



Virtual Beef

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The Origins and Impact of Antimicrobial Resistance

Tom Hamilton, Beef Systems Lead, OMAFRA, New Liskeard

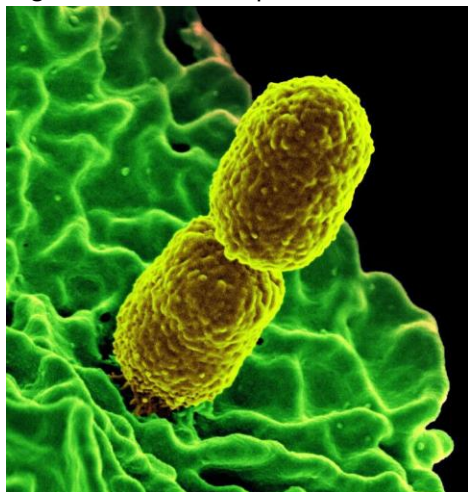
Microbes

Microbes are very small organisms visible only with the help of a microscope. They include bacteria and related organisms, viruses, and some types of fungi. Microbes inhabit almost all environments including soil and water, and live on the surfaces of larger organisms and within their digestive and respiratory systems. Although small in size, they may be present in great numbers – for example, in the average healthy adult human, there are **10 bacteria** for every **human cell**ⁱ. Most microbes are not harmful, and in fact many are beneficial to their hosts. Some assist in the digestion and absorption of nutrients, and even those which don't appear to have a specifically beneficial role serve to crowd out harmful species.

Pathogens and Antimicrobial Drugs

A few microbes are **pathogens** (disease causing) and although animals have an immune system to combat them, it may be outgunned or over-run. In these cases we have come to rely on **antimicrobial drugs (AMDs)** to help fight them and restore the health of the animal (or person). However, over time, a species or sub-species of microbe can acquire the ability to defend itself against an antibiotic to which it was formerly susceptible. This is called **antimicrobial resistance (AMR)**, illustrated in Figure 1. The occurrence rates of AMRs and the speed with which they are spreading across large distances have both been increasing. This is dramatically decreasing the usefulness of AMDs in both veterinary and human medicine.

Figure 1. Two carbapenem-resistant *Klebsiella pneumoniae* bacteria (yellow) and human white blood cell (green)



Credit - National Institute of Allergy and Infectious Diseases [digitally-colourized scanning electron micrograph]

Natural Antimicrobial Resistance

Prominent microbiologist Dr. Tim McAllister (AAFC, Lethbridge) recently described the origin and implications of AMR as part of a comprehensive presentationⁱⁱ. He stated that for millions of years before more complex organisms evolved, microbes were at war with each other for resources and living space. As part of an unending arms race, they produced various compounds which were toxic to competitors. The most successful of these antimicrobials killed almost all members of a competitive species. However, in some cases a few fortunate individuals who had an **inherent ability** (due to random **genetic mutations**) to resist the toxin would survive. They reproduced and passed on their resistance genes to future generations. This **selection** process created a **resistant population** against which that toxin was no longer effective. In essence, the **introduction** of any antimicrobial compound in a given bacterial population will select for the development of **resistance** to it.

Resistance to Antimicrobial Drugs

The antimicrobial drugs (**AMDs**) that we use today (such as penicillin and erythromycin) have their origins in compounds which previously existed in the natural world. Our **AMDs** are either purified naturally occurring antimicrobials; synthesized

versions of these compounds; or have been constructed with great similarity to natural antimicrobials. This means that even prior to the first use of a “new” AMD, it is likely that at least some bacteria somewhere already possess resistance genes, which will be at least partially effective in defending against it. One example of pre-existing resistance comes from bacteria sampled from a cave in New Mexico, which had been isolated from the rest of the world for 4 million yearsⁱⁱⁱ. Testing found several strains of bacteria with resistance to 14 of the antibiotic drugs currently in use, such as erythromycin, trimethoprim and streptomycin. This remarkable discovery showed conclusively that resistance to many veterinary and medical antibiotics existed in microbial populations long before they were used by humans.

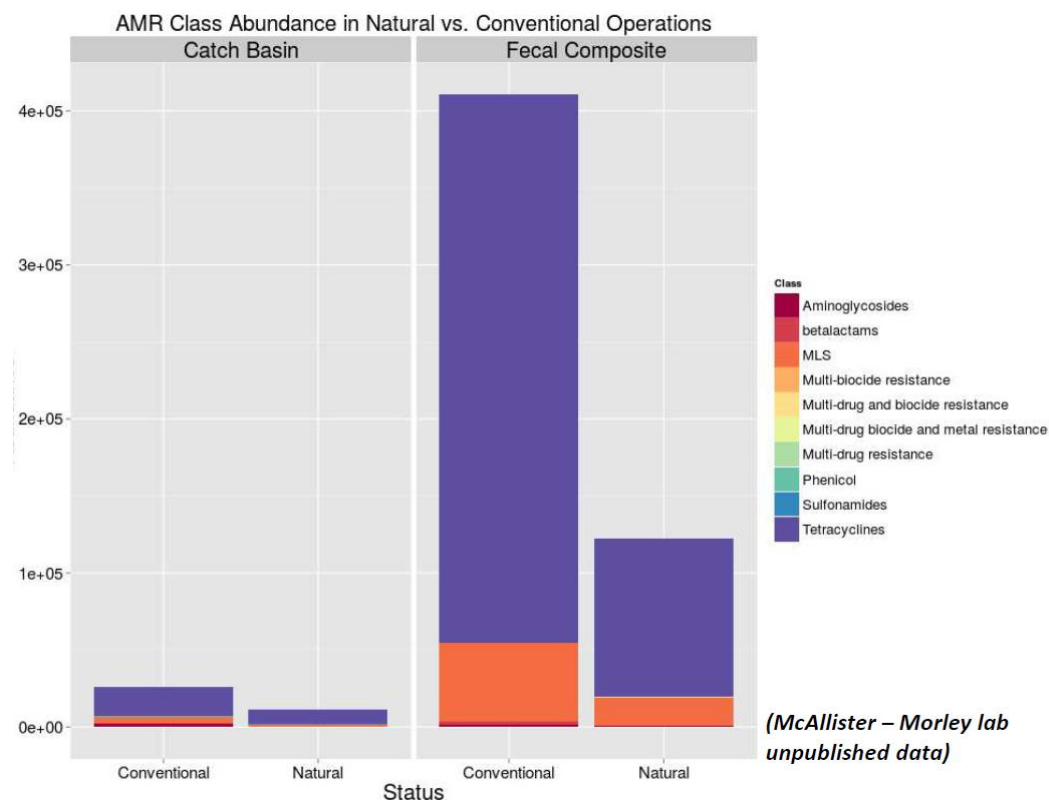
Scientists have developed a library of genetic resistance elements which have been found in various bacteria from different locations. Currently, this database contains 3,111 unique elements, indicating that a large array of resistance genes are scattered across the world in various bacterial species and strains. McAllister notes that the selection for and transfer of pre-existing resistance genes is responsible for almost all of the AMR we are seeing today. He asserts that new spontaneous mutations for resistance are relatively rare events in the natural world, although under laboratory conditions this can be accelerated.

How Does Antibiotic Resistance Spread?

Bacteria are much more adept at sharing AMR genetic elements than previously thought. They have several methods of conveying resistance among individuals, even without a direct challenge by an antimicrobial drug. This happens because adjacent individuals actively trade genetic resistance genes as part of normal “social” behaviour...similar to the trading of food recipes or workshop tips when people get together. Since different resistance genes may be located close together on the DNA, one transfer event may convey resistance to multiple antimicrobial drugs. In addition, this **sharing** can occur **between different species** of bacteria.

The spread of resistance genes can occur via microbes living in the soil and water. Resistance elements are passed sequentially through adjacent microbial populations across significant distances, and may appear in distant bacteria which have never been exposed to a particular antibiotic. These pathways can account for the presence of AMR bacteria in cattle on farms with no history of antibiotic use (see Figure 2). In this study, farms with a “natural” production system (no antibiotics used) had a high prevalence of tetracycline -resistant and MLS¹ - resistant bacteria in cattle fecal samples.

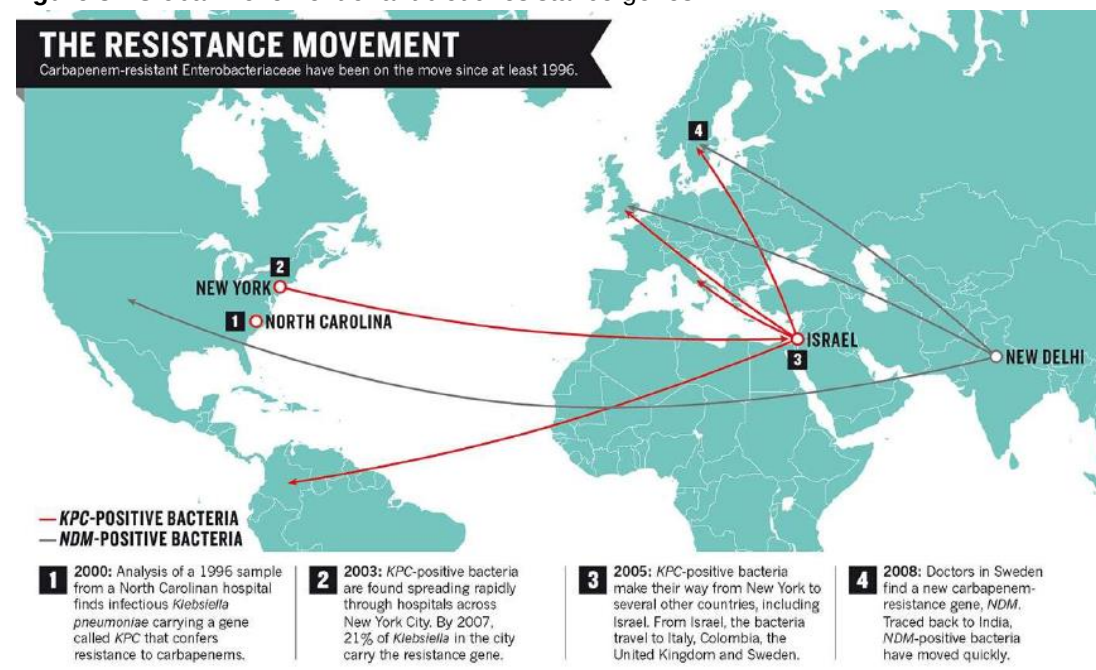
Figure 2 (1)iv



¹ MLS = Macrolides, lincosamides, streptogramins

Increasing air travel of people around the world has accelerated the transfer of resistance genes among continents. Geographic separation is no longer an effective buffer against resistance occurring in distant places. This is illustrated in Figure 3. The bacteria *Klebsiella pneumoniae* is a pathogen of humans, causing pneumonia. Carbapenems are antibiotics typically used to treat multidrug-resistant bacteria. The *KPC* gene, which confers resistance to carbapenems, was first found in *K. pneumoniae* in a hospital in North Carolina in 2000. By 2005 it had spread to three other continents. Figure 3 also shows how another carbapenem resistance gene (*NDM*) first reported in Sweden was traced back to India, and has spread to North America.

Figure 3. Global movement of antibiotic resistance genes.



Credit: Nature News <http://www.nature.com/news/antibiotic-resistance-the-last-resort-1.13426>

Summary and Implications

Cattle and humans are both mammals, with similar immune systems, and may be affected by similar types of microbial pathogens. Many of the antimicrobial drugs which have been developed are used both in veterinary and human medicine. **Resistance genes**, which can render specific antibiotics ineffective, occur in bacteria found in livestock, humans and the general environment. These genes can be **readily transferred** between individual bacteria within a species, as well as across microbial species, leading to the rapid development of bacterial populations that do not respond to drug therapies. This has serious health consequences for both livestock production and people.

Resistance genes can **flow through ecosystems**, mediated by many bacterial species. This includes bidirectional flow between livestock operations and human communities. They can also be transported across vast distances via modern air travel. The complexities of AMR occurrence, amplification and flow through the environment must be taken into consideration when formulating strategies to combat resistance. The development of AMR cannot be stopped, but it may be delayed as part of a strategy to preserve specific antibiotics for the treatment of serious disease.

Further Reading

Antimicrobial Resistance 101

<http://www.omafra.gov.on.ca/english/livestock/beef/news/vbn0715a4.htm>

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- ⁱⁱ McAlister, T. Dec. 2015. Overview of AMU, AMR and Alternative Research and emerging priorities. Beef Value Chain Workshop. Calgary AB.
- ⁱⁱⁱ Bhullar, K. et al. (2012) Antibiotic Resistance Is Prevalent in an Isolated Cave Microbiome. PLoS ONE 7(4): e34953. doi:10.1371/journal.pone.0034953
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Continuous Improvement

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“Sustainable Beef Production” is a term that is becoming much more common. As companies such as McDonalds and Walmart move towards marketing “sustainable beef”, we will hear more about how to achieve it. There are essentially three things that need to be considered to be sustainable: 1) the economic viability, 2) the environmental response, and 3) the social acceptance. In some respects, it is pretty simple, in that it is continuous improvement in “balancing environmental responsibility, economic opportunity and social diligence” (NCBA).

“Sustainable beef production can be defined as meeting current and future demand for safe, nutritious beef products while maintaining long-term business viability, stewardship of natural resources, and responsibilities to community, family, and animals. The optimum balance of the economic, environmental, and social aspects of sustainability will not be the same for each operation, due to differences across production systems including varying climates, available resources (financial capital, human capital, natural resources), and value judgements of both producers and consumers” (Sarah Place, Oklahoma State University).

Beef Production is very complex and diverse. There are a large number of links in the supply chain from conception to consumer and continuous improvement should be made in all of them(see figure1). Because of the diversity of operations, there is not one solution for all, but everyone in the supply chain needs to do their part.



Figure 1: Components of the Beef Production System

Source: National Cattlemen’s Beef Association (USA).
Undated. Sustainability – Executive Summary
<http://www.beefresearch.org/CMDocs/BeefResearch/Sustainability%20White%20Papers%20and%20Infographics/SustainabilityExecutiveSummaryWeb1.pdf>

There is some good news, as studies have shown improvement for beef production.

By simulating data from the beef production system of the USDA Meat Animal Research Centre (MARC), Rotz et al. (2013) found that the carbon footprint was reduced 6% from 1970 to 2011. Capper (2011) estimated that the U.S. beef carbon footprint was reduced by 16% from 1977 to 2007. Producing beef has reduced resources and thus has become more sustainable. Jude Capper reported that in 2007 it took four animals to produce the same amount of beef as five animals in 1977. Raising beef has become more efficient. Optimizing efficiency across the entire beef chain will be vital in striving for sustainability.



Figure 2: Beef Industry Stakeholder Definitions of Sustainability. Figure 2 indicates what USA stakeholders listed when defining sustainability. Continuous improvement in all of these components is necessary.

National Cattlemen's Beef Association (USA). Undated. Sustainability – Executive Summary <http://www.beefresearch.org/CMDocs/BeefResearch/Sustainability%20White%20Papers%20and%20Infographics/SustainabilityExecutiveSummaryWeb1.pdf>

The National Cattlemen's Beef Association (NCBA) has conducted the first and largest sustainability assessment in agriculture under the leadership of their Executive Director of Global Sustainability, Dr. Kim Stackhouse-Lawson. The production of beef is very complex as it probably has more biological processes involved than any other food product when accounting for all of the inputs and outputs of the entire life cycle. The study made a comparison of 2011 compared to 2005 and looked at the entire life cycle.

Highlights from this study include:

1. Lower energy use
2. Lower water use
3. Lower land use
4. Decrease in the number of working accidents, fatalities and illnesses associated with industries related to beef production.
5. Improved animal welfare at the feedlot and cow-calf sectors with adoption of Beef Quality Assurance as reflected in a third-party audit of packing plants.
6. Lower nuisance odours with installation of covered lagoons
7. Identifying the need to quantify the value of open space and wildlife habitat.
8. Where a significant amount of the feed used for beef production is inedible to humans, consideration must be given to the conversion of this feed to human edible protein. There are other things like gelatin based foods, medicines, pet food all dependent on animal agriculture, suggesting the carbon footprint is kept low.

These improvements have been accomplished via

- Improved crop production practices and increased crop yields
- Improved animal performance with better feed efficiency
- Usage of distillers grains

- Improvements in packing plant water efficiency
- Use of right sized packaging
- Optimizations in the case ready phase
- Increased use of biogas capture
- Conversion from diesel to natural gas

Keeping it Simple – An Action Plan

Here are a few examples of things producers can do to become more sustainable

1. Get enrolled for updates like OMAFRA *Virtual Beef* and the Bulletin Board from Beef Farmers of Ontario (BFO). There are also a multitude of other newsletters available. Scan the articles and look for ideas which you can implement to improve at least one of the three pillars of sustainability – profit, environment and social.
2. Attend educational workshops such as cattle handling by Dylan Biggs and implementing the Beef Cattle Code of Practice by Dan Ferguson of BFO.
3. Improve feed efficiency in your operation (this will be my article in the next issue of *Virtual Beef*).
4. Plant trees. Place the trees where they will be of most advantage to you. Most farms can use more windbreaks.

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<http://www.beefboard.org/news/files/FY2015/SustainabilityExecutiveSummaryWeb1.pdf>

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Traceability: Improve your Bottom Line and Protect Ontario's Beef Industry

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What is traceability?

Traceability is the ability to follow animals and food products through all stages of the supply chain – from farm to retail counter. It is an effective method for tracking an animal or a product, along with its attributes such as “locally raised” as it moves between locations.

Traceability for livestock business operators:

- Enhances operational efficiency such as labour improvements
- Reduces operational costs
- Informs management and genetic improvement decisions
- Increases sales

When the information collected by individual operators is shared (reported) and managed properly, as outlined by the Canadian Livestock Traceability Systems operated by the Canadian Cattle Identification Agency, traceability can be beneficial to the whole industry. More information about the benefits of traceability can also be found at TraceCanada's website (tracecanada.ca).

Traceability for the livestock industry:

- Allows for effective and efficient animal health incident management
- Increases market access, competitiveness and consumer confidence
- Protects your business and reduces market risk.

How does traceability work?

Effective traceability hinges on three key pillars:

- 1) Premises Identification
- 2) Animal Identification and
- 3) Animal Movement Recording and Reporting.

1. Premises identification:

Premises are identified with a Premises Identification Number (PID), which is a unique identifying number assigned to a parcel of land on which farming or food processing activities take place. There are more than 7,500 premises registered for beef cattle in Ontario.

Why should I get a PID?

- Premises identification can strengthen your business' traceability system, which in turn improves your ability to market your products and protect your brand.
- Retailers are starting to require traceability from their suppliers; having a PID means you will meet this growing market expectation.
- In the event of an animal disease outbreak or a contaminated food product, the provincial government can swiftly respond to incidents that could financially harm your business.
- Having a PID enables you to participate in funding programs offered by the Ontario Ministry of Agriculture, Food and Rural Affairs.

How do I register my premises?

Registering for a PID is quick, easy and free. You can register and/or update your premises information online by visiting www.ontarioppr.ca or by calling 1-855-MY-PPR-ID (1-855-697-7743).

2. Animal identification:

Since 2001, individual animal identification using a Radio Frequency Identification (RFID) tag has been mandatory for cattle in Canada under the federal Health of Animals Act, enforced by the Canadian Food Inspection Agency (CFIA). A RFID number can be linked to any number of facts about an animal including: information about genetics, which animals were housed together, what they were fed, medications used and when they entered a herd. RFID tag numbers are essential for tracking marketable attributes and very useful for providing individual carcass information where available. In Ontario, some livestock operators are using RFID tag numbers as part of their traceability systems to help reduce the cost of operation and efficiently manage their herd.

3. Movement recording and reporting:

Recording and reporting movement and events of identified animals between identified premises allows traceability information to benefit the livestock industry as a whole. This reduces the time it takes to respond to an animal health event or possible food product contamination. Collected information can also be used to meet the growing information demands of consumers, enhance consumer confidence and increase the overall competitiveness of the industry.

A popular tool, used voluntarily by many in the livestock industry to record animal movements, is the Ontario Livestock Manifest. To learn more about the Ontario Livestock Manifest, call the Agricultural Information Contact Centre at 1-877-424-1300 or send an e-mail to ag.info.omafra@ontario.ca.



How can traceability improve your bottom line and protect the broader Ontario beef industry?

Traceability offers individual businesses, partnerships and value chains opportunities to improve their bottom line over time by leveraging the power of information to enhance operational efficiency, support product claims and access markets. Working together cow-calf, backgrounder and feedlot operators can share information that leads to more intentional genetic selection and the development of plans that get steers to market at the best time of the year. Whether you want to sell locally, or sell branded beef into one of Canada's many export markets, being able to back up your claims through whole chain traceability gives you credibility in these markets, enhances your competitiveness and improves your bottom line.

As an industry, individual producers can take steps to improve on-farm traceability and movement reporting of animals to ensure the impacts of diseases and emergency incidents can be fully mitigated. Think of the industry level traceability system as a chain, with individual traceability systems forming the links. The industry's ability to efficiently and effectively manage incidents of diseases and emergencies is based on the reliability and accuracy of each link, and an efficient information collection and sharing system. In fact, the Ontario beef industry's protection from the impact of animal disease and emergency incidents is only as strong as your traceability system: **a chain is only as strong as its weakest link.**

Traceability is a priority both from an emergency management perspective and as an opportunity to improve business performance. Growing Forward 2, a federal-provincial-territorial initiative, offers a range of project options for beef farmers who are considering a traceability project. The initiative offers 35 per cent cost sharing of up to \$100,000 to implement traceability for your beef operation. There are also funding opportunities for traceability training, assessments, testing and planning. Funding is also available for projects that use traceability to meet desired outcomes such as improved animal health management, increased automation and labour productivity, enhanced production efficiencies and financial management.

Interested in learning more about how traceability can strengthen your business? Take advantage of the Ontario Soil and Crop Improvement Association's (OSCIA) free traceability workshops for producers. Register online today at www.ontariosoilcrop.org or call 1-800-265-9751.

Upcoming workshop dates and locations for winter 2016:

January 22, January 29 at 10:00 am
Ridgetown, Ontario

January 27, February 3 at 10:00 am
Colborne, Ontario

February 24, March 2 at 10:00 am
OMAFRA Simcoe, Simcoe, Ontario

FRENCH – February 29, March 7 at 10:00 am
Sarsfield, Ontario

March 3, March 10 at 10:00 am
Spring Bay, Manitoulin, Ontario

March 17, March 24 at 10:00 am
Elora, Ontario



Figure 1. Tagging a beef cow for traceability.

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Seminal Proteins Hint at Sexual Maturity and Feed Efficiency in Young Beef Bulls

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Background

The proteome is the entire set of proteins produced by a cell, tissue, or complete organism. Proteomics is the study of the structure, function and interactions of proteins in a diversity of biological samples. There is a growing interest in the proteins associated with fertility (FAP) that are present in seminal plasma of bulls. These proteins are essential for sperm survival, sperm fertilizing capacity and other functions (**Table 1**). These proteins are also related to puberty onset and sexual maturity; in fact, there are studies proposing the use of FAP as indicators of bull fertility (Kumar et al., 2012).

A recent publication from our group provides evidence of an antagonistic relationship between improved feed efficiency and measures related to fertility in young bulls (Fontoura et al., 2016). The “repro-traits” evaluated were semen quality, testis texture (via ultrasound), testis micro-structure (via histology) and scrotal circumference. We also collected seminal plasma of the same bulls, and using proteomics, furthered our understanding of the associations between the following:

- 1) fertility-related measures with seminal proteins
- 2) feed efficiency and seminal plasma proteins

Table 1. Selected fertility associated proteins (FAP) and respective metabolic functions.

Protein	Metabolic functions
Acidic seminal fluid protein (aSFP)	Associated with sperm motility, metabolism & membrane integrity
Acrosin (ACR)	Positively associated with sperm motility and semen concentration
Cathepsin D (CathD)	Promotes seminiferous tubule maturation
Epididymal sperm-binding (ESBP1)	Binds and tags sperm cells which would be dead upon ejaculation
Glutathione peroxidase (GPX)	Promotes homeostasis and prevents cellular oxidative stress
Niemann-Pick type C2 (NPC2)	Related to sperm cholesterol metabolism and semen concentration
Osteopontin (OPN)	Facilitates the acrosome reaction and sperm-oocyte interaction
Phosphoglycerate kinase 2 (PK2)	Promotes homeostasis and sperm motility, prevents oxidative stress
Prosaposin (PSAP)	Associated with the structural development of the testis
Protein C inhibitor (PCI)	Protects sperm from premature acrosome reaction and degradation
Seminal plasma protein 1 (BSP1)	Similar to BSP3, also regulates sperm energy use for motility
Seminal plasma protein 3 (BSP3)	Binds sperm, forms sperm reservoir in the female reproductive tract
Spermadhesin Z13 (SZ13)	Has sperm decapacitating properties, related to low fertility

Bull evaluation, sampling and proteomic analysis

Crossbred bull calves sourced from both the Elora Beef Research Center and New Liskeard Research Station were fed a corn-based ration and submitted to a routine performance evaluation with assessment of individual feed intake. Feed efficiency was determined using residual feed intake (RFI) adjusted for body composition, and bulls were grouped as efficient (low-RFI) or inefficient (high-RFI).

At an average age of 12.5 months bulls were submitted to a breeding soundness evaluation, along with testis ultrasonography. A portion of the semen collected was prepared for proteomic evaluation. Analyses were conducted at the SPARC BioCentre (Hospital for Sick Children, Toronto). Over 500 proteins were identified in seminal plasma of the bulls and a portion of them were evaluated in more detail based on the existing scientific literature on fertility associated proteins (FAP).

At slaughter, the reproductive tract was collected and dissected to obtain testis and epididymis weight. Testis samples were also collected for histological analysis, which determined the abundance of seminiferous tubules at distinct stages of maturity, see Figure 1.

What are the seminal proteins telling us?

Seminal proteins are associated with several biological processes and reproductive tissue development. Table 1 summarizes some of these aspects relevant to young bulls. The seminal proteins PK2, PSAP and SZ13 are associated with reproductive organ development. Our study showed significant correlations between some of these proteins and scrotum circumference, testis weight and epididymis weight (Table 2). Interestingly, PK2 seems to play a role in reproductive organ development and size in addition to its known functions in cell homeostasis and motility scores. In the case of PSAP, the opposite association with organ size might be explained by its activity in the proper development of reproductive organs. Basically, smaller reproductive organs still in development are associated with higher amounts of PSAP. The negative associations demonstrated between SZ13 and fertility-related measures are expected, as this is an anti-fertility protein and organ size is highly related to sperm-producing capacity.

Table 2. Correlations between seminal proteins and reproductive organ development (%)

Traits	PK2	PSAP	SZ13
Scrotal circumference	56	-38	-66
Testis weight	58	-40	-63
Epididymis weight	39	-48	-65

*Correlations can range from -100% to +100%. Negative and positive values denote antagonism and synergism, respectively.

Sperm motility was positively correlated with both aSFP (39%) and BSP1 (45%). These proteins are related to energy use and conservation by the sperm and relate to the fertilizing capacity of the sperm. Semen concentration was positively associated with ACR (49%) and NPC2 (37%). These proteins have a well-known positive relationship with semen concentration in other species as well. Thus, seminal plasma with higher aSFP, BSP1, ACR and NPC2 is associated with better semen quality in bulls.

Testis structure was assessed using testis ultrasonography and is positively associated with BSP1 (43%) and SZ13 (40%). These associations are probably due to the fact that these abundant proteins in the seminal plasma can increase the echogenicity of the organ, making the ultrasound images whiter. These observations are of practical relevance, since testis ultrasonography is a quick and easy assessment and can be conducted on commercial farms.

Testis microstructure (histology analysis of seminiferous tubules that house the sperm production) was correlated with several proteins (**Figure 1**). This is important, as testis microstructure is an indicator of sexual maturity. The association between CathD and seminiferous tubule maturity is demonstrating that this protein, along with BSP3, may aid in proper development of testis microstructure. In the same way, OPN and GPX are associated with mature tubules. Previous studies indicate that OPN is associated with better sperm performance, while GPX helps overcome oxidative stress that is detrimental to semen quality.



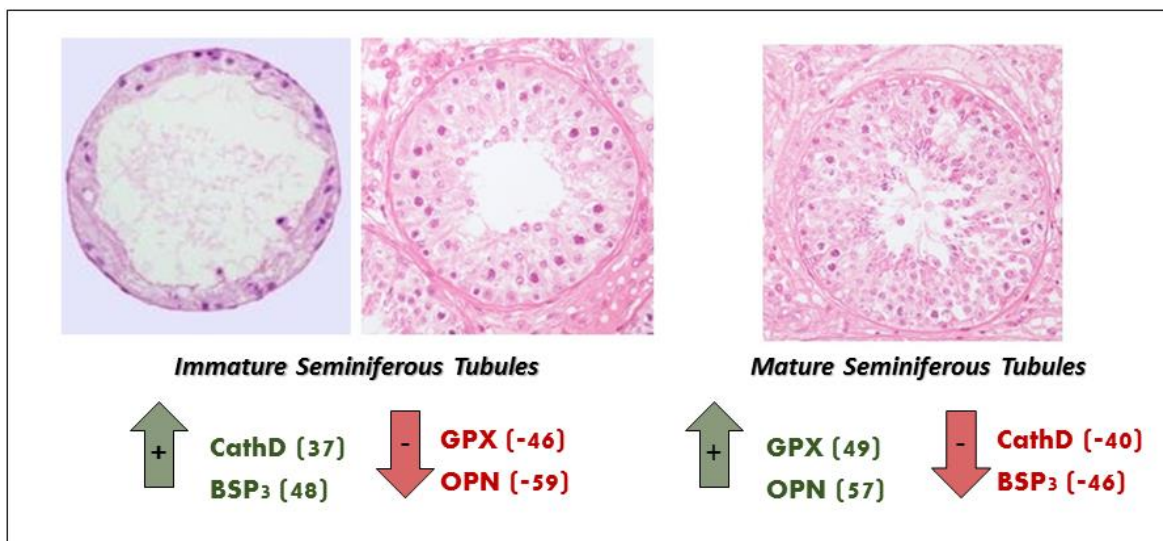


Figure 1. Correlations (%) between abundance of proteins and maturity of seminiferous tubules found in testis of young bulls. Images are cross-sections of seminiferous tubules, 400x magnification.

In addition to the associations between the structure of reproductive organs and semen quality, seminal proteins are also associated with feed efficiency. Figure 2 shows the relative abundance of seminal proteins in efficient and inefficient bulls. Three of these proteins (ESBP1, GPX and NPC2) are associated with diminished semen quality. ESBP1 is known to be strongly associated with the number of dead sperm in the ejaculate and NPC2 is a precursor of this protein. There is evidence indicating that increased GPX is also associated with certain sperm defects. Conversely, PCI is associated with sperm preservation and improved fertility. These results indicate that inefficient bulls had a more desirable profile of seminal proteins related to fertility, compared to the efficient bulls.

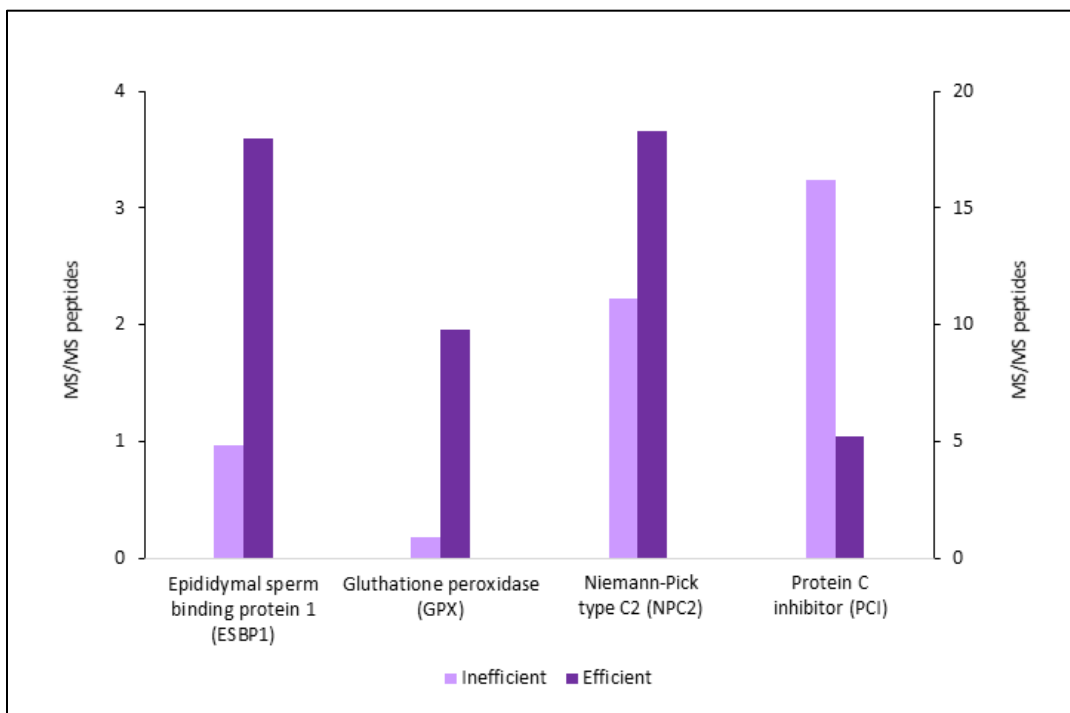


Figure 2. Different protein expression among young bulls by feed efficiency groupings

Take home messages

- Fertility-associated proteins from seminal plasma of young bulls relate to sexual maturity based on fertility-related traits (organ size, sperm quality and testis ultrasound and histology).
- Key fertility-associated proteins differ between feed efficient and inefficient young bulls. These proteins should be considered in the evaluation of feed efficiency and fertility potential.
- The differences in seminal proteins between feed efficient and inefficient young bulls support the association of delayed sexual maturity and improved feed efficiency.
- Research should focus on strategies to identify bulls with high feed efficiency accompanied by early sexual maturity and proven fertility still as young bulls.

Acknowledgements

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Testing Feeds: A Recurrent Procedure for Animal Performance and Well-being

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Analyzing Feed

Test your feed. You have heard it over and over again. But do you do it enough? To some degree it is the results of the report that can indicate how often, or not, you should sample your feed.

Feeds are sampled and analyzed for different reasons. Commonly, we all want to know the nutrient concentrations, as they can vary considerably. Some may decide to feed high quality feeds to the most productive livestock, whereas the low quality feed is used for animals with lower nutritional requirements. Those who cash crop use the nutritional value to establish a dollar value for selling the crop. However, testing can also be a means to determine the time of harvest, whether extra nutrients should be applied on the field, or approaches to maintain or improve storage and feed-out techniques.

Sampling is the First and Most important step

In a recent Ruminant Feed Industry meeting, Ron Piett of A & L Laboratories stated that sampling is the first and most important step of the entire analysis process. He indicated that the purpose of sampling a product is to determine the quality, through laboratory analysis, to identify the nutritional and anti-nutritional components. Both are just as important. For example, a mineral may need to be added if results are lower than expected, or steps may be taken to reduce the levels if they are too high. The analysis is what eventually is used to “facilitate the creation of a ration designed to maintain good health or optimum performance of the species” says Piett.

Common Mistakes

Laboratories get their fair share of samples that are difficult to analyze and in some cases impossible. Nelmy Narvaez, of SGS Laboratories commented on common errors that are seen when forage samples arrive at the laboratory. These samples may give an inaccurate representation of the feed from which it was taken, and as a result may not supply the required nutrients for the animal.

Errors seen in samples that arrive at the laboratory for testing are as followed:

1. Pulling hay samples from an intact bale causing samples to consist of stems, and no leaves. A large amount of hay samples that arrive at the laboratory are not cored- this is recommended for a representative sample.
A core sampler is a long hollow cylinder that is attached to a drill, or used by hand depending on type, to drive into bales to sample from several locations. For round bales, sample towards the middle of the bales. To sample square bales point the rod at a 90 degree angle so that multiple layers are obtained within a sample.
2. Samples are unrepresentative. Take samples from multiple spots; mix them to get a homogeneous sample, and then sub-sample approximately 500 gram.
3. Too much oxygen left in the sample bag. Remove all air from the sample by pressing the air out before closing it. Oxygen left in the bag will allow aerobic microorganisms to proliferate. The sample bag may generate pressure, causing the sample bag to tear.
4. Samples sizes are too big and bags are overfilled. It is difficult to properly mix these, and require more sub sampling in the lab. Overfilled bags can open up during shipping. Therefore, 500g samples are recommended.
5. Samples send out to the laboratory on Friday. This often results in samples sitting in a warehouse over the weekend. The fresher the sample, the better!
6. Improper labelling. To ensure proper analysis is done, label the samples clearly. Labelling should include what feed it is, date of sampling, and your name or farm name.

How often should I be sampling feeds?

In addition to errors, thought must be given to whether there were any issues at the time of harvest, or storage that would result in inconsistent results. “How often you sample these feeds will depend on the variability within the bunk or silo, and how quickly it is likely to change based on the rate you are feeding it. With greater variability, more samples will be required to understand the composition of what you are feeding”, says Chris Roelands of Honeyland Ag Services. “Common causes of increased variability are the growing and harvesting conditions, multiple cuts and/or different varieties stored in the same bunk, and storage conditions, to name a few. Are there any uncertainties with respect to any of the previously mentioned- if you don’t know, find out! And when you do, determine how often you should be sampling and what changes you can make, if any, to avoid this in the future”.

William Weiss and Normand St Pierre from the Ohio Agricultural Research and Development Center stated, “We need to start thinking about feed composition data in terms of probabilities rather than actual, absolute concentrations. In other words, how confident are you (or should you be) that the number you have actually represents the true concentration of a nutrient in a feed?”



NIR versus Wet Chemistry analysis

Sample request forms require you to indicate what analysis you would like to have done. Both wet chemistry and Near Infrared Spectroscopy (NIR) are methods commonly used. Wet chemistry measures the nutritional value using heat and chemicals to break down the forage. For example, NDF is the fiber portion that is not broken down when boiled in a neutral pH solution. This is weighed prior to and following the process and difference is calculated. Although accurate, it is time consuming and not as cost-effective as using NIR.

NIR estimates the nutritional value of the feed using light reflection rather than chemistry to identify and measure amounts of compounds in a sample. The reflectance values are entered into calibration equations which estimate nutrient values. The equations are based on studies which compare split samples for wet chemistry with NIR reflectance. This provides fast, reproducible and cost-effective results with minimal sample preparation by the laboratory providing the service, and allows for timely return of analytical results for the customer. However, if your feed was grown under conditions that are significantly different from those in the calibration set, the accuracy of NIR estimates may decrease

What's New?

Lately, a new term 'aNDFom' has been thrown around in terms of neutral detergent fibre (NDF) evaluations. It varies from NDF in that it is free of ash, which makes it on an 'organic matter basis'. Some laboratories may be giving you aNDFom values, whereas other laboratories still indicate NDF values. An ashing furnace is used to heat samples to extreme temperatures, leaving a residue of ash, which contains the minerals. This is then weighed and subtracted from the NDF portion, giving the 'ash-free' NDF, or aNDFom. Why does this matter? Well, when the NDF is determined, residues of ash are often perceived as part of the NDF value. The variability between NDF and aNDFom varies, as some may have higher ash content due to splashing of soil on leaves due to rainwater, areas prone to flooding, or soil picked up during harvest. This extra step to obtain aNDFom may delay results, but can be valuable to know when evaluating the feed.

Each phase of growth, harvest, storage, or feed-out of a feed involves a quality change, and you have the opportunity to obtain its nutritional value as you see fit. However, to get the most out of your feed, have your feed tested on a regular basis. A simple analysis can go a long way in increasing your bottom line.

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