

co-ordinated with the Director of the Institute / Research Unit

Institute of Computational Biology

PSP-Element:

G-503800-001

Person to contact for further enquiries:

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Title of the highlight:

Genome-wide association analyses identify 18 new loci associated with serum urate concentrations

Keywords:

GWAS, urate, gout, metabolomics

Central statement of the highlight in one sentence:

This GWAS on a combined set of population cohorts (>140,000 individuals) identified new genetic loci associated with serum urate, and possible implications for gout.

Text of the highlight:

This study combined samples from a series of different population cohorts, resulting in a total of over 140,000 individuals to study the influence of common genetic variants on serum urate levels. In this genome-wide association study (GWAS), we identified 18 novel regions that displayed a significant effect on urate. Moreover, the effect of the identified loci on the development of gout was investigated. Using network analysis, we identified the inhibin-activin pathway as well as glucose metabolism to be specifically involved in serum urate control. The results may have implications for the treatment and prevention of gout through future studies.

Publication:

Köttgen et al.. Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, 45(2):145-54, 2013

Taking account of the HMGU mission:

Determining the genetic influence on risk factors like urate and, subsequently, on widely spread disease like gout lays the basis to understand and eventually treat the disease. The project fits into the series of other projects at the HMGU that deal with metabolic diseases.

The internal HMGU co-operation partners with whom the highlight was compiled, if appropriate:

Eva Albrecht, Christian Gieger: IGE