modernizing their swine production towards the end of the 20th century and needed sows bred to produce larger litters of piglets, which were only available from the US, Canada, and Europe. Imported swine had to be documented to be free of certain pathogens such as African swine fever, but most pigs were not tested for influenza or quarantined. Because influenza frequently infects pigs asymptomatically, it makes an excellent stowaway. How had influenza viruses reached geographically isolated areas such as Western Australia, with its stringent quarantine requirements for imported animals? We were learning that the story of the 2009 pandemic had a twist. Yes, one H1N1 influenza virus had managed to jump from a pig to a human to spark the 2009 pandemic. But humans also transmitted influenza viruses to swine in what's known as reverse zoonosis, all over the world en masse, including in Australia. Humans may also have infected swine with influenza virus at agricultural fairs and state fairs—and that the risk of another influenza pandemic arising from pigs had only increased since 2009.

At first, the introduction of human viruses into swine herds created a disease problem largely restricted to pigs. But in each country, the human-sourced pandemic viruses quickly reassorted with other endemic swine viruses to create novel strains, some of which began to infect people. For example, during the summer of 2012, more than 300 American children, primarily in Ohio and Indiana, were infected by viruses from their show pigs, and my colleagues and I found that the viruses involved in that outbreak contained a piece of genetic material introduced into US herds by humans during the pandemic. This later round of zoonotic infections never established human-to-human transmission, so the strains never went global. But the scare was a wake-up call that new infectious diseases can arise at any time from unexpected sources—even from America’s wholesome state fairs—and that the risk of another influenza pandemic arising from pigs had only increased since 2009.

Still, the origins of the 2009 pandemic remained mysterious—and, frankly, a bit confusing. My collaborators sequencing flu viruses from Latin American pig herds turned up plenty of new viruses of human origin, but none contained genetic material from the Eurasian lineage that had donated two crucial segments to the pandemic virus. The more countries in the Americas that failed to sequence a match to the pandemic virus, or even a shred of evidence that Eurasian viruses had made it there, the more doubtful I became that the pandemic could have originated in the West. Had it come from Asia after all? Pigs can fly

Even though I found no support for my hypothesis about the pandemic’s swine origins being in the West, six years of digging had not been wasted. By 2015, labor-intensive viral collection, diagnostic testing, lab prep, genetic sequencing, and genetic analyses had revealed how the world’s billion swine move within and between countries, spreading flu viruses efficiently. We also discovered that most routes are not round-trip. Every pig that legally crosses international borders is reported to the United Nations Comtrade database, yielding data on the numbers of live swine traded between various countries each year. So I collaborated with NIH epidemiologist Cécile Viboud to build simulations from trade data to predict whether a virus residing in one country’s swine population is likely to spread to neighboring countries, or overseas. This simulation, published in 2015 in Nature Communications, predicted that countries such as the US that export many pigs act as “sources” for swine influenza around the world. Other countries, including China and Mexico, act as “sinks”—destinations that receive many pigs but where few pigs travel out. In sink areas, imported viruses can take root and evolve into new forms that go undetected without targeted surveillance. In other words, from the perspective of swine influenza, Mexico is like Vegas: what happens there stays there—at least, until it jumps to another species.

Ultimately, this means swine viruses in the US, Canada, and major exporting countries in Europe readily disperse along international trade routes, creating hubs of viral diversity across Asia and in countries such as Mexico. China was not the only country where the classical, Eurasian, and triple-reassortant lineages likely circulated and combined to create new viruses. And, because some of these countries, including Mexico, export few live animals, they could host new viruses for decades that never spread elsewhere. This could create niches for the hidden evolution of viral lineages—which, in theory, could explain the 2009 virus’s novelty and why it was so hard to pinpoint its origin.

And yet, while sampling Mexico’s swine herds in the years following the pandemic did uncover new Mexico-specific viruses, the