

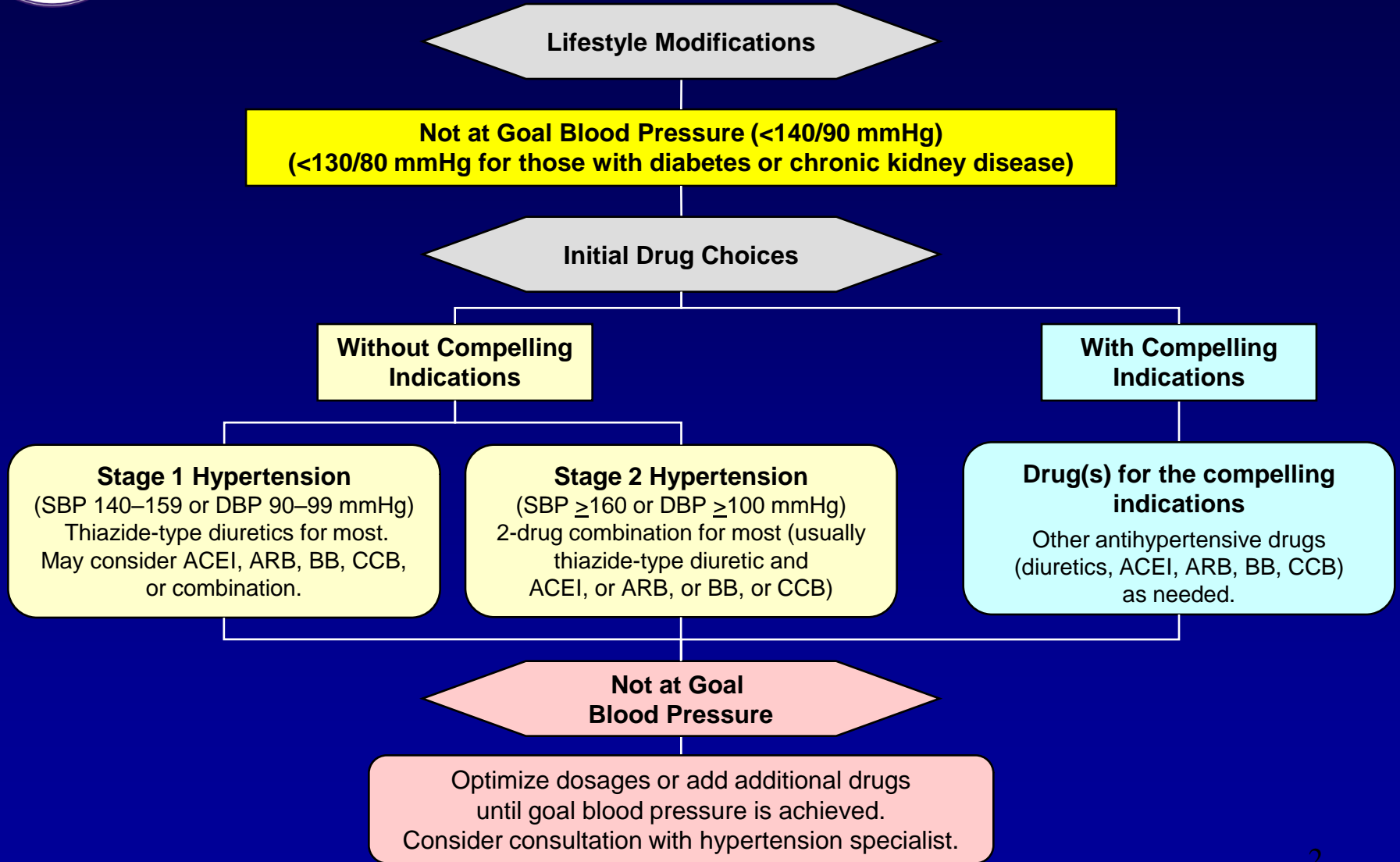
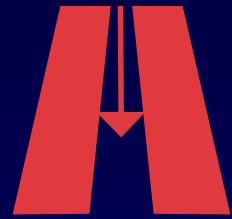


Scientific Evaluation of the Impact of Interventions Associated with Genetic Risk Factor Information

**Barry R. Davis, M.D., Ph.D.
University of Texas School of Public Health
NIH Workshop
December 17, 2008**

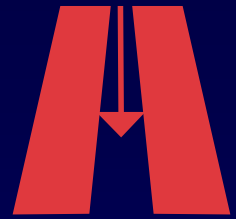


Algorithm for Treatment of Hypertension





Compelling Indications for Individual Drug Classes



Compelling Indication	Initial Therapy Option
Heart failure	THIAZ, BB, ACEI, ARB, ALDO ANT
Post myocardial infarction	BB, ACEI, ALDO ANT
High CAD Risk	THIAZ, BB, ACEI, CCB
Diabetes	THIAZ, BB, ACEI, ARB, CCB
Chronic kidney disease	ACEI, ARB
Recurrent stroke prevention	THIAZ, ACEI

Pharmacogenetics

Can we use genetics to guide antihypertensive therapy?

Pharmacogenetic approaches to hypertension therapy: design and rationale for the Genetics of Hypertension Associated Treatment (GenHAT) study

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ABSTRACT

The **Genetics of Hypertension Associated Treatment (GenHAT)** study will determine whether variants in hypertension susceptibility genes interact with antihypertensive medication to modify coronary heart disease (CHD) risk in hypertensives. GenHAT is an ancillary study of the Antihypertensive and Lipid Lowering Treatment to Prevent Heart Attack Trial, ALLHAT, a double-blind, randomized trial of 42 418 hypertensives, 55 years of age or older, with systolic or diastolic hypertension and one or more risk factors for

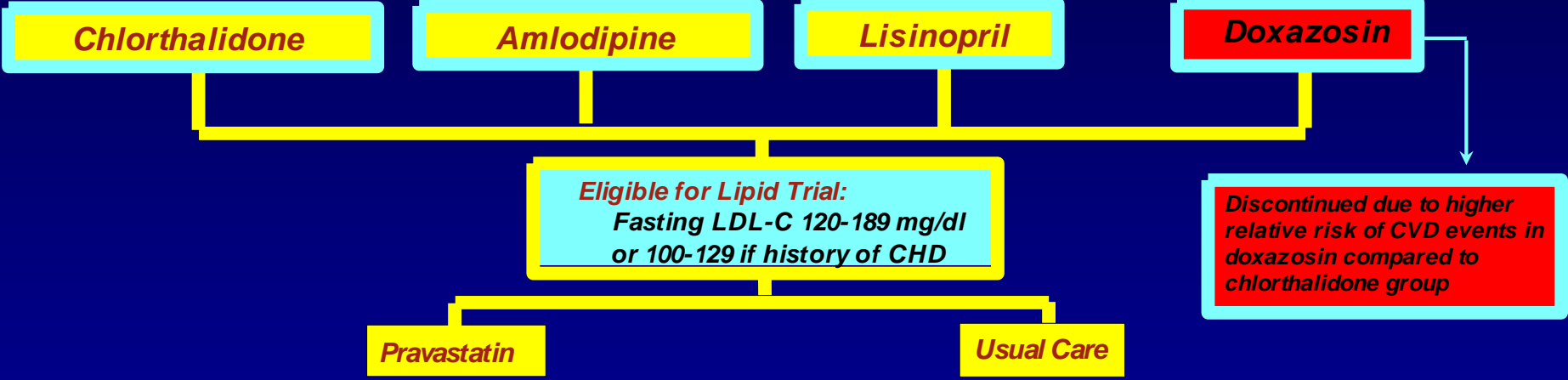
Antihypertensive and Lipid-Lowering Treatment to Prevent Heart Attack Trial (ALLHAT)



Eligible for BP trial:
Hypertension
>55 years
At least 1 other CVD risk factor →

H/O MI or Stroke
Revascularization procedure
Major ST depression/T wave inversion
ASCVD
Type II Diabetes Mellitus
HDL < 35 mg/dl X2
LVH
Current smoker

42,418 Eligible Participants Enrolled & Randomized to 5 years of Double-Blind Treatment



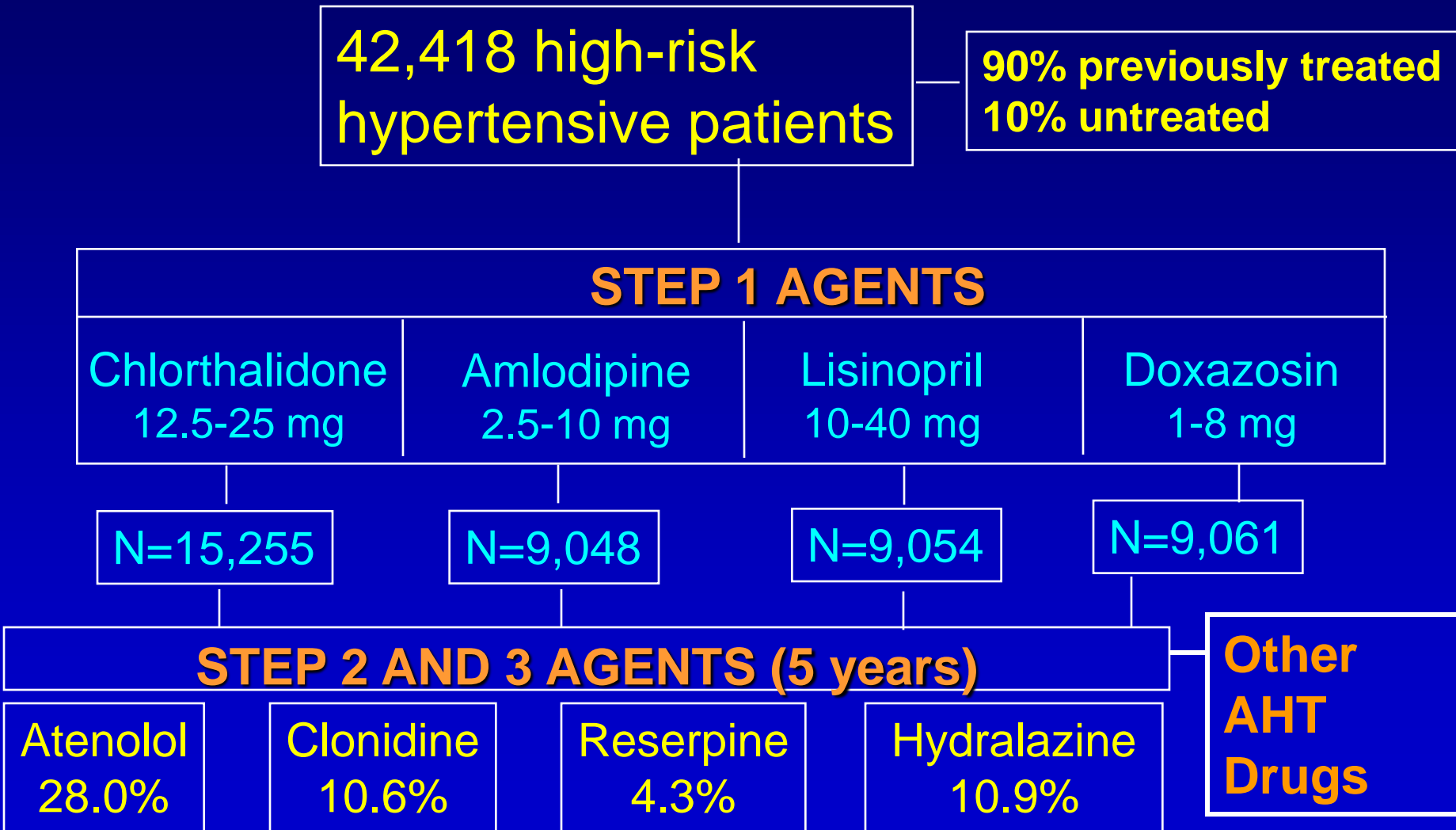
BP Trial Primary End Points:
-Fatal CHD & Non-Fatal MI
BP Trial Secondary End Points:
-All-cause mortality
-Stroke

Predefined Subgroups
-Age (<65 y; 65+y)
-Gender
-Race (Black; Non-Black)
-Diabetes (Diabetic; Non-Diabetic)

-Combined CHD – Fatal CHD, non-fatal MI, coronary revascularization, hospitalized angina
-Combined CVD – combined CHD, stroke, lower extremity revascularization, treated angina, fatal / hospitalized / treated heart failure (HF), hospitalized or outpatient peripheral arterial disease (PAD)
-Other – renal (reciprocal serum creatinine, ESRD, estimated GFR) and cancer



Randomized Design of ALLHAT Hypertension Trial





Genetics of Hypertension Associated Treatment

- **GenHAT is ancillary pharmacogenetics study**
- **ALLHAT, randomized double-blind active-controlled, clinical outcome trial conducted between 2/94 – 3/02**
- **42,418 hypertensive patients (47% female, 36% Black), 55+ years old with 1+ CHD risk factors.**
- **Mean follow-up of 4.9 years**
- **DNA isolated from stored blood clots**
- **39, 144 available for genetic analysis**

- Isolate DNA
- Punch 1.5 mm disk, purify
- Amplify DNA
 - Negative control (water)
- Anonymize samples
- Genotype testing
 - includes known control samples
 - “no template” reaction (monitor contamination)
 - blind duplicates

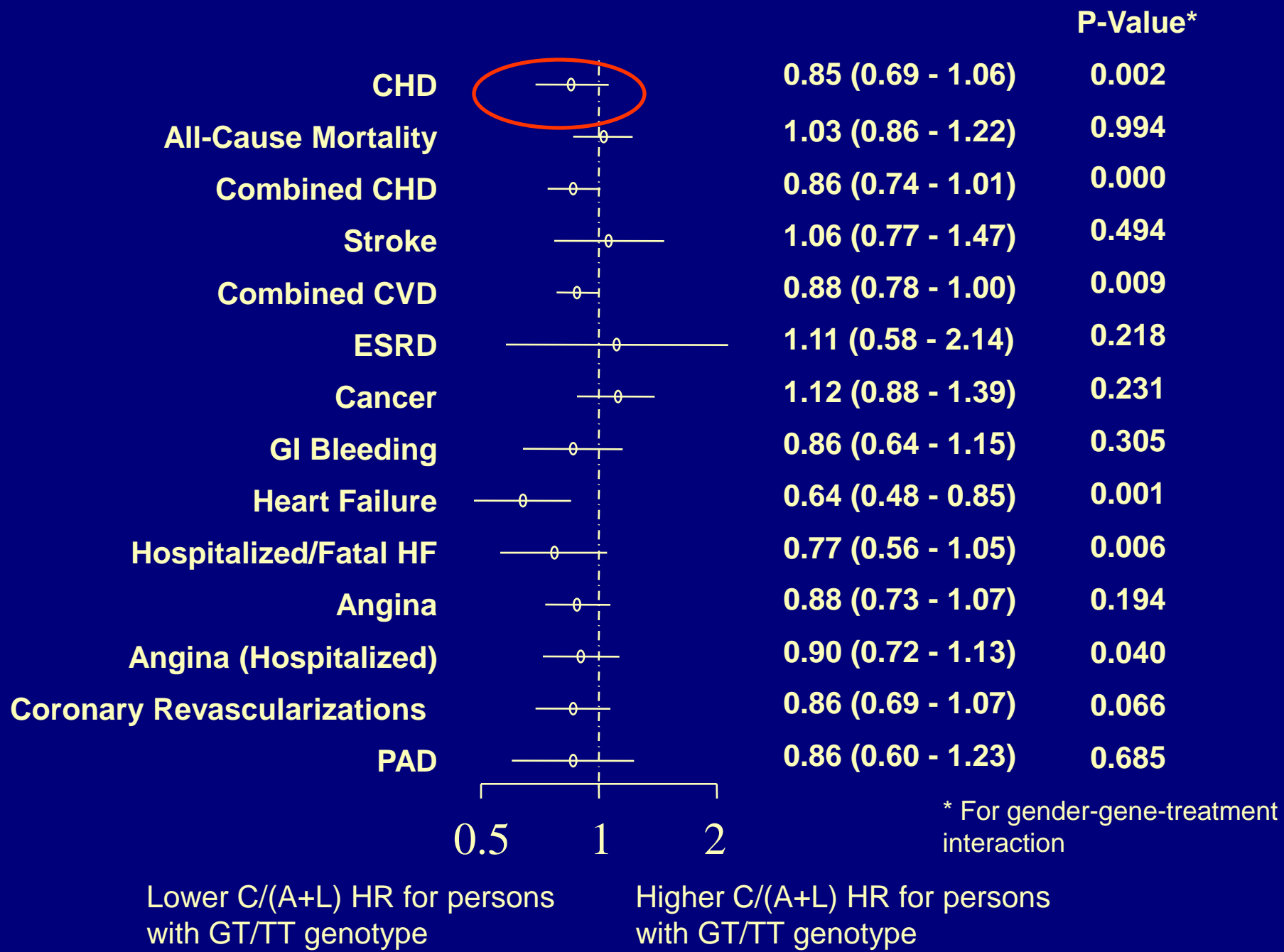
α -adducin gene

- **A genetic variant in α -adducin has been associated with renal sodium reabsorption and salt-sensitive hypertension**
- **Whether this genetic variant modifies the effect of diuretic therapy on the incidence of myocardial infarction (MI) and stroke is unknown.**

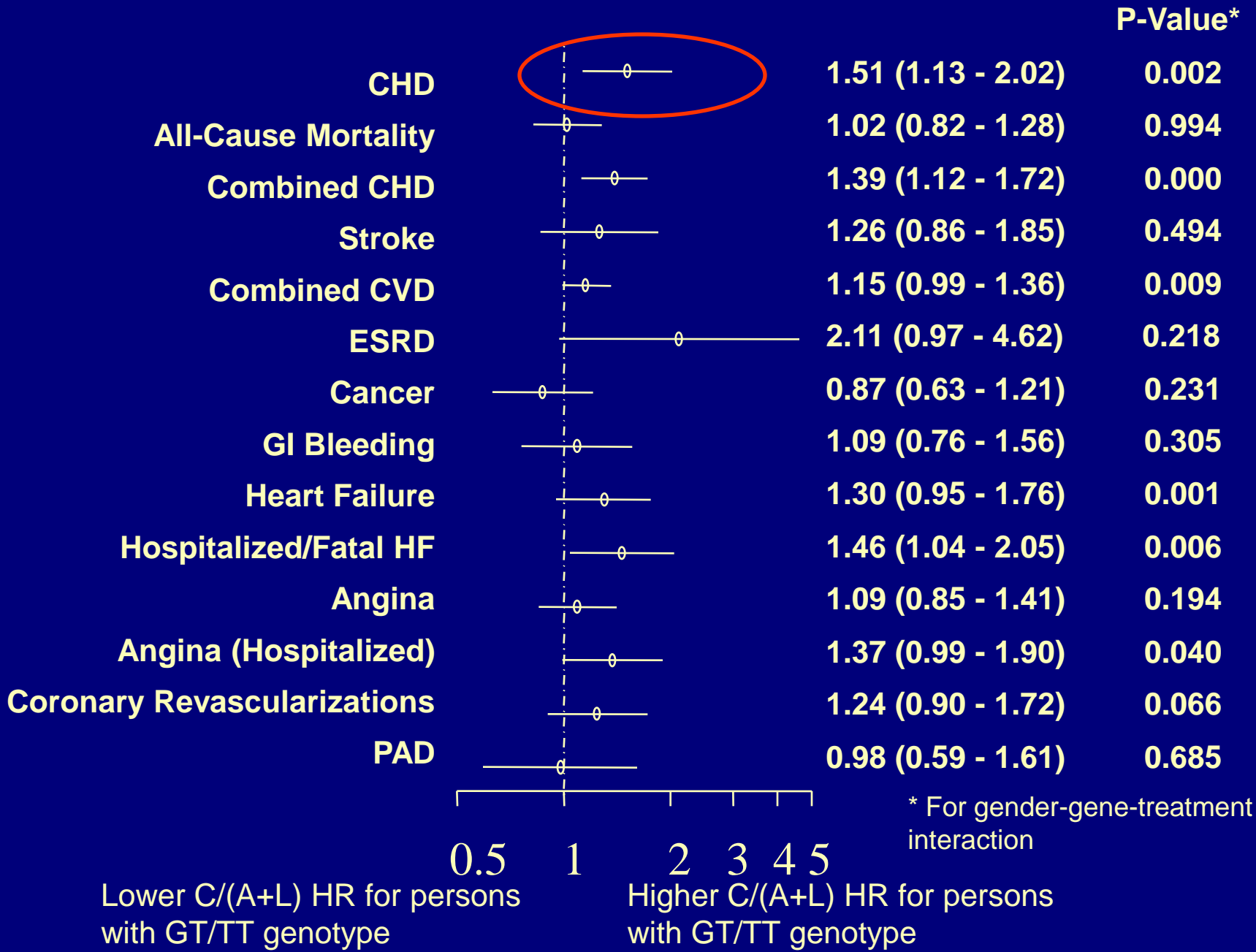
Davis BR, Arnett DK, Boerwinkle E et al.

The Pharmacogenomics Journal 2007; 7:112-122

Gene-Treatment Interactions in Men



Gene-Treatment Interactions in Women



Conclusions

- The α -adducin Gly460Trp polymorphism is not an important modifier of antihypertensive treatment on CV risk.
- Results suggest women Trp460 carriers may have increased CDH risk if treated with C vs. A+L.
- This finding needs to be confirmed in other studies to have implications for hypertension treatment.



ACE Insertion-Deletion (ID) Gene

Common variation in the gene that encodes the angiotensin converting enzyme is defined by the insertion(I) or deletion(D) of 287 bp of nonsense DNA in intron 16 resulting in 3 genotypes (DD, ID, II). The ACE I/D polymorphism can result in different levels of ACE activity.

Arnett DK, Davis BR, Boerwinkle E, et al.
Circulation 2005; 111:3374-3383.

Gene-Treatment Interactions for Clinical Outcomes (Interaction Hazard Ratios)

	L vs. C+A	L vs. C	L vs. A	L vs. D
CHD	1.04	1.06	1.00	0.84
Total mortality	0.99	0.99	0.98	0.89
Combined CHD	1.00	0.99	1.02	0.90
Stroke	0.93	0.96	0.87	1.02
Combined CVD	0.99	0.99	1.00	1.03
ESRD	1.08	1.16	0.97	0.90
Heart failure	0.91	0.89	0.94	0.94

There were no significant gene-treatment interactions for any of the clinical outcomes.

GenHAT Conclusions

- The association between type of antihypertensive medication and CHD or other major ALLHAT secondary outcomes (total mortality, combined CVD, HF, etc.) in high-risk hypertensives does not differ across genotypes of the ACE I/D polymorphism



NPPA T2238C Gene

- The *NPPA* gene encodes the precursor from which atrial natriuretic polypeptide (ANP) is derived.
- ANP acts as a diuretic in that it controls extracellular fluid volume and electrolyte homeostasis.
- Given the diuretic action of ANP, it is possible that individuals with a "high risk" phenotype (minor C allele of *NPPA T2238C* → impaired production of ANP) might have more favorable outcomes with a diuretic than other antihypertensive drug classes.

Lynch AI, Davis BR, Boerwinkle E, et al.
JAMA 2008; 299: 296-307

Genotype (NPPA T2238C) x Treatment Interaction Results – CHL vs AML HRs by Genotype for Clinical Outcomes

	CHD	Stroke	All-Cause Mortality
TT	1.09	1.26	1.12
TC	0.90	0.82	0.98
CC	0.86	1.18	0.87
P value for interaction	.03	0.01	0.05



Conclusions

- The NPPA T2238C variant was associated with modification of antihypertensive medication effects on cardiovascular disease and BP.
- Minor C allele carriers experienced more favorable outcomes (CHD, stroke, mortality) on a diuretic (vs. calcium channel blocker), whereas TT allele carriers had more favorable outcomes on a calcium channel blocker (vs. diuretic).

Genetic Variants Included in Gene Panel Predicting CHD Risk Score in GenHAT

Chlorthalidone

NOS3 -690

AGT -6

ICAM1 *gly214agr*

SELE *ser128agr*

Amlodipine

MMP1 -1607

F5 *arg506gln*

NPPA T2238C

PDE4D SNP3

PON1 -108

MMP9 R668Q

Lisinopril

PAI1 -675

AGT -6

PON1 -108

MMP12 N122S



Conclusions

- The pharmacogenetic study of complex disease phenotypes such as hypertension and its sequelae is illustrated by GenHAT
- There are logistical demands
 - tens of thousands of participants
 - long-term follow-up
 - multiple outcome phenotypes
 - subgroup analysis
- But there is the potential of identifying clinically useful genetic markers



Conclusions

- **May not have immediate clinical implications**
- **It moves us along the path toward individualized treatment guided by genetics**
- **Given the leap from pharmacogenetic knowledge to clinical practice, it is essential that**
 - **findings such as those in GenHAT be replicated**
 - **gene x gene and gene x environment interactions be thoroughly explored**
 - **cost-benefit analyses be conducted**