# NIDDK

## Genomic Opportunities for Studying Sickle Cell Disease

#### Griffin P. Rodgers, M.D., M.A.C.P. Director

National Institute of Diabetes and Digestive and Kidney Diseases

December 8-9, 2011

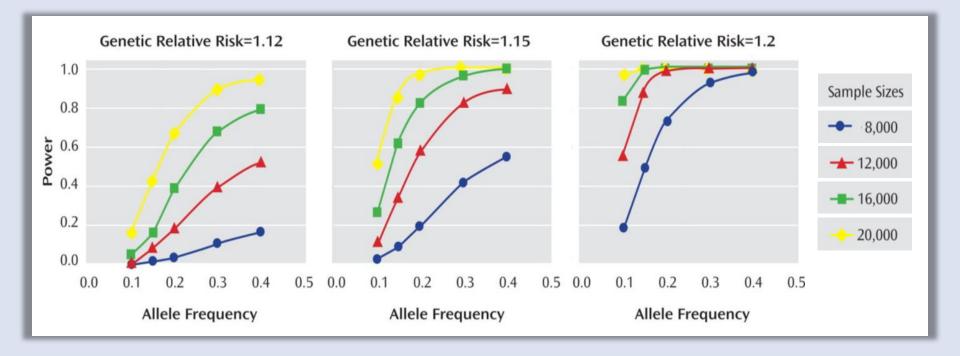




### Finding Modifier Genes for Single Gene Traits May Require Large Cohorts

The study of modifier genes is crucial to understanding why patients with the same mutation often have widely varying clinical courses, as in SCD.

As with all complex traits, having a large sample size is crucial to find lower frequency alleles with modest effects.







American Journal of Psychiatry 166: 540-556, 2009.

## Large Cohorts in GWAS

There are several NIDDK consortia assembling large cohorts for important GWAS studies, including some with recent successes:

Type 1 Diabetes Genetics Consortium (T1DGC)

> 7,514 cases and 9,045 controls

Inflammatory Bowel Disease (IBD) Genetics Consortium

➤ 3,230 cases and 4,829 controls

Chronic Kidney Disease (CKDGen)

67,093 individuals including 5,807 individuals with CKD

Kidney disease in Type 1 Diabetics (GENIE)

➤ 1,726 cases





## **Lessons Learned**

Assembling large cohorts is difficult, especially if it involves aggregating existing collections. It is very important to consider:

Phenotype(s)

Finding the right phenotype is critical for gene discovery

Logistical challenges

Availability of samples and data in usable and sharable forms
Ethical challenges

Consents and IRB approvals may differ widely among cohorts
Resource building

How can the collection remain useful for subsequent analyses?





The importance of the initiative being planned is that it aims to identify new genes that play a role in the clinical manifestations of SCD.

The NIDDK looks forward to helping support the difficult follow-on work that will investigate each new gene of interest in the context of normal and SCD physiology.





#### NATIONAL INSTITUTE OF **DIABETES AND DIGESTIVE** AND KIDNEY DISEASES

AND KIDNEY DISEASES





