## How Could Metagenomics Impact the Cattle Industry?

## Season 1, Episode 39

[Intro music]

**Kiernan Brandt:**

Welcome to Cattle HQ, a podcast from industry experts and progressive producers discussing cutting edge info about the cow calf sector to keep cattlemen and women in the know and positively affect their bottom line.

**Robin Salverson:**

Welcome to Cattle HQ, brought to you by South Dakota State University Extension. I am Robin Salverson, cow/calf field specialist, living the life in Lemmon, South Dakota. I am joined by Drew Lakamp, University of Nebraska graduate student and recently the winner of the Beef Improvement Federation Shark Tank competition. I’m excited to learn what the great scientific project caught the eyes of the sharkster in this competition. So, Drew, I’m really excited to have you. Before we jump in to the project and what made you award winner, could you share a little bit about yourself and why you are where you are today?

**Drew Lakamp:**

Sure thing. First of all, I’m happy to be here. I am from a small town in the middle of Illinois. So, if you’ve ever seen a cornfield, that’s exactly what everything looked like everywhere. Basically, I grew up showing Shorthorn cattle and we didn’t have a whole lot of money to buy really good cattle, but I figured out early that it was cheaper to breed cattle into the show ring or into the winter circle. So, I decided that ’10 or ’12, I was going to be a doctor of cow genetics and breed the best cow. Now, my definition of best cow has changed since then, but I am still well on my way to achieving that goal. I get my undergraduate work at Southern Illinois University in Carbondale. I took a couple of years, I entered the workforce after that. I hit companies that you probably know. I worked for Monsanto for a little while. I worked for a company called SD Genetics. I’m in the Wisconsin laboratory for a little while, and then I went to Kansas State University where I had the pleasure of working with Dr. Ralph in the animal breeding and genetics lab there. Then I have a great honor of working under Dr. Matt Spangler at the University of Nebraska Lincoln. Moving from cornfield to these really big beef/cattle states is where I’ve ended up.

**Robin Salverson:**

Someday you are going to have your doctorate of cow genetics.

**Drew Lakamp:**

Correct. I want mine.

**Robin Salverson:**

So, you will be a doctor of cow genetics.

**Drew Lakamp:**

Correct, a doctor of cow genetics.

**Robin Salverson:**

[Laughter] Sounds way better than PhD.

**Drew Lakamp:**

Right.

**Robin Salverson:**

Doctor of cow genetics. Well, we are really glad that you came from the cornfield and came to the plains of Nebraska to really start diving into some of this information on metagenomics. So, an article in Tri-State Livestock News really caught my eye, and it was titled “Magic of Metagenomics wows judges at BIF Shark Tank Competition.” It happened to be written by a person I know, Connie Groop. In this article, you were quoted, “My overall scientific idea focuses on the power of metagenomics and why it should be routinely used by cattle producers.” So I just have to ask because I’m not the smartest tool in the toolbox, really, what is metagenomics.

**Drew Lakamp:**

Oh, I’m not the smartest either, but when you go into it a little bit – so the first idea we have to cover before we get into metagenomics is the idea of a microbiome, and a microbiome is just a collection of microorganisms at a certain location. So, let’s take beef/cattle and focus on that for the instance. A lot of work is in the rumen microbiome. Anybody who’s taking a rumen at nutrition class or has ever fed cattle knows you don’t feed the cow, you feed the bugs. So, the formal term for the bugs is the microbiome. Right? Metagenomics, as opposed to regular genomics or just genomics is the idea of all of the genomic information of a certain sample. So, let me break that down for you. Most of your producers are going to know genomics. You take blood or hair or whatever, you send that off, you get that animal genotyped. Metagenomics is – let’s say you take a swab of a cow’s mouth, very similar to doing, I guess, a DNA dog swab, if you’ve ever done. Same idea. So, your swab now has animal DNA, animal cells, and then all of the microbial cells on that swab, and then what metagenomics is, is you just sequence all of the DNA you find there. That is metagenomics, is sequencing all of the DNA from a single sample, and that includes both cell, so cow cell, and then all of the microbial cells. That’s the idea of metagenomics.

**Robin Salverson:**

That’s pretty cool. How long has this research been going on with metagenomics? Has it been a while? Like you said, we hear of genomics but not as much about metagenomics. So, how long has it really been around?

**Drew Lakamp:**

So, metagenomics, really, as most things, you start in human space, and don’t hold me to this number, but about 2008, and then it came – we moved over to the animal side or livestock side about 2013. So, 10 to 11 years, but that still makes it young in some ways as far as a scientific field of study.

**Robin Salverson:**

Absolutely. It’s very new in our space, really. I mean, when we think about the world of genetics and AI, it started a long time ago, and now we’ve progressed into this. It’s very amazing, and it’s thanks to people like you that are doing this research. The next part of that little quote that you had said, “Producers should be routinely using this type of technology.” Why should cattle producers be using this idea that you had in the shark tank competition?

**Drew Lakamp:**

Excellent question. So, here are the highlights. When you do metagenomics, you get a lot of information for one sequencing cost. If you think about genomics, you pay your sequence at $35.00, $55.00, whatever that price is, and you get just the genotype of that animal. If you do metagenomics, you’re getting the microbiome information and the animal information at the same time. Here’s the plus side of that, is the microbiome information is a tool that we don’t routinely use in the livestock space but has been shown to be highly influential on traits that we consider important. I’m talking dry matter intake, average daily gain, fertility even. If we start looking at the vaginal microbiome – I have a project going on right now that is about the ocular microbiome. So, the eye in beef calves, and it looks like some of those microorganisms play a role in pink eye, and we’re really trying to start to unravel that whole mess. Anybody who’s dealt with pink eye before knows that it is a pretty complex disease. So, we’re coming at it from a few different angles.

Robin Salverson:

That’s very exciting, Drew, by the way, because I think that’s the most common question I get through my office, is how do I deal with pink eye? If we can understand the basis behind it and what you’re doing, this will be – this will revolutionize the pink eye industry – [Laughter] not the industry, revolutionize, help producers, I should say.

**Drew Lakamp:**

Absolutely. Unfortunately, I don’t have a good answer for you yet, but I can tell you we are working on it.

**Robin Salverson:**

Perfect.

**Drew Lakamp:**

That’s the benefit of microbial information. Right? I’m sure a lot of your listeners are familiar with the benefits of genomic information, but I’ll just hit those again real quick, is you get more accurate estimated breeding values or EPDs, which is one half of estimated beef biome. Right? So, more accurate EPDs, and then you get those accuracy increases sooner in life so you can make a decision earlier. And then, all of that fun stuff is, like I said, packaged in one go. Let me give you an example here. Take for instance that you have a group of heifers that you have just weaned off, okay? Now, you need to make a decision, “Who’s going to stay as my replacement heifers?” Well, we know that keeping and feeding out a replacement heifer is not inexpensive, right? So, we want to make sure that the ones that are most likely to breed are the ones that stay. Let me give you a hypothetical. If you could do a vaginal swab, take a swab, run it along the vagina, and send that off to a lab, you could get – you could genotype those animals for that, and then you get microbial information which some studies have shown that the microbial information is partially predictive of reproductive success. Now, that’s been a few studies. To what degree? We won’t have to argue X or Y, but it is possible. And so, you can identify those heifers that are unlikely to breed basically right after you wean them, selling the feeder calves, and not have to feed them out and find out that you ended up with an open heifer at the end of the breeding season. Right? That’s one potential application of this kind of technology. Another is if you identify, you start – if you’re on the feedlot end, you start grouping animals based on how similar they are to grow at the same rate, to finish at the same rate, those types of ideas. That was my general argument for the sharks was. You can leverage a whole bunch of information for one kind of standardized cost, and then you make decisions. Not just breeding decisions, but management decisions fairly early on before we invest too much.

**Robin Salverson:**

Going back to those replacement heifers example that you shared, could you also do the vaginal swab to understand conception rates in those heifers, but can you also do – get something in regards to the rumen microbiome for – because we know that if we can match that cow to that environment better, it can stay in our herd longer. Because longevity is really an issue in our beef industry. Keeping most females in our herd longer so they actually start making us money. Along first getting them bred as heifers, but then also staying in the herd. Could there be like a combo package that will help us predict not only heifer consumption rate but longevity?

**Drew Lakamp:**

Excellent question. The honest “PhD answer” is “I don’t know,” but let’s go down this line. Here’s the idea, is if you want to get rumen microbial information, the easiest way to do it is actually do an oral swab because cattle are ruminants, they regurgitate. If you want to get strictly technical, the oral microbiome and the rumen microbiome are not the same, but you could use – for ease of use, the oral sample will work. I don’t know of any studies that have studied longevity specifically, but you could probably make an argument that there is maybe something there based on the rumen microbiome that matches a better forage types. Maybe there’s something there that’s definitely worth looking into, but at this time, I can’t say definitive.

**Robin Salverson:**

Sure. It’s definitely a research for the future, I think.

**Drew Lakamp:**

Oh, you just wrote my next grant.

**Robin Salverson:**

[Laughter] Perfect, perfect. I have to admit that the work that you’re currently doing with understanding the ocular microbiome is huge. Pink eye really is something that – I’m going to use the word “plagues” our industry, and so can really affect performance of those animals, and so understanding that – I’m excited to hear the results when they come out from you.

**Drew Lakamp:**

I’ll give you a little inside information. What I’m doing with that research specifically is I’m looking at – we have ocular microbiome information so we know what bacteria and archaea live there, and then are the abundances of those bacteria genetically controlled? So, are they heritable? So, it seems to be for the whole microbiome in and of itself is under some sort of genetic control, and we’re starting to pull apart what abundance is of what bacteria at what point in time are heritable. That’s another thing that I think is definitely worth mentioning, is microbiomes are static. They are robust in the sense of if you move them, they’ll generally return to a similar state as before, but they are never the same. Take for contrast your genomics, my genomics, a cow’s genomics, whosoever, right? That is your DNA blueprint, that stays with you from conception till death. That never changes. Some of my molecular friends will argue the epigenome, but I deal with DNA sequence. DNA sequence stays the same. The microbiome does change in response to the environment, and so the easiest way to identify that is anybody who’s ever had a calf go acidotic, that’s because you changed their diets too quickly, all that lactic buildup, they weren’t ready for that much grain. Right? So, you can change it. You can change the rumen microbiome based on diet. The ocular microbiome changes with season. If they get a scratch on their eye then it get infected, that’s still a microbiome change. Those types of things. So, it’s harder to pin down the microbiome as to when do we take these samples. Right? When can we have a set point – animals are this age at this time of the year, where can we evenly compare across groups? That is still an open question. But circling back around to the pink eye idea is we see that the microbiome – what microbes are heritable does change with the age and timepoint, age and season that those samples were taken, but there’s some events that at least at some points in time, those bacteria that we think cause pink eye or are related to pink eye are under some genetic control. So, that’s good news. Fully flushing that out is going to take a few more years.

**Robin Salverson:**

So, what you’re saying is you’re going to be a PhD student for the rest of your life then? [Laughter]

**Drew Lakamp:**

I’m sure some people would love that, but…

**Robin Salverson:**

My next question then for you is really, how far down the road do these ideas that you just shared really become a reality for producers, and I think you gave us a little foresight that the microbiome is everchanging and you’re trying to figure that out, but is there a timeframe for reality or not?

**Drew Lakamp:**

Good question. Now, a lot of it depends on a few things. Number one is commercial and producer support. Right? If this is something that the public wants, given our cattle society, we shall give them, right? What I envision as a more consumer-applicable idea is what we described earlier with these hypothetical replacement heifers, or these hypothetical feedlot animals, right? A predictive tool. That, I can see being – I hesitate to put exact numbers on things, but 10 to 15 years, if the push is there. That requires a few things. That requires a database of animals with similar information taken on them that you can look at and say, “Okay. My new animals are similar to these animals I’ve seen before, so they’re probably going to act the same.” Right? That’s the whole idea of genomics, is these animals with these genes look a lot like animals with these genes or are related, which is our definition. Right? So, they’re probably going to act similar, generally. Right? The microbiome is just another layer on top of that. “This microbiome looks a lot like this microbiome that I’ve seen before. This one that I’ve seen before gained three and a half pounds a day. This one’s probably also going to get close to three and a half pounds per day just based on that information.” Something like that. That idea is probably closer to forthcoming. Let me back up. The mathematics and the chemistry to get this going are there. The bigger hurdles are getting a reference database and what I call the infrastructure. Who is going to hold all this information? Is it going to be the breed association, is going to be a private company? Who’s going to be in charge of that? And then number two, we’re talking about a lot of information here. The microbiome and the metagenome as a whole gets you a lot of information. I’m talking libraries full of information. Where are we going to put all that? Whose computer is going to hold all that? We need to figure those kinds of things out before we really start commercializing any sort of application.

**Robin Salverson:**

You said you need to get more reference datapoints. How do you accomplish that when you say that?

**Drew Lakamp:**

The reference database is essential to any sort of genomic or metagenomic study, and that just requires going out, selecting both phenotype and metagenomic information, right? We all know, at the end of the day, genomics are cool, but phenotype is king. So, I can’t do a whole lot with genomics if I don’t know what phenotype they relate to. That’s how we build the reference database, is we collect – a lot of those phenotypes are collected at universities or by really savvy producers or by other – something in feedlots or whoever else, where we collect dry matter intake, average daily gain, weaning weight, whatever. Right? That infrastructure already exists. Then it’s just a matter of, “All right. Well, let’s do that and get metagenomic information on them,” and then we can start to relate the two together, and once we’ve established that, then we can start to predict based on just metagenomic information.

**Robin Salverson:**

Makes a lot of sense. Yes, you’re really relying on the industry, like you said, and that was one of the points you made a little bit ago, about relying on the industry and how much they are vested into it also because they’re the driving force.

**Drew Lakamp:**

Absolutely. It’s the same idea as we saw with genomically-enhanced EPDs. This is a really neat tool. It helps a lot to make management decisions, but we rely a lot on the industry to help us get better accuracies, get better predictions based on the phenotypes and data that they feed in.

**Robin Salverson:**

Well, thank you, Drew. I think we’re going to be winding down this particular episode, but I need to ask this last question. So, what does your career path look like for you in the future? I know you want to be a doctor of cow genetics, you have been since you were 12 years old, and so what does the future path look for you?

**Drew Lakamp:**

That is a great question. The philosophy I have at the moment is I’m open to any opportunity that is interesting, and I work with good people. That is one of my main priorities, is as long as I’m working with a great group of people and it’s something that interest me, I can go with it.

**Robin Salverson:**

Okay. Well, I wish you the very best as you continue down the PhD road and you receive your degree, and look forward to hearing all of the research that comes out because you’re really working on some very exciting things. So, thank you, Drew for joining us.

**Drew Lakamp:**

Thanks so much, Robin.

**Robin Salverson:**

Once again, this has been Cattle HQ, brought to you by SDSU Extension, headquarters for all things beef/cattle. Visit extension.sdstate.edu for the latest beef information. Until our next episode. Remember, a smile is happiness you’ll find right under your nose.

**Kiernan Brandt:**

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[Outro music]