

Delivering Sequencing Results Quickly and at a Competitive Price

The NextSeq[®] 500 System enables the DNA Sequencing Facility at Cambridge University to offer high-demand applications and compete successfully for sequencing projects.

Introduction

When the DNA Sequencing Facility was founded at the University of Cambridge, genomics was still in its infancy. Operations began in 1989 when a small group in the Department of Biochemistry bought its first automated sequencer, an Alpha machine from Pharmacia. Although the group just sequenced DNA relating to its own research initially, it expanded in 1993 to accept customers from other departments in the university and outside institutions. In those early days, the entire facility had one full-time employee, current Facilities Manager, John Lester.

In the 20 years since the sequencing facility opened for business, Lester has witnessed a sea change in genomic sequencing technology. "When I started sequencing, we were still using radioactive isotopes. There were no machines to do it for you and it was very tedious stuff," Lester said. "When the first automated sequencers came out that was a real head-turner. You started to obtain longer reads and got away from radioactivity. I mean, who in their right mind wants to work with radioactivity?"

Lester's facility is a self-funded division at the university. Other than the building space in the Department of Biochemistry, Cambridge contributes nothing towards its operation. "We buy all the equipment and pay for all the wages from the money we make out of the machines," Lester said.

His team and the sequencers they use must be extremely efficient. While the facility uses sequencing systems from several different companies, in recent years they have been turning to Illumina next-generation sequencing (NGS) machines, including the MiSeq[®] and NextSeq 500 systems. These systems enable Lester to provide customers with good value and a fast turnaround, the backbone of the facility's service offering.

Recently, iCommunity sat down with Lester to discuss advances in DNA sequencing technology and how Illumina MiSeq and NextSeq 500 systems are helping his facility stay at the forefront of the genomics revolution.



The DNA Sequencing Facility team at the University of Cambridge is led by Facilities Manager John Lester (far left), and includes (from left to right) Reidun Lillestol, Carolina Velez, Reda Deglau, Nataliya Scott, Anna Efimova, Shilo Dickens, and Markiyan Samborskiy.

Q: What departments in the University or other institutes and organizations in the area do you perform services for? John Lester (JL): We'll perform services for anyone at Cambridge University. We also perform sequencing studies for other universities, and even institutes in other countries. Visiting scientists at Cambridge will use us while they are here and when they return home, they'll often get back in touch with us and ask if we can perform a sequencing project for them.

Q: What is it that you offer that other core facilities don't? JL: We offer a good price, a fast turnaround time, and great results. We've got some great people working for us and they're very diligent. They all have the same work ethic and I'm proud of them.

Q: Over the years, what sequencing machines have you used in your lab?

JL: We started with an ABI 373 DNA sequencer and subsequently used several generations of ABI sequencers before acquiring a capillary electrophoresis machine. Six years ago, we bought the Roche 454, when it first came onto the scene. As things progressed, the Roche people didn't do that much with the 454 system. It was an excellent machine, but pricing was abysmal. We had many people who wanted to use it, but they couldn't afford to.

Q: What made you decide to purchase your first Illumina sequencing system?

JL: We started to look into Illumina machines because we had more customers asking us to provide them with Illumina data. The HiSeq[®] systems are very large output machines, and while they suited huge projects in large institutes, they didn't necessarily suit providers like us who cater to researchers who have a smaller data requirement. With a HiSeq system, you have to wait a long time to fill them up, yet most of our customers just want a little bit of data. We were hearing stories of nine-month lead times, which never fit in with our ethos of providing quick results. We generally have a very fast turnaround, and that's always been an important consideration. Our customers always come first – quality with fast turnaround. Nine months is just too long to wait in research.

We kept looking at other things, but nothing really was suitable until Illumina introduced the MiSeq system. When we saw it was so easy to use, we dove in and purchased one.

Q: Why did you decide to purchase a NextSeq 500 system?

JL: We had the MiSeq system and knew how easy it was to run with its cartridges and everything. We also knew that we wanted a system that completed sequencing runs in a day and not one that takes two weeks. The NextSeq 500 system fits our needs perfectly.

When Illumina announced it, we said 'this is for us' and ordered one the same day. We were the first people in Europe to get one. We now have a couple of MiSeq systems and the NextSeq 500 system, and it's going well.

"Science exists on speed these days. We want to be there for our customers."

Q: Given the fact that you're a self-contained core lab, how important was the run cost in your decision?

JL: It's important because we want to be able to compete with companies like BGI in China. A lot of people here were sending their sequencing projects to China. If we can do it for the same price, I think they'd rather have results in a week rather than in two or three weeks' time. Science exists on speed these days. We want to be there for our customers.

With the NextSeq 500 system, we can deliver quick results at a competitive price. It's performed brilliantly. The running costs are so low that it puts us in place to undercut our competition on price. We're certainly looking forward to reaping the benefits of that. Q: How did the installation of the NextSeq 500 system go? JL: The NextSeq 500 system was installed and we started using it almost the same day. In fact, the installations of the MiSeq and NextSeq 500 systems went very well. These are good solid platforms and we've had no problem with them at all.

"Now that we have the NextSeq 500 system, we can compete with core laboratories and deliver results quickly at a competitive price."

Q: What kinds of sequencing do you perform for your customers?

JL: Anything they want. We sequence *de novo* organisms, usually bacterial, but we do some fungal, and perform amplicon sequencing. In the future, our lab will be conducting large scale *de novo* work where we'll be sequencing large numbers of genomes. The NextSeq 500 system will be ideal for those projects.

For customers that want a larger amount of data, we use the NextSeq 500 system. We've done a lot of whole-genome sequencing, mainly 8 Mb genomes. RNA-Seq work is popular and more people are requesting it.

Q: What library preparation kits are you using with the NextSeq 500 System?

JL: Nextera[®] Library Prep kits are fast and very popular. They're easy to set up and quick to run. We also have people who request that we use TruSeq[®] Library Prep kits. It all depends on what the customer wants.

Q: Have you seen the number of sequencing projects grow now that you have the NextSeq 500 System?

JL: We've expanded the types of projects we're doing. Before the NextSeq, we were getting inquiries for projects that the MiSeq system couldn't handle. Now that we have the NextSeq 500 system we can compete with core laboratories and deliver results quickly at a competitive price.

I think sequencing begets sequencing. Certainly the MiSeq is becoming increasingly popular and I think in due course so will the NextSeq 500 system.

Q: Could you have imagined a decade ago that sequencing systems could accomplish what the NextSeq 500 system can?

JL: Easily. It's been in the cards for a long time. The size of sequencers is really going to become smaller. The police are already starting to use portable sequencers to perform roadside DNA sequencing of suspects and to identify people.

I think sequencers will become a fairly basic thing, just like computers are now. No one really understands NGS, but everyone will use it. People want to have their own genomes sequenced. There are a number of reasons why. Some want to see what DNA mutations there may be in their genomes. Others want to know about where they've come from. There are many questions people would like to know about themselves that can be answered by genome sequencing.

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