AURORA

From Alaska to Ukraine, gene-sequencing professor chases viruses

By Sam Bishop

*Above: Associate professor Devin Drown, left, discusses a flow cell with **Logan Mullen '17**, who works in the Genomics Core Lab. The flow cell holds genetic material for sequencing in the search for coronavirus variants. UAF photos by Leif Van Cise unless otherwise noted.*

Devin Drown jumped into tracking variants of the COVID-19 virus after the pandemic arrived in Alaska in early 2020. With a doctorate in genomics and two decades of

experience in the field, the UAF associate professor's background fit the moment.

Drown began staying up late into the night compiling weekly reports on variants in Alaska and their spread. The reports went to hospitals and public health authorities to help explain what was happening.

New case numbers, sometimes at a few hundred a day, seemed shocking as he worked on the reports through the winter and spring of 2020-2021.

Then, in January of this year, the numbers grew to an almost surreal plateau.

Devin Drown

“There’s so much going around that’s quite hard to avoid at this point,” Drown said in January, “especially given current practices and low vaccination rates.”

He spoke as the latest coronavirus variant — omicron — tore through the state, nation and world. On Jan. 24, Alaska’s average new daily case count across the previous seven-day period crested at 2,595, far above anything seen to date.

At the same time, across the nation, deaths from the coronavirus were shooting up again. During the omicron surge, the seven-day average daily death rate topped out at 2,677 on Feb. 2. Every day, a few Alaskans were among the dead.

Drown, a specialist in genome sequencing, helped track omicron's spread in Alaska, just as he'd done with other, earlier variants. He and others working in his lab in the West Ridge Research Building are part of a federally funded team that sequences and analyzes coronavirus samples provided by the Alaska State Virology Laboratory on the Fairbanks campus.

The team includes fellow UAF associate professor Jack Chen, who, as deputy director of the state lab, has been the driving force behind the state and university effort to sequence the genes of coronavirus variants in Alaska, Drown said. UAF professor Brian Barnes, as head of the Alaska IDeA Network of Biological Research Excellence, is lead investigator on the grant. Others on the team are University of Alaska Anchorage researchers Jason Burkhead, Cindy Knall and Eric Bortz.

Their work tells doctors and public health authorities what Alaskans are dealing with, allowing those officials to better recommend treatments such as monoclonal antibodies and other measures to battle the virus.

Variants rise fast

While omicron has been less deadly than other variants, Drown said, it still has devastating consequences for real people.

“We say ‘Oh well, omicron isn’t so bad,’” he said in January, “but it is for the 2,000 people that died yesterday. It’s terrible for them. And it’s terrible for their families that they’ve left behind.”

By mid-April, deaths and infections among Americans and Alaskans had dropped drastically. But the virus still infected more than 100 Alaskans every day. And the state recorded 15 deaths from COVID-19 among Alaskans in March 2022. In some parts of the country, cases were on the rise again in April as a new omicron variant, BA.2, spread.

Total cases were not rising in Alaska, as of mid-April, but they also weren't declining as fast as they might have, absent BA.2.

"The wave would have had a steeper decline if it wasn't for this new variant," Drown said.

The new variant is a twist on the original omicron virus.

"BA.2 is a subvariant of it, but genetically it's quite different," Drown said. "It does have a noticeable increase in transmissibility."

So, as with earlier variants such as delta and omicron BA.1.1, the BA.2 version of omicron quickly pushed out its predecessors.

Alaskans can expect more such cyclical peaks and valleys in infections as long as vaccination rates remain stuck at current levels — about 65% both in Alaska and nationwide, Drown said. That allows viruses to thrive, which in turn creates more opportunities to mutate into new forms.

“If we didn’t have so much virus, then we wouldn’t have this enormous pressure that provides the opportunity for more mutations,” he said.

Drown said he expects that the virus that causes COVID-19, officially called SARS-CoV-2, is here to stay, like the annual flu virus.

“And the vaccines are providing a really effective protection from hospitalization and severe illness and death, which is great, and our flu vaccines do the same,” he said. “But I think we still need to stay vigilant. We still need to be worried about the next variant arriving that is much more deadly.”

When variants show up, his genomics lab finds them and adds them to an online data dashboard that lets anyone see what is happening in Alaska.

The fancy microscope

Most sequencing of the genetic material, which allows identification of virus variants, occurs at

the state virology lab in the Biological Research and Diagnostics Facility on the Fairbanks campus. **Jayme Parker '19** heads the effort.

But a portion of sequencing also occurs in a several-square-foot box that sits on a counter in Drown's Genomics Core Lab on the second floor of the West Ridge Research Building.

Clockwise from top: Logan Mullen holds a flow cell; Mullen describes information on the screen of the machine that sequences genetic material that he has dropped into a flow cell; Mullen inserts a cassette that contains chemical reagents that attach fluorescent chemicals to nucleotides in the genetic material, giving each type of nucleotide a specific color that can be detected and recorded by the sequencer.

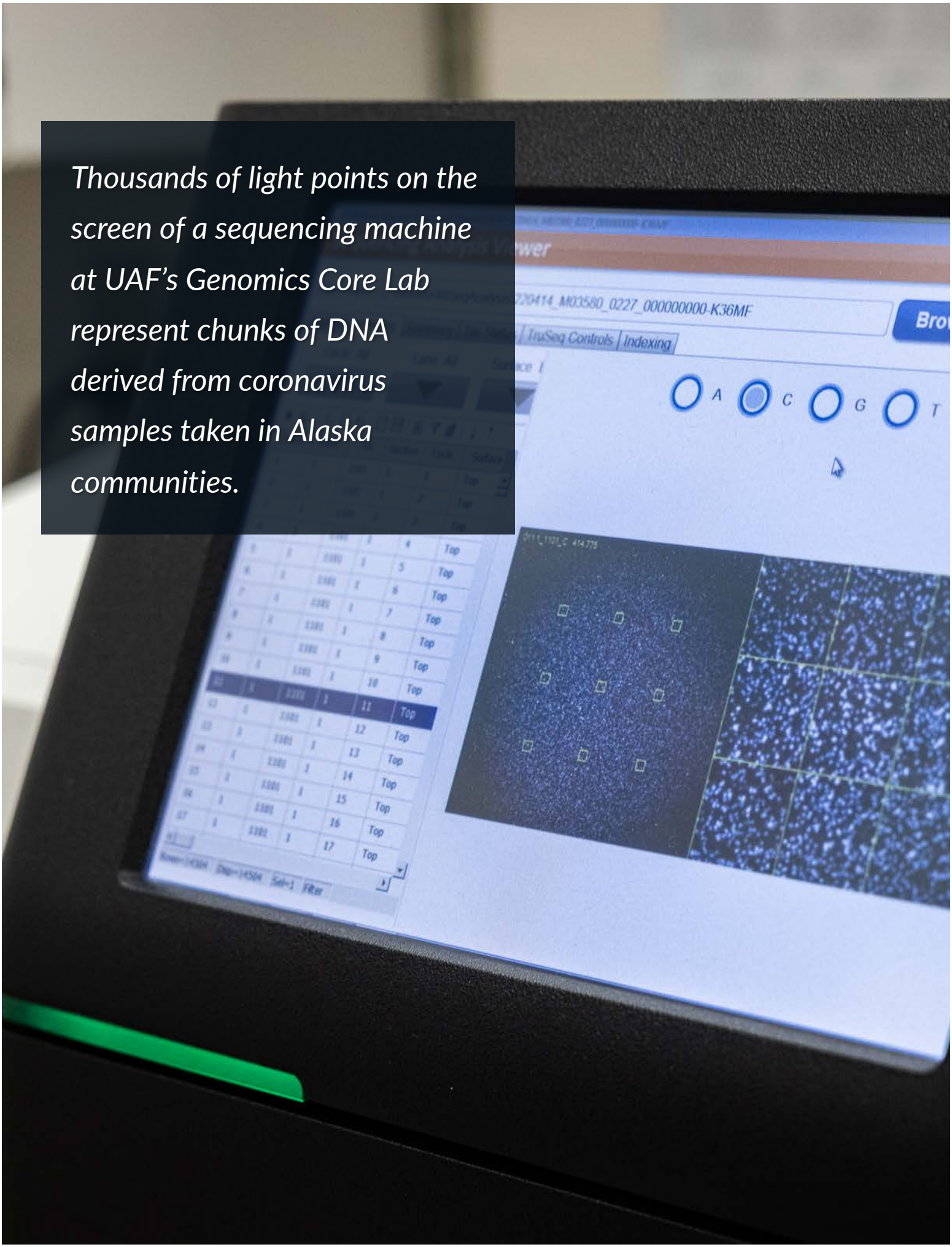
Clockwise from top: Logan Mullen holds a flow cell; Mullen describes information on the screen of the machine that sequences genetic material that he has dropped into a flow cell; Mullen inserts a cassette that contains chemical reagents that attach fluorescent chemicals to nucleotides in the genetic material, giving each type of nucleotide a specific color that can be detected and recorded by the sequencer.

A generic plastic case common to modern computer equipment garbs the instrument. A small door opens on the box's left side, allowing the operator to insert a glass slide, called a flow cell. The flow cell holds a solution containing coronavirus genetic material, which has been chopped into small segments and rendered noninfectious in another building on campus.

Logan Mullen, a former UAF entomology graduate student who Drown now employs to operate the lab's equipment, pointed to a computer screen mounted on the front of the box.

“The entire instrument is essentially a fancy microscope that’s taking pictures of what’s on that slide and translating those pictures into the sequencing data,” Mullen said.

The screen’s black background displayed thousands of tiny dots, something like a blurry telescope image of dense stars in a night sky. Each dot represented a section of genetic material containing a few hundred nucleotide pairs, the building blocks of DNA.



Thousands of light points on the screen of a sequencing machine at UAF's Genomics Core Lab represent chunks of DNA derived from coronavirus samples taken in Alaska communities.

Inside the box, a series of chemicals, called reagents, had washed over that DNA and attached fluorescent molecules to each nucleotide. The specific colors in the fluorescence reflect the presence of adenine, cytosine, guanine or thymine, the four base molecules that all DNA contains, and how they're paired within the nucleotides.

"A thousand little clusters, or pieces of DNA, are what the camera is photographing," Mullen said. "It can see the light given off by each little patch."

The computer compiles these tens of millions of data points to start to create a picture of the genetic material.

"The sequences we make, they're only 200-300 nucleotides long, but we have to assemble them together into a sequence that will eventually be 29,000 nucleotides long," Drown said.

The computer can properly piece together the data representing the shorter segments because it records the relative placement of the four base molecules, ACGT. Their positions, when mapped

across hundreds of nucleotides, reveal exactly where the segment should lie in the larger DNA molecule.

“Four positions in the order of 300 nucleotides — that’s a very unique sequence,” Drown said. “So then you can match it up.”

The computer does the matching up, and the resulting unique, longer sequence tells Drown and his research team which coronavirus variant is present.

Variant info helps treatments

In mid-summer 2021, as cases from the delta variant began to surge, keeping medical professionals up to date also kept Drown up late. They told him they needed what he was providing.

“That really kind of inspired me to stay up at 2 a.m. working on this while my household was asleep,” he said. “It was pretty tiring work, and that kind of kept me going, knowing that

somebody cared enough to read this thing, that they were using this."

Hospitals were studying the variant data to help them decide what type of monoclonal antibody treatments they needed for their patients.

> *"That really kind of inspired me to stay up at 2 a.m. working on this while my household was asleep."*

"Different monoclonals were more appropriate for different kinds of infections, and so I got emails from folks up on the North Slope, hospital directors, saying you know 'Hey your data is kind of limited here, can you tell us anything else?'" Drown said.

As recently as July 2021, Drown was hand-typing reports on the variant data every week and distributing them.

In August, he was able to stop compiling those reports after a master's student working in his

lab created an online tracking dashboard for the data.

"**Tracie Haan ('18, '21)** is the genius behind the dashboard," Drown said. "She has been winning awards for her talks and posters for a long time."

The dashboard allows a user to rapidly break down all of Alaska's sequencing information in multiple ways to see where, when and how fast variants are moving.

Identifying the variant can help health care professionals know how to treat patients.


Logan Mullen, at left, stands outside the West Ridge Research Building, where he works. At right, Mullen uses a multichannel pipette in the Genomics Core Lab.

For example, knowing that the omicron variant now accounts for almost 100 percent of the cases allows doctors to avoid prescribing ineffective monoclonals.

“One of the things that’s happened with omicron is it’s eliminated many of the monoclonal antibody treatments,” Drown said in January.

Drown’s team has applied for funding from the National Institutes of Health to continue the sequencing and maintain the dashboard. The first grant brought $770,000 to the team in July 2021, and the members hope to secure a similar second grant for another year of work.

“I think the genomic evidence is still of interest and of benefit to the public and public health measures,” Drown said.

Ukraine work

The pandemic wasn’t the only international news that became relevant to Drown in late January.

Russian military forces were surrounding Ukraine, where he worked from 2017 to 2019 on a project to genetically sequence African swine fever viruses to help stop their spread.

Eric Bortz, Drown's colleague on the coronavirus sequencing team at UAA, also worked in Ukraine on the project.

Bortz reported that colleagues in Kyiv and Kharkiv were subdued as they watched Russia's forces gather, Drown said in January.

"I listen with a keen interest to the news stories that we're hearing every day," he said. "You know, I'm telling my kids to be quiet at the breakfast table so I can get the latest announcement. It's something that's really at the forefront of my mind, because I know folks there and I care about them."

Drown, who grew up in New Hampshire, earned his Ph.D. at Washington State University and came to UAF in 2015 after a few years of working as a postdoctorate at Indiana University.

“I never thought I would be a researcher whose work was affected by a global pandemic and then, you know, potentially, political unrest,” he said in January.

That potential became reality in late February when Russia invaded Ukraine.

Drown said his work in Ukraine had no military application. The goal was to identify variants of the African swine fever virus and build Ukraine’s capacity to continue the effort. He and colleagues published their work, “Complete genome sequence of virulent African swine fever virus isolated from a domestic pig in Ukraine,” in the journal Microbiology Resource Announcements in 2019.

Humans can’t be infected with African swine fever, but it’s bad news for hogs. “I always think about it as Ebola for pigs,” Drown said.

Ukraine and other countries in the region rely upon pork for food. If a virus killed large numbers of the pigs, it could destabilize the area. The possibility worried the Pentagon’s Defense Threat Reduction Agency enough that it

provided initial funding for Drown, Bortz and others to travel to Ukraine.

“We worked with fantastic scientists, students — they all had a real keen interest in learning the science and technology,” Drown said.

Drown said he and Bortz are still in contact intermittently with the Ukrainian researchers. Bortz sent Drown a photograph of the research lab in Kharkiv, taken sometime after the invasion.

“Every window in the building had been blown out,” Drown said.

Still, the work went on. On Friday, April 22, the journal Viruses accepted a paper written by a graduate student with whom Drown worked in Ukraine and who collaborated with one of his UAF graduate students. The student had submitted the paper to the journal after the invasion.

“They were putting the final touches on it from the bomb shelter in Kharkiv,” Drown said.

Pipetting equipment hangs above Logan Mullen's work area in the Genomics Core Lab.

Aurora home