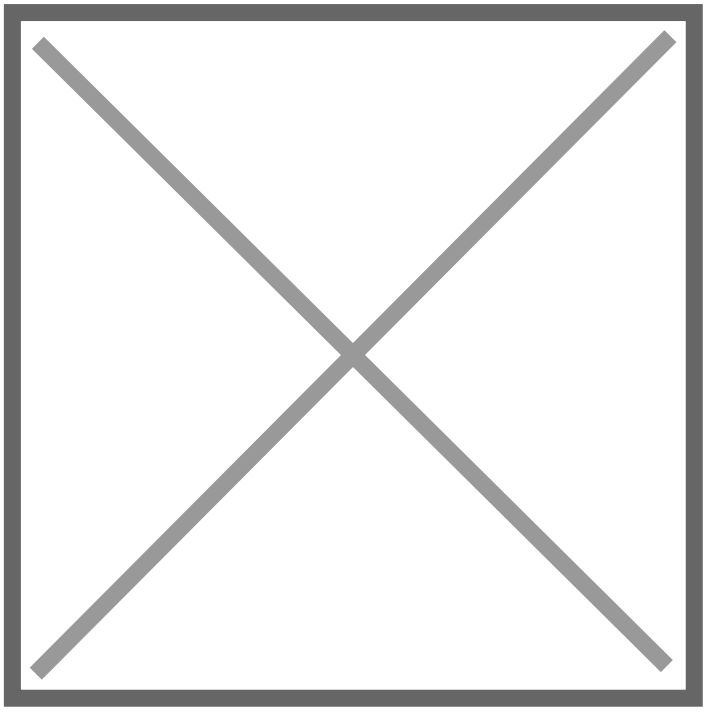
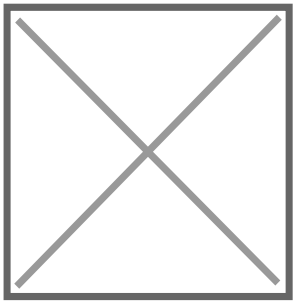
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The virus race

19 May 2003 | News



In recent times, there have been some exciting announcements such as the complete mapping of the human genome, claims about the birth of the first cloned human baby. Many scientific teams in organizations across the world have raced against each other to be the first to accomplish these tasks. And they had toiled over these projects for years. But the mid-April



announcement of the first mapping of the genome sequence of the SARS (severe acute respiratory syndrome) virus by a Canandian research team, which competed with a dozen other such global teams, has been nothing short of spectacular as they mapped the nearly 30,000 genes of the virus in just six days. The world has called this "stunning." A report about the truly amazing scientific feat.

When the history of the SARS virus is written, a small laboratory room in Vancouver in Canada's British Columbia province will find a special mention. For it was here, in a 100,000 sq.ft lab, where a group of 20 scientists toiled non-stop for six days, living on pizzas, doughnuts and aerated drinks and sleeping on chairs in the corridors, took the first step to solve the mystery surrounding the SARS virus by mapping its genome.

Things happened rapidly in weeks for what would have been a project that would have taken a few years to complete in normal times. Scientists at the Genome Science Center stopped every other work and responded to the Canadian Cancer Agency's call (this agency runs the center) to take the first step in tackling the mysterious illness that had spread to Toronto from an infected Chinese businessman.

From the moment they got the blood samples from one of the infected patients, the team of scientists, with an average age of 23 or 24, took up the job in right earnest. They knew they were not the only ones working on the project. Twelve other top research teams around the world, including a much acclaimed team across the
Canadian border at one of the Centers for Disease
Control (CDC)in the US, were on to it.

But at 4 am on 12th April, the Canadian team won the race, so to say, when they made public the sequences of the 29,736 genes that made up the SARS virus which belonged to the coronavirus family. This family of viruses, called so due to their crown shape, have been known mostly to cause mild illnesses and cold. But for three weeks, scientists had speculated that an unknown member of this family of virus was the most likely culprit behind the SARS scare sweeping parts of the world.

The samples were first cultured in primate cells at the National Microbiology Laboratory in Winnipeg, Manitoba. The "sensitive, very delicate" work of converting the sample's RNA into DNA took about five days by a two-person team, Dr Marra said, while "the rest of us reorganized the laboratory so it could run rapidly." Of course, the American team was breathing behind their neck and announced their own version of the gene sequence of the virus three days later.

And together, these scientists have helped the world take the first tentative steps to develop diagnostic kits and drugs in the coming months and prepare the world to tackle the menace. Scientists from both teams said the virus's startling novelty could make it harder to trace what animal or bird it came from, if it did jump from another species.

A spokesman for the World Health Organization called the speed at which the gene was sequenced "stunning"."It was just three weeks ago that the coronavirus was identified as the likely cause," said the spokesman, Dick Thompson. "Don't forget that it took several years to find the virus that causes AIDS. The way people worked together is just great."

The virus appears to be unique. "It doesn't look any more like one known coronavirus than another," the center's director Dr Marco Marra said. With 29,736 base pairs of nucleotides, he said, "it's a biggie for a coronavirus." Viruses usually have thousands of these base pairs, while bacteria have millions and the human genome has over three billion.

The CDC sequence was nearly identical to that determined by a Canadian laboratory .The significant difference was that the CDC-determined sequence has 15 additional nucleotides, which provides the important beginning of the sequence, CDC scientists said.

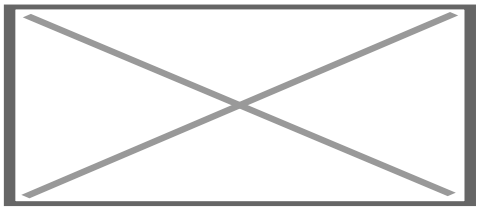
The results came just 12 days after a team of 10 scientists, supported by numerous technicians, began working around the clock to grow cells taken from a throat culture taken from one of the SARS patients in Vero cells (African green monkey kidney cells) in order to reproduce the ribonucleic acid (RNA) of the disease-causing coronavirus. The new sequence has 29,727 nucleotides, which places it well within the typical RNA boundaries for coronaviruses. Members of this viral family tend to have between 29,000 and 31,000 nucleotides.

Identifying the genetic sequence of a new virus is important to efforts to treat or prevent it, said Dr Julie Gerberding, CDC director. "Research laboratories can use this information to begin to target antiviral drugs, to form the basis for developing vaccines, and to develop diagnostic tests that can lead to early detection."

In sequencing the genome, CDC scientists worked closely with coronavirus experts at academic institutions across the United States. "This is an active, working community of scientific experts who have been contributing their knowledge and expertise throughout this investigation," said William Bellini, Ph.D., SARS laboratory team coordinator.

The nearly identical findings in the US and Canada were important because they were derived from different individuals who were infected in different countries. This suggests that the virus probably originated from a common source. The CDC's analysis of the virus was far from finished, officials emphasized. Because coronaviruses have the ability to mutate rapidly, scientists will compare the sequences from viruses isolated in cell culture to those obtained from diseased tissues taken from SARS patients.

"This is essentially a draft. Now we need to see if what we have identified in the laboratory matches what's causing disease in patients," Bellini said. But the groundbreaking work of isolating the genomic sequence speeds the task of comparison. In fact, this has already started to happen. A week later, Chinese scientists have announced that significant differences between virus samples from patients in Guangzhou and in Beijing, indicating that the virus is mutating rapidly.



Yang Huanming, one of China's top geneticist, at the Beijing Genomics Institute has sequenced the SARS virus in a joint project with the Institute of Microbiology and Epidemiology of the Academy of Military Medical Sciences.

He said samples already sequenced in the United States and Canada were similar to the Guangzhou samples because the American and Canadian samples came from people who caught the disease in southern China. But when researchers did sequencing of samples collected in Beijing, about 1,200 miles to the north, they detected significant differences from the viruses known as southern strain.

The coronaviruses are prone to mutations. "These mutations may cause the virus to become more virulent, or alternatively the mutations may cause the virus to become less virulent," Michael Lai, a coronavirus expert at the University of Southern California, told Washington Post. "It will take more analysis to know." The mutations were seen in all five of the viruses' known functional genes, with most of them occurring in the gene that carries the instructions for the distinctive spikes that jut from the outside of the virus, according to Siqi Liu, associate director at the Beijing Genomics Institute, part of the Chinese Academy of Sciences.

patients in Beijing.

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