

Gene linked with human kidney aging

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A gene has been associated with human kidney aging, according to researchers from Stanford University, the National Institute on Aging, the MedStar Research Institute, and the HudsonAlpha Institute for Biotechnology. In work published on October 16 in the open-access journal *PLoS Genetics*, the investigators claim that their approach, which combines sequential transcriptional profiling and eQTL mapping, can be applied to any phenotype of interest to help find other genetic associations.

Kidneys age at different rates, such that some people show little or no effects of kidney aging whereas others show rapid functional decline. Determining genetic factors associated with different rates of kidney aging contributes to the understanding of molecular mechanisms underlying the human aging process. Although family studies have shown that [genes](#) play a role in longevity, it has proven difficult to identify the specific genetic variants involved, until now.

The researchers, led by Dr. Stuart Kim, first used genome-wide transcriptional profiling to determine that 630 genes change expression with age in [kidney tissue](#). Next, they determined that 101 of these age-regulated genes contain DNA variations among individuals that associate with [gene expression](#) level. These 101 genes were tested for association with kidney aging in a combined analysis of two populations selected to study normal aging: the Baltimore Longitudinal Study of Aging and the InCHIANTI Study. One gene that encodes an extracellular matrix protein (MMP20) was revealed to be significantly associated with kidney aging, providing the first gene association with kidney aging.

Because data from both populations were combined in the kidney aging association analysis, the researchers stress that this finding needs to be replicated in additional populations. As more aging genes are discovered and confirmed, the particular genetic variants belonging to a person could one day be combined to better predict the aging trajectory of the kidney.

More information: Wheeler HE, Metter EJ, Tanaka T, Absher D, Higgins J, et al. (2009) Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. *PLoS Genet* 5(10): e1000685. [doi:10.1371/journal.pgen.1000685](https://doi.org/10.1371/journal.pgen.1000685)

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