

Gene is first linked to herpes-related cold sores

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A team of researchers from the University of Utah and the University of Massachusetts has identified the first gene associated with frequent herpes-related cold sores.

The findings were published in the Dec. 1, 2011, issue of the [Journal of Infectious Diseases](#).

Herpes simplex labialis (HSL) is an infection caused by [herpes simplex virus type 1](#) (HSV-1) that affects more than 70 percent of the U.S. population. Once HSV-1 has infected the body, it is never removed by the [immune system](#). Instead, it is transported to nerve cell bodies, where it lies dormant until it is reactivated. The most common visible symptom of HSV-1 reactivation is a cold sore on or around the mouth. Although a majority people are infected by HSV-1, the frequency of cold sore outbreaks is extremely variable and the causes of reactivation are uncertain.

"Researchers believe that three factors contribute to HSV-1 reactivation – the virus itself, exposure to environmental factors, and genetic susceptibility," says John D. Kriesel, M.D., research associate professor of infectious diseases at the University of Utah School of Medicine and first author on the study. "The goal of our investigation was to define genes linked to cold sore frequency."

Kriesel and his colleagues previously had identified a region of chromosome 21 containing six genes significantly linked to HSL disease

using DNA collected from 43 large families to map the human genome. In the current study, Kriesel and his colleagues performed intensive analysis of this chromosome region using single nucleotide polymorphism (SNP) genotyping, a test which identifies differences in genetic make-up between individuals.

"Using SNP genotyping, we were able to identify 45 DNA sequence variations among 618 study participants, 355 of whom were known to be infected with HSV-1," says Kriesel. "We then used two methods called linkage analysis and transmission disequilibrium testing to determine if there was a genetic association between particular DNA sequence variations and the likelihood of having frequent cold sore outbreaks."

Kriesel and his colleagues discovered that an obscure gene called C21orf91 was associated with susceptibility to HSL. They identified five major variations of C21orf91, two of which seemed to protect against HSV-1 reactivation and two of which seemed to increase the likelihood of having frequent cold sore outbreaks.

"There is no cure for [HSV-1](#) and, at this time, there is no way for us to predict or prevent cold sore outbreaks," says Kriesel. "The C21orf91 gene seems to play a role in cold sore susceptibility, and if this data is confirmed among a larger, unrelated population, this discovery could have important implications for the development of drugs that affect cold sore frequency."

Provided by University of Utah

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