New gene variant identified for nondiabetic end stage renal disease in African-Americans

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Scientists at Johns Hopkins schools of Public Health and Medicine have, for the first time, identified variants in the gene MYH9 that are associated with increased risk for non-diabetic end stage renal disease (ESRD,) which is the near-loss of kidney function leading to either dialysis of transplant. MYH9, located on the 22 chromosome, is the first gene identified for common forms of kidney disease. The study was published online September 14 in the journal *Nature Genetics* and will be published in the October print edition. In a separate study published in the same issue, researchers at the National Institutes of Health reported similar findings.

In the United States, about 26 million Americans have chronic kidney disease with nearly 427,000 Americans requiring dialysis or kidney transplant each year for the treatment of ESRD, according to U.S. government studies. African Americans are affected disproportionately as they have a four-times-higher incidence of end stage renal disease compared to European Americans.

"We are in the midst of an epidemic of chronic kidney disease, in which African Americans are disproportionately affected. This finding does not mean that non-genetic factors, such as socioeconomic indicators and other factors do not contribute to the higher risk of kidney disease in African Americans. It defines a subset of persons most likely vulnerable to the harmful effect of these factors," said study author Michael J. Klag, MD, MPH, dean of the Johns Hopkins Bloomberg School of Public Health.

"Our results show that in addition to environmental and behavioral risk factors, genetic factors play a role as well," said lead author, Linda Kao, PhD, MHS, associate professor in Bloomberg School of Public Health's Department of Epidemiology and the Welch Center for Prevention, Epidemiology and Clinical Research.

"While we know these genetic variations are common among African Americans, not everyone with the variations has disease and not everyone with disease has the variations. Therefore, it is imperative that we understand what other modifiable risk factors are interacting with the genetic risk factors to cause disease."

For the study, researchers used a technique known as admixture mapping to survey genomes of 1,372 African Americans with ESRD and a control group of about 800 African Americans without ESRD. The study identified several alleles, or variations, in the MYH9 gene that were highly associated with non-diabetic ESRD but not diabetic ESRD. These variants were not associated with diabetic ESRD. Even though the variations identified in this study are present in many populations, they are more frequent among individuals with West African ancestry.

"This finding suggests that the mechanisms leading from onset of chronic kidney disease to kidney failure may differ based on the inciting cause," said study author Rulan S. Parekh, MD, associate professor Johns Hopkins School of Medicine and the Welch Center. "Discovery of the gene and its association with kidney disease will lead to future studies to better understand the biology of kidney disease progression and ultimately may direct drug therapy and potential screening of patients."

Source: Johns Hopkins University