

Alexandria Real Estate Equities, one of the largest owners of commercial lab space in the region, says that 99% of its Cambridge properties are occupied. In such a competitive market, most landlords will choose established tenants over potentially unstable start-ups. Although Cambridge has added 465,000 square metres of lab space since 2007, most of that has gone to large firms, says Peter Abair, director of economic development and global affairs at the Massachusetts Biotechnology Council in Cambridge.

SHARED SPACES

The local community recognizes that start-ups need to be nurtured for the biotech hub to thrive, says Peter Parker, a co-founder of LabCentral in Kendall Square. One of several local projects created to provide lab space and equipment to help start-ups get off the ground quickly, LabCentral receives state funding as well as corporate sponsorship from large pharmaceutical firms. It plans to double its occupancy in the next two years. MITIMCo, a division of MIT that manages the institution's sizeable property holdings, has also committed to housing start-ups.

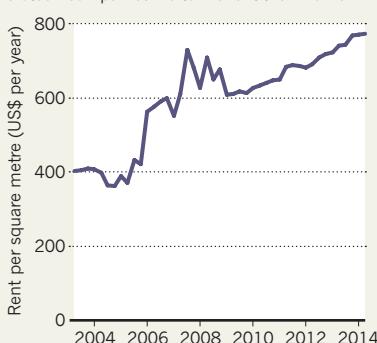
But start-ups may disperse to the suburbs anyway, says José Lobo, who studies urban economies at Arizona State University in Tempe. Kendall Square's story is an anomaly, he says — urban centres around the world have tried to replicate it, mostly without success. And in places where biotech is thriving, such as the San Francisco Bay Area in California and the outskirts of Washington DC, it is more spread out. Having run out of affordable space in Kendall Square, Boston's biotech firms may soon follow that pattern, he says: "I won't be surprised if they leave."

Some already have. Wilson says that Unum Therapeutics is now close to signing a lease on the outskirts of Cambridge. He suspects that more will do the same, forming new start-up clusters in the suburbs. "We'll see how it evolves," he says. "But it'll be a very different feel." ■

SOURCE: TRANSWESTERN R&B

UP AND AWAY

The price of lab space in the Kendall Square region of Cambridge, Massachusetts, has risen dramatically over the past decade as drug and biotech companies vie to make it their home.



A medical worker in South Korea handles a sample from a man suspected of having the MERS virus.

SOUTH KOREA

MERS cases spotlight lack of research

Outbreak of Middle East respiratory syndrome in South Korea is controllable, but how it infects humans is a puzzle.

BY DECLAN BUTLER

The world is watching South Korea as the latest outbreak of Middle East respiratory syndrome (MERS) unfolds. But how exactly the virus jumps to humans in the first place is still unknown, and clues to that puzzle lie thousands of kilometres away.

As *Nature* went to press, the cluster of hospital-associated cases in South Korea — the largest MERS outbreak outside the Middle East — had killed 7 people and infected 95, according to the World Health Organization (WHO). Hundreds of schools have been shut. Although the causal coronavirus, MERS-CoV, is considered a potential pandemic threat, specialists told *Nature* that they expect authorities to quickly bring this outbreak under control.

A much bigger challenge than emergency response, they say, is how to stop MERS being transmitted from animals to people in the Middle East, where it is endemic in camels. "The focus on South Korea would be better directed towards Saudi Arabia," says David Heymann, a researcher at the London School of Hygiene and Tropical Medicine and chair of Public Health England, to stop the cases that

continue to spark new outbreaks at the source.

Since it was first detected in Saudi Arabia in 2012, MERS-CoV has infected around 1,200 people worldwide, roughly 450 of whom have died, according to the WHO. The virus is thought to originate in bats and to jump to humans through an intermediate animal, such as camels. It does not easily spread between people, partly because it infects deep areas of the lungs, and is not coughed out. Most of the human infections, however, were the result of human-to-human spread, which can occur in hospitals when certain medical procedures combine with poor infection control to disseminate the virus. The latest clusters began when a South Korean man returned to Seoul from the Middle East, and visited four health-care facilities before he was diagnosed.

There is always a chance that as the virus spreads, it could acquire mutations that allow it to spread more easily between humans. But on 6 June, the South Korean health ministry announced that it had sequenced the virus in the current outbreak and that it was almost identical to past sequences from the Middle East. On the same day, the Chinese Center for Disease Control and Prevention posted a

► separate sequence to the publicly available GenBank database, from a man infected in the South Korean outbreak who then travelled to China, where he felt ill. Christian Drosten, director of the Institute of Virology at the University of Bonn Medical Centre in Germany has analysed this sequence and says that it shows only minor mutations compared with Middle Eastern strains, none in areas of the genome thought to influence infectiousness.

A stream of new cases in South Korea might create the impression that the disease is out of control. But all cases reported so far have clear transmission routes from the initial infection, says Ian Lipkin, an outbreak specialist at Columbia University in New York. The country is now intensively tracing and isolating the contacts of those infected, and implementing strict infection controls in hospitals. Were cases springing up outside of hospitals that would be cause for worry, but that is not happening, says Lipkin.

In the Middle East, however, the virus continues to jump from camels to humans leading to hospital outbreaks. Heymann, who in 2003 led the global effort to contain severe acute respiratory syndrome, or SARS, says that authorities in the Middle East should do more to investigate how people catch the virus from camels.

Such studies would involve investigating the recent activities of infected people, finding out, for instance, whether they had had contact with animal carcasses or bodily fluids, had consumed fluids such as camel milk or urine, or had been near bat colonies. "It's frustrating that all cases from animal infections have not been properly investigated," says Peter Ben Embarek, leader of the WHO's MERS team at the agency's headquarters in Geneva, Switzerland. One obstacle is cultural, in that Saudis tend to be averse to discussing what they consider private matters, he says.

The outbreak in South Korea will probably put pressure on Middle Eastern countries to accelerate research and control of MERS, says Drosten.

Another outstanding mystery is why human cases have not been detected in African countries with large camel populations: Somalia has 7 million camels, and Kenya 3 million, dwarfing Saudi Arabia's population of 260,000. "MERS is circulating in camels in many parts of Africa," says Ben Embarek, "so camel-wise, it's the same picture as in the Middle East." One possibility is that human cases are going undetected because of poor surveillance. Another possibility is that cases in Africa are less likely or less serious, because MERS tends to cause serious illness only in people who have diseases that result from modern lifestyles, such as diabetes, which are more common in Saudi Arabia. ■



NATALIA SHISHINA

The Yamnaya people are thought to have carried their burial practices and other traditions into Europe.

GENOMICS

DNA deluge reveals Bronze Age secrets

Population-scale studies of ancient genomes hint at roots of technology, languages and diet.

BY EWEN CALLAWAY

Only half a decade after a 4,000-year-old tuft of hair yielded the first ancient-human genome¹, researchers are starting to sequence ancient genomes by the dozen, much as they do with modern genomes.

Such population-scale sequencing is answering long-standing questions about the Eurasian Bronze Age. This tumultuous period between about 3000 BC and 1000 BC saw new technologies and cultural traditions — from the use of finely crafted weaponry and horse-drawn chariots to changes in burial practices — spread across Europe and Asia, starting in the steppe between the Black Sea and the Caspian Sea.

As DNA data flood in, researchers say, the mass-genome approach will paint an increasingly accurate picture of the past and show how ancient events shaped modern humanity — from what we eat to the diseases that ail us. "Christ, what does this mean?" says Greger

Larson, an evolutionary geneticist at the University of Oxford, UK. "In another five years, we'll be talking about tens of thousands of ancient genomes."

The dawn of ancient population genomics is the result of cheap DNA sequencing and the rise of boutique lab techniques that can separate highly degraded ancient DNA from contemporary contaminants.

A team led by palaeogenomicists Morten Allentoft and Eske Willerslev at the Natural History Museum of Denmark in Copenhagen has used these advances to sequence the genomes of 101 people who lived across Eurasia between about 3000 BC and AD 700 (ref. 2). "We could have stopped at 80," says Allentoft. But "we thought, 'Why the hell not? Let's go above 100.'"

The sequences allowed the team to tackle questions that have vexed archaeologists for decades, says Allentoft. For example, researchers have disagreed over whether the cultural changes of the Bronze Age were the result