CUSTOMER SPOTLIGHT

TWIST BIOSCIENCE

A Better Way to Detect Cattle Disease

Twist Custom Panels give researchers the diagnostic firepower to specifically identify dangerous pathogens and antibiotic-resistant strains.

The cattle business in Western Canada is a multi-billion dollar industry and a huge economic driver. Unfortunately, bovine respiratory disease (BRD), septic arthritis, joint infections, myocarditis, chronic pneumonia, and other conditions can cause enormous economic losses each year.[1, 2]

Cattle are particularly vulnerable in feedlots, where they go to be fattened for beef production. Feedlots are never entirely cleared of cattle, which means that once a pathogen settles into a facility, it can live there indefinitely.

While animals receive antibiotics, feedlot operators and veterinarians may have no idea which specific strains are in the cattle and whether they are antibiotic-resistant.[2]

To help solve this problem Andrew Cameron, PhD, a microbiologist at the University of Regina in Saskatchewan, and colleagues have been investigating new ways to detect pathogens, characterize their antibiotic resistance, and develop cost-effective tools to monitor cattle health.



In collaboration with Antonio Ruzzini, PhD, a microbiologist at the University of Saskatchewan, they developed an elegant and unobtrusive way to identify the strains floating around feedlots – water bowls. Cattle need lots of water and shed pathogen DNA into the bowls. Using this method, the researchers can readily pull samples without moving cattle in and out of their pens, a complicated process. By sequencing the genetic material in the water, they can get detailed information about the strains affecting the feedlot.

Still, these are complex metagenomic samples with irrelevant genetic material from cows and commensal bacteria, and only small amounts of pathogen DNA. Cameron needed a highly sensitive method to separate signal from noise.

The solution was Twist enzymatic fragmentation library preparation kits with custom next-generation sequencing (NGS) panels. By creating bespoke targeted sequencing panels, with only a narrow group of pathogen genes, they were able to cut through the noise and identify the strains that are causing so much damage. We recently chatted with Cameron and Daniel Kos, a research scientist in the Cameron lab, to learn more about this work and where they hope to go

When did you start using Twist tools?

Cameron: Our first experience with Twist's custom panels came in 2020 during COVID.[3] We wanted to understand viral diversity, and the scientists we assembled to design custom probe captures for coronaviruses had been using Twist for some time. They were quite pleased with the quality of the probes compared to what was available (and continues to be available) on the market.

Twist's ability to synthesize these highly specific, DNA-based probes fit our criteria perfectly. We also found the company is great to work with because they are so supportive, getting us the probes we need – exactly how we want them designed – when we need them. Twist has been our preferred and only provider.

You didn't start your bovine disease work using probe capture, describe the research evolution.

Cameron: We began with shotgun metagenomic sequencing, looking at BRD, but that was problematic on a number of levels. First, it's basically unaffordable at the feedlot level, particularly with our water samples. There was so much cattle DNA, as well as non-pathogenic microbial DNA, we couldn't consistently detect the respiratory pathogens. Custom capture panels allow us to identify those relatively rare sequences because they are just so much more sensitive.

Kos: Custom panels also helped us move beyond standard microbiology approaches. It's quite common to run PCR on the 16S gene, which is unique to bacteria, but then we're getting all kinds of bacteria that aren't particularly relevant to our research. The custom probes increase our odds of detecting the pathogens we want because we're looking at more than just one gene, and that gives us increased sensitivity.

With this approach, we can test for genes that identify specific strains, such as Mycoplasma bovis, a major player in BRD.2 It also helps us detect resistance mutations, which could be incredibly valuable for feedlots, so they can actually give the most effective antibiotics.

Cameron: I also want to note that when we target 16S sequences, we identify all the bacteria in a system. This approach is semi-quantitative, so it's dominated by all sorts of normal flora. Not only that but, when we get down to the genus/species level, we may have a genus that has a few real baddies in it, but we're also detecting the commensal, harmless bacteria in that same genus.

Overall, we can now detect things we weren't finding with shotgun metagenomics, helping us reduce so much of the noise. We're not sequencing a whole bunch of cattle DNA over and over again. We're focusing on those needles in a haystack, which are the few pathogens that are mixed in with all that cow and commensal bacteria DNA.

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Andrew Cameron, PhD

Microbiologist at the University of Regina in Saskatchewan

Tell us a little more about your approach.

Cameron: There's been a long tradition of using seven or eight genes we can count on to be present in our species of interest. If we can sequence a region from each of those genes and then put all those variants together, we can get a very specific sequence type.

We wanted to incorporate that traditional approach to microbiological epidemiology with capture so we detect the genes and know the pathogen is there. Also, by sequencing the capture genes, we get typing information to know this is a sequence type that may not have been detected in Western Canada before. Or maybe this is a new sequence type that hasn't been detected anywhere before.

A lot of times, microbiologists will try capture more of the genome, but in this case, less is more. We find a microbe's whole genome interesting, but it's impractical to capture and sequence it. If we really focus our targeting on these specific loci, we maximize our information to these core genes because they give us species and strain-level resolution.

Are these techniques limited to BRD or can they identify other conditions?

Kos: We started in BRD and have since moved into septic arthritis.[4] We applied our custom panel and got great coverage of our genes of interest, much better than shotgun metagenomics provided.

We want to get as much information as possible from the water. If we sample every day, we can track which strains are present and their antibiotic resistance. Eventually, we'd like to use these tools to look for myocarditis as well.

If we can define which pathogens and strains are present, that gives the industry tremendous knowledge to help develop vaccines. There are existing vaccination programs, but they're not always effective. Now, we can determine the strains in a feedlot, including resistance genes. That strain data could be enormously helpful, informing research into new animal vaccines.

How else might probe capture enhance the beef industry's ability to fight pathogens?

Kos: This is a big deal for the industry. They have been working to manage diseases at these feedlots for more than 40 years. Current industry methods are quite cumbersome and not particularly effective. They open up a carcass, take a picture and send that image to a vet to diagnose the disease. Or they take lung tissue and culture it, which is slow, expensive and inefficient, and they have to repeat that process for multiple animals.

Now, we have this fast and highly sensitive way to look at the water and identify the pathogens in the feedlot. We get a lot of queries from feedlot operators wanting to know what we found in their water.

But we're still not there yet. We can identify the pathogens, the resistance genes and other traits, but that's for an entire feedlot. This is useful information, operators could change the antibiotics they administer based on our results. But it's still a really broad view.

Cameron: In the big picture, target capture is proving an excellent tool to study epidemiology in feedlots and other agricultural spaces. The ability to detect dangerous, sometimes antibiotic-resistant, pathogens in such a granular way could provide a variety of new epidemiological insights.

Ultimately, this research is a jumping off point to develop cheaper and better diagnostic approaches that can support assessment for groups of cattle in real time. We're talking about thousands of cattle so we need a fast, inexpensive tool that can identify sick cows to address disease on a more granular basis.

There are steps we could take to develop fast detection kits. The capture we're doing now is a bridge that provides foundational knowledge to develop better diagnostics. There's a really great analogy with COVID, with the rapid tests. If we could do that for feedlots, it would be a great economic benefit.

Note: this interview was edited for length and clarity.

Twist products are for research use only, not for diagnostic procedures. Results are specific to the institution where they were obtained and may not reflect the results achievable at other institutions.

REFERENCES

1. Canada A and AF. Cattle/Beef and Veal. agriculture.canada.ca. Published August 25, 2020. https://agriculture.canada.ca/en/sector/animal-industry/red-meat-and-livestock-market-information/cattlebeef-and-veal

2. Russell JN, Kos D, Yacoub E, et al. Enhanced metagenomic surveillance for bovine respiratory disease pathogens and antimicrobial resistance by hybridization capture sequencing. Appl Environ Microbiol. 2025;91(10):e0097725. doi:10.1128/aem.00977-25

3. Kuchinski KS, Loos KD, Suchan DM, et al. Targeted genomic sequencing with probe capture for discovery and surveillance of coronaviruses in bats. Elife. 2022;11:e79777. Published 2022 Nov 8. doi:10.7554/eLife.79777

4. Kos D, Warr B, Suchan DM, et al. Survey of bacteria associated with septic arthritis in beef feedlot cattle. Appl Environ Microbiol. Published online January 21, 2026. doi:10.1128/aem.01675-25

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