Pharmacogenetics of Tobacco Smoking and Lung Cancer

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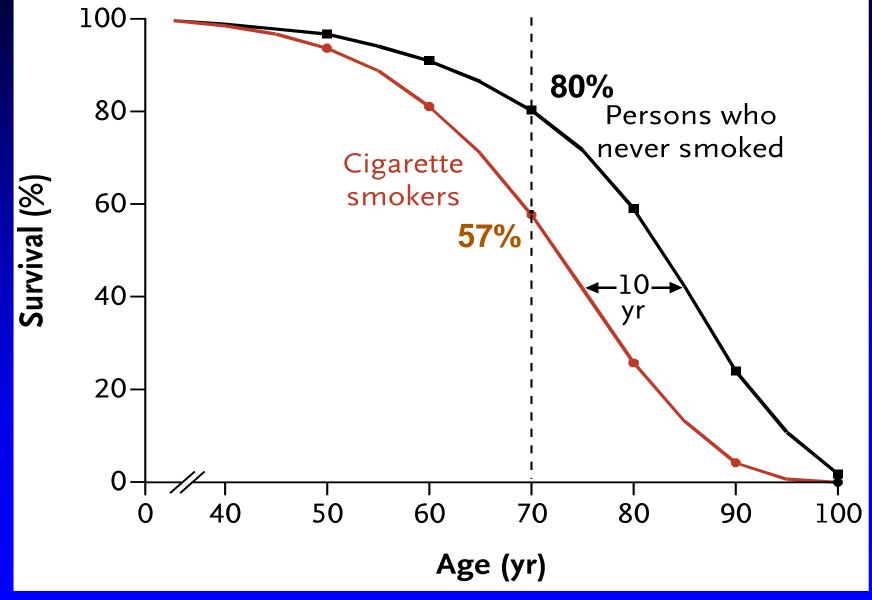
> Center for Genomic Medicine Geisel College of Medicine at Dartmouth



GAME-ON Consortium



Smokers live 10 years less



Peto et al., 2010

Smoking: a leading cause of premature death

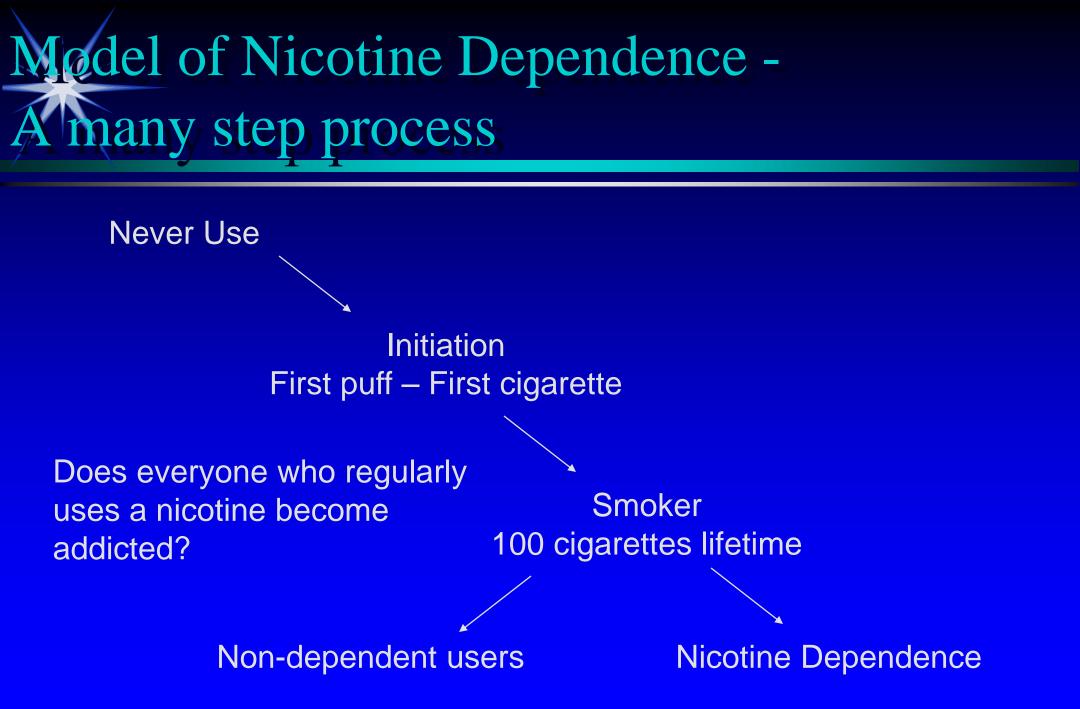
Currently: >1 billion smokers globally 6 million death each year

Projected: 1 billion deaths during 21st century

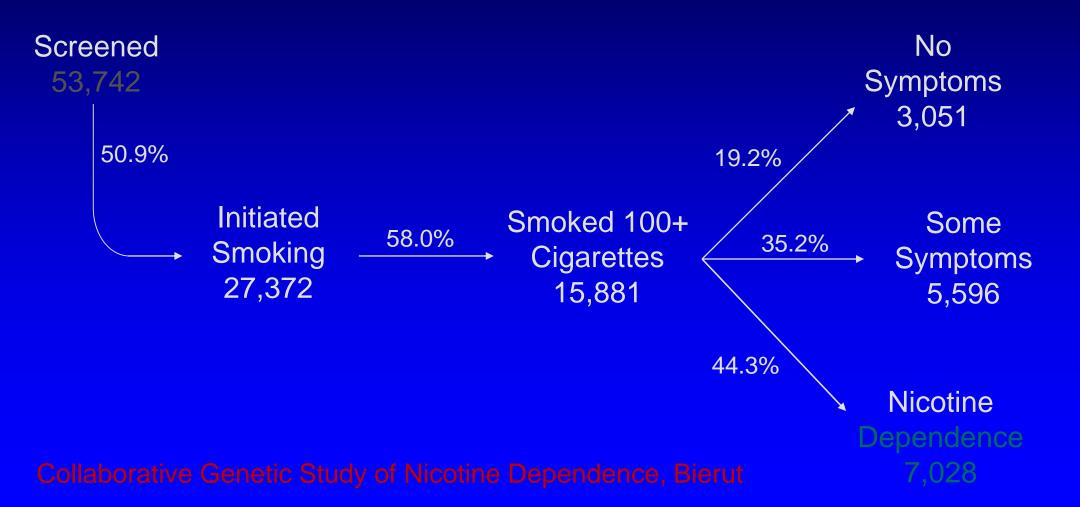
	Numbe	r of deaths	RR (95% CI)
	Current smoker	Never smoker	
Chronic lung disease (J40–44)	1789	121	35.3 (29.2–42.5)
Cancer of lung (C34)	5633	698	21.4 (19.7–23.2)
Aortic aneurysm (171)	330	164	— 6·32 (5·17–7·71)
Intestinal ischaemia (K55)	183	91	<u>5.58 (4.27–7.29)</u>
Cancer of mouth, pharynx, larynx, nasal cavity, or sinuses (C00–14,30–32)	204	91	<u> </u>
Coronary heart disease (I21–25)	2726	1732	4·47 (4·19–4·77)
Cirrhosis or alcoholic liver (K70,74)	478	256	→ 3·35 (2·84–3·94)
Cancer of bladder (C67)	178	156	<u> </u>
Cancer of oesophagus (C15)	450	397	_ 3·10 (2·68–3·58)
Pneumonia (J12–18)	494	408	_ 3·09 (2·68–3·56)
Cerebrovascular disease (I60–69)	1528	1458	
			Pirie et al., 2010

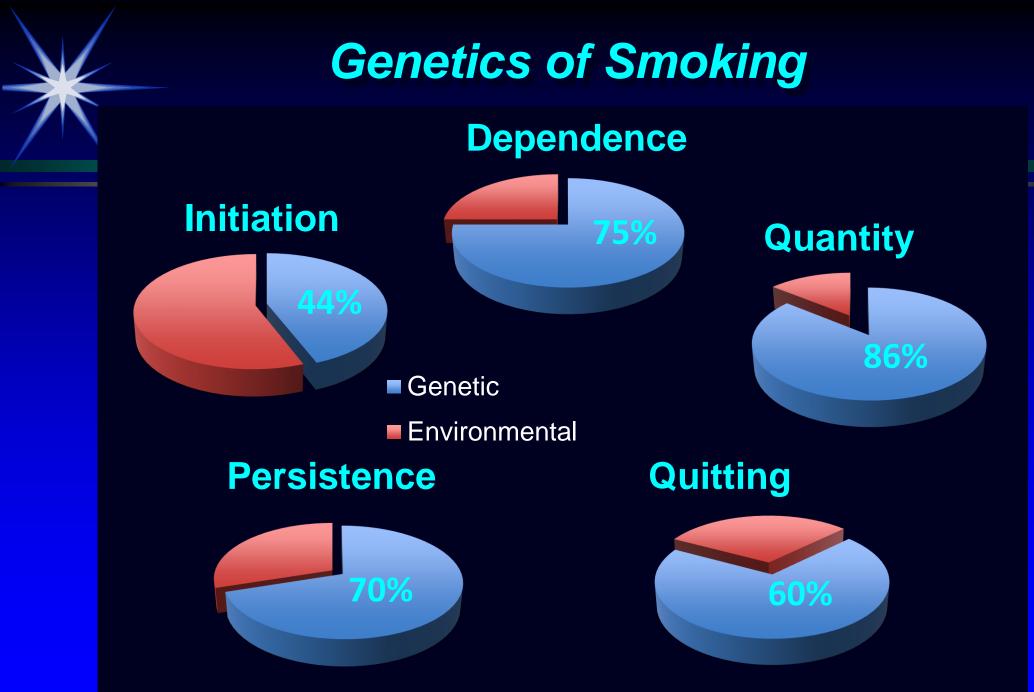
I miss my lung, Bob.

California Department Of Health Services. Funded By The Tobacco Tax Initiative.



U.S. Population Screening and Nicotine Dependence





Vink, et al. 2005; True, et al. 1997, Koopmans, et al. 1999

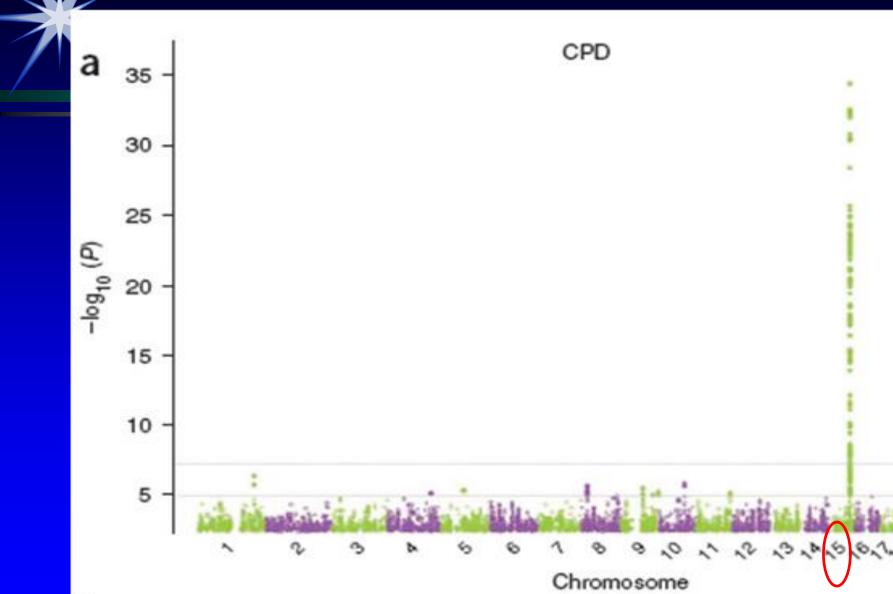
Table 1 Heritability estimates for different drugs of abuse

Heritability estimates		
28-84%		
45-86%		
31–75%		
26-48%		
50-58%		
50-70%		
45-58%		
8-50%		
43-60%		
29-58%		
42-74%		

Twin, family and adoption studies in humans, together with animal studies, have provided the foundation for genetic effects on substance use, abuse and dependence.

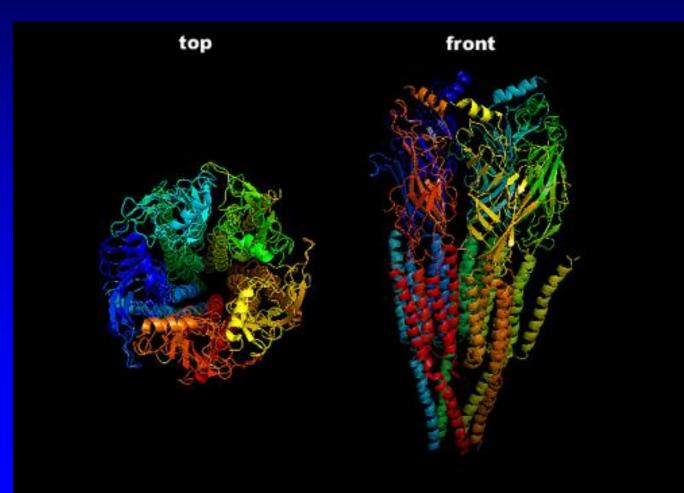
Ho, Goldman, Heinz, Kaprio, Kreek, Li, Munafò, Tyndale. Breaking barriers in the genomics and pharmacogenetics of drug addiction. Clin Pharmacol Ther. 2010 Dec;88(6):779-91.

Chromosome 15q25 Is Important for Smoking



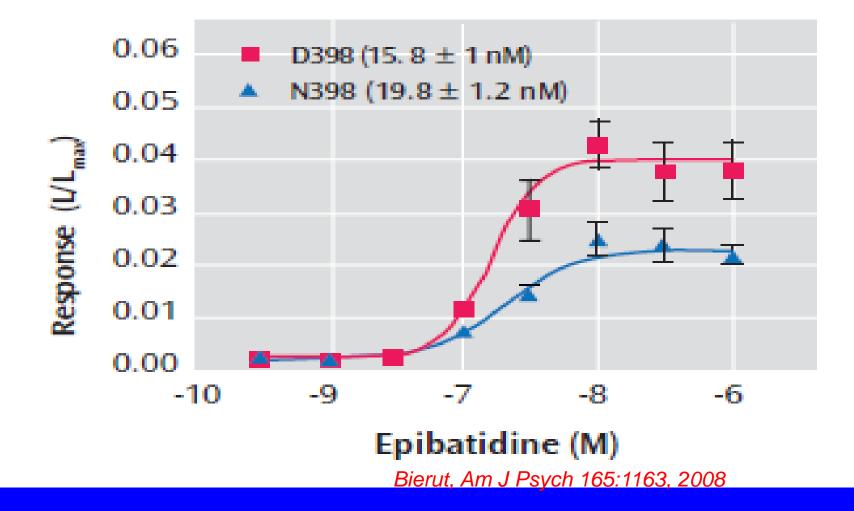
The Tobacco and Genetics Consortium (2010) Nature Genetics

Nicotinic Receptors are Homo- or Heteropentamers

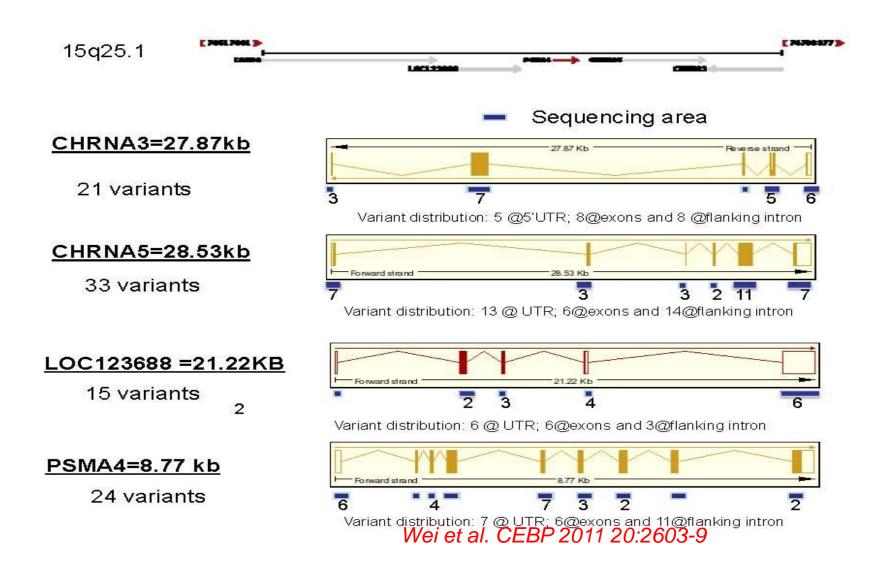


 α_3 β_4 α_5 low level expression in brain

SNP rs16969968 affects maximal response to agonist



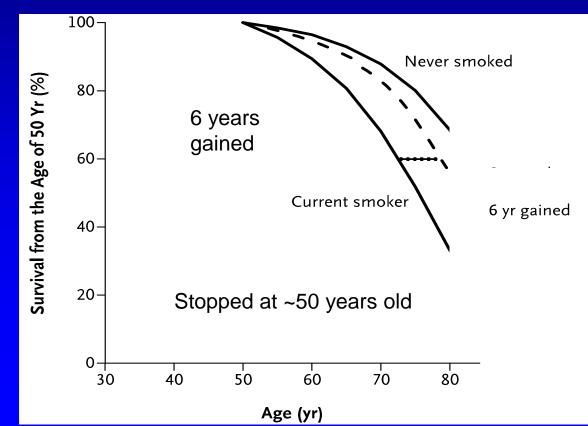
Chromosome 15_q25.1 region contains specialized nicotinic receptor variants



Smoking Cessation

> 70% of smokers say they would like to quit

- 40% quit for at least 1 day each year, but 80% of them relapse within a month
- Only 3% of smokers quit successfully each year



Benowitz et al., 2010; Jha et al., 2013

Is CHRNA5-A3-B4 involved in cessation?

Study Design

U Wisconsin - TTURC

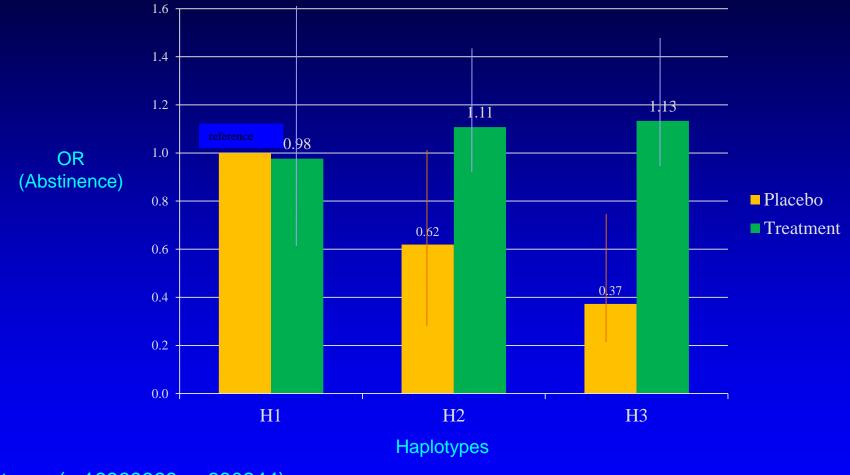
- ↗ N=1073, European Ancestry
- Pharmacotherapy arms (Bupropion, NRT, combo) and one placebo arm

Cessation
 Abstinence at 60 days
 Time to relapse over 60 days

CHRNA5-A3-B4 Haplotypes

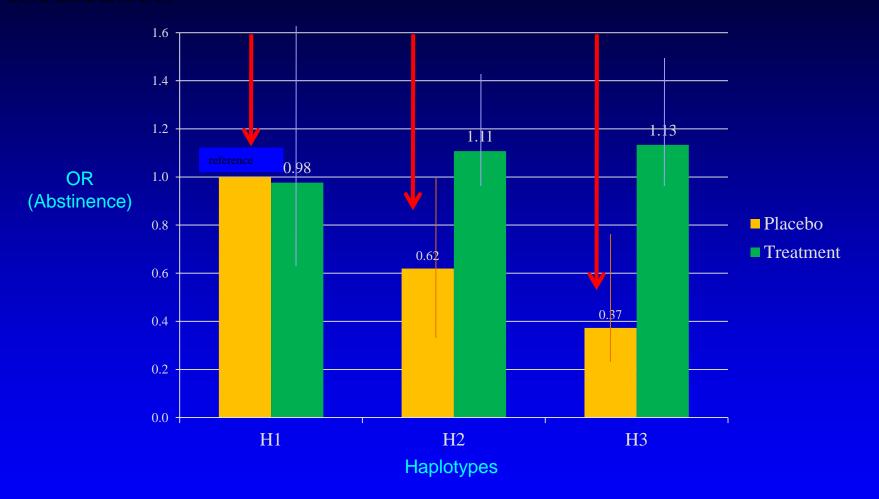
- rs16969968
 Non-synonymous coding, Amino acid change in *CHRNA5*
- rs680244 CHRNA5 mRNA levels in brain and lung
- Combination of 2 variants
 - ↗ H1 (G_C, 20.8%)
 - → H2 (G_T, 43.7%)
 - ↗ H3 (A_C, 35.5%)

Haplotypes predict cessation and response to medication

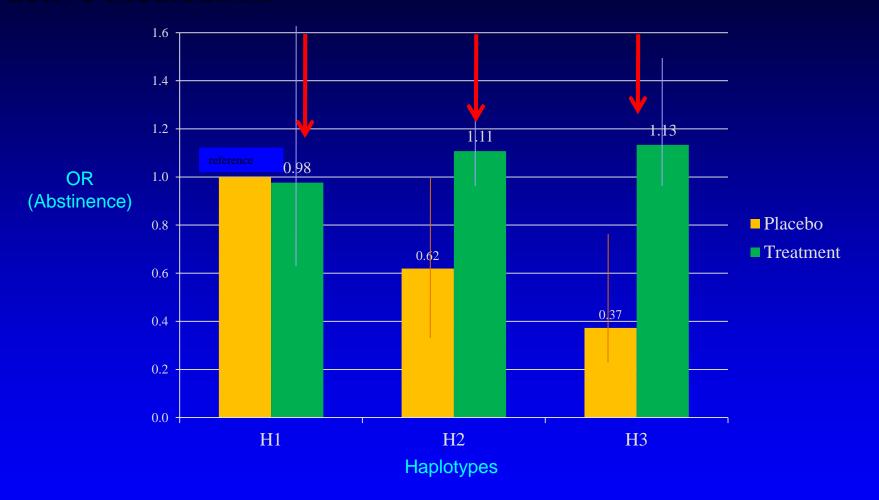


Haplotypes (rs16969968, rs680244): H1=G_C(20.8%) H2=G_T(43.7%) H3=A_C(35.5%)

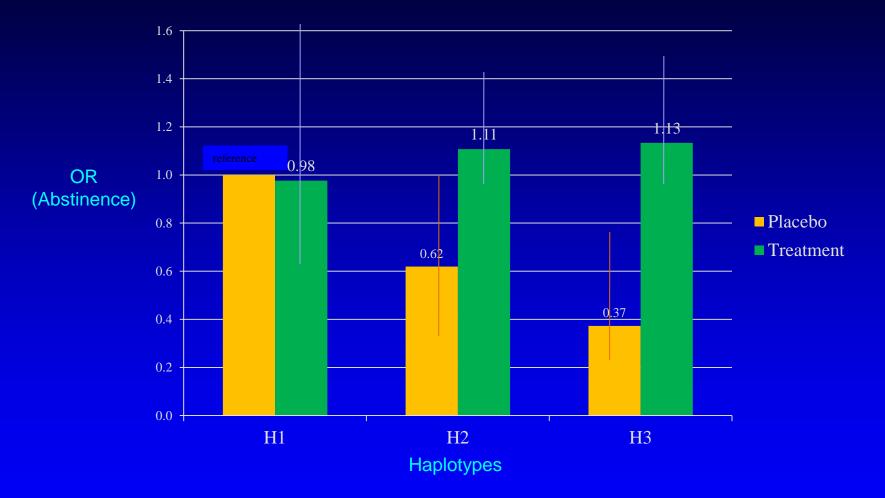
Haplotypes predict abstinence in individuals receiving placebo medication



Haplotypes do not predict abstinence in individuals receiving active medication



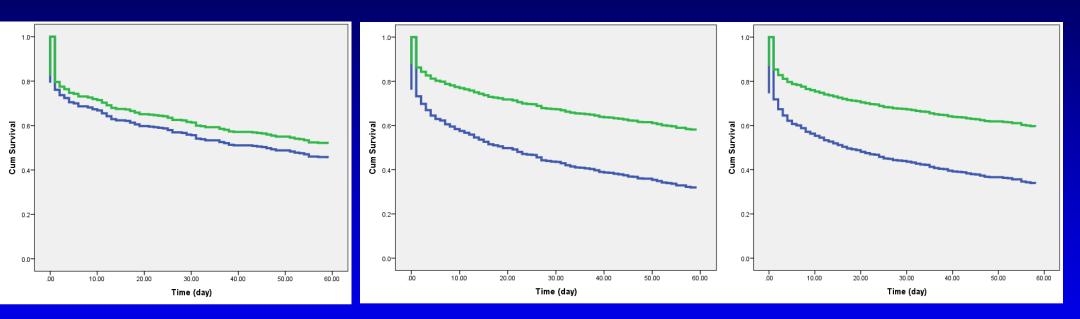
A Significant Genotype by Treatment Interaction



The interaction of haplotypes and treatment is significant (X²=8.97, df=2, p=0.011)

Response to Treatment Differs by Haplotype

a. Haplotype H1 (G_C) RH=0.83, p=0.36 **b. Haplotype H2 (G_T)** RH=0.48, p=2.7*10⁻⁸ **c. Haplotype H3 (A_C)** RH=0.48, p=9.7*10⁻⁷



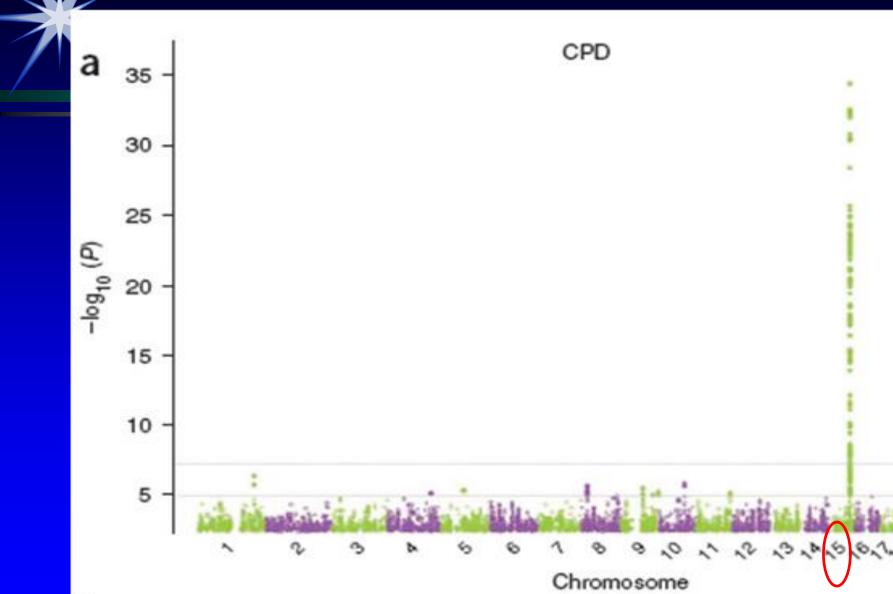
Placebo Active Treatment

Genetics can predict prognosis & inform treatment

Smokers with the low risk haplotype (H1/G_C)
 can quit more successfully without medication
 do not benefit from medication

- ↗ have more difficulty quitting without medication
- can benefit from medication with a 3-fold increase in cessation success

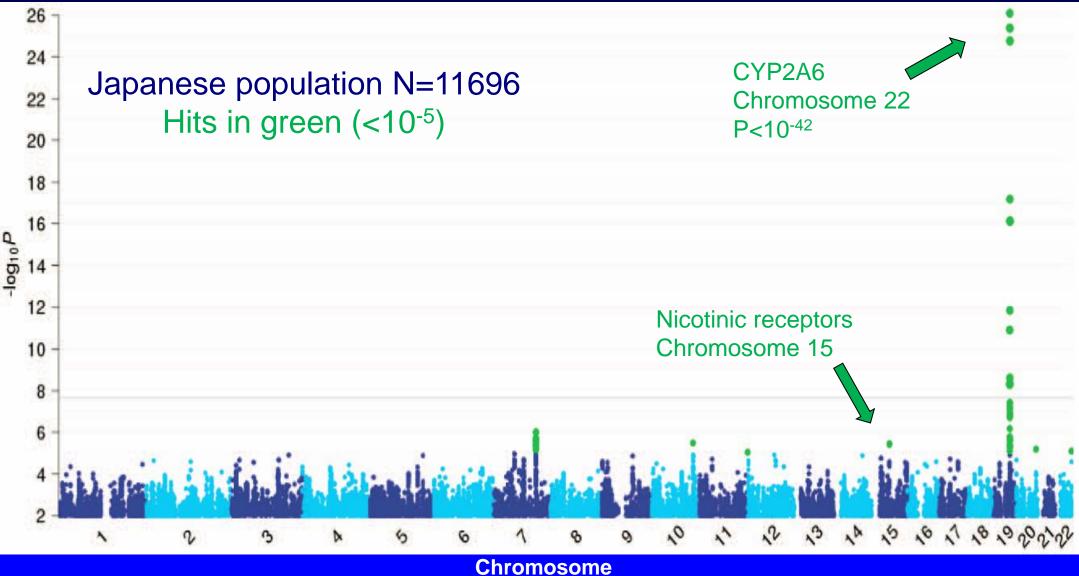
Chromosome 15q25 Is Important for Smoking



The Tobacco and Genetics Consortium (2010) Nature Genetics

Manhattan plot for all CNPs and SNPs in the genome-wide analysis of Cigarettes per day

Kumasaka, Aoki, Okada, Takahashi, Ozaki, Mushiroda, Hirota, Tamari, Tanaka, Nakamura, Kamatani, Kubo, PLOS one 2012

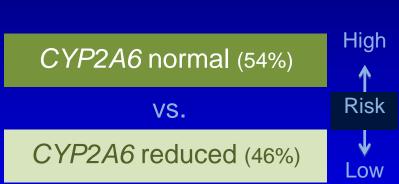


CYP2A6 Genotyping and Statistical Methods

CYP2A6 genotyping:



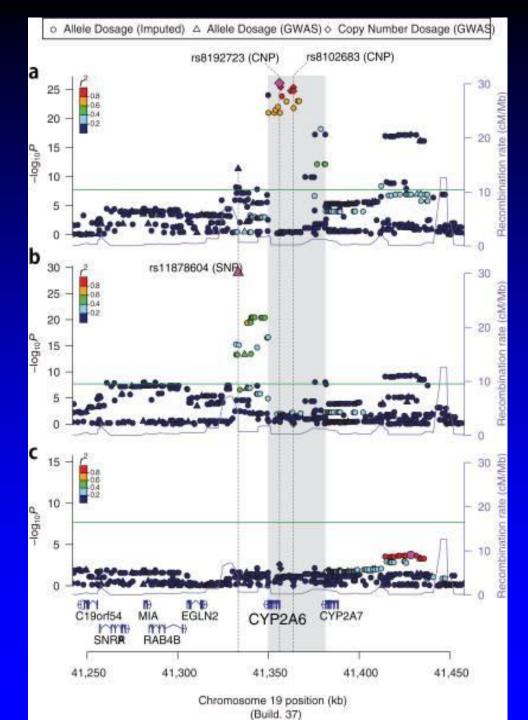
- Reduced or null activity alleles (CYP2A6*4, *9, *17, *20, *23-*27, *31, *35)
- Grouped by predicted metabolic activity



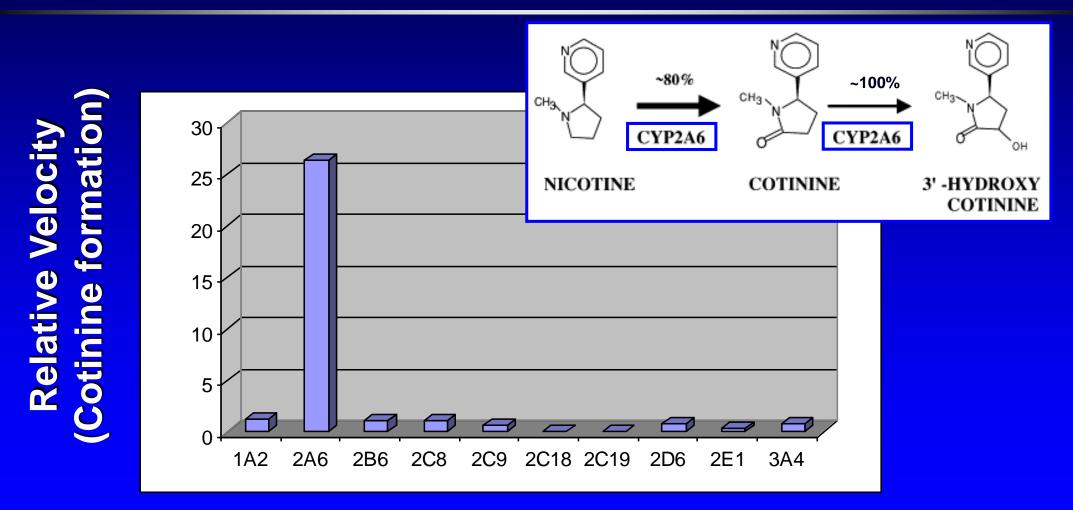
a) Before conditioning

b) After conditioning on rs8102683 (CNV)

c) After conditioning on rs8102683 and rs11878604



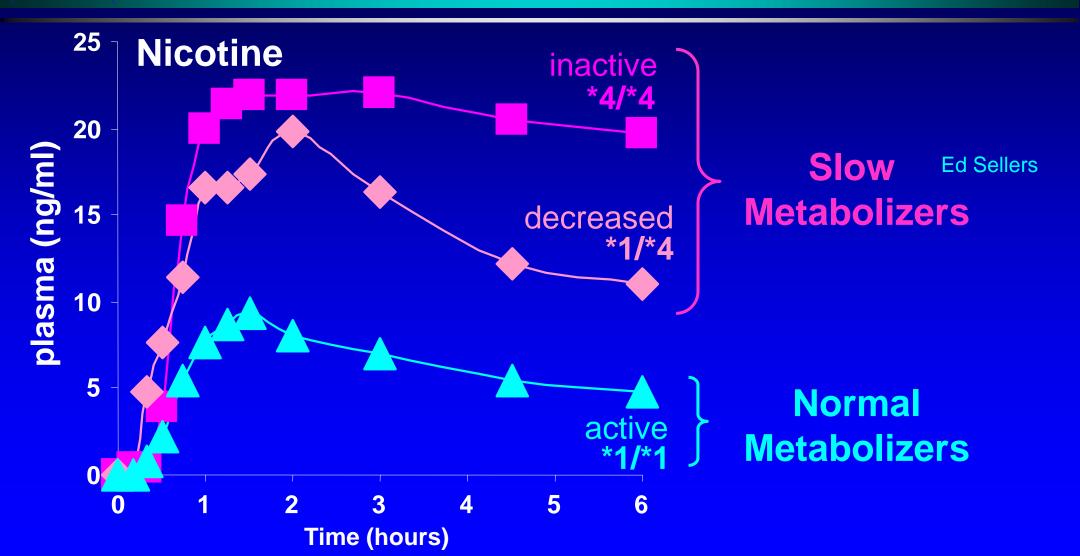
Relative Nicotine (61 μM) metabolism by Expressed CYPs (Baculovirus): CYP2A6



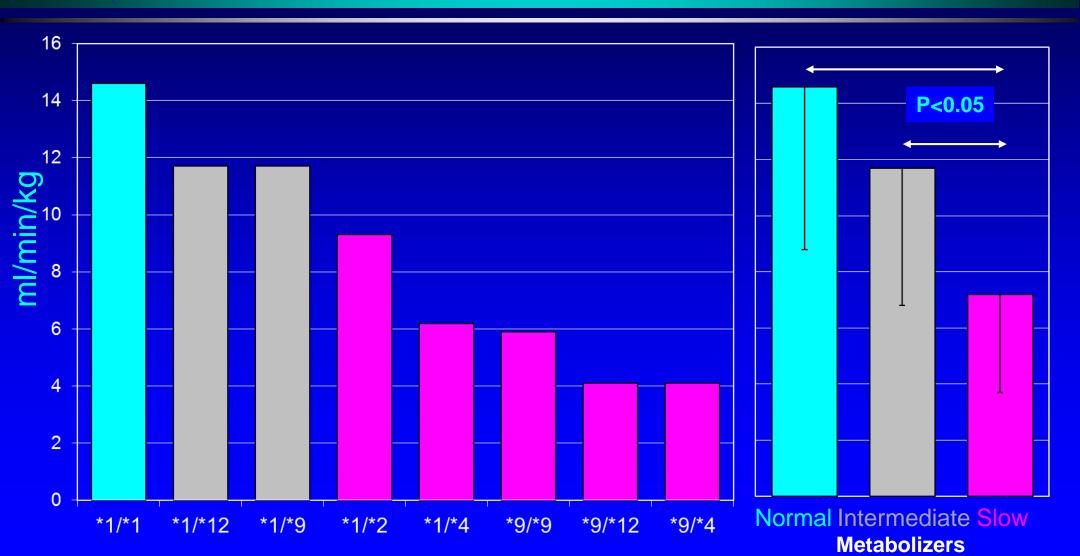
Type of CYP

Genetically Reduced CYP2A6 increases nicotine plasma levels

Nicotine 4 mg base, oral Japanese subjects



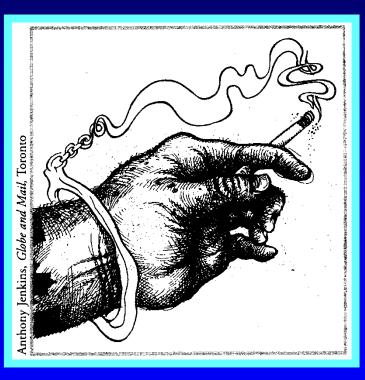
CYP2A6 Genotype: Fractional Clearance of Plasma NIC to COT (Twin NIC infusion cohort) Benowitz CPT 2006



Does slow nicotine inactivation alter the amount smoked?

Rationale:

- Dependent smokers adjust their smoking behavior to maintain nicotine levels
- ➤ Amount smoked ≈ 85% genetic
 - Koopmans JR et al, Behav Genet 29(6): 383-93., 1999.
 - Kaprio J et al, Int J Epidemiol 11(4): 378-86., 1982.

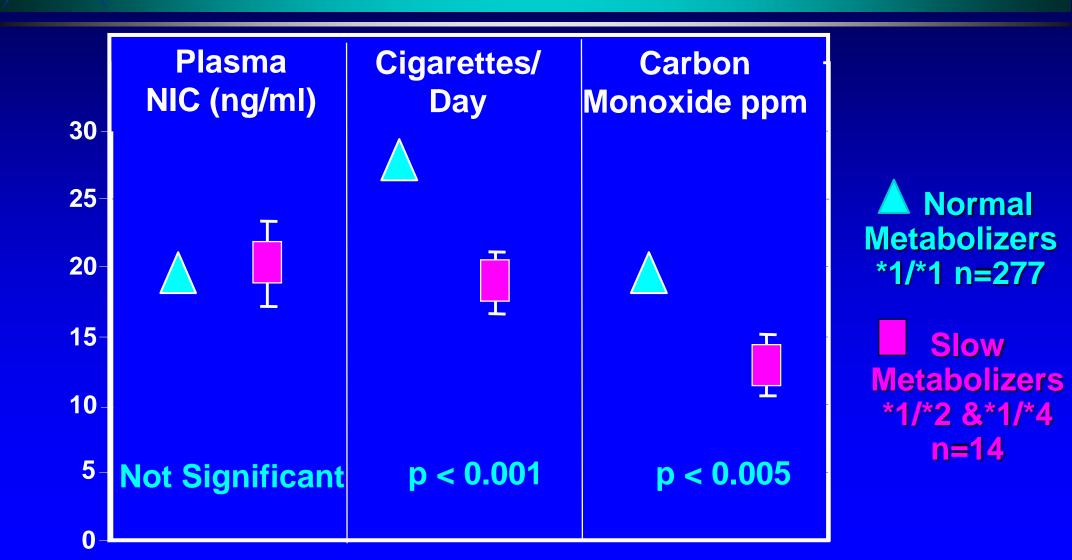


Hypothesis:

Genetically slow nicotine metabolizers who are dependent smokers will smoke fewer cigarettes per day

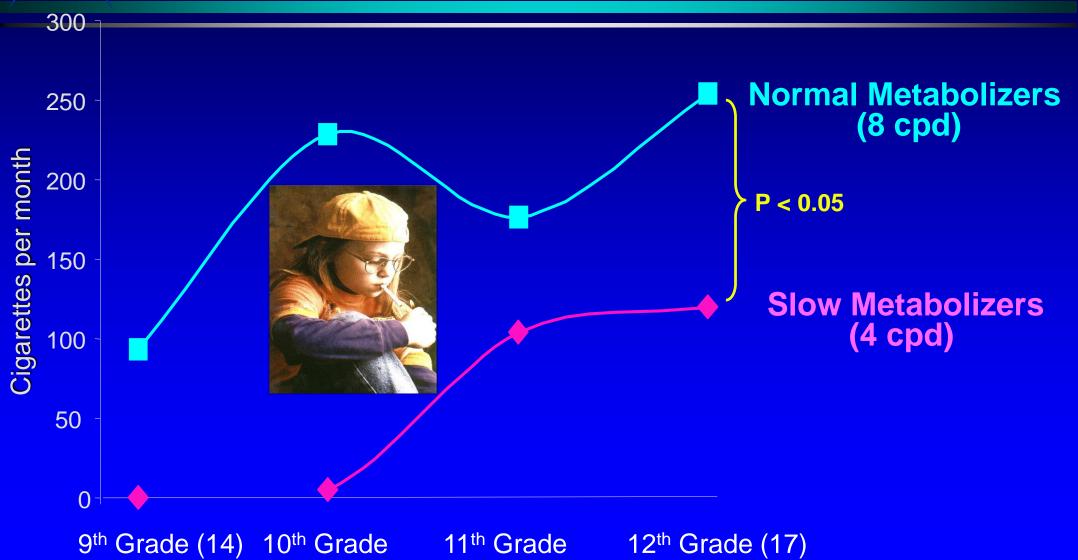
Slow metabolism decreases smoking (# of cigarettes smoked and breath CO)

Rao et al., Mol Pharm 2002



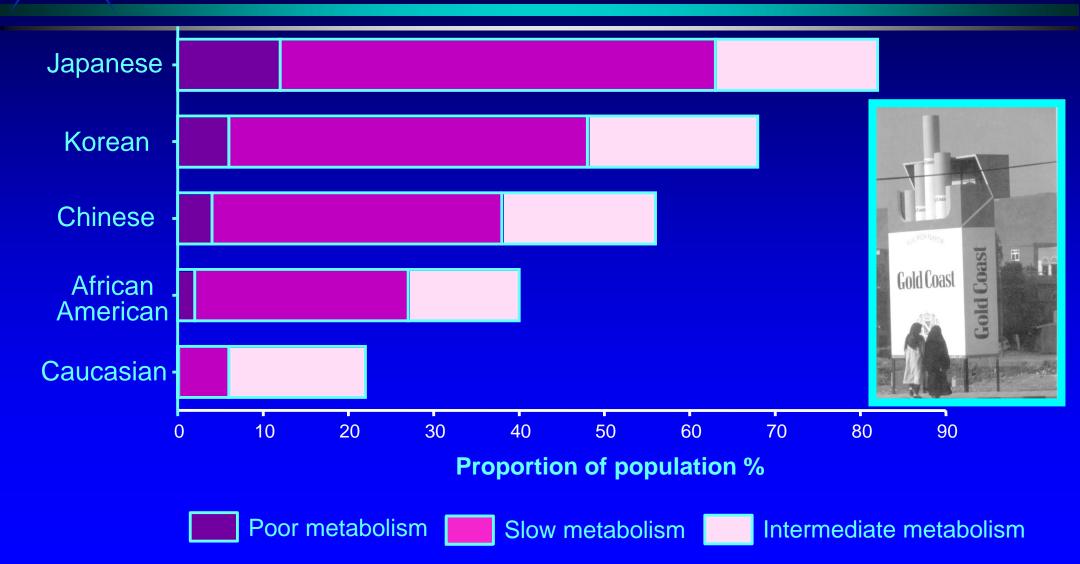
Slow metabolizers smoke fewer cigarettes, Even at very early stages of smoking

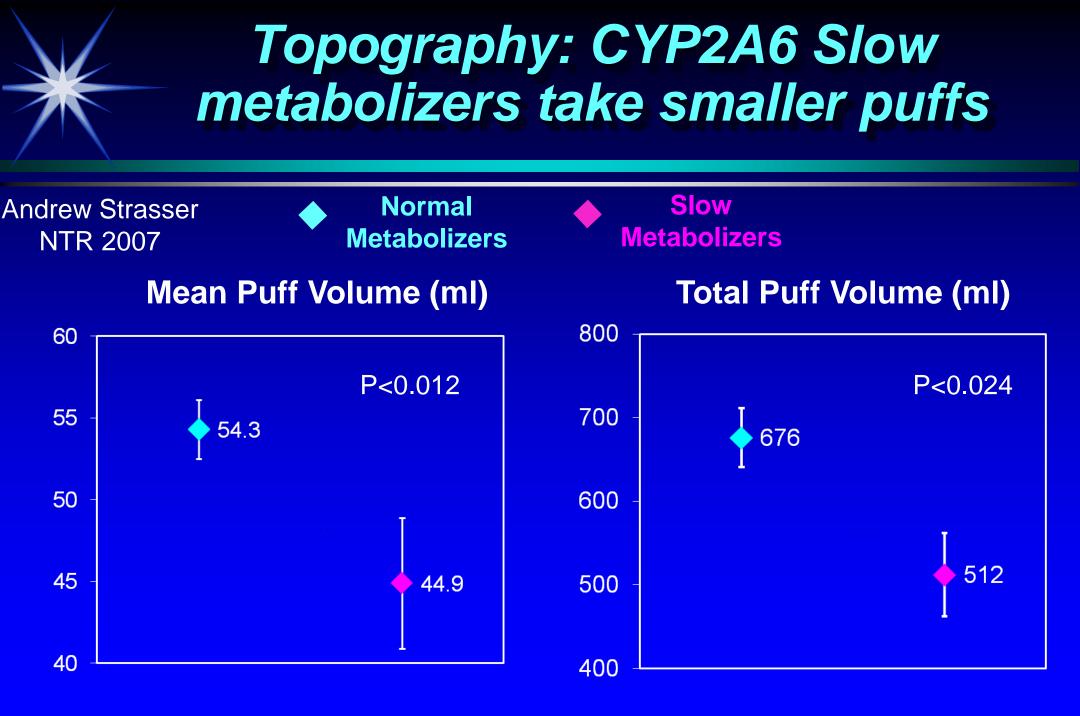
Audrain-McGovern, Pediatrics 2007



Frequencies of CYP2A6 activity groups varies among ethnic groups (*2, *4-*10,*12, *17) N=2000

Malaiyandi et al, CPT 2005; Mwenifumbo et al., PG &G 2005, DAA 2007







THE RIGHT STUFF: Personal but pricey health profiles may help doctors prescribe

DRUGS JUST FOR YOU

BUSINESS

Genetic testing can tell what drugs work best, and fastest, for whom

Pharmacogenetics of Treatment

Current treatment: low efficacy

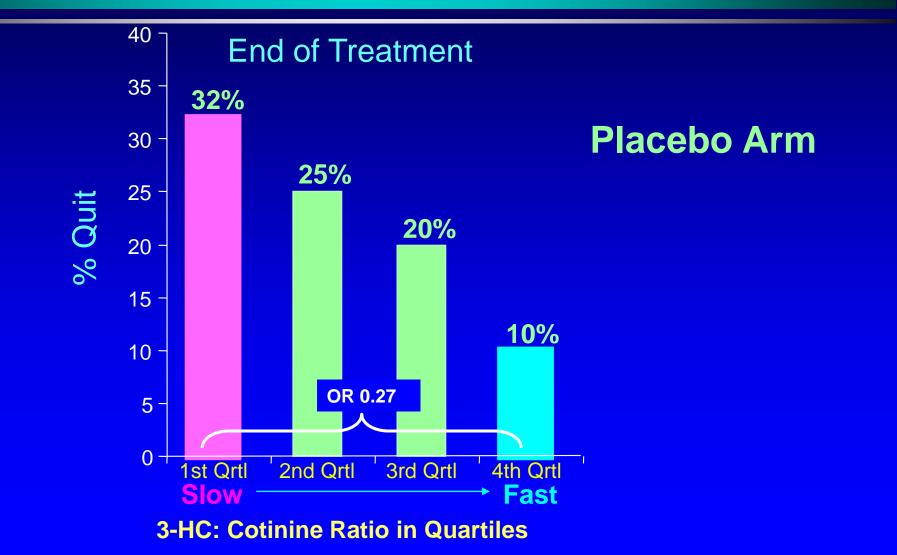
- Genetic variation in response
- Tailor medication to genetic make-up
- Discover novel targets for drug development

MacLeans Feb 18, 2008

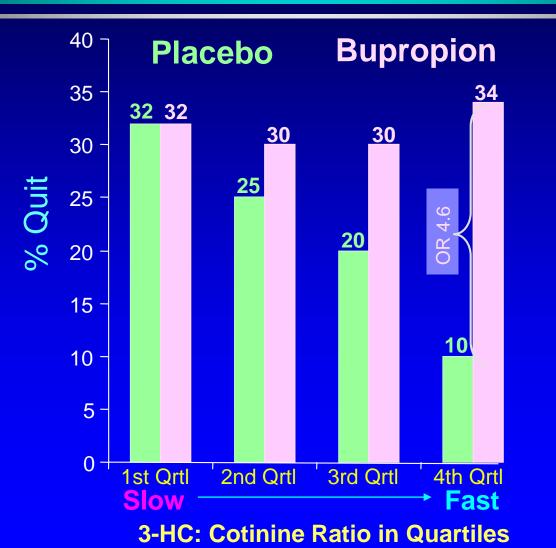
THE BEST MEDICINE THAT YOU CAN'T HAVE

Why breakthroughs in genetic testing don't help actual patients

Slow Metabolizers have better quit rates on placebo Patterson et al 2008



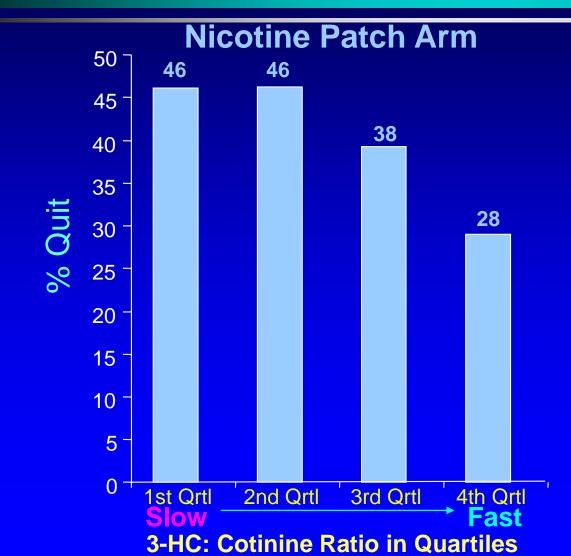
Fast Metabolizers quit poorly on placebo, but respond well to Bupropion



End of Treatment

Slow metabolizers respond well to Nicotine Patch

Lerman et al., Clin. Pharm. Ther. 2006, 2010



Replicated in multiple retrospective studies

Also looked at extended treatment

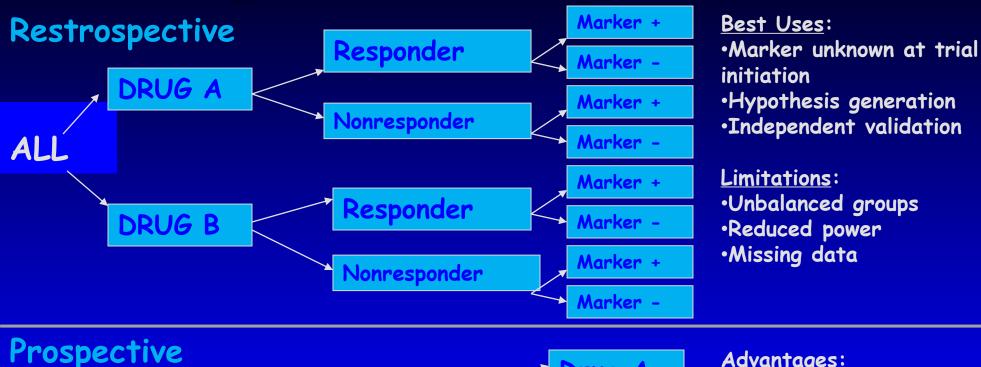
- even better for slow metabolizers
- no gain for fast metabolizers

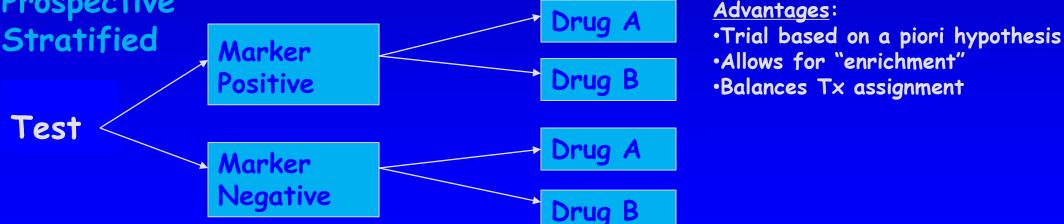
Higher dose nicotine patch (pilot)may help faster metabolizers

Identification of a reliable marker for nicotine addiction treatment

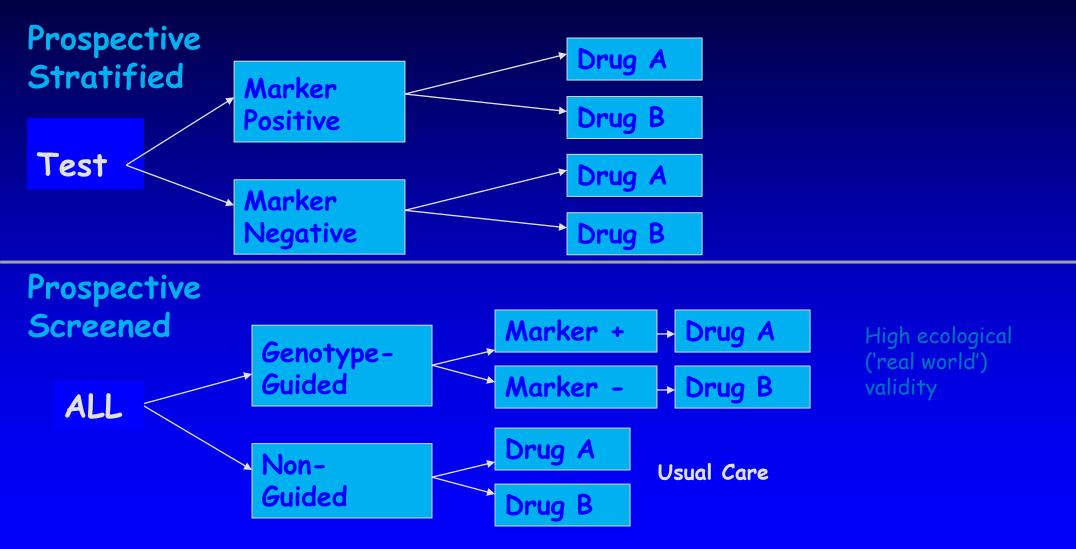
Marker development		Proof of Association		F	Proof of Efficacy and Utility			
	tine PK: tability			YP2A6/NMR		Prospective stratified clinical trial		
	CYP2A6 variants			sociations with sponse to Rx		Cost-effectiveness analysis		
	CYP2A6 & metabolism		Replication ir independent tr			Mechanistic studies		
Deve	elop functiona test-NMR	ıl	2005 2010			2010-2015 PNAT2: Clinical utility		
			2005-2010			PINATZ. Chinical utility		

Pharmacogenomic Trial Designs





Pharmacogenomic Trial Designs



True Test of Whether Personalized Medicine is Effective?

Lost in Translation?

Increase generalizability to clinical practice settings

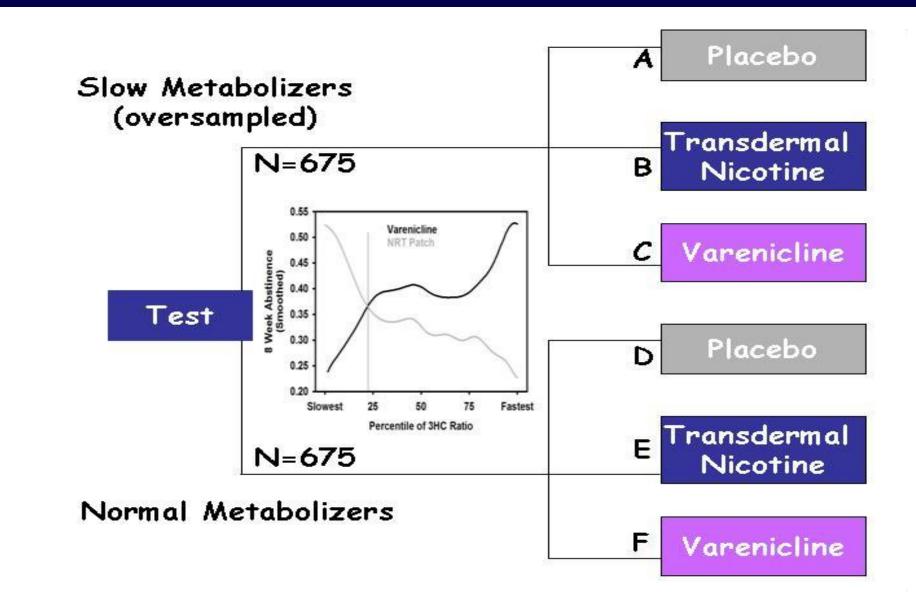
 Demonstrate improvement of health outcomes and cost-effectiveness

Establish evidence-based guidelines

Enhance adoption in clinical practice

Khoury, Genomic Medicine, 2009

Prospective Randomized Trial



Smokescreen® Genotyping Array



A platform for genetic research on smoking, addiction, and treatment approaches

<u>Summary</u>

- Genotyping array with 646,247 markers designed for studies of addiction, smoking, downstream consequences and treatment
- Developed as part of a SBIR contract with the National Institute on Drug Abuse (NIDA)
- ◄ High coverage in multiple populations (African, Asian, European)
- Available companion services by BioRealm
 - Unified quality control and analysis
 - → Software interface to results
 - Genotyping at partner labs

GAME-ON OncoArray



Common Content – 40K

Fine-mapping of common cancer susceptibility loci (*TERT*, 8q24 (proximal and distal to *MYC*), *HNF1B*, *TET2*, *RAD51B*, 11q13, *MERIT40*, *MDM4*)
Ancestry Informative Markers
Cross-Site meta analysis
Pharmacogenetic components
eQTL (Height, Weight, BMI, WHR, Menarche, Menopause etc)
Other cancers published GWAS variants
Chromosome X and mitochondrial DNA variants



Challenges in application of pharmacogenetics for smoking cessation

- Two different loci, each having multiple variants, influence smoking cessation. Genetic markers are effective for CHRNAs but serum markers may be better for characterizing CYP2A6 variation.
- Will smokers seeking to quit wait for test results before starting therapy?