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Nova Scotian researcher sheds light on Boston COVID-19 superspreader event

Bronwyn MacInnis was senior author of a study published in the journal Science

[Vernon Ramesar](#) · CBC News · Posted: Dec 13, 2020 1:37 PM AT | Last Updated: December 13





Nova Scotian Bronwyn MacInnis was senior author of a study tracking a COVID-19 superspreading event in Boston (Stephen Schaffner)

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A scientist originally from Nova Scotia was part of a Massachusetts-based team that used genetic fingerprinting to track the devastating spread of COVID-19 from a single event.

A Biogen corporate conference held at a Boston hotel in February led to an estimated 245,000 infections in 29 U.S. states and several countries around the world by Nov. 1.

Bronwyn MacInnis, director of pathogen genomic surveillance at the Broad Institute in Cambridge, Mass., led a team that used genetic fingerprinting to track the spread of the virus from the Boston conference.

MacInnis grew up in Lower Sackville and credits her high school biology teacher, Roger O'Neil, with sparking her love of biology and curiosity about the natural world.

Studied at Dalhousie

That passion led her to complete an undergraduate degree in biology at Dalhousie.

MacInnis said it was an exciting time in genomics as it was moving from being a theoretical field to one with real-world applications.

Inspired by the life-saving possibilities of genomic research, she went on to complete graduate degrees in molecular and cellular genetics at University of Alberta.

After following work opportunities in California and the U.K., she said the "gravitational force" of Nova Scotia drew her back to the East Coast.

When an opportunity arose for her to continue her work in Boston, a major biotech centre, she jumped at the opportunity to be closer to her family.

"It's now either a short flight or a long drive home depending on how you look at it," she said, adding that if an opportunity ever arose to work in Nova Scotia she would move back in a heartbeat.

She is the senior author of the study that was published in the journal *Science* on Dec. 10. The study paints a disturbing picture of how easily and quickly COVID-19 spreads.

"We're looking at little genetic markers, like a genetic fingerprint, that enable us to distinguish the virus in one infection in one individual from another," she said.

"This is a new kind of approach to infectious disease epidemiology, where we use the DNA, the genetic sequence of the pathogens and viruses, to understand how they're evolving and spreading through communities."

She said the process was akin to building a virus "family tree."

A perfect storm

MacInnis said when COVID-19 cases started to pop up in the state, the Massachusetts Department of Public Health and the Massachusetts General Hospital would send samples to her institute to be sequenced.

After looking at the genomic sequence of the viruses and identifying the COVID-19 variant, they were able to track the spread back to the conference and follow its progress.

She described the circumstances that led to the spread of the virus following the conference as a "perfect storm of unfortunate events."

Because the conference was held in the early days of the pandemic, measures like physical distancing, avoiding large gatherings and mask wearing were not yet in place.

"There was just a lot of opportunity for the virus to spread undetected widely at that time," MacInnis said.

Conference participants from across the U.S. and around the world returned home when the event ended, taking the virus with them.

It also led to widespread community transmission throughout the Boston area as well, including to homeless shelters and other high-risk communities.



The study estimates that a Biogen conference in Boston may have led to 245,000 COVID-19 cases worldwide (Brian Snyder/Reuters)

Superspreader event

The Boston conference is categorized as a superspreader event.

In a year when most people have been exposed to a slew of pandemic-related terms, MacInnis said the term has a specific meaning in the context of the study.

"Epidemiologically, we use that word when a single individual case leads to many onward infections in a very short amount of time and often associated with a particular event or gathering," she said.

MacInnis said although the extent of the spread from a single event was dramatic, it wasn't shocking to her as it reflects infectious disease epidemiology at work.

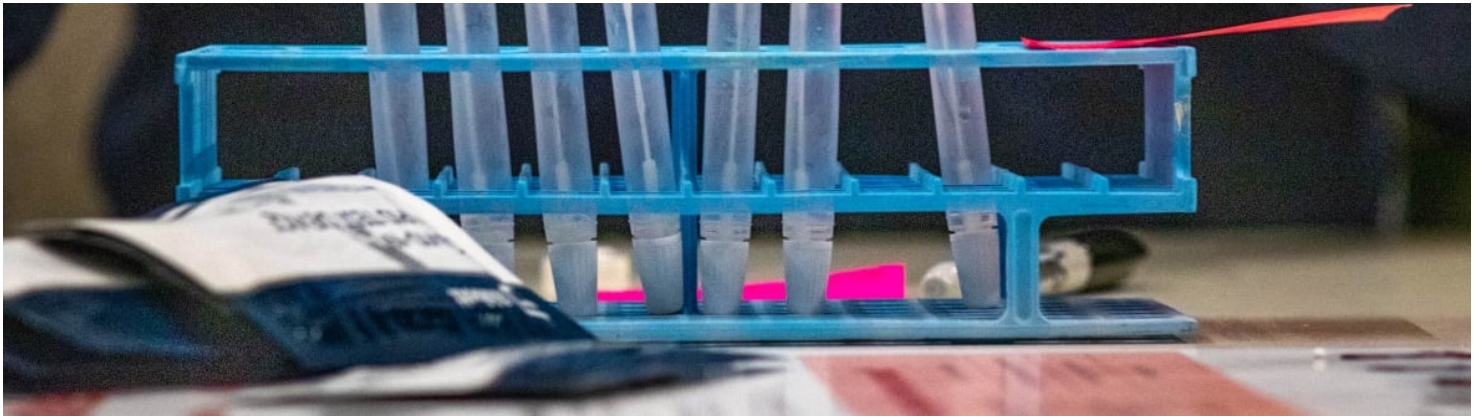
She described seeing the transmission and reconstructing it with data as "kind of mind blowing."

Cautionary tale

MacInnis said there are practical applications of this new genetic approach to tracking infectious diseases and said it is a new tool in the toolkit in the fight against COVID-19.

She said this study in particular offers an important "cautionary tale" in terms of public awareness and public health messaging, especially in the holiday season.





MacInnis said Nova Scotia has done well in its efforts to contain the pandemic. (Robert Short/CBC)

Impressed by Nova Scotia

In the case of her home province, MacInnis said she was "deeply impressed" and very proud of Nova Scotia's ability to keep COVID-19 in check.

She said while there are features of the province, like a relatively small and fairly isolated population, that made containment easier, the political and public will also played a big role.

MacInnis said she often refers her colleagues to Nova Scotia when discussing preventative measures and the "receptivity of the public to take them up and enforce them."

"I have no doubt that those practices have largely protected the province from the devastating experience that others are grappling with," she said

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