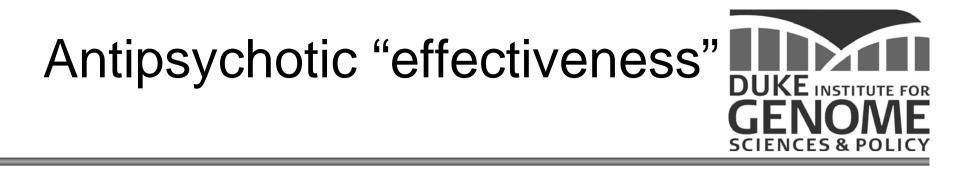


Personalized medicines: Lessons from neuropsychiatric pharmacogenetics

David Goldstein Center for Population Genomics and Pharmacogenetics Institute for Genome Sciences & Policy Duke University Medical Center



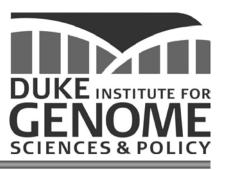
CLINICAL ANTIPSYCHOTIC TRIALS OF INTERVENTION EFFECTIVENESS

 The CATIE trial compared the effectiveness of atypical antipsychotics (olanzapine, quetiapine, risperidone, ziprasidone) with perphenazine in 1493 patients from 57 US clinical sites

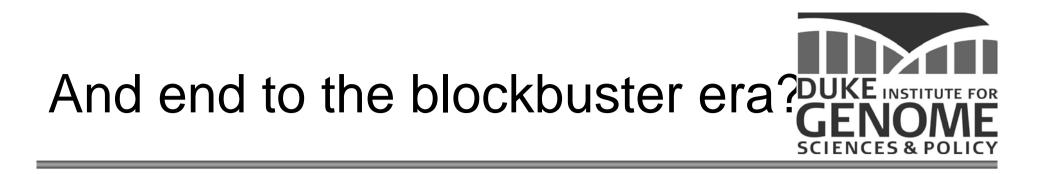
Discontinuation

64

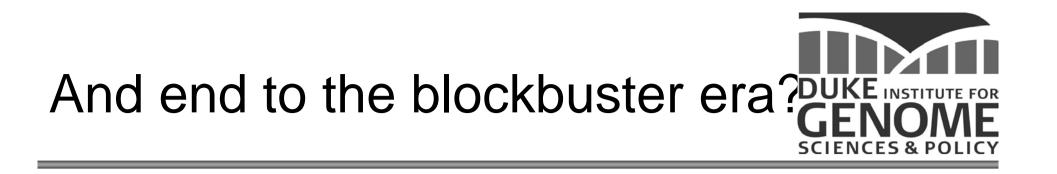
74



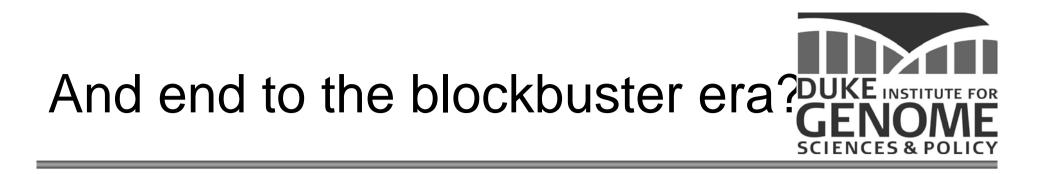
- Olanzapine
- Quetiapine 82
- Risperidone
- Ziprasidone 79
- Perphenazine 75



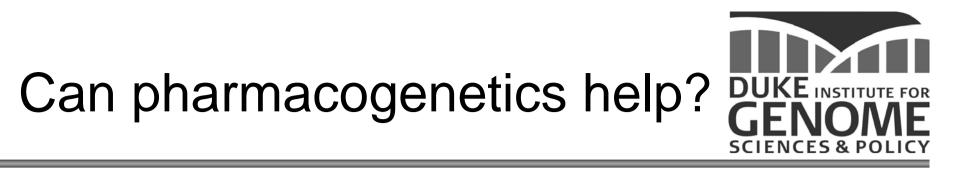
 No drug, or even drug class, is much better than the others



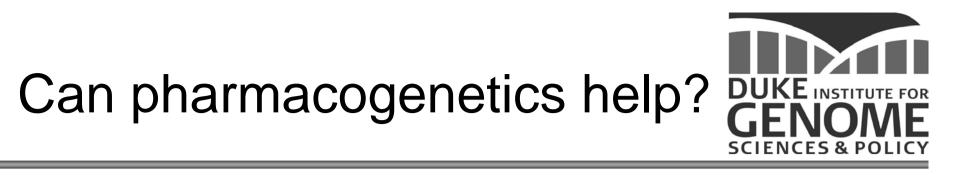
- No drug, or even drug class, is much better than the others
- Certain drugs however are much better (or worse) for certain patients



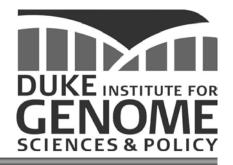
- No drug, or even drug class, is much better than the others
- Certain drugs however are much better (or worse) for certain patients
 - 30 % of patients on olanzapine increase body wt > 7%
 - Similar proportion on many of the typical antipsychotics develop TD



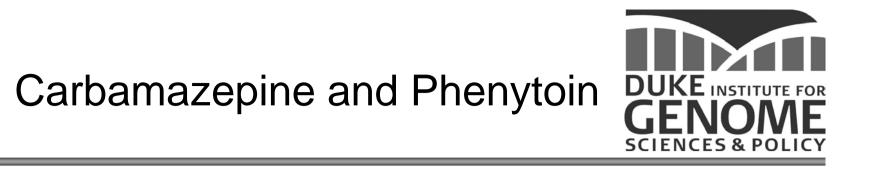
- Genetic differences may predict efficacy and sensitivity to adverse reactions and efficacy
- Genetic differences may predict appropriate doses for individual patients



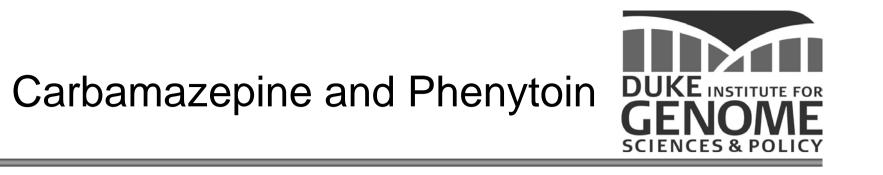
- Genetic differences may predict efficacy and sensitivity to adverse reactions and efficacy
- Genetic differences may predict appropriate doses for individual patients
- There have been no serious efforts to find such variants for the vast majority of marketed medicines



Lessons from Anti Epileptic Drugs

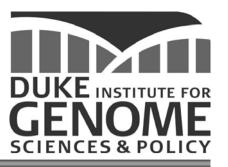


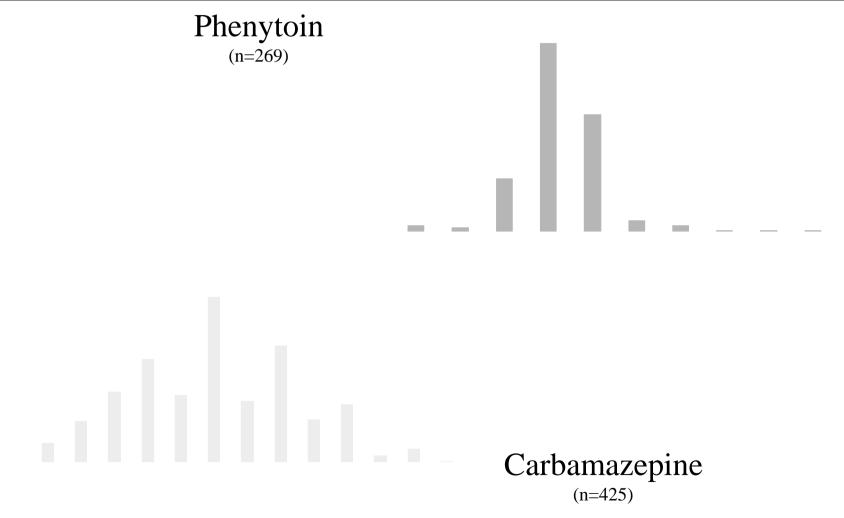
- Widely used (especially Carbamazepine)
- Inexpensive
- Effective



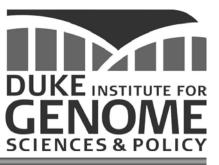
- Widely used (especially Carbamazepine)
- Inexpensive
- Effective
- Appropriate doses can take months to find

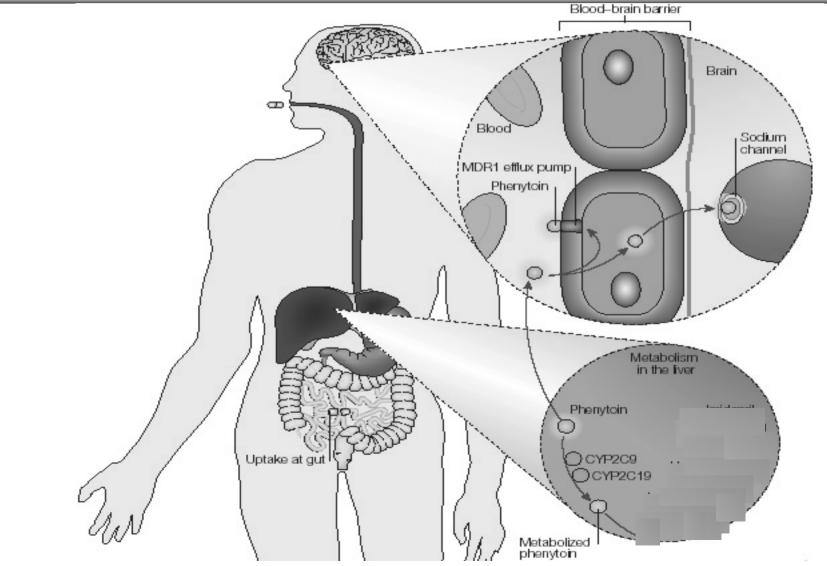
Maximum doses





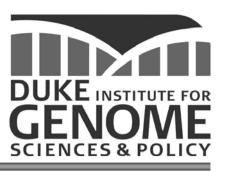
Phenytoin Pathway





Tagging SNPs

to represent common (known & unknown) variation

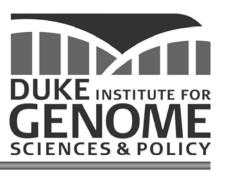


Haplotype

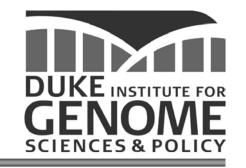
1	С	С	т	т	т	Α	С	С	С	т	т	С
2	С	С	Т	Т	Т	Α	С	С	С	Т	Α	Α
3	С	G	Т	Т	Α	G	С	G	С	Т	Т	С
4	Т	С	Т	Т	Т	Α	С	С	G	Т	Т	С
5	Т	С	Α	Α	Α	G	G	G	G	Α	Т	С
	Haploty	vne										
	Haplot	ypc	1	C	С	Т	Т	Т				
			2	C	С	Т	Т	Α				
			3	C	G	Т	Α	Т				
			4	T	С	Т	Т	Т				
			5	Т	С	Α	Α	Т				

Figure taken from: Tate, S. K. & Goldstein, D. B. Pharmacogenetics and the treatment of cardiovascular disease. *Handbook of Experimental Pharmacology: Cardiovascular Pharmacogenetics* **160**: 25-37 (2004)

Results



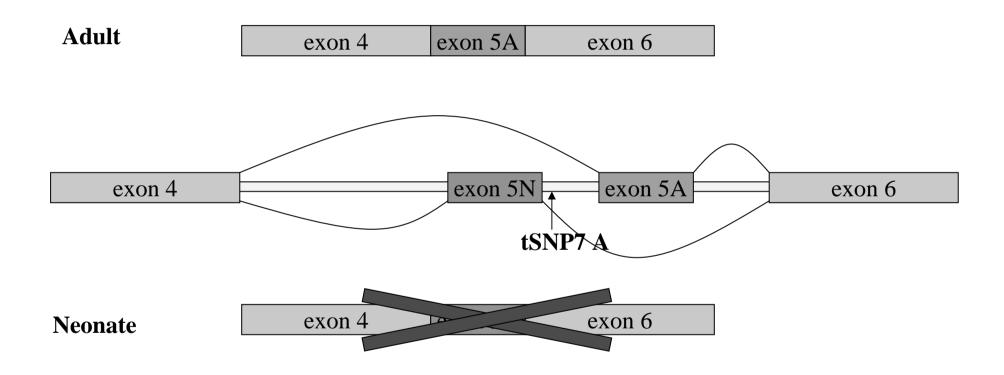
CYP2C9 Allele	Freq. (%)	Average F	Sig.		
		wt/wt	wt/var	var/var	Cigi
*2	11.9	357	339	317	0.38
*3	9.7	362	304	250	0.005



SCN1A – "tag 7"

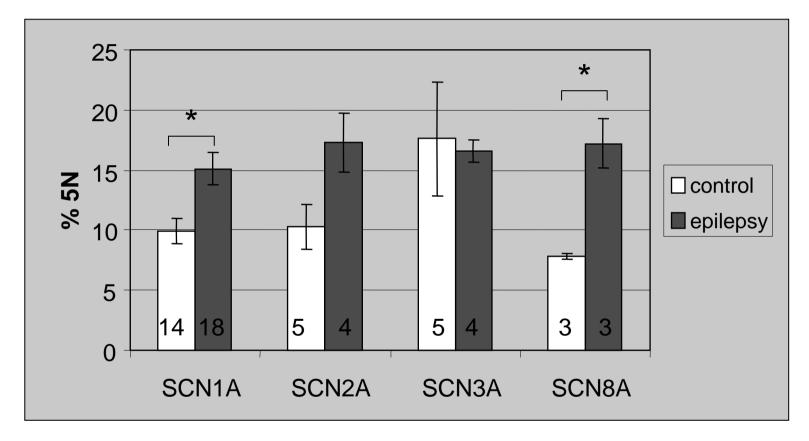
	AA	AG	GG	Significance
Phenytoin	373	340	326	p=0.005
Carbamazepine	1312	1225	1083	p=0.001

tSNP7 may affect SCN1A splicing **DUKE** INSTITUTE FOR in humans

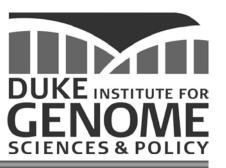


tSNP7 A = splice site disrupted, expression of exon 5N altered altered 5A/5N ratio?

Exon 5N is up-regulated in SCN genes in human epileptic tissues

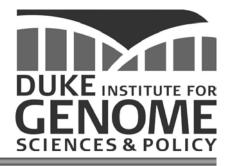


- Control RNA was purified from tissues in the Parkinson's Brain Bank
- For all but SCN1A, sample sizes are small
- SCN5A and SCN9A were not reliably detected in these tissues

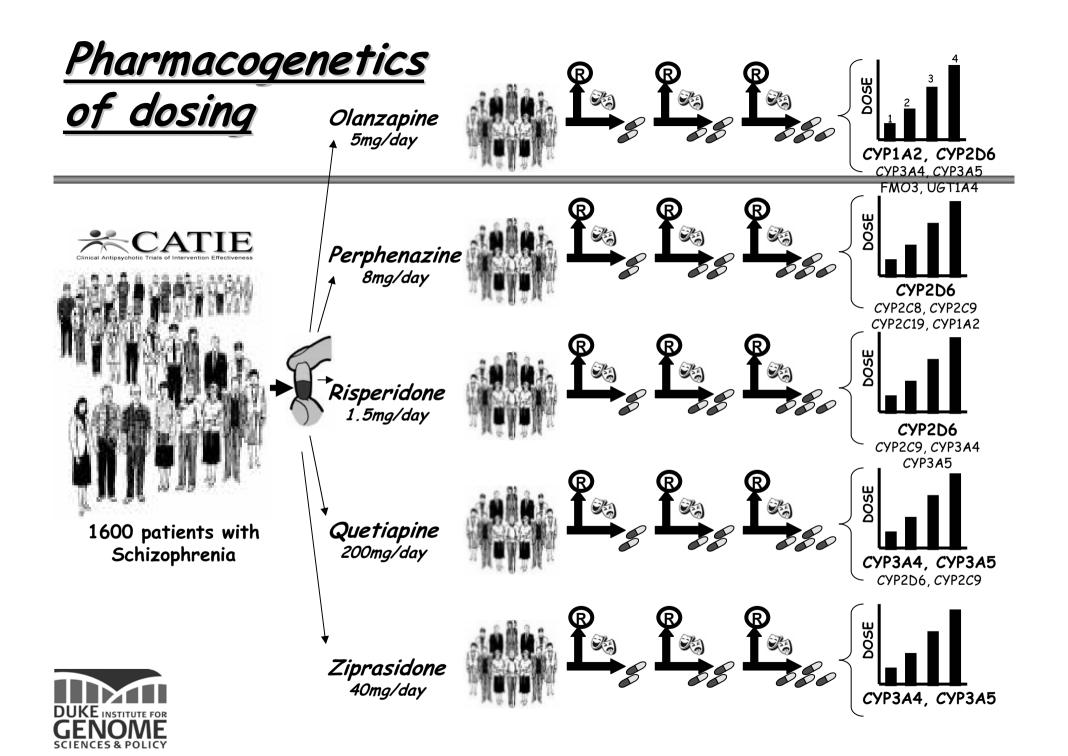


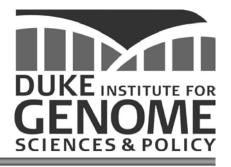
Patients Cohorts

- Standard measures of clinical responses (all aspects)
- Sufficient numbers to accommodate clinical complexity and identify variants of modest effect

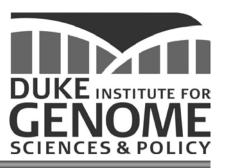


 Whenever large cohorts have been assembled, with carefully assessed drug responses measures, gene variants are identified that influence response



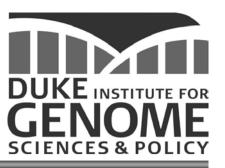


 It is reasonable to conclude that a careful pharmacogenetic study would lead to improvements in the clinical use of most medicines



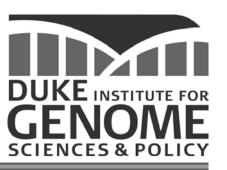
Well defined pathways providing compelling candidate genes

- Pharmacodynamics:
- Pharmacokinetics: drug metabolizing enzymes, transporters
- Genes known to affect pathways relevant to ADRs, e.g. weight gain, long QT syndrome



Systematic characterisation of candidate genes

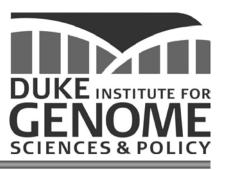
- Analyse all relevant genes in pathway, not just famous ones
- Analyse all variants in the genes, (including variation from multiple populations if sample is mixed) until knowledge permits study of only functionals
 - tagging
- Gene-gene interactions
- Gene-environment interactions



Best practise

- Stratification checks
 - Genomic control
 - Ancestry informative markers
- Replication, replication, replication
- Functional follow-up of implicated variants
 - Alternative splicing, expression, activity, abundance/ distribution of protein

Ackowledgments



Gianpierro Cavalleri Anna Need **Nicole Walley** Iris Grossman **Stephanie Schorge** Nicole Soranzo Sarah Tate Asra Siddiqui Mike Weale Ley Sander Mari Wyn Burley **Richard Marguerie** Nicholas Wood Sanjay Sisodiya

Patrick Sullivan CATIE advisory committee