

Increased prevalence of lupus in Non-Europeans has a genetic basis, study confirms

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Non-Europeans have a higher frequency of the gene variants that increase the risk of lupus as compared to the European population, a new study from researchers at the National Institute for Health Research (NIHR) Biomedical Research Centre at Guy's and St Thomas' and King's College London, has confirmed.

The findings, which are published today in *Nature Genetics*, could lead to the development of tests to predict if an individual is more likely to develop lupus and may also contribute to the development of personalised treatments for the difficult to treat autoimmune condition the affects more than five million people worldwide.

The study was led by Professor Tim Vyse, an expert in genetics and molecular medicine at King's College London and an honorary consultant rheumatologist at Guy's and St Thomas' NHS Foundation Trust, who said:

"Lupus is a very poorly understood condition. The confirmation that the condition's increased prevalence in non-Europeans has a [genetic](#) basis is an important step towards developing better predictive and diagnostic tools and may eventually help us to develop personalised treatments too."

The research team searched genetic data gathered from 22,670 Europeans, 13,174 Chinese as well as data from South Asian, east Asian

and African recorded in the 1000 genomes. Analysis of the data revealed that non-European populations have a higher number of the gene variants, known as alleles, which are thought to contribute to the risk of developing lupus, amongst the Chinese population.

While the study establishes that lupus is highly hereditary, researchers believe there is still a large 'environmental' component which plays a significant role. Dr David Morris, a researcher at King's College London and one of the study's co-authors, said:

"For the first time we've shown that Chinese populations have a higher number of risk alleles than their European counterparts, but we don't understand why this susceptibility hasn't diminished over time for non-Europeans.

"When thinking about whether someone might develop lupus, we use evidence from Twins studies which has shown that genetic factors account for two-thirds of the picture and [environmental factors](#) make up the final third. Our study advances our understanding of the genetic component, but more work needs to be done to better understand the environmental factors."

Further analysis of the data also uncovered 10 additional risk alleles associated with lupus, bringing the total of known lupus-related alleles to 88. Dr Morris said:

"Identifying more [lupus](#)-related risk alleles gives us a clearer picture of the genetic triggers. It's possible that we may never identify all of these triggers, but we are moving closer to a threshold that when crossed will help us to more effectively predict and treat this debilitating and poorly understood condition."

The team is keeping a track of these genes on its website

<http://insidegen.com/>.

More information: Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus, *Nature Genetics*, [DOI: 10.1038/ng.3603](https://doi.org/10.1038/ng.3603)

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