IN BRIEF

GENETICS

The genetic contribution to blood pressure variation is largely unexplained. Now, however, two genome-wide association studies of systolic and diastolic blood pressure and hypertension published in *Nature Genetics* have identified multiple loci associated with interindividual blood pressure variation. The identification of these genes will help improve our understanding of the regulation of blood pressure. The findings might also be useful for the development of novel treatments and for identifying individuals at high risk of hypertension.

Original articles Levy, D. *et al.* Genome-wide association study of blood pressure and hypertension. *Nat. Genet.* doi:10.1038/ng.384 (2009). Newton-Cheh, C. *et al.* Genome-wide association study identifies eight loci associated with blood pressure. *Nat. Genet.* doi:10.1038/ng.361 (2009).

GENETICS

Although several studies have indicated a genetic component to kidney disease, common variants associated with susceptibility to chronic kidney disease have been difficult to detect. Using genome-wide association studies among participants of four population-based cohorts of European ancestry, however, researchers have now identified mutations in several genes that are associated with susceptibility for kidney dysfunction and chronic kidney disease. One of the genes, *UMOD*, encodes Tamm–Horsfall protein, the most common protein in healthy human urine. "Studies to understand the production and functions of Tamm–Horsfall protein are warranted and may eventually lead to novel prevention and intervention options to reduce CKD risk," state the authors.

Original article Köttgen, A. *et al.* Multiple loci associated with indices of renal function and chronic kidney disease. *Nat. Genet.* doi:10.1038/ng.377 (2009).

GENETICS

A genetic sequence variant that is associated with both kidney stones and reduced bone mineral density has been identified by researchers. Thorleifsson and colleagues conducted a genome-wide association study in 3,773 cases and 42,510 population controls from Iceland and The Netherlands. They identified common variants in the *CLDN14* gene that were associated with both kidney stones and with reduced bone mineral density at the hip and spine. Further research is required to understand the biological pathways that connect kidney stones, reduced bone mineral density and *CLDN14*, which is expressed in the kidney and encodes a protein involved in the regulation of paracellular permeability at epithelial tight junctions.

Original article Thorleifsson, G. *et al.* Sequence variants in the *CLDN14* gene associate with kidney stones and bone mineral density. *Nat. Genet.* doi:10.1038/ng.404 (2009).