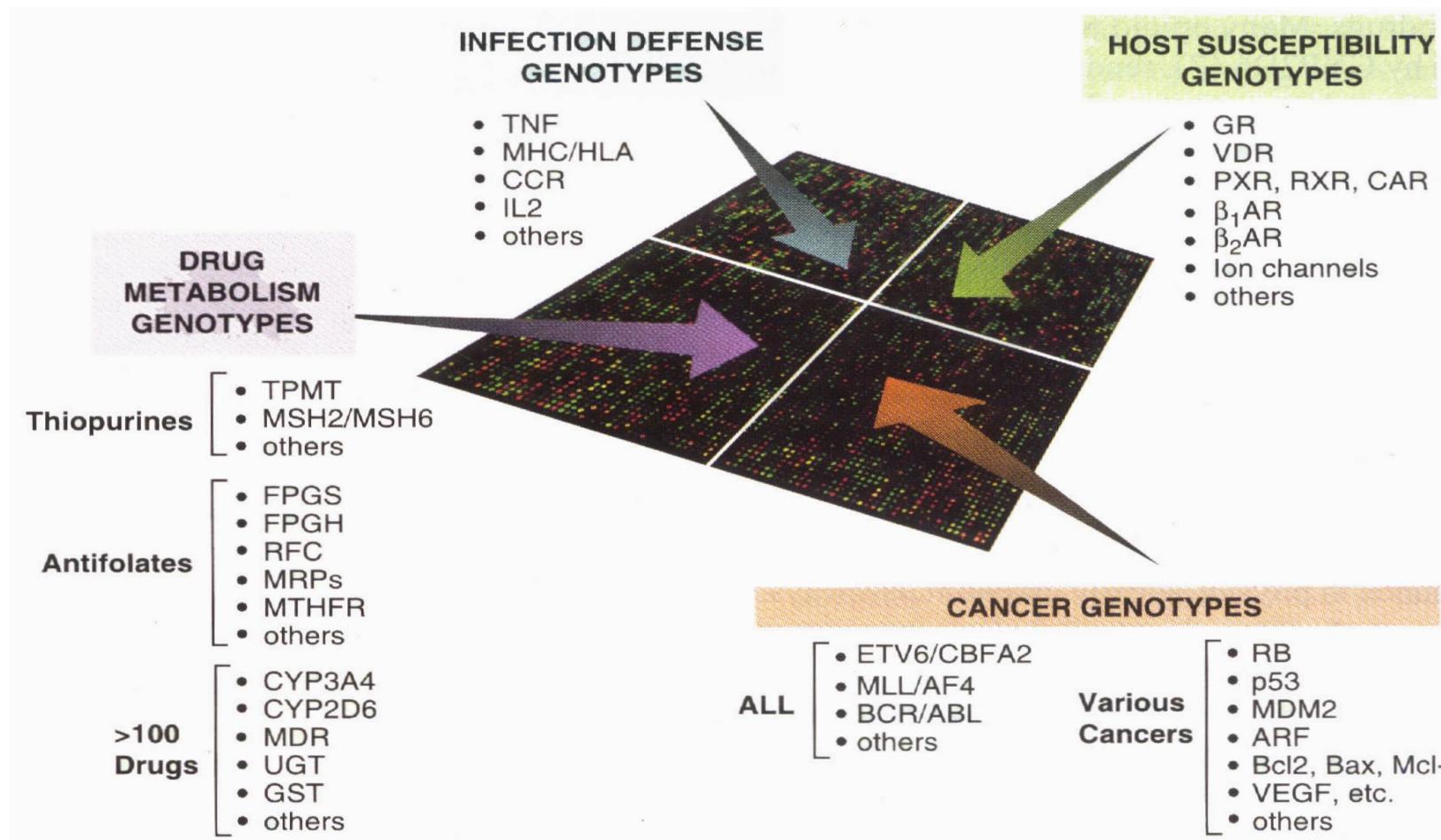
Outcomes - Efficacy & Safety



- Dose of drug **increase** (metabolism, more drug **destruction**; drug-*enalapril*, enzyme - *ACE* SNPs)
- Dose of drug **decrease** (metabolism, more drug **activation**; *codeine*; *CYP2D6* SNPs)
- **Toxicity** of drugs (adverse events; anti-depressants *Imipramine* & *CYP2D6* SNPs)
- Response to **drug changes** (targets, FEV1 variation; Albuterol changes with SNPs in *beta-2 adrenergic receptor* = *ADRB2*) - forced expiratory volume in one second
- **Disease subtypes**, drug response (disease response change; *Herceptin* and *Her2neu*)
 - Breast cancer subtype

Pharmacogenomics V

Complexity of Genetic Variations



D528–D532 Nucleic Acids Research, 2004, Vol. 32, Database issue
DOI: 10.1093/nar/gkh005

SNP500Cancer: a public resource for sequence validation and assay development for genetic variation in candidate genes

Bernice R. Packer*, Meredith Yeager, Brian Staats, Robert Welch, Andrew Crenshaw,
Maureen Kiley, Andrew Eckert, Michael Beerman, Edward Miller, Andrew Bergen¹,
Nathaniel Rothman¹, Robert Strausberg² and Stephen J. Chanock³

Intramural Research Support Program, SAIC-Frederick, NCI-FCRDC, Frederick, MD, USA, ¹Division of Cancer Epidemiology and Genetics, ²Office of Cancer Genomics, National Cancer Institute, Bethesda, MD, USA and
³Section on Genomic Variation, Pediatric Oncology Branch, National Cancer Institute, National Institutes of Health, Gaithersburg, MD, USA

Received July 8, 2003; Revised and Accepted August 7, 2003

SNP500Cancer: Home Page - Microsoft Internet Explorer

檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(I) 說明(H)

上一頁 → 搜尋 我的最愛 地圖 電子郵件 http://snp500cancer.nci.nih.gov/home_1.cfm?CFID=471564&CFTOKEN=47465521 移至 連結 »

網址(1) http://snp500cancer.nci.nih.gov/home_1.cfm?CFID=471564&CFTOKEN=47465521 移至 連結 »

Google SNP500Cancer 搜尋 新! PageRank 1 已擋截 7465521 選項 SNP500Cancer

NATIONAL CANCER INSTITUTE CGAP Cancer Genome Anatomy Project SNP500Cancer Database

NCI > CGAP > SNP500Cancer > Home Genome build 35 v1, dbSNP build 125

Home

Search by Gene/
Chromosome/
Pathway

Search by SNP

List Assays

FTP

Links

Log In

NEW!

What is SNP500Cancer?

The goal of the SNP500Cancer project is to resequence 102 reference samples to find known or newly discovered single nucleotide polymorphisms (SNPs) which are of immediate importance to molecular epidemiology studies in cancer. SNP500Cancer provides a central resource for sequence verification of SNPs. For more information, see [SNP500Cancer background](#).

WHAT'S NEW with SNP500Cancer?

Search for SNPs in SNP500Cancer database

You can search for SNPs using SNP identifier, gene symbol, gene alias, chromosome location, or gene ontology pathway.

- by SNP identifier**
to display SNP details, allele and genotype frequencies

Enter the dbSNP ID or internal SNP ID: Search [search hints](#)

- by Gene**
to display SNPs on the gene, and haplotype data

Enter gene symbol, alias, or GenBank ID: Search [search hints](#)

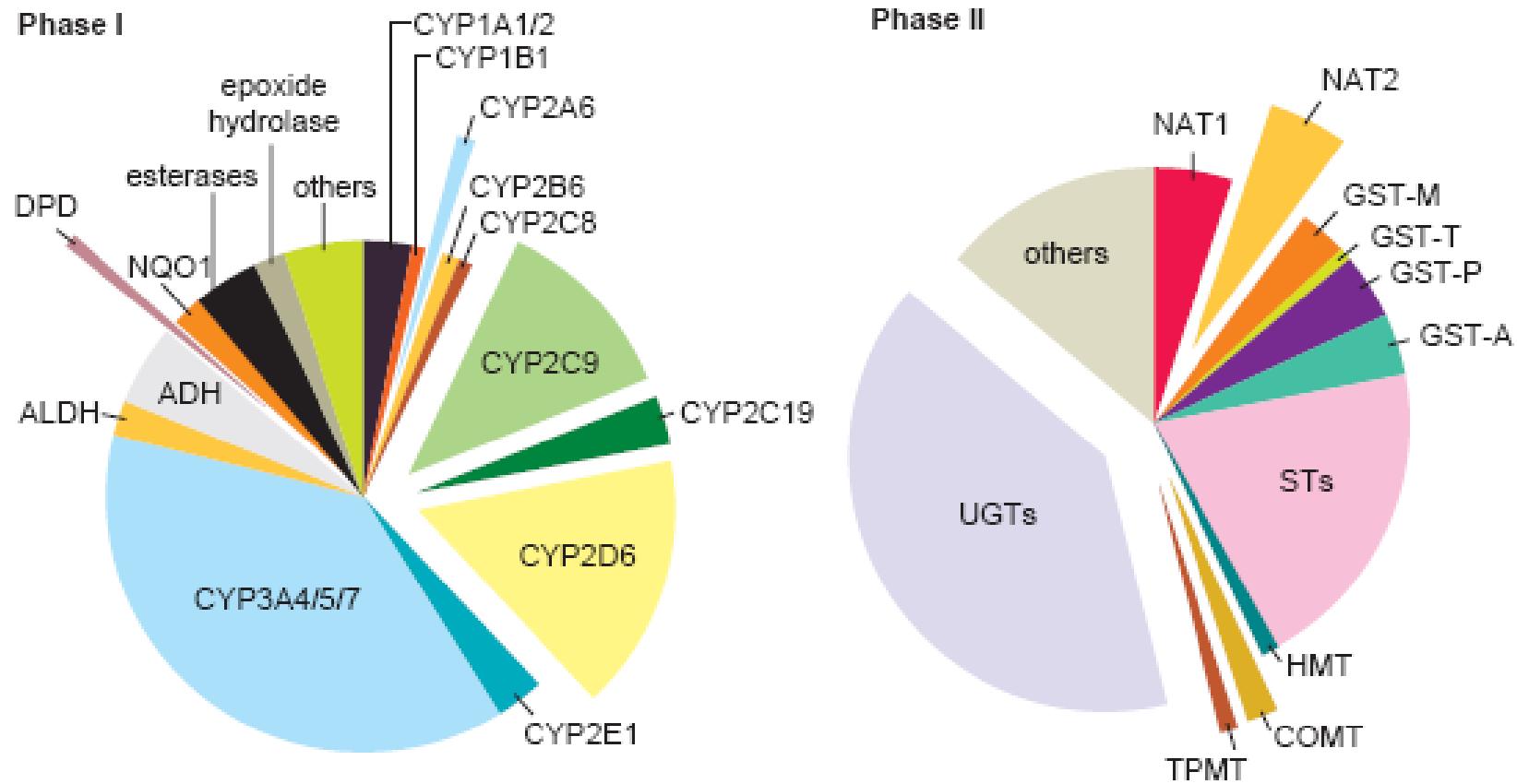
or: List genes with analyzed SNPs Get list

or: List genes with pending SNPs Get list

Enter chromosome number: Search [search hints](#)

Phase I: Major human enzymes responsible for modification of functional groups

Phase II: Conjugation with endogenous substitutents (置換基) or Phase I metabolites that are readily excreted in the urine or bile



Genetic Variations in Drug-metabolizing Enzymes (1)

- ✗ At least one of these allele → alters the activity of the encoded protein
 - ✗ **Cytochrome P450 genes** (*CYP2D6*, *CYP3A4*)
 - ✗ Specify enzymes responsible for drug metabolism in the liver
 - ✗ **Terfenidine** is metabolized by P450 enzymes *CYP2D6* & *CYP3A4*
 - ✗ 6-10% Caucasian population; homozygous for non-functional *CYP2D6* mutant alleles
 - ✗ **Terfenidine** is metabolized by *CYP3A4* in these individuals
 - ✗ *CYP3A4*: is inhibited by
 - ✗ Several commonly prescribed antibiotics
 - ✗ **Grapefruit juice**

Genetic Variations in Drug-metabolizing Enzymes (2)

- ✗ *Terfenidine* is administered with a *CYP3A4* inhibitor
 - ✗ High levels of *terfenidine* accumulate → life-threatening cardiac arrhythmia (心率不整)
 - ✗ Has been removed from the US market (Kurth 2000)

SNPs in Drug-metabolizing Enzymes

- ✗ *CYP2D6*
 - ✗ **Mutant alleles:** responsible for **individual variability** in pain relief by opioid analgesics (止痛劑)
 - ✗ *E.g., Codeine* (可待因)
 - ✗ Require **activation by CYP2D6**
 - ✗ Individuals with **non-functional CYP2D6 mutant alleles** → resistant to the effects of opioid analgesics
 - ✗ Several mutant alleles of the *CYP2D6* gene coding for **debrisoquine 4-hydroxyase** predispose to **toxicity** with
 - ✗ Metaprolol, timolol, nortriptyline, perhexeline, propafenone and **codeine**
 - ✗ **Genetic tests (genotyping):** to prevent potential toxicity by **lowering dosages** or **not** prescribing certain drugs → selection of **optimal drug therapy**

Cytochrome P-450 Multiplicity (1)

- ✗ **Superfamily:** current estimates > 1,000 genes
- ✗ Some of these are "pseudogenes"
- ✗ Humans: current estimates
 - ✗ ~57 distinct P450's in 17 families
 - ✗ Initially simple P-450's cholesterol & FA's form membranes
 - ✗ Millions of years, evolved endogenous ⇒ endogenous + exogenous compounds

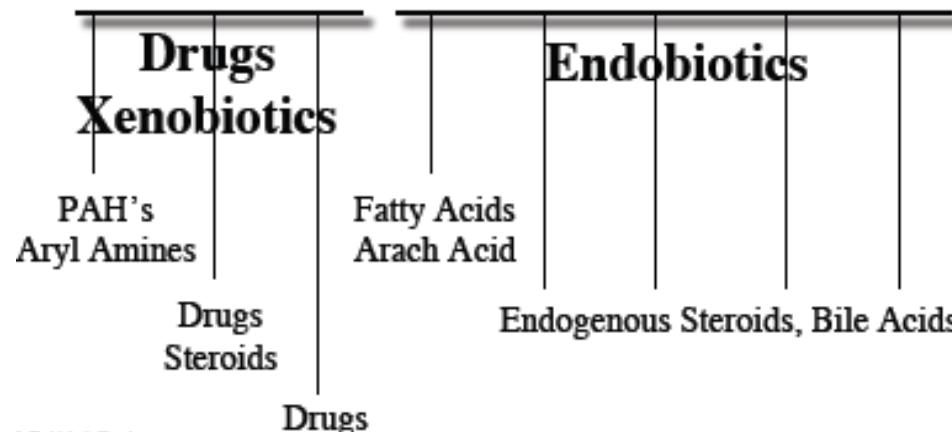
Cytochrome P-450 Multiplicity (2)

- ✗ Superfamily nomenclature
- ✗ *CYP2D6*
 - ✗ C: Cyt P450
 - ✗ 2: Family (>40% homology)
 - ✗ D: subfamily (>55% homology)
 - ✗ 6: individual form

Human P-450 Multiplicity

CYP1	CYP2	CYP3	CYP4	CYP11	CYP17	CYP19	CYP21
1A1	2A6	3A3	4A9	11A1			21A2
1A2	2A7	3A4	4A11	11B1			
	2B6	3A5	4B1	11B2			
	2C8	3A7	4F2				
	2C9		4F3				
	2C10						
	2C18						
	2C19						
	2D6						
	2E1						

CYP1	CYP2	CYP3	CYP4	CYP11	CYP17	CYP19	CYP21
------	------	------	------	-------	-------	-------	-------



Genetic Variations in Drug-metabolizing Enzymes (3)

- ✗ Some drugs require metabolism **before** exerting their **effect**, e.g.,
 - ✗ Antileukemic agents
 - ✗ Mercaptopurine (MP)
 - ✗ Thioguanine (TG)
 - ✗ Immunosuppressant
 - ✗ Azathiopurine
- ✗ Polymorphisms in genes encoding the metabolizing enzymes may produce adverse drug effects

Genetic Variations in Drug-metabolizing Enzymes (4)

- ✗ MP & TG ∈ inactive prodrugs
 - ✗ Require metabolism to thiopurine nucleotides to exert cytotoxicity
 - ✗ Undergo S-methylation catalyzed by thiopurine S-methyltransferase (TPMT)
 - ✗ High TPMT activity results in less activation to thioguanosine phosphates (TGNs), a competitive metabolic pathway
 - ✗ Patients with inactivating TPMT mutation (1/300 inherited deficiency)
 - ✗ Accumulate high TGNs concentration in erythrocytes ⇒ potentially fatal hematopoietic toxicity if full doses are administrated
 - ✗ 10% Caucasians & African-Americans are heterozygous for active TPMT ⇒ at intermediate risk of thiopurine toxicity

Genetic Variations in Drug-metabolizing Enzymes (5)

- ✗ Genotyping (DNA microarray)
 - ✗ To identify *TPMT*-deficient patients → successful treatment at a reduced thiopurine dosage
- ✗ Most drug-metabolizing enzymes exhibit clinical relevant genetic polymorphisms (next slide)

Gene/Enzyme	Drug	Quantitative Effect
<i>CYP2C9</i>	Tolbutamide, warfarin, Phenytoin, nonsteroidal anti-inflammatoies	Anticoagulant effect of warfarin
<i>CYP2D6</i>	Beta blockers, antidepressants, antipsychotics, codeine, debrisoquin, dextromethorphan, encainide, flecainide, guanoxan, methoxyamphetamine, N-propylajmaline, perhexiline, phenacetin, phenformin, propafenone, sparteine	Tardive dyskinesia from antipsychotics; narcotic side effects, efficacy, & dependence; imipramine dose requirement; beta-blocker effect
Dihydropyrimidine dehydrogenase	Fluorouracil	Fluorouracil neurotoxicity
Thiopurine methyltransferase	Mercaptopurine, thioguanine, azathioprine	Thiopurine toxicity & efficacy; risk of second cancers
<i>ACE</i>	Enalapril, Lisinopril, captopril	Renoprotective effects, cardiac indices, blood pressure, immunoglobulin A nephropathy
Potassium channels		
<i>HERG</i>	Quinidine	Drug-induced long QT syndrome
<i>KvLQT1</i>	Cisapride Terfenadine, disopyramide, mefloquine	Drug-induced torsade de pointes Drug-induced long QT syndrome
<i>hKCNE2</i>	Clarithromycin	Drug-induced arrhythmia

Drug Target Polymorphisms (1)

- ✖ Affect drug
 - ✖ Pharmacodynamics
 - ✖ Efficacy
- ✖ Genes involve in
 - ✖ Determine the plasma concentration (extent of drug activation)
 - ✖ Determine the sensitivity of the drug receptor at any given concentration

Drug Target Polymorphisms (2)

- ✗ Drug-metabolizing enzymes
- ✗ Receptors
- ✗ Both homozygous wild-type
 - ✗ High probability of therapeutic efficacy
 - ✗ Low probability of drug toxicity
- ✗ Both homozygous mutants
 - ✗ Low probability of efficacy
 - ✗ High probability of drug toxicity

Receptor Polymorphisms (Example) (1)

- ✗ Kuivenhoven *et al.* (1998) N Engl J Med 338, 86-93.
- ✗ Background
 - ✗ Higher high-density lipoprotein (HDL) cholesterol concentration is inversely related to the risk of coronary artery disease
 - ✗ The Cholesteryl Ester Transfer Protein (CETP) has a central role in the metabolism of HDL → alter the susceptibility to atherosclerosis (動脈硬化症)
- ✗ *CETP* polymorphisms
 - ✗ B1 variant
 - ✗ B2 = without B1 variant

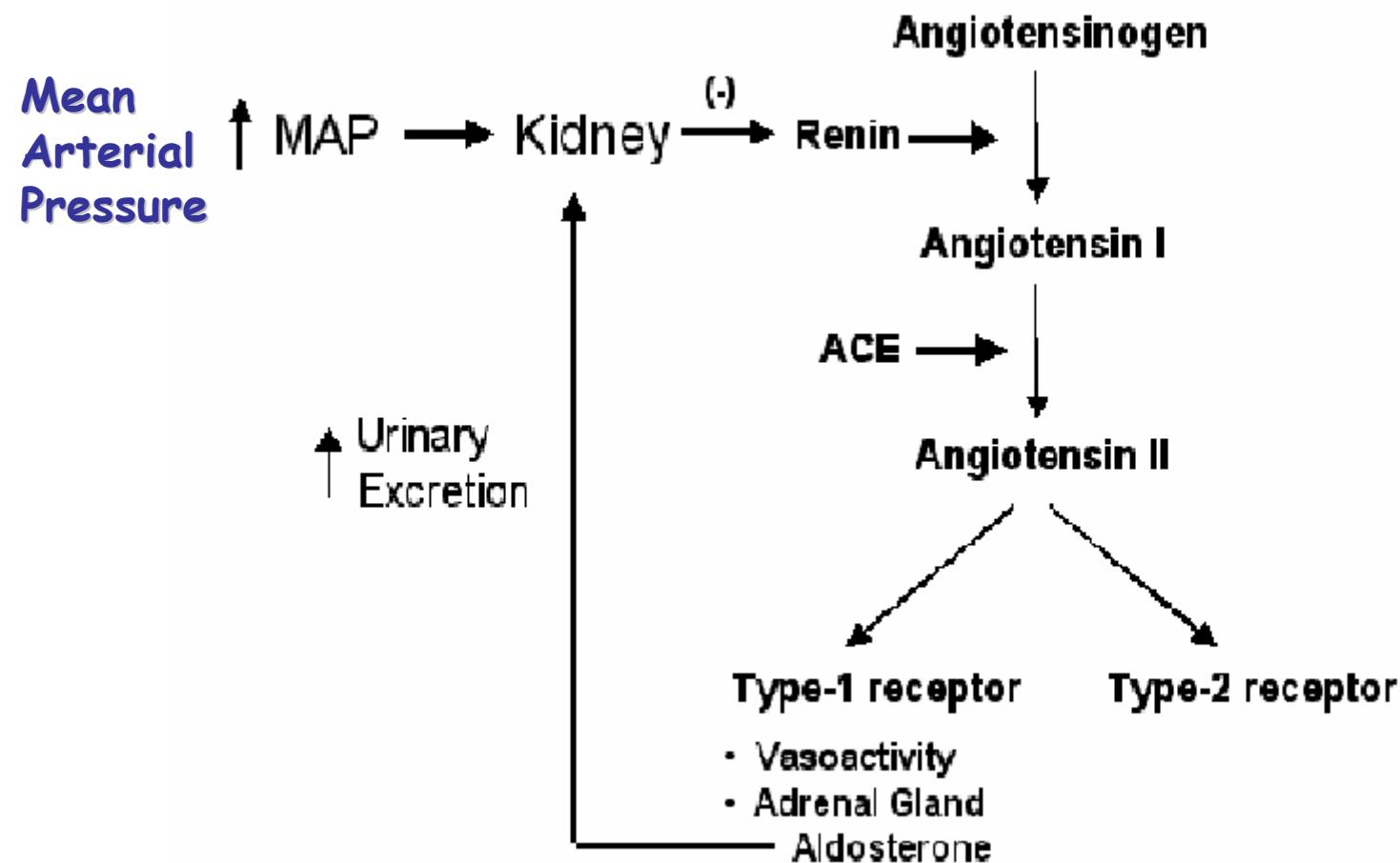
Receptor Polymorphisms (Example) (2)

- ✗ 807 patients
 - ✗ Antiographically documented coronary atherosclerosis
 - ✗ Participated in a cholesterol-lowing trial designed to induced the regression of coronary atherosclerosis
 - ✗ Randomly assigned to treatment with either (2 years)
 - ✗ *Pravastatin*
 - ✗ *Placebo*
 - ✗ **B1** variant of the *CETP* gene was associated with
 - ✗ Higher plasma CETP conc.
 - ✗ Lower HDL cholesterol conc.
 - ✗ *Pravastatin* therapy slowed the progression of coronary atherosclerosis in **B1B1 carriers** but not in **B2B2 carriers**

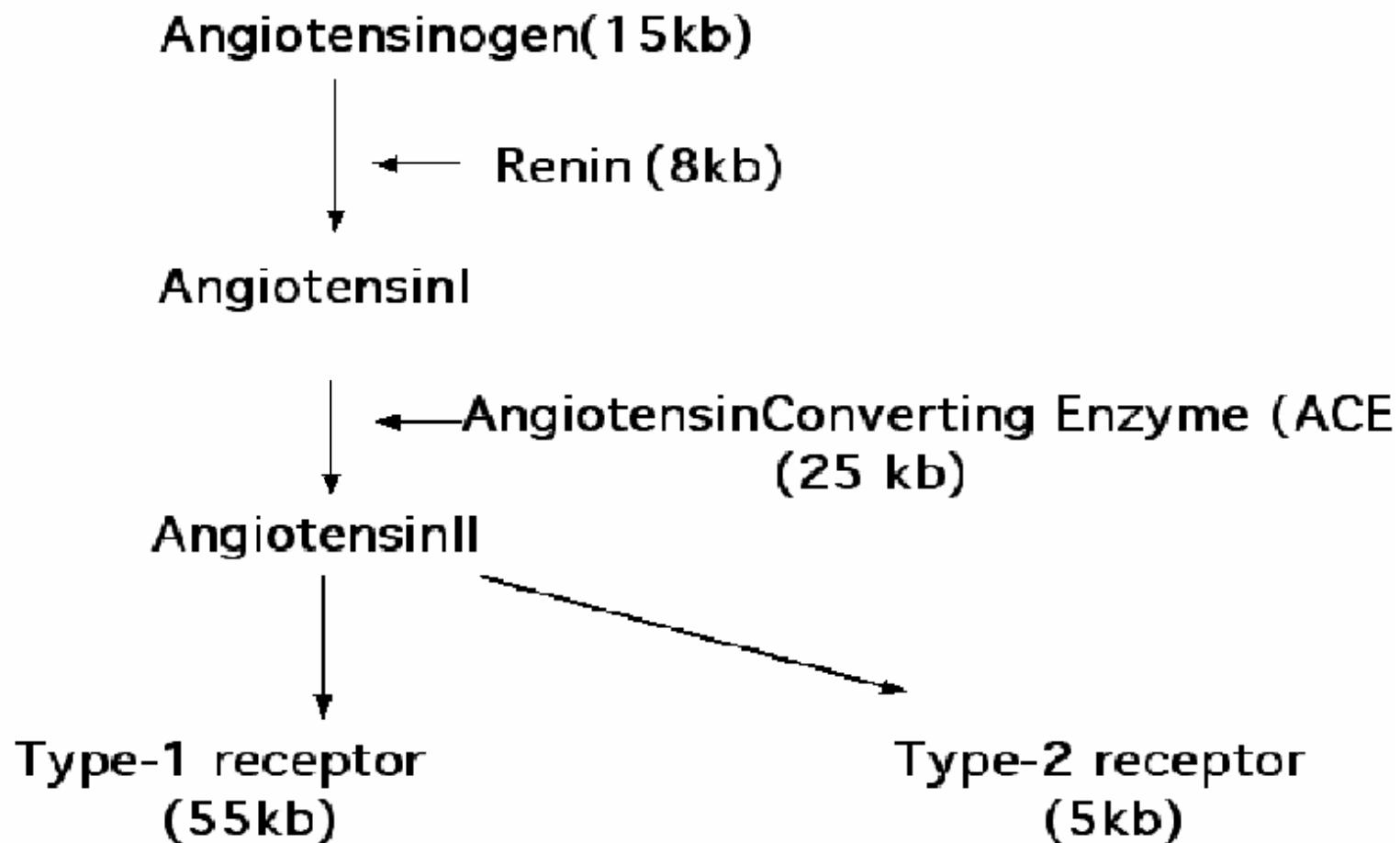
Example: *ACE*

- × Patients **homozygous** for an allele with a **deletion in intron 16** of the gene for **angiotensin-converting enzyme (*ACE*)** showed **no benefit** from the **hypertension drug *enalapril*** while other patients did benefit

Renin-Angiotensin System: Physiology

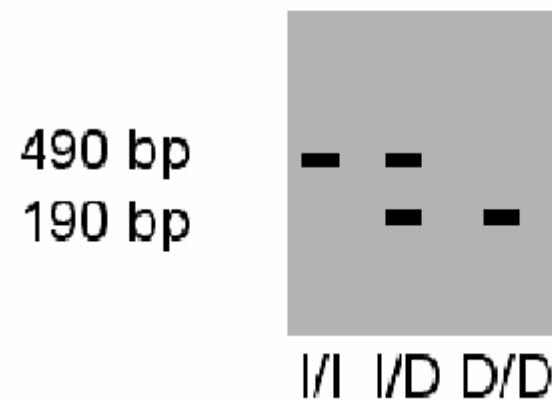
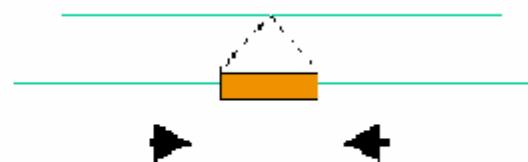


Renin-Angiotensin System



ACE: Candidate Gene

Two alleles: Deletion (D)
Insertion (I)



- ✗ "D" allele: ↑enzyme activity, hypertension, LVH, CAD, renal disease, longevity
- ✗ "I" allele: ↑LV mass, elite endurance /athletic performance

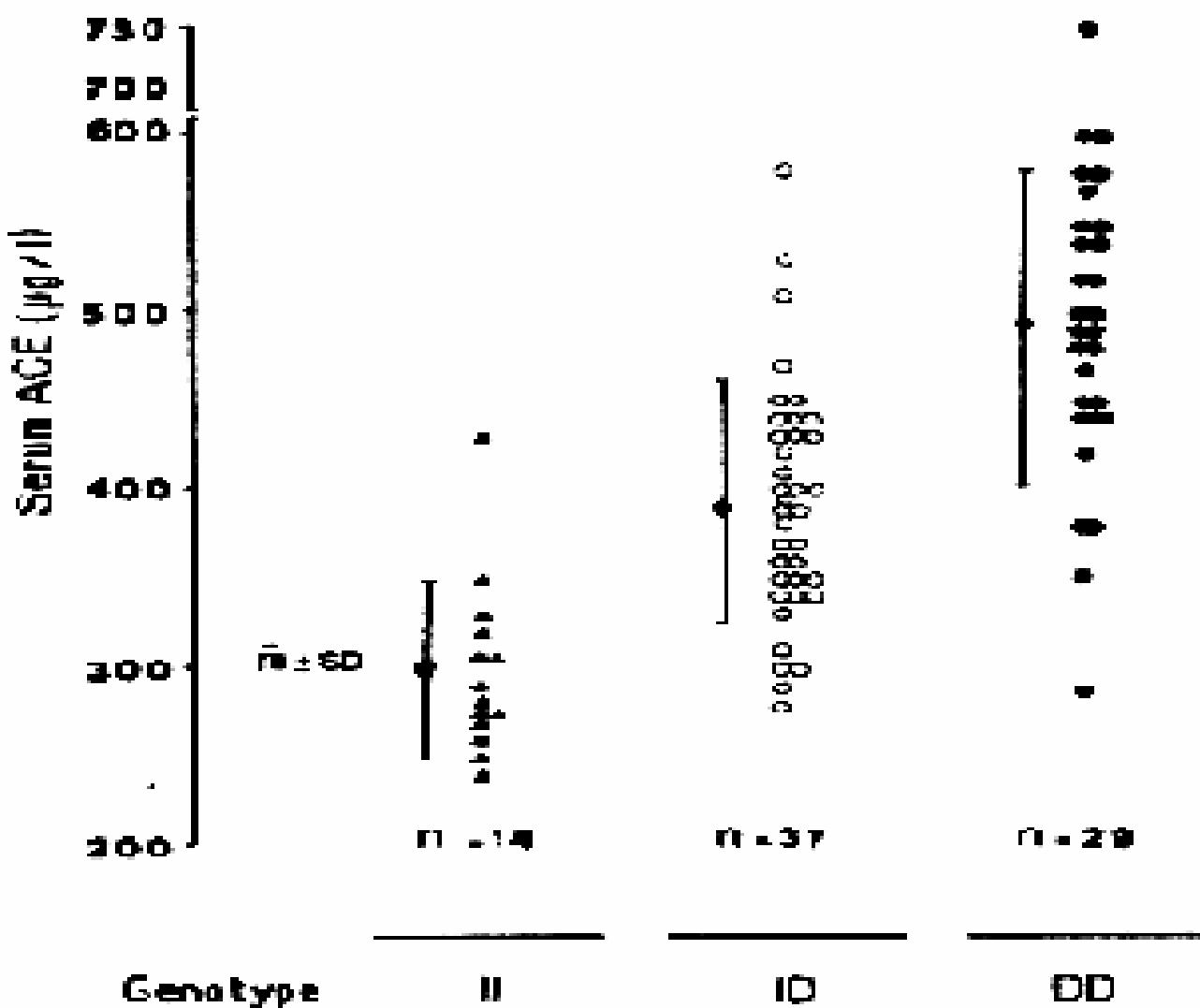


Figure 2. Serum immunoreactive ACE concentrations ($\mu\text{g/liter}$) for individual with the II, ID, and DD genotypes, respectively, shown in left, middle, and right panels. Solid vertical bars indicate mean concentration and standard deviation for each group.

Rigat et al. *J. Clin. Invest.* 1990

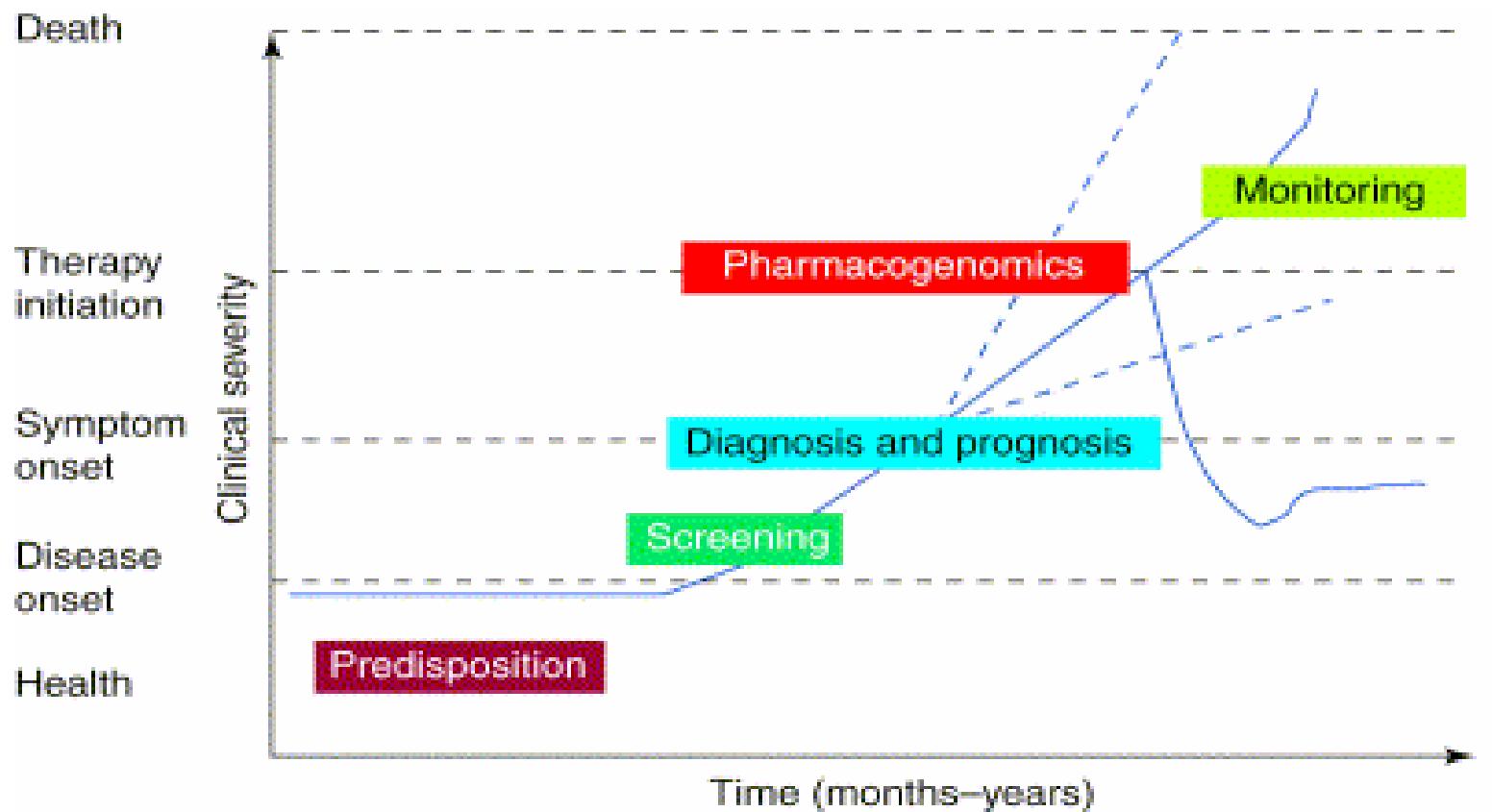
The Value of Pharmacogenomics

- ✗ Drug discovery: enhanced
- ✗ Patient drug therapy: optimized
- ✗ Patient vary in drug response
 - ✗ To identify polymorphisms in drug-metabolizing enzymes
 - ✗ To identify drug targets in order to tailor drug therapy
- ✗ Pharmacogenomics → to create small molecules with greater specificity and efficacy
 - ✗ Rational drug design
 - ✗ Combinatorial methods

Real World Applications

- ✗ Most of the major pharmaceutical companies are currently collecting pharmacogenomic data in their clinical trials
 - ✗ Data is yet to be published
- ✗ **Genetic indications** for drug use are still a few years away

Impact of Pharmacogenomics on Chronic Diseases



TRENDS in Biotechnology

Trends Biotech. 19, 491-496 (2001)

Pharmacogenomics - A new Script for Prescriptions

- ✖ **Information**
 - ✖ Unique variations in an individual's **genetic makeup**
 - ✖ Resulting highly variable **responses** to drug
 - ✖ Metabolism
 - ✖ Effectiveness
 - ✖ Toxicity
- ✖ **Everybody must**
 - ✖ Get up and ready for pharmacogenomics