

# Could COVID-19 Have Escaped from a Lab?

The world's preeminent scientists say a theory from the Broad Institute's Alina Chan is too wild to be believed. But when the theory is about the possibility of COVID being man-made, is this science or censorship?

By Rowan Jacobsen, *Boston Magazine*, 9 September 2020

In January, as she watched the news about a novel virus spreading out of control in China, Alina Chan braced for a shutdown. The molecular biologist at the Broad Institute of Harvard and MIT started stockpiling medicine and supplies. By the time March rolled around and a quarantine seemed imminent, she'd bought hundreds of dollars' worth of fillets from her favorite fishmonger in Cambridge and packed them into her freezer. Then she began to ramp down her projects in the lab, isolating her experimental cells from their cultures and freezing them in small tubes.

As prepared as she was for the shutdown, though, she found herself unprepared for the frustration of being frozen out of work. She paced the walls of her tiny apartment feeling bored and useless. Chan has been a puzzle demon since childhood, which was precisely what she loved about her work—the chance to solve fiendishly difficult problems about how viruses operate and how, through gene therapy, they could be repurposed to help cure devastating genetic diseases. Staring out her window at the eerily quiet streets of her Inman Square neighborhood, she groaned at the thought that it could be months before she was at it again. Her mind wandered back to 2003, when she was a teenager growing up in Singapore and the first SARS virus, a close relative of this coronavirus, appeared in Asia. It hadn't been anything like this. That one had been relatively easy to corral. How had this virus come out of nowhere and shut down the planet? Why was it so different? she asked herself.

Then it hit her: The world's greatest puzzle was staring her in the face. Stuck at home, all she had to work with was her brain and her laptop. Maybe they were enough. Chan fired up the kettle for the first of what would become hundreds of cups of tea, stacked four boxes on her kitchen counter to raise her laptop to the proper height, pulled back her long dark hair, and began reading all of the scientific literature she could find on the coronavirus.

It wasn't long before she came across an article about the remarkable stability of the virus, whose genome had barely changed from the earliest human cases, despite trillions of replications. This perplexed Chan. Like many emerging infectious diseases, COVID-19 was thought to be zoonotic—it originated in animals, then somehow found its way into people. At the time, the Chinese government and most scientists insisted the

jump had happened at Wuhan's seafood market, but that didn't make sense to Chan. If the virus had leapt from animals to humans in the market, it should have immediately started evolving to life inside its new human hosts. But it hadn't.

On a hunch, she decided to look at the literature on the 2003 SARS virus, which had jumped from civets to people. Bingo. A few papers mentioned its rapid evolution in its first months of existence. Chan felt the familiar surge of puzzle endorphins. The new virus really wasn't behaving like it should. Chan knew that delving further into this puzzle would require some deep genetic analysis, and she knew just the person for the task. She opened Google Chat and fired off a message to Shing Hei Zhan. He was an old friend from her days at the University of British Columbia and, more important, he was a computational god.

"Do you want to partner on a very unusual paper?" she wrote.

Sure, he replied.

One thing Chan noticed about the original SARS was that the virus in the first human cases was subtly different—a few dozen letters of genetic code—from the one in the civets. That meant it had immediately morphed. She asked Zhan to pull up the genomes for the coronaviruses that had been found on surfaces in the Wuhan seafood market. Were they at all different from the earliest documented cases in humans?

Zhan ran the analysis. Nope, they were 100 percent the same. Definitely from humans, not animals. The seafood-market theory, which Chinese health officials and the World Health Organization espoused in the early days of the pandemic, was wrong. Chan's puzzle detectors pulsed again. "Shing," she messaged Zhan, "this paper is going to be insane."

In the coming weeks, as the spring sun chased shadows across her kitchen floor, Chan stood at her counter and pounded out her paper, barely pausing to eat or sleep. It was clear that the first SARS evolved rapidly during its first three months of existence, constantly fine-tuning its ability to infect humans, and settling down only during the later stages of the epidemic. In contrast, the new virus looked a lot more like late-stage SARS. "It's almost as if we're missing the early phase," Chan marveled to Zhan. Or, as she put it in their paper, as if "it was already well adapted for human transmission."

That was a profoundly provocative line. Chan was implying that the virus was already familiar with human physiology when it had its coming-out party in Wuhan in late 2019. If so, there were three possible explanations.

Perhaps it was just staggeringly bad luck: The mutations had all occurred in an earlier host species, and just happened to be the perfect genetic arrangement for an invasion of humanity. But that made no sense. Those mutations would have been disadvantageous in the old host.

Maybe the virus had been circulating undetected in humans for months, working out the kinks, and nobody had noticed. Also unlikely. China's health officials would not have missed it, and even if they had, they'd be able to go back now through stored samples to find the trail of earlier versions. And they weren't coming up with anything.

That left a third possibility: The missing phase had happened in a lab, where the virus had been trained on human cells. Chan knew this was the third rail of potential

explanations. At the time, conspiracy theorists were spinning bioweapon fantasies, and Chan was loath to give them any ammunition. But she also didn't want to play politics by withholding her findings. Chan is in her early thirties, still at the start of her career, and an absolute idealist about the purity of the scientific process. Facts were facts.

Or at least they used to be. Since the start of the pandemic, the Trump administration has been criticized for playing fast and loose with facts—denying, exaggerating, or spinning them to suit the president's political needs. As a result, many scientists have learned to censor themselves for fear that their words will be misrepresented. Still, Chan thought, if she were to sit on scientific research just to avoid providing ammunition to conspiracy theorists or Trump, would she be any better than them?

Chan knew she had to move forward and make her findings public. In the final draft of her paper, she torpedoed the seafood-market theory, then laid out a case that the virus seemed curiously well adapted to humans. She mentioned all three possible explanations, carefully wording the third to emphasize that if the novel coronavirus did come from a lab, it would have been the result of an accident in the course of legitimate research.

On May 2, Chan uploaded the paper to a site where as-yet-unpublished biology papers known as “preprints” are shared for open peer review. She tweeted out the news and waited. On May 16, the Daily Mail, a British tabloid, picked up her research. The very next day, Newsweek ran a story with the headline “Scientists Shouldn't Rule Out Lab as Source of Coronavirus, New Study Says.”

And that, Chan says, is when “shit exploded everywhere.”

Chan had come to my attention a week before the Newsweek story was published through her smart and straightforward tweets, which I found refreshing at a time when most scientists were avoiding any serious discussion about the possibility that COVID-19 had escaped from a biolab. I'd written a lot about genetic engineering and so-called gain-of-function research—the fascinating, if scary, line of science in which scientists alter viruses to make them more transmissible or lethal as a way of assessing how close those viruses are to causing pandemics. I also knew that deadly pathogens escape from biolabs with surprising frequency. Most of these accidents end up being harmless, but many researchers have been infected, and people have died as a result.

For years, concerned scientists have warned that this type of pathogen research was going to trigger a pandemic. Foremost among them was Harvard epidemiologist Marc Lipsitch, who founded the Cambridge Working Group in 2014 to lobby against these experiments. In a series of policy papers, op-eds, and scientific forums, he pointed out that accidents involving deadly pathogens occurred more than twice a week in U.S. labs, and estimated that just 10 labs performing gain-of-function research over a 10-year period would run a nearly 20 percent risk of an accidental release. In 2018, he argued that such a release could “lead to global spread of a virulent virus, a biosafety incident on a scale never before seen.”

Thanks in part to the Cambridge Working Group, the federal government briefly instituted a moratorium on such research. By 2017, however, the ban was lifted and U.S.

labs were at it again. Today, in the United States and across the globe, there are dozens of labs conducting experiments on a daily basis with the deadliest known pathogens. One of them is the Wuhan Institute of Virology. For more than a decade, its scientists have been discovering coronaviruses in bats in southern China and bringing them back to their lab in Wuhan. There, they mix genes from different strains of these novel viruses to test their infectivity in human cells and lab animals.

When word spread in January that a novel coronavirus had caused an outbreak in Wuhan—which is a thousand miles from where the bats that carry this lineage of viruses are naturally found—many experts were quietly alarmed. There was no proof that the lab was the source of the virus, but the pieces fit.

Despite the evidence, the scientific community quickly dismissed the idea. Peter Daszak, president of EcoHealth Alliance, which has funded the work of the Wuhan Institute of Virology and other labs searching for new viruses, called the notion “preposterous,” and many other experts echoed that sentiment.

That wasn’t necessarily what every scientist thought in private, though. “They can’t speak directly,” one scientist told me confidentially, referring to the virology community’s fear of having their comments sensationalized in today’s politically charged environment. “Many virologists don’t want to be hated by everyone in the field.”

There are other potential reasons for the pushback. There’s long been a sense that if the public and politicians really knew about the dangerous pathogen research being conducted in many laboratories, they’d be outraged. Denying the possibility of a catastrophic incident like this, then, could be seen as a form of career preservation. “For the substantial subset of virologists who perform gain-of-function research,” Richard Ebright, a Rutgers microbiologist and another founding member of the Cambridge Working Group, told me, “avoiding restrictions on research funding, avoiding implementation of appropriate biosafety standards, and avoiding implementation of appropriate research oversight are powerful motivators.” Antonio Regalado, biomedicine editor of MIT Technology Review, put it more bluntly. If it turned out COVID-19 came from a lab, he tweeted, “it would shatter the scientific edifice top to bottom.”

That’s a pretty good incentive to simply dismiss the whole hypothesis, but it quickly amounted to a global gaslighting of the media—and, by proxy, the public. An unhealthy absolutism set in: Either you insisted that any questions about lab involvement were absurd, or you were a tool of the Trump administration and its desperation to blame China for the virus. I was used to social media pundits ignoring inconvenient or politically toxic facts, but I’d never expected to see that from some of our best scientists.

Which is why Chan stood out on Twitter, daring to speak truth to power. “It is very difficult to do research when one hypothesis has been negatively cast as a conspiracy theory,” she wrote. Then she offered some earnest advice to researchers, suggesting that most viral research should be done with neutered viruses that have had their replicating machinery removed in advance, so that even if they escaped confinement, they would be incapable of making copies of themselves. “When these precautions are not followed, risk of lab escape is exponentially higher,” she explained, adding, “I hope the pandemic motivates local ethics and biosafety committees to think

carefully about how they can reduce risk.” She elaborated on this in another tweet several days later: “I’d also—personally—prefer if high biosafety level labs were not located in the most populous cities on earth.”

Chan had started using her Twitter account this intensely only a few days earlier, as a form of outreach for her paper. The social platform has become the way many scientists find out about one another’s work, and studies have shown that attention on Twitter translates to increased citations for a paper in scientific literature. But it’s a famously raw forum. Many scientists are not prepared for the digital storms that roil the Twitterverse, and they don’t handle it well. Chan dreaded it at first, but quickly took to Twitter like a digital native. “Having Twitter elevates your work,” she says. “And I think it’s really fun to talk to nonscientists about that work.”

After reading her tweets, I reviewed her preprint, which I found mind-blowing, and wrote her to say so. She thanked me and joked that she worried it might be “career suicide.”

It wasn’t long before it began to look like she might be right.

Speaking her mind, it turns out—even in the face of censure—was nothing new for Chan, who is Canadian but was raised in Singapore, one of the more repressive regimes on earth. Her parents, both computer science professionals, encouraged free thinking and earnest inquiry in their daughter, but the local school system did not. Instead, it was a pressure-cooker of a system that rewarded students for falling in line, and moved quickly to silence rebels.

That was a bad fit for Chan. “You have to bow to teachers,” she says. “Sometimes teachers from other classes would show up and ask me to bow to them. And I would say, ‘No, you’re not my teacher.’ Back then they believed in corporal punishment. A teacher could just take a big stick and beat you in front of the class. I got whacked so many times.”

Still, Chan rebelled in small ways, skipping school and hanging out at the arcade. She also lost interest in her studies. “I just really didn’t like school. And I didn’t like all the extracurriculars they pack you with in Singapore,” she says. That changed when a teacher recruited her for math Olympiads, in which teams of students compete to solve devilishly hard arithmetic puzzles. “I really loved it,” she says. “You just sit in a room and think about problems.”

Chan might well have pursued a career in math, but then she came up against teams from China in Olympiad competitions. “They would just wipe everyone else off the board,” she says. “They were machines. They’d been trained in math since they could walk. They’d hit the buzzer before you could even comprehend the question. I thought, I’m not going to survive in this field.”

Chan decided to pursue biology instead, studying at the University of British Columbia. “I liked viruses from the time I was a teen,” she says. “I remember the first time I learned about HIV. I thought it was a puzzle and a challenge.” That instinct took her to Harvard Medical School as a postdoc, where the puzzle became how to build virus-like biomolecules to accomplish tasks inside cells, and then to Ben Deverman’s lab at the

Broad Institute. “When I see an interesting question, I want to spend 100 percent of my time working on it,” she says. “I get really fixated on answering scientific questions.”

Deverman, for his part, says he wasn’t actively looking to expand his team when Chan came along, but when “opportunities to hire extraordinary people fall in my lap,” he takes them. “Alina brings a ton of value to the lab,” he explains, adding that she has an ability to pivot between different topics and cut to the chase. Nowhere was that more on display than with her coronavirus work, which Deverman was able to closely observe. In fact, Chan ran so many ideas past him that he eventually became a coauthor. “She is insightful, determined, and has the rare ability to explain complex scientific findings to other scientists and to the public,” he says.

Those skills would prove highly useful when word got out about her coronavirus paper.

If Chan had spent a lifetime learning how to pursue scientific questions, she spent most of the shutdown learning what happens when the answers you come up with are politically radioactive. After the Newsweek story ran, conservative-leaning publications seized on her paper as conclusive evidence that the virus had come from a lab. “Everyone focused on the one line,” Chan laments. “The tabloids just zoomed in on it.” Meanwhile, conspiracists took it as hard evidence of their wild theories that there had been an intentional leak.

Chan spent several exhausting days putting out online fires with the many people who had misconstrued her findings. “I was so naive,” she tells me with a quick, self-deprecating laugh. “I just thought, Shouldn’t the world be thinking about this fairly? I really have to kick myself now.”

Even more troubling, though, were the reactions from other scientists. As soon as her paper got picked up by the media, luminaries in the field sought to censure her. Jonathan Eisen, a well-known professor at UC Davis, criticized the study in Newsweek and on his influential Twitter account, writing, “Personally, I do not find the analysis in this new paper remotely convincing.” In a long thread, he argued that comparing the new virus to SARS was not enough to show that it was preadapted to humans. He wanted to see comparisons to the initial leap of other viruses from animals to humans.

Moments later, Daszak piled on. The NIH had recently cut its grant to his organization, EcoHealth Alliance, after the Trump administration learned that some of it had gone to fund the Wuhan Institute of Virology’s work. Daszak was working hard to get it restored and trying to stamp out any suggestion of a lab connection. He didn’t hold back on Chan. “This is sloppy research,” he tweeted, calling it “a poorly designed phylogenetic study with too many inferences and not enough data, riding on a wave of conspiracy to drive a higher impact.” Peppering his tweets with exclamation points, he attacked the wording of the paper, arguing that one experiment it cited was impossible, and told Chan she didn’t understand her own data. Afterward, a Daszak supporter followed up his thread with a GIF of a mike drop.

It was an old and familiar dynamic: threatened silverback male attempts to bully a junior female member of the tribe. As a postdoc, Chan was in a vulnerable position. The world of science is still a bit medieval in its power structure, with a handful of institutions

and individuals deciding who gets published, who gets positions, who gets grants. There's little room for rebels.

What happened next was neither old nor familiar: Chan didn't back down. "Sorry to disrupt mike drop," she tweeted, providing a link to a paper in the prestigious journal *Nature* that "does that exact experiment you thought was impossible." Politely but firmly, she justified each point Daszak had attacked, showing him his mistakes. In the end, Daszak was reduced to arguing that she had used the word "isolate" incorrectly. In a coup de grâce, Chan pointed out that actually the word had come from online data provided by GenBank, the NIH's genetic sequence database. She offered to change it to whatever made sense. At that point, Daszak stopped replying. He insists, however, that Chan is overinterpreting her findings.

With Eisen, Chan readily agreed to test her hypothesis by finding other examples of viruses infecting new hosts. Within days, a perfect opportunity came along when news broke that the coronavirus had jumped from humans to minks at European fur farms. Sure enough, the mink version began to rapidly mutate. "You actually see the rapid evolution happening," Chan said. "Just in the first few weeks, the changes are quite drastic."

Chan also pointed out to Eisen that the whole goal of a website such as bioRxiv (pronounced "bioarchive")—where she posted the paper—is to elicit feedback that will make papers better before publication. Good point, he replied. Eventually he conceded that there was "a lot of interesting analysis in the paper" and agreed to work with Chan on the next draft.

The Twitter duels with her powerful colleagues didn't rattle Chan. "I thought Jonathan was very reasonable," she says. "I really appreciated his expertise, even if he disagreed with me. I like that kind of feedback. It helped to make our paper better."

With Daszak, Chan is more circumspect. "Some people have trouble keeping their emotions in check," she says. "Whenever I saw his comments, I'd just think, Is there something I can learn here? Is there something he's right about that I should be fixing?" Ultimately, she decided, there was not.

By late May, both journalists and armchair detectives interested in the mystery of the coronavirus were discovering Chan as a kind of Holmes to our Watson. She crunched information at twice our speed, zeroing in on small details we'd overlooked, and became a go-to for anyone looking for spin-free explications of the latest science on COVID-19. It was thrilling to see her reasoning in real time, a reminder of why I've always loved science, with its pursuit of patterns that sometimes leads to exciting revelations. The website CNET featured her in a story about "a league of scientists-turned-detectives" who were using genetic sequencing technologies to uncover COVID-19's origins. After it came out, Chan added "scientist-turned-detective" to her Twitter bio.

She's lived up to her new nom de tweet. As the search for the source of the virus continued, several scientific teams published papers identifying a closely related coronavirus in pangolins—anteater-like animals that are heavily trafficked in Asia for their meat and scales. The number of different studies made it seem as though this virus was ubiquitous in pangolins. Many scientists eagerly embraced the notion that the

animals might have been the intermediate hosts that had passed the novel coronavirus to humans. It fit their preexisting theories about wet markets, and it would have meant no lab had been involved.

As Chan read the pangolin papers, she grew suspicious. The first one was by a team that had analyzed a group of the animals intercepted by anti-smuggling authorities in southern China. They found the closely related virus in a few of them, and published the genomes for that virus. Some of the other papers, though, were strangely ambiguous about where their data was coming from, or how their genomes had been constructed. Had they really taken samples from actual pangolins?

Once again, Chan messaged Shing Hei Zhan. “Shing, something’s weird here,” she wrote. Zhan pulled up the raw data from the papers and compared the genomes they had published. Individual copies of a virus coming from different animals should have small differences, just as individuals of a species have genetic differences. Yet the genomes in all of the pangolin papers were perfect matches—the authors were all simply using the first group’s data set. Far from being ubiquitous, the virus had been found only in a few pangolins who were held together, and it was unclear where they had caught it. The animals might have even caught it from their own smuggler.

Remarkably, one group of authors in *Nature* even appeared to use the same genetic sequences from the other paper as if it were confirmation of their own discovery. “These sequences appear to be from the same virus (Pangolin-CoV) that we identified in the present study.”

Chan called them out on Twitter: “Of course it’s the same Pangolin-CoV, you used the same dataset!” For context, she later added, “Imagine if clinical trials were playing fast and loose with their patient data; renaming patients, throwing them into different datasets without clarification, possibly even describing the same patient multiple times across different studies unintentionally.”

She and Zhan posted a new preprint on bioRxiv dismantling the pangolin papers. Confirmation came in June when the results of a study of hundreds of pangolins in the wildlife trade were announced: Not a single pangolin had any sign of a coronavirus. Chan took a victory lap on Twitter: “Supports our hypothesis all this time.” The pangolin theory collapsed.

Chan then turned her Holmesian powers on bigger game: Daszak and the Wuhan Institute of Virology. Daszak had been pleading his case everywhere from *60 Minutes* to the *New York Times* and has been successful in rallying sympathy to his cause, even getting 77 Nobel laureates to sign a letter calling for the NIH to restore EcoHealth Alliance’s funding.

In several long and detailed “tweetorials,” Chan began to cast a cloud of suspicion on the WIV’s work. She pointed out that scientists there had discovered a virus that is more than 96 percent identical to the COVID-19 coronavirus in 2013 in a mineshaft soon after three miners working there had died from a COVID-like illness. The WIV didn’t share these findings until 2020, even though the goal of such work, Chan pointed out, was supposedly to identify viruses with the potential to cause human illnesses and warn the world about them.

Even though that virus had killed three miners, Daszak said it wasn't considered a priority to study at the time. "We were looking for SARS-related virus, and this one was 20 percent different. We thought it was interesting, but not high risk. So we didn't do anything about it and put it in the freezer," he told a reporter from Wired. It was only in 2020, he maintained, that they started looking into it once they realized its similarity to COVID-19. But Chan pointed to an online database showing that the WIV had been genetically sequencing the mine virus in 2017 and 2018, analyzing it in a way they had done in the past with other viruses in preparation for running experiments with them. Diplomatic yet deadpan, she wrote, "I think Daszak was misinformed."

For good measure, almost in passing, Chan pointed out a detail no one else had noticed: COVID-19 contains an uncommon genetic sequence that has been used by genetic engineers in the past to insert genes into coronaviruses without leaving a trace, and it falls at the exact point that would allow experimenters to swap out different genetic parts to change the infectivity. That same sequence can occur naturally in a coronavirus, so this was not irrefutable proof of an unnatural origin, Chan explained, "only an observation." Still, it was enough for one Twitter user to muse, "If capital punishment were as painful as what Alina Chan is doing to Daszak/WIV regarding their story, it would be illegal."

Daszak says that indeed he had been misinformed and was unaware that that virus found in the mine shaft had been sequenced before 2020. He also says that a great lab, with great scientists, is now being picked apart to search for suspicious behavior to support a preconceived theory. "If you believe, deep down, something fishy went on, then what you do is you go through all the evidence and you try to look for things that support that belief," he says, adding, "That is not how you find the truth."

Many of the points in Chan's tweektorials had also been made by others, but she was the first reputable scientist to put it all together. That same week, London's Sunday Times and the BBC ran stories following the same trail of breadcrumbs that Chan had laid out to suggest that there had been a coverup at the WIV. The story soon circulated around the world. In the meantime, the WIV has steadfastly denied any viral leak. Lab director Yanyi Wang went on Chinese television and described such charges as "pure fabrication," and went on to explain that the bat coronavirus from 2013 was so different than COVID that it could not have evolved into it this quickly and that the lab only sequenced it and didn't obtain a live virus from it.

To this day, there is no definitive evidence as to whether the virus occurred naturally or had its origins in a lab, but the hypothesis that the Wuhan facility was the source is increasingly mainstream and the science behind it can no longer be ignored. And Chan is largely to thank for that.

In late spring, Chan walked through the tall glass doors of the Broad Institute for the first time in months. As she made her way across the gleaming marble foyer, her sneaker squeaks echoed in the silence. It was like the zombie apocalypse version of the Broad; all the bright lights but none of the people. It felt all the weirder that she was wearing her gym clothes to work.

A few days earlier, the Broad had begun letting researchers back into their labs to restart their projects. All computer work still needed to be done remotely, but bench scientists such as Chan could pop in just long enough to move along their cell cultures, provided they got tested for the virus every four days.

In her lab, Chan donned her white lab coat and took inventory, throwing out months of expired reagents and ordering new materials. Then she rescued a few samples from the freezer, took her seat at one of the tissue-culture hoods—stainless steel, air-controlled cabinets in which cell engineers do their work—and began reviving some of her old experiments.

She had mixed emotions about being back. It felt good to free her gene-therapy projects from their stasis, and she was even more excited about the new project she and Deverman were working on: an online tool that allows vaccine developers to track changes in the virus's genome by time, location, and other characteristics. "It came out of my personal frustration at not being able to get answers fast," she says.

On the other hand, she missed being all-consuming by her detective work. "I wanted to stop after the pangolin preprint," she says, "but this mystery keeps drawing me back in." So while she waits for her cell cultures to grow, she's been sleuthing on the side—only this time she has more company: Increasingly, scientists have been quietly contacting her to share their own theories and papers about COVID-19's origins, forming something of a growing underground resistance. "There's a lot of curiosity," she says. "People are starting to think more deeply about it." And they have to, she says, if we are going to prevent future outbreaks: "It's really important to find out where this came from so it doesn't happen again."

That is what keeps Chan up at night—the possibility of new outbreaks in humans from the same source. If the virus emerged naturally from a bat cave, there could well be other strains in existence ready to spill over. If they are closely related, whatever vaccines we develop might work on them, too. But that might not be the case with manipulated viruses from a laboratory. "Someone could have been sampling viruses from different caves for a decade and just playing mix-and-match in the lab, and those viruses could be so different from one another that none of our vaccines will work on them," she says. Either way, "We need to find where this came from, and close it down."

Whatever important information she finds, we can be sure Chan will share it with the world. Far from being shaken by the controversy her paper stirred, she is more committed than ever to holding a line that could all too easily be overrun. "Scientists shouldn't be censoring themselves," she says. "We're obliged to put all the data out there. We shouldn't be deciding that it's better if the public doesn't know about this or that. If we start doing that, we lose credibility, and eventually we lose the public's trust. And that's not good for science." In fact, it would cause an epidemic of doubt, and that wouldn't be good for any of us.