Experts: Mild swine flu could quickly turn deadly

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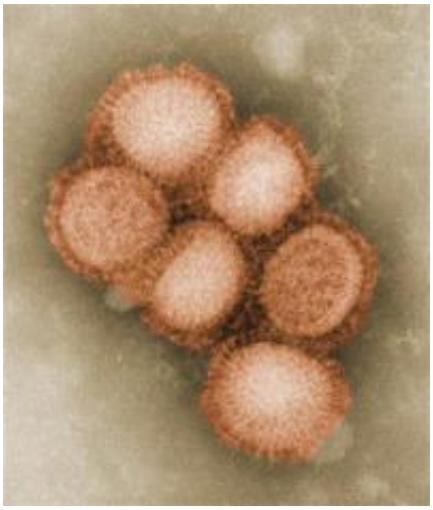

FILE - This 2009 file microscope image originally provided by the Centers for Disease Control and Prevention, shows a negative-stained image of the swine flu virus. In this year's swine flu, changes in the virus have helped it spread more easily among people, but also made it less deadly than distant ancestors. More mutations, dangerous ones, could come later this year. And that's why scientists are watching it so closely. (AP Photo/Centers for Disease Control and Prevention, C. S. Goldsmith and A. Balish)

(AP) -- A flu virus is a powerhouse of evolution, mutating at the maximum speed nature allows. A mild virus can morph into a killer and vice versa.

One change already made this year's swine flu more of a problem,

helping it spread more easily among people. The big question is: What mutations are next? That's why scientists are watching it so closely.

"There are no rules to flu viruses; they are just so mutable," said Dr. Paul Glezen, a flu epidemiologist at the Baylor College of Medicine in Houston. "The fact that it changes all the time really confounds our efforts to control it."

Think of flu's evolution like a family tree: In the current flu's distant ancestry are last century's three pandemics. But its more immediate relatives are swine flu strains that were no big deal to humans.

The good news right now is that this flu has lost some of the most dangerous genetic traits of past pandemics. The bad news is that it's gained something its parents didn't have: the ability to spread from human to human.

Flu reproduces about every eight hours, said Dr. Raul Rabadan, professor of computational biology at Columbia University. That means this morning's flu is a parent by the afternoon, a grandparent by the evening, and a great-grandparent by the next day.

Instead of complex double-helix DNA - nature's basic biological instruction book - flu has a simpler, single strand of genetic code. Normal DNA has a spellcheck-like system that reduces mistakes in replicating the code; the flu virus does not. So mutations come more often. If the mutations are good for the virus, they multiply, and voila, you have a new and sometimes nastier flu.

Scientists are trying to piece together swine flu's ever-changing genome, its genetic ancestors and the random mutations that in this instance turned a simple pig disease into something that scares billions.

They also don't know how the virus is going to mutate next.

In the world's most devastating global flu epidemic in 1918, the first wave of cases in the spring were mild. Then, the virus evolved and came back in the fall as a strain that proved truly deadly, flu experts say. So scientists today are watching to see if that could happen again.

Also troubling is the possibility that this virus could develop resistance to anti-flu drugs, and flu trackers are watching for such changes, Centers for Disease Control and Prevention flu chief Dr. Nancy Cox said.

It's impossible to know where this swine flu strain began exactly, Cox said. But flu trackers do have clues to its closest ancestral genes.

"Its two parents were swine viruses that we know and love," said virologist Dr. Richard Webby, a researcher at St. Jude Children's Research Hospital in Memphis, Tenn.

The mother of the swine flu was a surprising genetic event that went unnoticed except by a few scientists a little over a decade ago. Three influenza strains - some pig, some bird, some human - combined in pigs to form two new strains of swine flu. This new flu was unusual. Virus hunters called it a "triple reassortment."

That 1998-99 flu in pigs first hit a farm in North Carolina, then spread to Iowa, Texas, Oklahoma and eventually to at least 23 states. No more than 4 percent of the swine died. But the disease was in more than one-quarter of tested pigs. A handful of people who were in close contact with the hogs got slightly sick when they caught this flu from pigs, but they didn't die and didn't spread it to others.

In 2005, a 17-year-old Wisconsin boy caught that triple reassortment flu virus from "respiratory secretions" of a pig he had been helping his

brother-in-law butcher, according to the CDC. He recovered and didn't pass it on to others.

There have been about 10,000 generations of that virus since. Six of the eight genetic segments of the current swine flu can be traced to that triple combination, Rabadan said.

The rest of the swine flu parentage is more of a mystery. The other two of the eight genetic segments can be traced to pig viruses in Europe and Asia that were seen from time to time in the 1990s, Rabadan said. Scientists don't quite know if those other two segments combined with the triple reassortment at the same time or separately.

How the triple reassortment genes and the European and Asian genes met and mixed is not known, Webby said.

The three global flu epidemics of the past, including the 1918 event, all passed on traits to ancestors of this flu, Rabadan said. But there have been many changes in the thousands of generations since.

A specific gene for virulence that was seen in the 1918, 1957 and 1968 pandemics was notably absent in this swine flu, said Dr. Peter Palese, a prominent flu researcher for Mount Sinai Medical Center in New York. He said when he removed that gene from other viruses of the past, they weren't as dangerous.

Rabadan suggests the way to think of this flu is like a homemade car with parts from different vehicles. The parts have all been in several different vehicles before. Sometimes the combination of parts is a dud and the car doesn't move. And sometimes you get a race car. A pandemic is a race car.

All eight of the new flu's genetic segments have been in different viruses

before. But this is the first time this specific combination has been seen. The big question is: Why is this particular swine virus spreading so fast among people when past swine viruses haven't?

One possibility is that it's just this particular combination of the eight parts that makes it spread among people, Webby said. But a more logical explanation is that a small mutation within the individual genetic segments changed things.

These tiny changes are possible because there are about 13,000 individual letters, or bases, in the flu genetic code, Rabadan said. That's tiny compared to more than 3 billion in humans.

One prime suspect is the surface protein hemagglutinin, the "H" in the virus' H1N1 name. It is "probably the most important gene determining virulence and immunological characteristics," according to Palese.

In flu viruses, scientists have so far identified 16 hemagglutinins. Only three - H1, H2 and H3 - commonly infect humans. The other surface protein, neuraminidase, has nine variations. Palese said scientists are seeing more different types of flu strains because of better surveillance and increases in bird, pig and human populations.

"These genetic processes of mutation and genetic reassortment occur all the time," he said, "and every once in a time, it's a lottery winner."