New genetic risk factors of lupus found in study of African-American women

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Researchers from Boston University's Slone Epidemiology Center have found four new genetic variants in the major histocompatibility complex (MHC) that confer a higher risk of systemic lupus erythemathosus ("lupus") in African American women. The study, which currently appears on-line in *Human Genetics*, is believed to be the first to comprehensively assess the association between genetic variants in the MHC region and risk of lupus in African American women.

The findings were based on the ongoing Black Women's Health Study, a prospective study of the health of 59,000 African American women conducted by the researchers since 1995.

African American women have a higher risk of lupus compared with white US women. It has been known that the MHC region in chromosome 6 carries genetic factors associated with several auto-immune disease, and recent studies have reported several genetic variants in the MHC region associated with risk of lupus. However, these previous studies were carried out in European and Asian ancestry populations.

The researchers genotyped more than 1,500 genetic variants single nucleotide polymorphisms (SNPs) in 400 lupus cases and 800 controls. They found four independent SNPs associated with higher risk of lupus. Through the construction of a genetic score consisting of those four SNPs, the researchers found that risk of lupus increased by almost 70 percent for each extra high risk allele. One of the SNPs reported in the

present study was also found in a study in Chinese women, and the researches were also able to replicate some previous findings from a study in women of European ancestry.

According to the researchers, their results show the presence of several independent genetic risk factors in the MHC region in African American women. Some of those genetic variants may be shared among women of different genetic ancestries.

"Taken together, our results and previous genome-wide association studies in European and east Asian ancestry populations show that women of different ancestral origins may share some genetic components for the risk of lupus," said lead author Edward A. Ruiz-Narvaez, ScD, an assistant professor of epidemiology at Boston University School of Medicine. "The identity of the causal variants that are being tagged by the reported SNPs is still unknown. Further studies are needed to narrow the position of the potential causal variants," he added.

The researchers point out that the identified genetic variants are not necessarily the ones directly involved in the pathogenesis of lupus, and further research is needed to identify the true causal genetic variants. Identification of the true causal genetic variants should lead to a better understanding of the biology of lupus.

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