needing the hard-to-make antibodies.

For Julia Maxson, a cell biologist at Oregon Health & Science University in Portland, finding glycobiologists to get tips from and bounce ideas off was key. Several years ago, she was trying to determine how a gene mutation causes rare leukaemias. The mutation affects a receptor on the surface of immune cells by disabling where it attaches to a large glycan. Without the sugar, the receptor can trigger the cell to grow uncontrollably — a unusual cancer-causing pathway.

But when Maxson submitted the manuscript for publication, a reviewer wanted clearer evidence for the modification, called *O*-linked glycosylation. She wondered whether Bertozzi's labelling strategy might help and e-mailed her for advice on how to use it for her research.

With Bertozzi's counsel and a deeper understanding of how sugars can trigger rare leukaemias, Maxson won an NIH fellowship for postdocs transitioning to faculty positions. Today she works with Bertozzi to characterize sugar structures found uniquely on cancer cells. They hope that their findings can lead them to therapeutic strategies that precisely target tumour cells, which could pique industry interest and create research opportunities. Indeed, as scientists get a better handle on studying glycans in the lab, companies are exploring therapeutic ramifications, which should fuel growth in industrial research jobs.

"Glycobiologists are important in most biological drug programmes."

Most biologics — medical products derived from natural sources — are glycosylated, which drives interest in investigating how the sugar structures influence the safety and effectiveness of therapies being developed for cancer and other diseases, Williams says.

Analytical glycobiology is so crucial, in fact, that Deng's boss is looking to hire another researcher with these skills. And just as in his case, Deng says, it looks likely that such a candidate could land a job without even formally applying. ■

Esther Landhuis *is a freelance journalist in Pleasanton, California.*

CORRECTION

The Spotlight article 'China's Silicon Valley' (*Nature* **545,** S29–S31; 2017) erroneously stated that Ali Muhammad moved to Shenzhen from India. In fact, he moved from Pakistan.

TURNING POINT
Single-cell mapper

Biotechnologist Andrew Adey developed a high-throughput method for mapping the genomes of single cells. The advance, reported in January, allows for the identification of diverse cell populations in tumours, and so paves a path towards precision medicine. To develop it, Adey, now at Oregon Health & Science University in Portland, relied on HeLa cells, a prolific cancer-cell line biopsied in the 1950s from Henrietta Lacks, who had cervical cancer, and used widely in biomedical research without her consent.

MIKE LISKAY

How has single-cell biology advanced?

In the mid-2000s, next-generation sequencing was just starting, so today's version of single-cell biology was non-existent. Today, researchers can look at genome-wide properties or other aspects of single cells.

How did you use HeLa cells?

I knew nothing about the history of HeLa, just that it was a cancer-cell control line that grew really well. We wanted to understand how different copies of chromosomes influence cells. Once we developed technology to do this in normal cells, we set out to see how those copies act in cancer cells, and so applied it to HeLa. We learned more about HeLa — notably, that multiple copies of a genome can act differently — and worked out the genomic changes that enable an aggressive cancer to reproduce so readily.

What was your role in the privacy debate over publishing HeLa sequence information?

As we were readying a paper in 2013 (A. Adey *et al. Nature* **500,** 207–211; 2013), we didn't know how we were going to publish genetic information that could have consequences for Lacks's descendants. Ultimately, the US National Institutes of Health reached an agreement with the Lacks family that accompanied our paper, and that granted researchers access to the cells while maintaining the Lacks's privacy. HeLa is a unique case — one not only at the forefront of medical advances but also about the ethical informed consent that is crucial to medical practice.

Can you explain the technique put forth in your January paper?

Initially, our platform could fully sequence only the portion of the genome that regulates gene expression in single cells (S. A. Vitak *et al. Nature Meth.* **14,** 302–308; 2017). We wanted to progress to whole-genome sequencing from single cells. But when you target regulatory elements, you typically have access to only 1–4% of the genome. We had to work out how to free up the DNA to convert the entire genome into sequenceable molecules.

What were the main obstacles?

At one point, it seemed like we were playing 'whack-a-mole'. Every time we altered one fixed property of the protocol, something else that had been working fine would stop. It was challenging, because the genome is packed nicely into nuclei. We needed to destroy the proteins that packaged the DNA inside the nucleus, without destroying everything else. Most of the time, everything would just explode and we'd lose the ability to look at single cells.

What's next?

We've already improved our method from what we published in January. It's even more reproducible, and we can get more data from single cells. Half of my lab does technology development; the other half applies those methods to answer questions of interest. This method was the first step to examining other aspects at the single-cell level. We're now using these technologies to explore cell identity. For example, how does a cell respond when treated by a cancer drug?

How will your method affect cancer treatment?

With a single-cell focus, we can start to profile an individual's tumour and identify molecularly distinct subpopulations in a tumour. If we can then profile large cohorts and tumours at the single-cell level, we can learn how certain subpopulations will respond to specific drugs to better home in on effective treatments. ■

INTERVIEW BY VIRGINIA GEWIN

This interview has been edited for length and clarity.