Metabolomics: predicting sheep productivity

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Abstract

The scientific study of a set of small molecules present within a cell, tissue or an organism is referred to as metabolomics. This study of the unique chemical fingerprint of an organism has been widely applied in biomedical research for disease diagnosis and prognosis. Application of metabolomics in livestock research, specifically in sheep, is by far behind the potential it offers. We have initiated three projects using metabolomics to assess sheep feed efficiency and carcass merit, pregnancy and litter size, and parasitic infection. Our main objective is to identify biomarkers within individual animals that are predictive for their parasite infection status, productivity level and/or pregnancy condition. Ultimately, these biomarkers are intended for use in the development of a portable "pen-side" device that would use a few drops of blood to identify and/or predict efficient sheep. This device will help farmers save money on other costs (e.g., ultrasound), save time (with user-friendly application), be more efficient (by real-time data collection, centralizing in a computer-friendly interface and adopting a better management plan in advance) and be more independent. We have conducted preliminary laboratory analyses using nuclear magnetic resonance spectroscopy to evaluate serum samples (n=35) collected from lambs and ewes. Initial results have identified potential markers that distinguish between high and low feed efficient lambs, parasite infected and non-infected sheep, and open and pregnant ewes with a single fetus or multiple fetuses. We are currently investigating a larger cohort of samples (n=1720) using 4 different analytical platforms to validate these initial results.

Selection Response for Total Post-Weaning Weight in Rideau-Arcott Sheep

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Abstract

The total litter post-weaning weight is a single composite trait that has been proposed to be used as a biological index for overall ewe reproductive success, which can balance the genetic improvements for the growth and the reproductive component traits. Such a composite trait can be improved by both direct and indirect selection. The goal of this research was to predict and evaluate the response of selection for total post-weaning weight based on: a) direct selection for the trait, b) indirect selection based on single component traits, and c) combining growth and reproductive traits in a selection index. Estimates of genetic and phenotypic parameters for growth and reproductive (at first and later lambings) traits including birth weight, weaning weight, post-weaning weight, number of lambs born, number of lambs weaned, total weaning weight, and total post-weaning weight were used to predict selection response. The results indicated that single-trait selection based on weaning weight or post-weaning weight yields higher selection response than direct selection for total post-weaning weight. However, such selection would be accompanied by unfavorable response on the number of lambs born. On the other hand, when growth and reproductive component traits were combined into a selection index, the selection response for total post-weaning weight was the highest, with no negative response in number of lambs born. Therefore, the use of selection index was the most effective selection method to improve total post-weaning weight and its component traits.

Correlation of pre-breeding CarLA® with periparturient and late lactation fecal gastrointestinal nematode egg count and hematocrit in Ontario sheep

Research team   Emma Borkowski, Stéphanie Bourgon, Andrew Peregrine, Niel Karrow, Brandon Lillie, Paula Menzies

Abstract

Gastrointestinal nematodes (GINs) are an important cause of morbidity, mortality and financial loss on Ontario sheep farms. Anthelmintic resistance among GINs has become widespread, and selection of breeding animals with superior immune response is an attractive alternative strategy for controlling GINs. One method of identifying sheep with improved immunity to GINs is through assessment of salivary antibody to carbohydrate larval antigen (CarLA®), a marker on the surface of infective larvae. This strategy is used successfully in New Zealand; however, to date this method of selection has not been evaluated under Ontario grazing conditions. In this study, CarLA® antibody was measured in 106 ewe lambs on a commercial sheep farm during their first grazing season. These lambs were followed through their first lambing and lactation as part of a two-year investigation into the immune response of sheep to GINs under Ontario grazing conditions. Periparturient and late lactation GIN fecal egg counts (FECs) and hematocrit (a measure of anemia) were correlated with pre-breeding CarLA in order to determine whether pre-breeding CarLA was predictive of peri- and postparturient parasitism. A weak, significant negative correlation was identified between pre-breeding CarLA and late lactation hematocrit; no correlation was found between pre-breeding CarLA and GIN FEC or periparturient hematocrit. These findings indicate that pre-breeding CarLA is not predictive of parasitism in periparturient or lactating Ontario sheep.

Comparison of deep amplicon nemabiome sequencing with morphological identification to quantify species proportions of gastrointestinal larvae isolated from small ruminant feces

Research team   Emma Borkowski, Elizabeth Redman, Russell Avramenko, Rebecca Chant, Jacob Avula, Niel Karrow, Paula Menzies, Brandon Lillie, Andrew Peregrine, John Gilleard

Abstract

Gastrointestinal nematode (GIN) parasitism has a significant impact on health and productivity of sheep and goats worldwide. Fecal GIN-type egg counts are widely used for monitoring infection levels and anthelmintic resistance within a flock; however, the eggs of many nematode species, including the most commonly identified species in Ontario (Haemonchus contortus, Teladorsagia circumcincta and Trichostrongylus spp.), are identical in morphology. This necessitates larval culture to determine the species involved. The traditional method involves morphologic speciation of third-stage (L3) larvae cultured in feces following incubation for 7 days. However, morphologic differences are often subtle and results are consequently prone to error. In addition, culture for this duration can bias species composition. A new approach to quantify the relative proportions of parasite nematode larvae isolated from fecal samples, called nemabiome sequencing or metabarcoding, has been recently described for cattle GINs. This is based on deep amplicon next generation sequencing of the internal transcribed spacer (ITS)-2 ribosomal DNA locus. We have applied this approach to populations of first-stage (L1) larvae cultured for 48 hours following isolation of eggs from small ruminant feces. This study compared species composition of pooled small ruminant fecal samples determined using traditional morphologic identification of L3 larvae with results of this new L1 deep amplicon sequencing approach. The L1 culture method displayed significantly improved larval recovery and similar speciation results compared to the traditional method. Thus, speciation of L1 GIN larvae using DNA sequencing offers an objective and rapid alternative to morphologic speciation of L3, with comparable species composition.

Tales from the grave: how dead sheep can help you and your vet help your farm

Research team   Jeanette Cooper[1], Dr. Andria Jones-Bitton[1], Dr. Paula Menzies[1], Dr. Sherilee Harper[1], Dr. Jocelyn Jansen[2], Dr. Maria Spinato[3]

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Abstract

The project "Distance support for on-farm investigation of adult small ruminant mortalities" is designed to encourage producers and veterinarians to perform postmortems on adult sheep and goats that die unexpectedly or for unknown reasons on-farm. Improved postmortem techniques achieved through this project will result in better diagnostic outcomes and enhanced disease surveillance in Ontario's small ruminant populations. Improved diagnostic information will also allow veterinarians and producers to create a tailored health management strategy to decrease sheep and goat mortalities and therefore, increase producer profits.

This project has thus far accepted postmortems from 8 sheep and 15 goats with unknown causes of death. Diagnoses were made in all 8 sheep cases. These include: copper toxicity (2), nasal tumours (3), haemonchosis (2) and monensin (Rumensin®) toxicity (1). Diagnoses from goat cases include: Johne's disease (1), enterotoxaemia from clostridial infection (2), caprine arthritis encephalitis (CAE) (1), pneumonia (4), uterine infection (2) and copper toxicity (2). Diagnoses were unable to be made in 3 goat cases.

Many of the diagnoses, both in sheep and goats, can have impacts on overall flock/herd health, with the potential to cause multiple mortalities. The diagnostic information gained from a proper postmortem can provide the basis for the design of

Leveraging transcriptomics and systems biology to understand the genes and metabolic pathways associated with resistance of sheep to gastrointestinal nematodes

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Abstract

Haemonchus contortus infection has been previously identified as a common cause of morbidity and mortality in Ontario grazing sheep. Due to increasing anthelmintic resistance, chemical control alone is inadequate to control these infections. In addition, changes in climate and climate variability will not only affect the sheep's ability to fight off infection, but also the life cycle, parasite load, and pasture contamination of H. contortus. All of these factors make it critical for more tools to be developed, such as genetic selection for sheep resistant to H. contortus infection that can be used as part of a sustainable integrated parasite management program. Selecting sheep that develop immunity to gastrointestinal nematode (GIN) parasites more rapidly for breeding purposes will result in lower levels of clinical disease and reduced fecal shedding of eggs in Ontario sheep populations.

Our project will be collecting abomasum tissues, the primary target tissue of H. contortus, from previously phenotyped HIGH and MIDDLE stress responding sheep (n=30), HIGH and LOW immune responding sheep (n=30), and control sheep (n=16), to examine the abomasum transcriptomic profile associated with the parasite resistance. Differential gene expression analysis within groups, single nucleotide polymorphism (SNP) and transcript discovery analysis will be performed in order to identify functional SNP associated with immune response. We will also be collecting climate data over two grazing seasons, to examine a correlation between climate conditions and H. contortus pasture contamination and host load.

Determining phenotypic trait correlations with an indicator of Haemonchus contortus resistance in Rideau Arcott sheep

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Abstract

The blood-sucking parasite, Haemonchus contortus, has caused flock illness, production loss, and death throughout the Canadian sheep population. While the industry attempts to select for more resistant individuals in order to reduce the parasitic infestation, the impact of this selection on the various production traits of the Rideau Arcott breed remain unknown. To determine associations between parasite resistance and other production traits, producer data was obtained on 29 traits, including fecal egg counts (FEC), from 455 Rideau Arcott sheep between the years of 2012 to 2016. Statistical Analysis Software (SAS) was used to determine the significance and strength of correlations between FEC and production traits, as well as within the production traits themselves. Significantly correlated traits had a p-value of less than 0.05 and the strength of their correlation was determined using a Pearson correlation coefficient. Results show that reproductive traits, including the number of lambs born at the first lambing, the lambing interval, and the number of lambs born at the later lambings, were correlated significantly (p-value <0.05) with FEC. Number of lambs born at first lambing, lambing interval, and number of lambs born at later lambings were all positively correlated with FEC, with Pearson correlation coefficients of 0.101 (p=0.032), 0.093 (p=0.049), 0.099 (p=0.035), respectively. More FEC data and production trait measurements will be needed in order to further investigate the correlations between FEC and other economically important production traits, to increase the accuracy of selection in the Ontario sheep industry.

Exploring the practicality of using FAMACHA scoring in Southern Ontario sheep farms

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Abstract

Anthelmintic resistance has become an overwhelming issue for Ontario sheep producers. Therefore, novel approaches to control or prevent anthelmintic resistance in parasite populations are needed to improve production efficiency in the Ontario sheep industry. Selection of sheep that are genetically resilient or resistant to parasite infection may offer a novel approach to prevent anthelmintic resistance, however, parasite resistance phenotypes may be difficult and expensive to collect. To address this concern, we investigate the on-farm feasibility of using FAfa MAllan CHArt (FAMACHA), as opposed to the traditional Fecal Egg Count (FEC), for selecting sheep that are resistant or resilient to Haemonchus contortus. Traditionally, FAMACHA is used as a tool for selective deworming of small ruminants. It consists of scoring the severeness of anemia by examining the animal's submucosal eyelid and comparing it to images on a reference card. The FAMACHA technique was used to score sheep at two different commercial farms in Ontario. The FEC test was carried out using the McMaster technique on two groups, mature ewes and young sheep from a single farm. Our results indicated that FAMCHA is an easier and quicker method to assess the possibility of Haemonchus contortus infection. Through further evaluation, producers may be able to apply more effective, less time-consuming and more economical measures to proactively control anthelmintic resistance in Ontario sheep flocks.

Risk assessment for the incursion and establishment of Orbiviruses in Ontario: Serosurveillance in cervids and cattle and characterization of current vector composition and distribution

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Abstract

Epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) are vector-borne Orbiviruses representing imminent threats to Ontario's wildlife and livestock. Environmental factors and associated vector expansion appear to be spreading the distribution of these viruses northward in the USA. Ontario is at high risk for EHDV/BTV incursion and establishment, with confirmed outbreaks in white-tailed deer near the Ontario-U.S. border, BTV-seropositive cattle in Ontario, and the Ontario presence of Culicoides sonorensis, an EHDV/BTV vector. Ontario ruminants are immunologically naïve to these viruses; thus, their introduction may have significant negative impacts on wild cervid populations and livestock (farmed cattle, sheep and deer) through morbidity, mortality and production loss. Our research seeks to characterize Culicoides spp. vector distribution and composition and assess for possible ongoing transmission (i.e., serosurveillance) in wild cervids and livestock in high-risk regions of Ontario. LED light traps will be placed on cattle farms and in natural areas across southwestern Ontario, then Culicoides vectors identified taxonomically and molecularly. Sera from wild cervids and will be screened for EHDV/BTV antibodies by ELISA, and the serotypes of positive samples will be determined by serum neutralization assay. Data will undergo spatial analysis to reveal regional and seasonal-temporal patterns in vector distribution, as well as statistical analyses to detect disease associations among animal age, sex, and season. This information supplements the data from ongoing annual bovine serological surveillance and the nationwide targeted Culicoides survey conducted by the CFIA and help to better identify the threat of EHDV/BTV to Ontario wildlife and livestock.

Development of a vaccine against Toxoplasma gondii for small ruminants

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Abstract

Toxoplasma gondii is one of the leading causes of abortion of sheep and goats in Ontario. The environment becomes contaminated from infected cat feces, and the parasites survives well in the environment, even at extreme temperatures. The eggs (oocysts) are then ingested by small ruminants and enter the digestive tract. Pregnant ewes can then abort, or give birth to weak lambs with or without congenital defects. Toxovax (Merial) is a vaccine available in Australia and the UK, and is made of the attenuated parasite. While it is effective in prevention of abortions, it's short half-life, zoonotic potential, and the fact that the vaccine is not licensed for use in North America make its routine use difficult to impossible. There are no effective means for prevention available in Canada. Viruses are useful for vaccine development as they can elicit robust immune responses. In our lab, we engineer viruses to express foreign antigens and act as vaccine vectors. We have developed two viruses which express Toxoplasma gondii antigens and our next step is to evaluate the safety and efficacy of our vaccine in mice. Once we have demonstrated that our vaccine can elicit a strong immune response and decrease parasite burden in mice, we will test our vaccine in sheep. Our final goal is to engineer a vaccine that reduces the incidence of Toxoplasma gondii abortion in sheep and goats.

Price Transmission in the Ontario Lamb Market

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Abstract

Small but not insignificant, the Ontario lamb market has struggled to meet the increasing demand for lamb by Canadian consumers. Since local lamb is more expensive to consumers than lamb imported from Australian and New Zealand, it appears that the incentives associated with sustained growth in demand for lamb may not be reaching Ontario lamb producers. How do different segments of the vertically linked lamb market respond to changes in prices at any level?

While price transmission in agri-food markets has received significant research attention in recent years, the results are inconclusive and vary across commodities, countries and time periods considered (Vavra and Goodwin, 2005; Frey and Manera, 2007). Only a few studies focused on vertical price transmission in the market for lambs (Griffith and Piggott, 1994; Tiffin and Dawson, 2000; Ben-Kaabia and Gil, 2007 and Shadmehri and Ahmadi, 2010) and the results appear to be contradictory. To the best of our knowledge, no price transmission study has been done for the Ontario lamb market. This paper attempts to bridge the gap by studying the nature of vertical price transmission in the Ontario lamb market.

Weekly average prices from four main auction yards, as well as wholesale and retail prices, from 2008 to 2016 are used in this study. The results suggest that the price transmission in the Ontario lamb market is of "demand pull" type and that the price transmission is asymmetric.

Evaluating direct and indirect selection for genetic improvement of carcass yield and quality in Canadian sheep

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Abstract

Continuous improvement of carcass yield and quality are necessary for the Canadian sheep industry to remain competitive. New research has shown that carcass traits are moderately heritable in the Canadian sheep population (0.17-0.32), indicating that there is potential to improve carcass characteristics through genetic selection, but how? In the future, genetic evaluations may allow direct selection to improve carcass yield and quality, however, direct selection for carcass traits may be unfeasible for producers that market on a live weight basis. Indirect selection, in which a target trait is improved through selection on a genetically related trait, could offer an alternative to direct selection. For example, the higher selection intensity and heritability of post-weaning weight (0.28 ± 0.01), could result in greater improvement of hot carcass weight (0.17 ± 0.02) through indirect selection. Therefore, the objectives of this research were: (1) to examine the influence of current selection for growth and ultrasound traits on carcass yield and quality and (2) to evaluate the relative efficiency of direct and indirect selection to improve carcass traits. Genetic parameters estimated from weaning weight (n= 29,082), post-weaning weight (n= 26,763), ultrasound loin and fat depth (n= 1,299), and carcass (n= 14,441) records (hot carcass weight, fat depth, saleable meat yield and carcass conformation) were used to predict expected direct and correlated response to selection and to determine their relative efficiency. The results of this research will provide insight into the efficiency of direct and indirect selection for genetic improvement of carcass yield and quality.

Determining the prevalence and distribution of Eimeria species infecting lambs on Ontario sheep farms

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Abstract

Coccidiosis, caused by protozoan parasites in the genus Eimeria, has not been studied systematically in Canada since 1985 (Dohoo et al., 1985) despite a recent survey by the Ontario Animal Health Network identifying coccidiosis in lambs as a top clinical issue (Ontario Animal Health Network, 2016). There are ~15 named Eimeria spp. that infect sheep and the variety of resultant clinical signs are species dependent (Taylor and Catchpole, 1994). The identification of individual species, particularly those that cause severe clinical signs, is information crucial for effective and targeted anticoccidial treatment. Less pathogenic species can be excreted at large numbers without causing clinical effects therefore it is difficult to determine the actual severity of infection using conventional oocysts enumeration methods (McDougald, 1979). The objectives of this project include: 1) to develop an economical assay for the identification of Eimeria species present in feces; and, 2) determine the prevalence and distribution of Eimeria species in lambs on Ontario sheep farms. To date, at least 5 distinct Eimeria species have been identified in Ontario sheep, frequently in mixed infections. Collectively, parasite identification and enumeration can guide specific management practices, feed, and treatment options to decrease the impact of coccidiosis.

Development of a low-density array from SNPs located in genes expressed in the sheep's mammary gland

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Abstract

The availability of Single Nucleotide Polymorphism (SNP) arrays facilitates the study of genetic architecture of livestock traits. The appearance of SNP chips was possible by the availability of animal genome sequences due to the development of Next generation sequencing technologies (NGS). In sheep, there are currently different commercial SNPs chips developed mainly by Illumina and Affymetrix. However, the growing power and the reducing costs of NGS in the last years sparked an enormous range of applications and enabled the development of an increasing number of custom SNP chips developed by individual laboratories. The objective of this study was the development of a low-density custom SNP panel by using the functional variants from milk somatic cell RNA-Seq data in two commercial dairy sheep, Assaf and Churra. Firstly, genetic variants (SNPs and indels) were identified in two breeds with different phylogenetic origin: Assaf (n=4) and Churra (n=4), obtaining 212,742 polymorphisms. Then, we kept the SNPs with a minor allele frequency (MAF) higher than 0.125 in both breeds, obtaining 91,683 SNPs. Among these, we selected 1,161 SNPs that were classified by Variant Effect Predictor software with a high or moderate impact and located within milk protein and fat candidate genes and sheep QTL regions (https://www.animalgenome.org/cgi-bin/QTLdb/OA/index). Finally, we covered the gaps between the selected SNPs with additionally markers showing a MAF higher than 0.125 every 1,000,000 bp. The final SNP panel had 3,194 SNPs. The development of a custom chip panel on functional data will allow us its use on commercial populations of dairy sheep with the aim of identifying potential associations of these functional variants with dairy productive traits.

Combating Haemonchus contortus infection with fecal egg counts

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Abstract

Haemonchus contortus, or Barber's Pole Worm, is a costly worldwide challenge in sheep industries. Drenching is no longer a sufficient defense against this parasite as H. contortus has developed resistance within all major groups of dewormers. Fecal egg counts (FEC) can be used to select breeding stock that are more resistant to H. contortus. An Ontario farm has incorporated FEC into their breeding program since 2012. The farm's median FEC has been decreasing over the past 4 years. When FEC values were adjusted to account for variation due to year sample was taken, litter size at birth, age at measurement, and dam age, sire was significantly associated with FEC and explained 38% of the variation. In 2014, sire was associated with FEC (p <0.0001), and two sires had a significantly higher progeny FEC than a third sire. In 2015, sire was associated with FEC (p <0.0001), and there were also significantly different progeny FECs between sires. Some sires produce offspring with lower average offspring FEC than others, and this may provide legitimate reasoning for choosing one sire over another. FEC was significantly associated with management group, body condition score, and age at measurement, which shows that FEC is a complex trait partially mediated by management practices. A heritability estimate of 0.10 ± 0.08 for the population provides further evidence of a genetic component to FEC. The results of this research suggest that FEC could be a useful tool for genetic selection to improve parasite resistance on Canadian sheep farms.