Disease genes that followed the Silk Road identified

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Scientists have identified key genes responsible for a severe inflammatory disease that has spread along the old silk trading routes from the Far East to the edge of Europe.

University of Manchester researchers, working as part of a large international consortium, have revealed some of the genetic mutations that lead to Behçet's disease. The group's findings are published in Nature Genetics.

Behçet's is a vascular disease where the body's normal inflammatory immune response becomes overactive and destroys blood vessels resulting in severe mouth and genital ulcers and skin lesions. The eyes can also be affected by the condition and this can lead to blindness.

The condition, sometimes referred to as the 'Silk Road disease' due to the way its prevalence has spread along the old silk trading routes, is rare in Western Europe but is a major disease in Far- and Middle-Eastern countries, as well as in Greece and, particularly, Turkey, where it affects four in every 1,000 people.

"Our research has for the first time in a large-scale study identified the genes responsible for Behçet's disease," said Bill Ollier, Professor of Imunogenetics and Director of the University's Centre for Integrated Genomic Medical Research (CIGMR).

"The condition is relatively rare in the UK, mainly affecting those of

Asian and Middle-Eastern descent, but its hereditary nature has seen its prevalence spread westward from the Far East as trading routes opened and populations migrated."

The researchers carried out genetic tests on almost 2,500 Turkish volunteers, 1,215 people with Behçet's disease and 1,278 healthy individuals. The scientists compared their results with additional data from a further 5,000 people in Turkey, the Middle East, Europe and Asia.

The team found an increased risk of disease was associated with three genes - HLA-B51, IL10, IL23R-IL12RB2. There is also evidence to suggest the involvement of two further genes in this condition. The discovery could pave the way for new treatments for Behçet's in the future.

Professor Ollier said: "Through establishing this major international collaboration between research groups from all over the world we have managed to identify and confirm some of the genes involved in this terrible condition.

"Hopefully, if we can collect larger numbers of patients, we will be able to go on to identify further genes which contribute smaller levels of risk. By identifying the genetic factors in Behcet's disease we will be in a position to establish the biological and biochemical pathways that cause the disease pathology. Only by doing this, will we be able to design the right drugs to correct these pathways and treat the patients.

"Our other long-term ambition is that we could use genetic testing to identify early cases in families with a history of the disease and predict which patients will have a more severe disease course and consequently require a more aggressive therapy."

More information: 'Genome-wide association study identifies variants in the MHC class I, IL10, and IL23R-IL12RB2 regions associated with Behçet's disease,' *Nature Genetics*.

Provided by University of Manchester