

Epigenetic studies provide intriguing results, but are hard to replicate

Obesity may be written not only in the genes, but also on top of them. One of the largest studies so far to probe the human epigenome — the collective name for the patterns of chemical groups that adorn DNA sequences and influence their activity — has found some tags that are linked to differences in body mass index (BMI).

Chemical alterations in a gene thought to be involved in metabolism were identified in the blood and fat cells of more than 2,500 people, scientists reported last month. The work, led by Nilesh Samani at the University of Leicester, UK, is part of an emerging line of research that is probing disease through epigenome-wide association studies (EWAS). Those in the field hope that because many epigenetic changes are influenced by the environment, such studies will reveal mechanisms of disease that have remained elusive. However, many scientists remain sceptical.

But many scientists say that the field of EWAS, which is less than a decade old, has yet to show that it can yield real insight. “The problem with EWAS is that there’s so much more that can confound an outcome compared with a GWAS,” says John Greally, an epigeneticist at Albert Einstein College of Medicine in New York. For instance, epigenetic alterations vary drastically between cells of the same tissue, and it can be difficult to determine whether an alteration is a cause or consequence of a disease.

Read the full, original story: [Epigenomics starts to make its mark](#)