Drilling down on the roots of chronic fatigue syndrome? 200 genetic variants now linked to the disorder

Scientists have discovered possible genetic risk factors involved in chronic fatigue syndrome (CFS), also known as myalgic encephalomyelitis (ME).

ME/CFS is a poorly understood condition characterised by persistent fatigue and brain fog. It is thought to affect around 17 million people worldwide.

To better understand its cause, Steve Gardner at UK biotechnology company PrecisionLife and his colleagues analysed DNA samples from 2382 participants of the UK Biobank study, all of whom had been diagnosed with ME/CFS.

Most genetic studies look for differences in single DNA letters, known as single nucleotide polymorphisms (SNPs). In contrast, Gardner and his colleagues searched for differences in combinations of SNPs, allowing them to identify genetic traits that may only be in a subgroup of people with ME/CFS.

The team identified 199 SNPs, of 14 genes, in 91 per cent of the participants with ME/CFS. A statistical analysis suggests this wasn’t a chance finding.

Previous studies have linked these genetic variants to our mitochondria – our cells’ energy powerhouses, as well as our circadian rhythm or body clock, and our overall stress response. People with these variants may also be at a heightened risk of catching viral and bacterial infections or developing certain autoimmune conditions, such as multiple sclerosis.

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