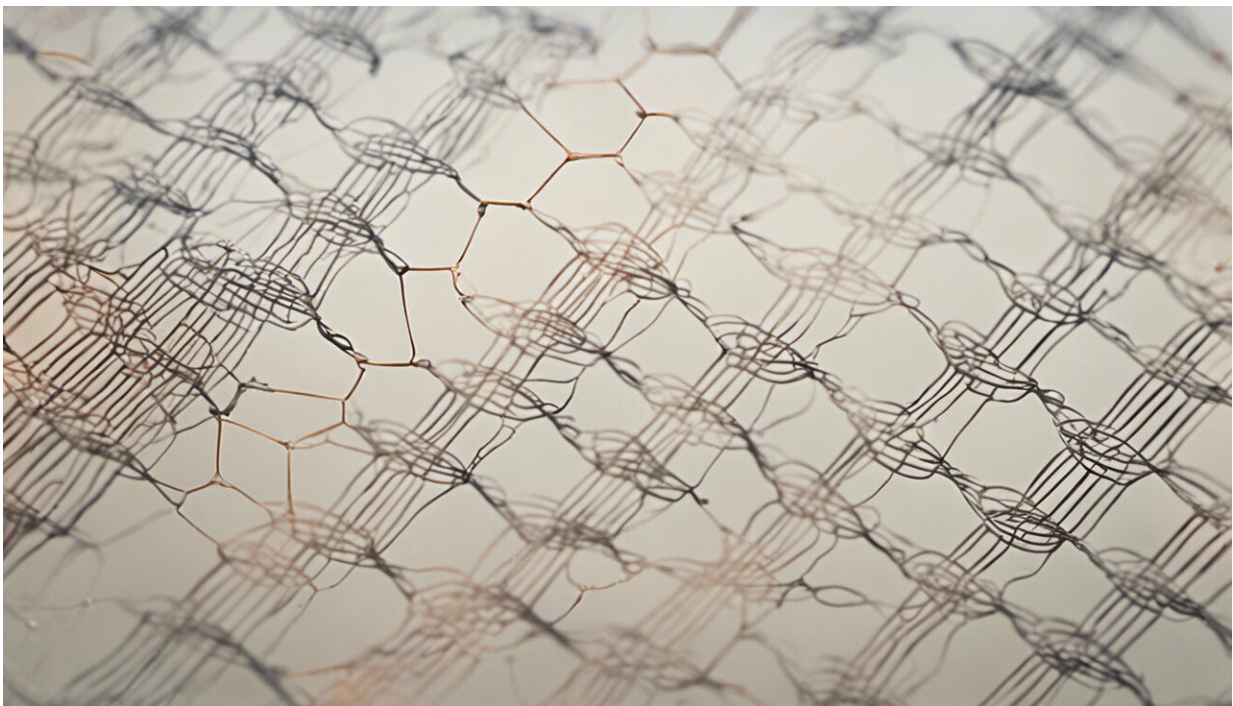


Geneticists uncover a trail of variants associated with kidney dysfunction, specifically among East Asian populations

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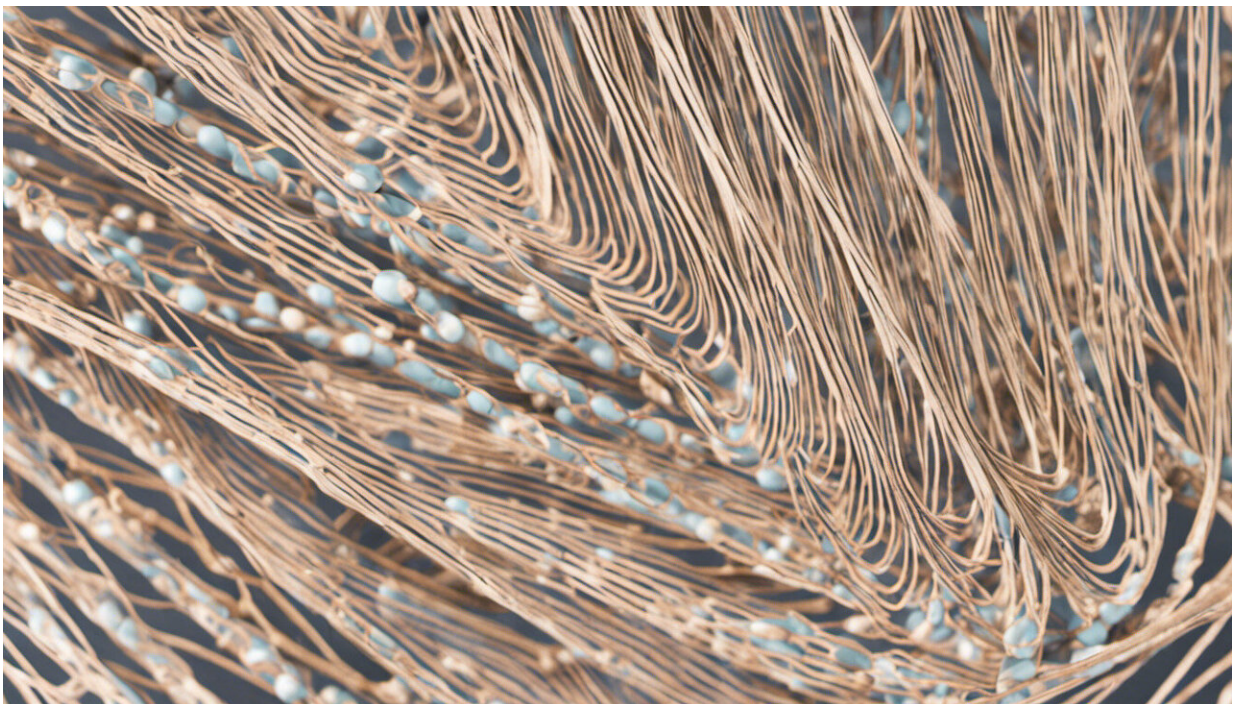


Credit: AI-generated image ([disclaimer](#))

The past decade has seen a steady torrent of data linking human genetic variants associated with disease risk, and yet many important gaps remain. For example, many of these studies have focused primarily on Caucasian populations in North America and Europe. The resulting data

may be less relevant to other ethnic groups that may have accumulated distinct subsets of risk factors over the millennia since our ancestors first parted ways in Africa.

The Asian Genetic Epidemiology Network (AGEN) was formed to address this issue by identifying disease risk loci specific to [Asian populations](#). A new study from AGEN-affiliated scientists has now identified 17 genomic sites that potentially predispose East Asian individuals to [chronic kidney disease](#) (CKD). CKD, which puts patients at risk of [kidney failure](#) and cardiovascular disease, encompasses a host of potential metabolic symptoms. Accordingly, project leaders Yukinori Okada and Toshihiro Tanaka of the RIKEN Center for Genomic Medicine designed their study to identify potential genetic variants linked with four different physiological manifestations of CKD.



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They performed what is known as a meta-analysis, conducting a broad examination of [genomic data](#) obtained from 11 previously-studied cohorts comprising over 70,000 East Asian individuals. In particular, they were interested in identifying tiny [genomic sequence](#) variations known as single-[nucleotide polymorphisms](#) (SNPs) that appear to be associated with CKD symptoms. This yielded 25 candidate loci, which the AGEN team then double-checked against another dataset obtained from nearly 20,000 more East Asian subjects.

Alongside several previously-identified potential risk factors, their analysis uncovered 17 loci that appear to be meaningfully linked with CKD. Importantly, only a subset of these showed equally strong association with CKD symptoms in datasets obtained from large numbers of Caucasians. They were also able to identify individual variants linked to multiple CKD manifestations, including SNPs within three genes that were significantly associated with all four symptoms selected for this study.

Several of the SNPs identified here were linked to genes involved in immunity and embryonic development, including one gene with an established role in the formation of the kidney. At least three others have been tied to kidney function in previous studies. For many of the other genes identified, however, the connection to kidney or metabolic disease remains unclear, and further study will be required to assemble these diverse data into a coherent map of CKD etiology and to understand which factors are particularly important 'red flags' for health risk in East Asian patients.

More information: Okada, Y., Sim, X., Go, M.J., Wu, J.-Y., Gu, D., Takeuchi, F., Takahashi, A., Maeda, S., Tsunoda, T., Chen, P. et al. Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. *Nature Genetics* 44, 904–909 (2012).

Provided by RIKEN

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