MedicalXpress

New genes linked to gout

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Researchers have identified two new genes – and confirmed the role of a third gene – associated with increased risk of higher levels of uric acid in the blood, which can lead to gout, a common, painful form of arthritis. Combined, the three genetic variations were associated with up to a 40-fold increased risk in developing gout. The findings suggest that genetic testing could one day be used to identify individuals at risk for gout before symptoms develop, as well as determine who might benefit from medications to prevent the development of gout.

"Association of three Genetic Loci with Uric Acid Levels and Gout Risk," is published online in *The Lancet* September 30. The study was supported by the National Heart, Lung, and Blood Institute (NHLBI) of the National Institutes of Health (NIH) and the Netherlands organization for scientific research (NWO). Additional support from the NIH's National Center for Research Resources and through the NIH Roadmap for Medical Research was provided.

The genes were identified using data from two large genome-wide association studies – genetic variations of nearly 7,700 participants from NHLBI's Framingham Heart Study SHARe (SNP Health Association Resource) and more than 4,100 participants in NWO's Rotterdam Study. Researchers then replicated their finding using data from nearly 14,900 participants in NHLBI's Atherosclerosis Risk in Communities Study (ARIC).

Caroline S. Fox, M.D MPH, NHLBI project officer and one of the senior authors of the study, is available to comment on these findings.

Christopher J. O'Donnell, M.D., MPH, scientific director of SHARe and senior advisor to the NHLBI director for genetics and genomics, is also available for interviews.

Nearly 3 million adults in the United States are estimated to have gout. Gout can develop when excess amounts of uric acid build up in the blood and form crystals, which accumulate in the joints causing swelling and pain. Left untreated over time, gout can permanently damage affected joints and, possibly, the kidneys.

The findings are the first published results of analyses of data from Framingham SHARe since the extensive Web-based dataset of genetic and clinical data was made freely available to researchers worldwide in October 2007. Framingham SHARe includes data on more than 9,300 participants spanning three generations. The Framingham Heart Study is funded by NHLBI in collaboration with Boston University School of Medicine (BUSM) and Boston University School of Public Health.

Source: NIH/National Heart, Lung and Blood Institute