

B.C. team unravels SARS

By Charlie Anderson
Staff Reporter

Scientists at the B.C. Cancer Agency have made a major breakthrough in solving the puzzle of the killer virus known as SARS.

The Vancouver scientists are the first to crack the genetic code of the Severe Acute Respiratory Syndrome virus — which will speed the diagnosing of victims of the often-fatal disease and help with the work of finding a vaccine.

The group, working out of the Michael Smith Genome Sciences Centre, made the discovery at 4 a.m. yesterday.

A spokesman for the World Health Organization in Geneva called it “an

inquotes

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— Anca Petrescu,
Vancouver biologist
with the team working
on SARS project

extraordinary step.”

“I knew it would happen quickly,” said Dick Thompson. “And frankly, I thought that the CDC [U.S. Centers for Disease Control in Atlanta] would get it done first.”

The local scientists have been working around the clock for the past six days.

Yesterday, some were still hard at it, their computers competing for space with the pizza and sugary snacks that fuelled their work.

The road to the discovery began in late March with a conversation between Dr. Marco Marra, director of the local centre, and Dr. Caroline Astell, the project’s leader.

“We were at a conference at UBC and Marco said, ‘Let’s do it,’” Astell recalls.

A trace of the virus was taken to the ultra-secure National Microbiology Lab in Winnipeg, where it was grown and purified.

The genetic material was then rushed to Vancouver.

Some 30 researchers temporarily dropped their regular cancer-genome investigation to get the work done as quickly as possible. Some got by with just two or three hours’ sleep.

“This was relevant to a public-health situation; it wasn’t a typical research program,” Marra said. “It was important to pro-



Nick Procaulo — The Province

Marco Marra (pointing), director of the Michael Smith Genome Sciences Centre, and Yaron Butterfield, assistant coordinator for sequencing, were part of the SARS project at the B.C. Cancer Agency.

duce it quickly.”

As soon as the genetic sequence was finished, it was posted on the World Wide Web for use by other international health researchers.

Its importance?

“It will lead to the rapid development of very sensitive diagnostic tests to determine if people are infected by the virus by looking at the genome of the virus,” said Astell.

“You’ll also be able to look to see if viral proteins are there, and also whether people have made antibodies to those viral proteins.

“It will allow people to use a more intelligent approach to designing anti-virals that might block the replication of the virus.”

Astell says the latest literature has pegged the corona virus as the most like-

SARS cases

The following is a breakdown of suspected or probable SARS cases worldwide:

- Canada: 274 cases, 13 deaths.
- China: 1,336 cases, 60 deaths.
- Hong Kong: 1,109 cases, 36 deaths.
- Malaysia: 51 cases, one death.

■ Singapore: 140 cases, nine deaths.

■ Taiwan: 23 cases, 0 deaths.

■ U.S.: 166 cases, 0 deaths.

■ Global total: 3,242 cases, 126 deaths.

Sources: World Health Organization, national health officials.

ly suspect in the SARS epidemic.

Anca Petrescu, a computational biologist with the team, said the team’s people were thrilled by the early-morning discovery.

“We had been working on the sequence and once the sequence came, we worked as much as we could,” said Petrescu.

“It’s so interesting, you don’t want to stop. It was great. We were elated.”

Astell said that Friday was a sleepless night for her, too.

“I checked my e-mails at 1 a.m. and there was nothing. I thought that was bad news.

“And then I checked at five [a.m.] and it was there. I think it’s an important achievement, but it doesn’t deter us from the cancer research we are doing.

“This is a fantastic group of people.”

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