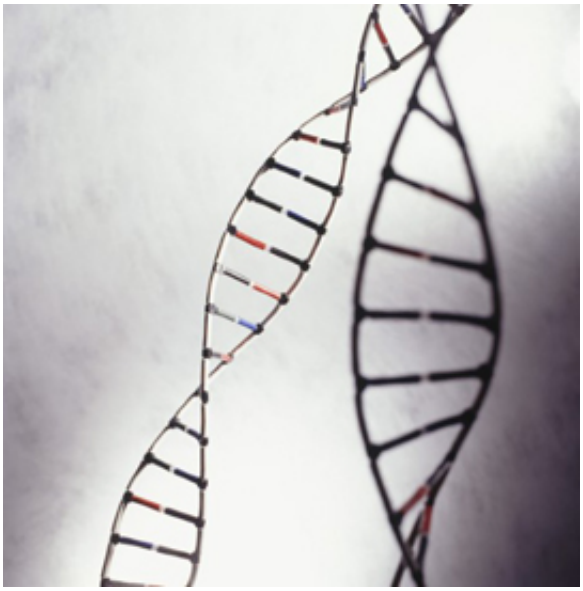
Medical Xpress

Genome studies can help identify lifestyle risks for diseases

February 12 2016



Credit: NIH

Genome wide association studies (GWAS) scan the entire genome in order to pinpoint genetic variants associated with a particular disease. The technique is employed to identify biological pathways - the series of actions and changes that have occurred in cells and genetic material - that can be linked to the causation of a disease.

A team of researchers from the University of Bristol and Oxford University have suggested, in a paper published this week in *PLOS Genetics*, that a GWAS for a disease should also identify genetic variants

that predict behaviours that increase the risk of the disease as well. If this is the case, GWAS may be useful places to look for potentially modifiable risk factors for disease, which could then be targeted by medics for interventions.

Professor Marcus Munafo, the study's lead author, said: "Genome-wide association studies of lung cancer have identified genetic variants that strongly predict smoking. It is possible these genetic variants have independent effects on both smoking and lung cancer, but it seems far more likely that this variant was seen because smoking causes lung cancer.

"Genetic predictors for lifestyle are still being identified. We already know about variants that predict smoking, alcohol or caffeine use, and research is ongoing to predict things like cannabis use. As larger GWASs of disease are carried out, more of these variants which indicate the causal modifiable risk factors for disease will be identified. This will help the development of more effective and better-targeted interventions.

"These discoveries really underline how valuable the investment in genetic studies is - more so than is often thought. Genetic studies can not only identify the biological risk factors for disease, but the behavioural risk factors as well"

More information: Suzanne H. Gage et al. G = E: What GWAS Can Tell Us about the Environment, *PLOS Genetics* (2016). DOI: 10.1371/journal.pgen.1005765

Provided by University of Bristol