

Scientists begin to unravel what makes pandemic H1N1 tick

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As the number of deaths related to the pandemic H1N1 virus, commonly known as "swine flu," continues to rise, researchers have been scrambling to decipher its inner workings and explain why the incidence is lower than expected in older adults.

In a study appearing online and in a future issue of [Proceedings of the National Academy of Sciences](#), a UT Southwestern Medical Center researcher and his collaborators in California show that the molecular makeup of the current H1N1 [flu strain](#) is strikingly different from previous H1N1 strains as well as the normal seasonal flu, especially in structural parts of the virus normally recognized by the [immune system](#).

Prior research has shown that an individual's immune system is triggered to fight off pathogens such as influenza when specific components of the immune system - namely antibodies, B-cells and [T cells](#) - recognize parts of a virus known as epitopes. An individual's ability to recognize those epitopes - spurred by past infections or vaccinations - helps prevent future infections. The challenge is that these epitopes vary among flu strains.

"We hypothesize that older people are somewhat protected because the epitopes present in flu strains before 1957 may be similar to those found in the current H1N1 strain, or at least similar enough that the immune system of the previously infected person recognizes the pathogen and knows to attack," said Dr. Richard Scheuermann, professor of pathology and clinical sciences at UT Southwestern and a co-author of the paper.

"Those born more recently have virtually no pre-existing immunity to this pandemic H1N1 strain because they have never been exposed to anything like it."

Between April and mid-October, the current H1N1 virus sickened roughly 22 million Americans and contributed to or caused about 4,000 deaths, according to the figures recently released by the Centers for Disease Control and Prevention. The deaths included 540 children. The CDC report also estimates the total number of hospitalizations at around 98,000 nationwide, with children accounting for 36,000 of the total.

For this study, researchers examined whether epitopes present in the seasonal flu strains between 1988 and 2008 also are found in the existing H1N1 strain. They used data catalogued in the Immune Epitope Database as well as information from the National Center for Biotechnology Information (NCBI) and the Global Initiative on Sharing Avian Influenza Data's (GISAID) influenza genetic sequence databases. Dr. Scheuermann said his team also analyzed the virus' genetic data using the NIH-sponsored Influenza Research Database, which he oversees at UT Southwestern.

The researchers found major genetic differences between the pandemic H1N1 strain and seasonal strains, potentially explaining why children and young adults are more susceptible to the H1N1 strain now circulating worldwide.

"Normally, older adults are generally more susceptible to pathogens like influenza, however, for the pandemic H1N1 strain this does not seem to be the case," said Dr. Scheuermann, who is also a member of the Cancer Immunobiology Center at UT Southwestern. "The antibody epitopes, which provide protection against disease, for the pandemic H1N1 strain are virtually all different from those present in recent seasonal strains, so young people have no built-in protective mechanisms. We speculate that

older adults may have been exposed to viruses in their youth in which the epitopes are more similar."

At this point, he said, scientists must continue to be vigilant about tracking the pandemic H1N1 strain as it continues to evolve.

"H1N1 has not mutated in such a way as to make people sicker, but it could happen," Dr. Scheuermann said. "It is important that individuals follow the public health guidelines regarding vaccination as the H1N1 vaccine becomes more widely available."

Source: UT Southwestern Medical Center ([news](#) : [web](#))

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