

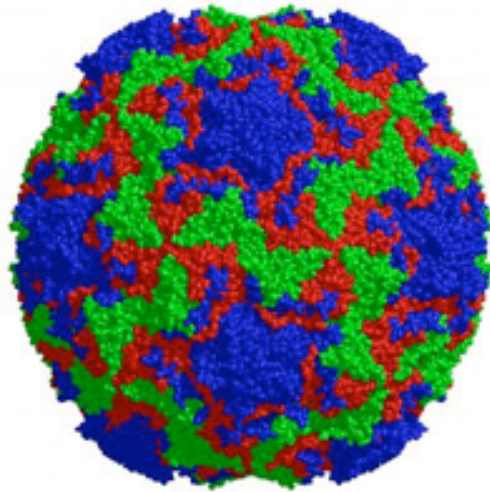
Researchers cracking code of the common cold

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Courtesy University of Maryland Medical Center and [World Science](#) staff

Scientists say they have put together the pieces of the genetic codes for all known strains of the pathogen responsible for the common cold, in work that could lead to the first effective treatments for the illness.

Researchers at the University of Maryland School of Medicine and the University of Wisconsin-Madison completed the genomic sequences of many strains of the virus, called the human rhinovirus, and assembled them into a “family tree” showing their relationships. The study appears in the online version of the journal *Science* on Feb. 12.



“There has been no success in developing effective drugs to cure the common cold, which we believe is due to incomplete information” about the genes, said the study’s senior author, Stephen B. Liggett of the University of Maryland School of Medicine.

“We generally think of colds as a nuisance, but they can be debilitating in the very young and in older individuals, and can trigger asthma attacks at any age. Also, recent studies indicate that early rhinovirus infection in children can program their immune system to develop asthma by adolescence,” said Liggett, a pulmonologist and molecular geneticist.

The researchers found that human rhinoviruses are organized into about 15 small groups that come from distant ancestors. The discovery of these multiple groups explains why a “one-drug-fits-all” approach for anti-viral agents doesn’t work. But, said Liggett, “Perhaps several anti-viral drugs could be developed, targeted to specific genetic regions of certain groups. The choice... would be based on the genetic characteristics of a patient’s rhinovirus infection.”

Liggett added that while anti-virals seem the best bet, “the data gathered from these full genome sequences gives us an opportunity to reconsider vaccines as a possibility.”

The analysis found that some human rhinoviruses result from the exchange of genetic material between different strains of the virus in one person. The viruses also mutate often, helping them avoid being hunted down by the immune system, according to Liggett.

“As we begin to accumulate additional samples... it is likely that hotspots for mutation or recombination [gene exchange] will become apparent,” said the study’s lead author, biochemist and virologist Ann C. Palmenberg of the University of Wisconsin-Madison. “This will provide clues as to how flexible the virus is” in its survival strategies.

Human rhinovirus causes half of all asthma attacks and is a factor in bronchitis, sinusitis, middle ear infections and pneumonia. The coughs, sneezes and sniffles of colds are estimated to cost the U.S. economy some \$60 billion annually.

Before this project, the genomes of only a few dozen rhinoviruses had been sequenced from a frozen collection of 99 different rhinovirus strains taken from patients over a span of more than two decades. The study by Palmenberg and colleagues adds 80 genome sequences to the rhinovirus library and 10 more acquired recently from people with colds. During the study, several other research groups began to report the full genomes of some of the viruses in the previous collection, as well as some odd rhinovirus-like strains from relatively sick patients.

“Now we can put together many pieces of the human rhinovirus puzzle to help us answer some fundamental questions,” Liggett said: “how these rhinoviruses might mutate as they spread from one person to another; which rhinoviruses are more associated with asthma exacerbations and why rhinovirus exposure in infancy may cause asthma later in life. With all this information at hand, we see strong potential for the development of the long-sought cure for the common cold.”

Image: Model of the outer structure of the human rhinovirus. (Courtesy Jean-Yves Sgro, U. of Wisconsin-Madison)