Food security, global health and environmental sustainability: challenges from increasing meat consumption

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Introduction   The increasing consumption of meat and other animal-sourced foods is one of the most important contemporary trends in the global food system. It matters because there is increasing evidence that the consumption of different types of meat and meat products have a variety of effects on human health, both good and bad, and because livestock production is one of the most significant ways in which agriculture affects environmental sustainability. The earth could not support a global population of around 10 billion consuming meat at anywhere near the levels found today in Europe and North America without radical changes in production methods.

Results   The talk will first explore recent evidence about the health effects of eating different types of meat. Epidemiological analysis of longitudinal cohorts shows that consumption of red and processed meat in particular is linked with negative health outcomes, though patterns that are significant at the population health level may nevertheless represent relatively marginal increases in personal risk. In some parts of the world, where diets are still deficient in calories, increased consumption of animal-sourced foods may be desirable. The talk will also explore the environmental consequences of different types of meat production. Meat, especially grain-fed ruminant meat, tends to be a particularly poorly performing type of food for its greenhouse gas emissions, while other types of meat production can perform much better across a range of environmental metrics.

In order to understand the complex interactions between economic, health and environmental processes quantitative modelling is essential. A brief summary of some modelling results using a new coupled economics and health model will be presented. The health and environmental consequences of different types of diet change will be explored, as well as the likely effects of climate change on health mediated through diets. Finally, the effects of carbon taxes on the price and consumption of different food types will be modelled, and their effects on greenhouse gas emissions and social equity studied.

Conclusion   The talk will conclude by asking what the livestock industry can do to mitigate the environmental and health effects of changing dietary patterns. It will also explore whether the industry should view the increasing attention being given to the health and environmental consequences of eating meat as a challenge to be resisted or an opportunity to be embraced.

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Impact of Brexit on the Irish Agricultural Sector

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Application   Economic Analysis of the impact of Brexit on the Irish agricultural sector

Introduction   The UK decision to leave the UK (Brexit) could have profound impacts on the Irish agriculture and food industry. The nature of the future post-Brexit trade relationship between the UK and the European Union is currently unknown. Recent research (Feng *et al*., 2017; van Berkum *et al*., 2016) has analysed the impact of Brexit on UK agriculture of different possible Brexit scenarios. In this paper we explore the possible impact of Brexit on Irish agri-food exports to the UK and on Irish farm incomes.

Material and methods   Highly disaggregated data on Irish agri-food trade with the UK, data on EU Most Favoured National tariff rates applicable to imports of agri-food products into the EU from non-EU origins and recent estimates of UK import demand elasticities (Imbs and Mejean, 2017) are used to assess the possible impact of Brexit on Agri-food trade between Ireland and the UK. Furthermore, results from recent research on the impact of Brexit on UK agriculture (Feng *et al*., 2017) are used to assess the possible impact of Brexit on Irish agricultural incomes within a static framework using microeconomic data from the Teagasc National Farm Survey.

Results   If, following Brexit the UK imposes the current EU MFN tariff schedule Ireland will lose the preferential access to the UK market that it currently enjoys. Using recent estimates of UK import demand elasticity for food products (Imbs and Mejean, 2017) the introduction of tariffs to Irish-UK trade is found to dramatically reduce many of the important agri-food export flows from Ireland to the UK. Such outcomes would be likely to have a profound impact on the level of Irish farm gate prices and on Irish agricultural sector incomes.
Using the simulated impact of Brexit on UK agricultural commodity prices (Feng *et al*., 2017) the impact on Irish farm level incomes of Brexit using Teagasc National Farm survey data is assessed. While Brexit, and the associated loss of preferential access to the UK market, will lead to reductions in the value of agricultural output produced in Ireland, the possible impact of Brexit on the value of direct payments received by Irish farmers from the CAP could significantly magnify the impact of Brexit on Irish farm income.

Conclusion   Ireland, and Irish agriculture specifically, has, over the course of its membership of the EU progressively reduced its dependence on the UK export market. Brexit could dramatically accelerate this process and impose significant economic losses on Irish Agriculture. The results illustrate the sensitivity of simulated trade impacts of Brexit on agri-food trade between Ireland and the UK with respect to a) the elasticity of import demand used and b) the magnitude of the tariff and non-tariff barrier to trade that will be faced by Irish exporters to the UK following Brexit.

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The impact of post-Brexit trade agreements on UK agriculture

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Application Quantification of the sectoral impacts of alternative trade agreements in the post-Brexit era.

Introduction The UK agricultural sector is deeply embedded within the European Union and hence the process of leaving the Union will potentially have profound implications for this sector within the UK. Analysis undertaken as part of the FAPRI-UK project has quantified the sectoral impacts on UK agriculture of alternative trade agreements following Brexit (Feng *et al.*, 2017). We analyse three possible post-Brexit trade arrangements: *Bespoke Free Trade Agreement with the EU*; *WTO default MFN tariffs*; and *Unilateral Trade Liberalisation*. The scenarios are designed to be illustrative of the impacts of the range of theoretical possible trade arrangements, rather than speculating on the final outcome of the Brexit trade negotiations.

Material and methods The modelling framework is based on a partial equilibrium methodology, which captures the dynamic interrelationships among the variables affecting supply and demand in the main agricultural sectors of England, Wales, Scotland and Northern Ireland. The UK model consists of a system of equations covering the dairy, beef, sheep, pigs, poultry, wheat, barley, oats, rapeseed and biofuel sectors. A key feature of the FAPRI-UK modelling system is its links within an EU-wide modelling system and a global modelling system (FAPRI Missouri's EU grain, oilseed, livestock and dairy (GOLD) model). The modelling system captures the impacts on commodity markets as a result of changes in trade flows with the EU and the rest of the world. It has been substantially updated to account for the fact that in the case of Brexit the UK and EU markets would no longer be fully integrated.

Results The results for the *Bespoke Free Trade Agreement with the EU* scenario indicate that the impact on producer prices varies across all commodities, but the changes are relatively small due to the limited disruption to trade.
In the absence of a Free Trade Agreement between the UK and the EU, the UK would fall back to *WTO default MFN tariffs*, at least in the short-run. Under this scenario, MFN tariffs are applied on UK exports to the EU and likewise imports from the EU to the UK. The MFN tariffs are very high, leading to significant disruptions to trade between the UK and EU-27; impacts depend on whether UK is a net importer or a net exporter of the relevant commodity.
Under the final scenario we consider a radical version of *unilateral trade liberalisation* in which the UK sets zero tariffs on imports to the UK from both the EU and the rest of the world. This scenario has a depressing impact on UK prices and output values across all commodities, particularly in the beef and sheep sectors where international competition is very strong.

Conclusion The analysis demonstrates the extent to which the type of trade agreement could result in different price and production impacts in the UK depending on the disruption to trade patterns. In addition, the results show variable impacts across sectors, reflecting the extent to which the UK is a net importer or exporter and the degree of international competition within specific sectors.

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Evolving views on bovine respiratory disease – an appraisal of potential challenges and solutions in livestock production

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Introduction Bovine respiratory disease (BRD) is one of the most commonly diagnosed causes of morbidity and mortality in cattle and interactions of factors associated with the animal, the pathogen and the environment are central to its pathogenesis. Emerging knowledge of a role for pathogens traditionally assumed to be minor players in the pathogenesis of BRD reflect an increasingly complex situation that will necessitate regular reappraisal of BRD pathogenesis and control. Blanket vaccination or mass medication provide inconsistent control and the effective tackling of BRD will require innovative, evidence-based and targeted interventions which, if employed sensibly, offer useful alternatives for addressing this disease.

An appraisal of selected pathogens The traditional model of primary viral infection followed by secondary bacterial opportunism has increasingly been challenged as being overly simplistic in failing to acknowledge the primary role of some pathogens that were previously considered of minor importance. The use of approaches in pathogen identification such as metagenomics has revealed the presence of some of these pathogens in bovine lungs which were rarely, or not previously, detected. Emerging knowledge of a potential role for these 'minor' players (e.g. bovine coronavirus, bovine rhinitis A virus) in the pathogenesis of BRD coupled with the polymicrobial nature of many cases, and the detection of many recognised BRD pathogens in the nasopharynx or lungs of healthy cattle (e.g. *M. bovis*), complicates BRD diagnosis and blurs the precise role played by specific pathogens in eliciting disease. The potential role of selected apparently 'minor' pathogens in BRD pathogenesis is discussed.

An appraisal of selected control measures Vaccination against bacterial and viral pathogens implicated in BRD is broadly accepted as an effective control measure and is widely practiced although supportive evidence of efficacy is sometimes lacking. Claims of vaccine efficacy are often based on biologically logical extrapolation from challenge studies rather than field efficacy data. Furthermore, differences in BRD pathogenesis between beef and dairy cattle are also significant in considerations of BRD vaccine efficacy. The age at which vaccination is typically performed, the potential effects of maternal antibody on the host response, the timing of vaccination relative to infectious challenge and the ability of high-risk animals to mount an appropriate response to administered vaccines must all be considered. Current knowledge suggests that we are making less than optimal recommendations on vaccine use.

Administration of antimicrobials to cattle to control BRD can be generally classified as therapeutic or preventative, with preventative use further subdivided into prophylactic and metaphylactic use. The decision to engage in either prophylactic or metaphylactic use of antimicrobials is influenced by many factors, among them the potential role of these essentially crude control instruments, which can obliterate whole ecosystems of microflora in the animal, as drivers for the development of antimicrobial resistance in commensal or pathogenic bacteria. With growing public aversion to the large scale use of antimicrobials in food animals, alternatives to metaphylaxis or prophylaxis have been sought. Some of these solutions have focused on the earlier detection of infected animals through the use of automated systems or the use of recently proposed alternatives to blanket antimicrobial administration at induction.

Conclusion In light of evolving knowledge regarding the role of specific pathogens in BRD pathogenesis we need to regularly reappraise our understanding of BRD pathogenesis and control. Emerging knowledge of pathogens traditionally assumed to play minor roles in BRD shows us that the 'playing field' for BRD is more crowded than previously thought and that the potential role of these pathogens, either alone or in concert with other BRD pathogen infections, should not be discounted. Furthermore, the limitations of specific control measures should prompt us to regularly reappraise our understanding of BRD control. Targeted interventions at the critical control point in BRD pathogenesis is the key in groups of cattle of all ages and in all husbandry systems and by expecting blanket interventions in highly stressed cattle to be effective in all situations we may be repeating many of the mistakes of the past. Innovative, evidence-based diagnostic and control measures, if employed sensibly, offer useful alternatives for addressing this disease.

Improving animal health and reducing the environmental footprint of animal systems via systems microbiology

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Recent technological advances led to the communalisation of nucleotide sequencing and next-generation sequencing platforms are now available at most universities and governmental institutions. The large amount of sequence data that is being generated for individual projects can today be analysed via cloud computing using open source software and the scientific community is now tasked to tackle the next significant challenge: converting large amounts of data (Big Data) into meaningful data (Deep Data). Once this transition is achieved successfully, metagenomics will have matured from a hypothesis-generating into hypothesis-testing approach and it will be possible to test complex hypotheses in microbial ecology. One step into this direction and towards the ability to build mechanistic models of complex microbial processes in the environment is the capability to *i)* reconstruct full-length genes and pathways from omics data and *ii)* the ability to differentiate between genes that are only present and genes that are actively contributing to the phenotype of an individual microorganism and complex microbial communities.

The seminar will discuss the strategies employed by Prof. Matthias Hess of UC Davis to identify several hundreds of putative fungal glycoside hydrolases that were expressed during biomass-degradation in the cow's rumen. Anaerobic fungi are an essential component in many biomass-degrading ecosystems, but they are currently poorly understood. Results from this work will contribute to a better understanding of the molecular machinery that is employed by anaerobic fungi to break down complex carbohydrates and provide the opportunity to improve currently available enzyme cocktails for improved feed digestibility.

Furthermore, results will be shown from an in-vitro experiment which tested the effect of macroalgae on methane emission from enteric fermentation and its potential as feed additive for more sustainable animal production systems.

Microbiome repair and rehabilitation: normalisation of gut function

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Gut health and its management is an intricate and complex area governed by numerous factors including nutrition, microbiology, immunology and physiology. When gastrointestinal health is compromised, nutrient digestion and absorption are affected, feed conversion becomes reduced, susceptibility to disease is heightened, all of which can have negative economic impacts. The overall population of microorganisms in the gut is referred to as the microbiome and is recognised as a very diverse community of bacteria, fungi, protozoa, and viruses. Its' diversity varies along the different regions of the GI tract, with regions having less tolerable conditions containing a reduced microbial diversity in comparison to regions more favourable to microbial growth. Within the GI tract, there are multiple interactions between the host, intestinal environment and microbial cells in addition to feed components. These interactions underline the critical role of the microbiota in the health and well-being of the host, although the exact way in which this is achieved is not yet fully understood. The diversity within the microbiome plays a critical role in gut health with beneficial microbes forming a protective barrier lining the gut, preventing the growth of pathogenic bacteria such as Salmonella, Campylobacter, Clostridia and Escherichia amongst others. Poor intestinal health is often associated with increased pathogen colonisation, susceptibility to infectious disease and increased mortality. While there is a need for therapeutic use of antimicrobials to treat disease, globally it is recognised that there is an urgent need to further limit and restrict their use in production settings. The main drawback of the therapeutic use of antimicrobials to combat poor intestinal health is their non-specific effects on the gut microbiome and the reduction in overall gut microfloral diversity noted with their administration. Without intervention, the use of antimicrobials can lead to a vicious cycle whereby their use reduces overall microfloral diversity and selects for the expansion of resistant species to the detriment of non-resistant commensal strains. This reduced diversity allows for the continued proliferation of resistant species and can have negative impacts on health and performance. One strategy to combat the negative consequences of therapeutic antibiotic use is to repair and rehabilitate the gut microfloral diversity. Profiling and understanding the role of intestinal microbial communities is important for the development and understanding of new and existing feed additives thus allowing the manipulation of diets to improve performance, health and welfare. Dietary supplements, which focus on rehabilitating or repairing the gut microflora to aid intestinal health and decrease the animal's susceptibility to disease will prove key in developing non-antibiotic pathogen control strategies.

Function and dysfunction of the gut, at the molecular, cellular and tissue level

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The gut is the central organ of animal health and production. The gut is the nutrient absorptive organ making it essential for efficient growth; it is also one of the main sites of pathogen entry, making a proper functioning gut important for maintaining disease free production. Within the gut are the resident microorganisms, the gut microbiota. These microorganisms and their combined genetic material, the microbiome, are just as important to health and production as any organ within the animal and are critical to the proper functioning of the gut.

Many of the measurements of function or dysfunction of the gut have focused on relatively crude outputs of whole animal response or pathogen load. For example, feed intake, live weight gain, feed conversion, mortality, villus height / crypt depth, or microbe count reduction have been classically used when considering the state of the gut. Given how much nutrition, metabolism and immunity is concentrated in the gut, a more detailed measurement of gut response is needed to fully characterize the various gut health interventions currently being studied.

The revolution in the study of the microbiota by high-throughput genetic techniques has significantly advanced our understanding of gut function and dysfunction. However, in these studies, the same comprehensive approach has not been applied to the host side of the host-microbiome analysis. The host-microbiome cross talk occurs at the molecular, cellular and tissue level and includes the immune system, metabolism, anatomic development, physiology, hormones and the gut-brain axis. Considering the host gut at a multi-omics systems biology level will inform our decisions on animal health, disease and production at least as much has the microbiome revolution has.

We have studied *Mycobacterium avium* subspecies *paratuberculosis* at a molecular and immune cell level, and have found targets for disease intervention. We have studied *Salmonella* infection of the chicken gut at a molecular, cellular and tissue level and found distinct phases in the chicken immune development and distinctions between the human and chicken response to this gastrointestinal pathogen. A mechanistic understanding of host-microbiome and host pathogen interaction can lead to targets of intervention and a more complete understanding of gut health in production animals.

Table Chicken responses to a *Salmonella* infection depending on age of inoculation

Characteristic	Early (4-48 hours)	Late (4-14 days)
Immune cells	Heterophils, macrophages	Tregs
Transcription factor activation	NF-κB	NFAT, Smad1-3
Cytokine mRNA expression	IL-1β, IL-6, IFN-γ	IL-10, TGF-β4
Metabolism	Anabolic	Catabolic
Characteristic metabolic processes	Glycolysis, protein synthesis	Oxidative phosphorylation
Energy balance	AMP:ATP	AMP:ATP
Regulatory enzyme activity	mTORC1 phosphorylation	AMPKα phosphorylation
Tissue phenotype	Pro-inflammatory	Anti-inflammatory (Tolerance)

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Nutritional innovations in pig production

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Introduction Innovations in pig production can take many forms and serve many purposes towards improving the economics, welfare and sustainability of pork production. Over the past 10 years, nutritional innovations could be categorised into specific nutrients and ingredients: fibre and energy, protein and amino acids, minerals, and additives. The objective of this abstract is to highlight some of these innovations, their impact on pig production, and suggest possibilities for future innovations.

Fibre and energy A consistent and universal definition for fibre does not currently exist and the benefits of dietary fibre are often limited to the type and concentration, as well as the age and production status of the pig. This provides an opportunity for better understanding of dietary fibre, methods to improve fibre fractions or utilisation in the diet, and the impact of fibre on fermentation, microbial populations and overall gut health and function (Lindberg, 2014).

Protein and amino acids Evaluation of amino acid requirements, ratios and N balance in pigs has been under investigation since at least the 1950s (Meade, 1956). However, availability of synthetic amino acids, novel protein-based feed ingredients, pig genetic improvements and improved techniques to capture microbial populations and emissions, has resulted in continued evaluations of amino acid requirements, ratios and N balance. As the use of antibiotics and growth promoting feed additives, such as ractopamine, become limited globally, the influence of amino acids, N and feed ingredients on gut function and the microbiome will become even more important. In this regard, innovative feed ingredients and formulation, as well as better understanding of the microbiome and amino acid (both essential and non-essential) requirements for growth, immune function and production (Wu *et al*., 2014), will be critical to maintain efficient and sustainable lean meat production.

Minerals Evaluation of mineral requirements and application of minerals in diets has received considerable attention recently. Data evaluating the digestibility of Ca in ingredients (Gonzalez-Vega *et al*., 2015) and the digestible Ca requirements of pigs are now available from 11 to 130kg (Gonzalez-Vega *et al*., 2016a, 2016b, Merriman *et al*., 2017). Subsequently, re-evaluation of the digestible P requirements and ratios to digestible Ca are ongoing. The results highlight that Ca and P requirements for growth are less than the requirements for skeletal development. They also suggest optimising Ca and P in the diet can lead to significant improvements in growth and efficiency. Other mineral applications, such as the ban on the use of pharmacological ZnO used to reduce post-weaning scour, will provide opportunities for innovative ingredients, additives or management practices to evolve over the next 5 years to mitigate post-weaning scour and improve nutrient digestion and growth.

Additives Feed additives such as enzymes, probiotics and prebiotics are not new. However, enzymes have evolved to be more efficacious and novel applications were developed to improve nutrient utilisation and pig growth and efficiency (Bedford and Walk, 2017). Probiotics and prebiotics are available with variable success at immune stimulation, pathogen binding, microbial mitigation and subsequent improvements in growth and efficiency. As with enzymes, these products will continue to evolve to be more efficacious and targeted to specific functions to improve gut function and health.

Summary and conclusions When considering nutritional innovations in pig production in the past 10 years, it is only natural to assume progress will continue. Nutritional requirements and determination of nutrient content of ingredients will become more precise, novel ingredients will be utilised, and new feed additives will become available. Factors not considered in this review, such as genetic selection, global trade and supply, animal welfare, consumer requirements and perceptions, government policies and sustainability will continue to provide opportunities for novel methods, processes and products in pig production.

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Nutrient requirements for growth, health and robustness in salmon farming

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Application A sustainable aquaculture needs to keep focus on the nutrient composition of the fish feeds for optimal growth, feed utilisation and robustness towards environmental challenges and infectious diseases. Practical diets with surplus nutrient supplementation may improve production and reduce production disorders in salmon farming.

Introduction Seafood production has been defined as part of the solution for global food security, meaning there is enough safe and nutritious food for the growing global population. As the wild fisheries are exploited to a full extent, the major future rise in seafood production has to come from aquaculture. Sustainable, suitable and affordable feed ingredients to support intensive aquaculture growth will have to come from lower trophic production levels, like marine and terrestrial plants. However, changes in major feed ingredients in fish feed may introduce risks for welfare issues, due to sub-optimal nutrient composition, changes in nutrient bioavailability, as well as new safety challenges from undesirables and anti-nutrients. The present communication presents practical nutrient requirement research in salmon, with focus on fish growth, health and welfare. One study illustrates the sensitivity of triploid salmon to environmental challenges that can be overcome by dietary means.

Material and methods Results of several feeding studies are presented where surplus supplementation of nutrients aim to improve salmon production and welfare. Examples include a) Long-term feeding studies with Atlantic salmon in freshwater and seawater using plant-based diets supplemented with increasing levels of a micronutrient package (vitamin and mineral mix and selected amino acids) (Hemre *et al*. 2017; Hamre *et al*. 2017). b) Adult salmon fed diets differing in lipid sources for 26 weeks after which they were exposed to a viral challenge with SAV3 causing pancreas disease (PD) (Holen *et al*. in press). c) Diploid and triploid salmon were reared at two temperatures during smoltification and fed two diets varying in the functional amino acid histidine to examine their sensitivity towards cataract development (Remø *et al*. 2014; Sambraus *et al*. 2017). Phenotypic outcomes in the experiments were supported by detailed analyses of nutrient status, histology, and biochemical and molecular analyses.

Results The feeding studies demonstrated the necessity for nutrients supplementation above the recommendations to improve growth and feed utilisation, and to prevent deficiency symptoms and welfare disorders like metabolic syndrome (fatty liver), bone deformities, cataracts and gill disorders (Hemre *et al*. 2017; Hamre *et al*. 2017; Remø *et al*. 2014). Dietary lipid source determined the outcome of disease resistance and immunological reactions (Holen *et al*. in press). Elevated dietary histidine alleviated cataract development to a different degree in diploid and triploid salmon, however less at elevated temperatures (Sambraus *et al*. 2017).

Conclusion Increased micronutrient and amino acid supplementations and selected fatty acids may be a necessity in future fish feeds to promote optimal growth, welfare and robustness in aquaculture, especially in triploid fishes and under changing farming conditions following local climate changes.

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Oilseed rape variety and heat intensity during oil extraction impact on nutritional value of oilseed rape co-products for pigs and poultry

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Application   Nutritional value of oilseed rape meals for fattening pigs and broilers can be improved through reducing heat intensity during oil extraction processes and through oilseed rape variety selection.

Introduction   Protein-rich oilseed rape (OSR) co-products are often used in farm animal diets, including pigs and poultry, with typical upper inclusion limit have long been assumed to be ~15% for rapeseed meal (RSM) in fattening pigs in the UK. However, more recent Canadian studies revealed greater levels of RSM derived from current OSR varieties in weaned pigs without performance penalties (Landero *et al*, 2011). Therefore, in this program of work, we revisited nutritional value and recommended upper inclusion levels of OSR co-products using current UK OSR varieties for pigs and poultry, in order to increase confidence in using OSR meals in pig and poultry diets as home grown alternatives for soya bean meal.

Approaches   Three types of OSR co-products were prepared from OSR batches of known variety. These were cold-pressed rapeseed expeller (RSE), hexane-extracted RSM under reduced (soft) heat intensity (sRSM), and hexane-extracted RSM under heat intensity as used under commercial conditions. Animal studies assessed their nutritional value in terms of levels of standardised ileal digestible amino acids (broilers and pigs), apparent metabolizable energy (broilers) and P bioavailability (broilers). This was underpinned with OSR co-product biochemistry to identify variation in glucosinolates, tannins, sinapine, phytic acid and fibre, also to assess correlations between nutritional value and these parameters, traditionally known as anti-nutritional factors. Digestibility studies were followed by growth performance trials with broilers and fattening pigs to assess upper inclusion levels of RSM from known OSR varieties as soya bean meal replacer.

Outcomes   Data collated over three seasons from almost 30 OSR varieties indicated that meals from modern OSR varieties continue to display significant variation in both nutritional factors (levels amino acid and residual oil) and anti-nutritional factors (especially glucosinolate), though variation in protein quality in terms of amino acids composition was rather small (Kightley *et al*, 2016). We also observed significant variation between OSR varieties in terms of amino acid standardised ileal digestibility (Kasprzak *et al*, 2016; 2017; 2018), energy metabolisability and P bioavailability (Olukosi *et al*, 2017). However, with the exception of fibre, OSR co-product biochemistry did not correlate with amino acid or energy digestibility, indicating that between-variety variation in tannin, phytic acid, glucosinolate and sinapine in modern OSR varieties is likely to be below a threshold to negatively impact nutritional value. Therefore, standardised ileal digestible amino acid and apparent metabolizable energy largely depends on the content of amino acids and energy (oil) in OSR co-products, respectively, although reducing fibre levels in OSR meals would be expected to improve nutritional quality for pigs. The comparison between RSE, sRSM and RSM confirmed that nutritional value reduces as heat intensity increases during processing (Kasprzak *et al*, 2016; 2017; 2018; Olukosi *et al*, 2017). Inclusion of RSM reduced feed intake in broilers (Olukosi *et al*, 2017) and growing pigs (Houdijk *et al*, 2017), most clearly above a threshold of 100 g/kg for broilers and 50 g/kg for growing pigs, but not for finishing pigs fed RSM up to 250 g/kg diet (Houdijk *et al*, 2017). However, both broilers and pigs all performed above breed and commercial targets at any RSM inclusion level.

Conclusions   The overall conclusion of our work is that there is opportunity to improve nutritional value of OSR meals through amending oil extraction processes and variety selection, with key informants being amino acid, residual oil and fibre levels, because classically considered key plant secondary metabolites did not inform on digestibility within currently available and tested varieties. However, intake constraints remain for the more sensitive stock, indicating upper limits for broilers to be ~100 g/kg and for growing pigs between 50 and 150 g/kg. However, for finishing pigs, upper limit may be well above 250 g/kg, which could contribute greatly to a reduced reliance on soya bean meal.

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Hexane-free rapeseed meals: feasibility of alternative techniques and their impact on protein quality

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Application Hexane extracted rapeseed meals are characterized by significant losses in lysine content and digestibility due to a desolventization process that was not designed for preserving the proteins solubility. Alternative hexane-free oil extraction techniques are being developed with beneficial impact on protein quality.

Introduction Desolventization of rapeseed meal is carried out at temperatures above 105°C in wet conditions and relatively long residence time. The process lead to meal with oil content below 3% but reduced proteins solubility (below 50% in KOH) and up to 20% loss of lysine. Disappearance of lysine is proportional to the temperature and the duration of exposure. Lysine represents 6.2% of the protein in native oilseed rape protein and can decrease to 4.5% after processing leading to a KOH protein solubility of 32%. Residual lysine has a reduced digestibility of about 50%. Therefore, in theory, it should be possible to have rapeseed meal with 22 g/kg of lysine when in reality, only 10-12 g/kg is digestible by pigs.

Alternative processing methods An alternative oil extraction process is cold pressing, which leads to meals having fat content in the range 12-20% depending on efficiency. It is used in small-scale oil mills using pressing eqipment not exceeding 2 t/hr in capacity. The pressing temperature is generally in the range 55-65°C but certain screw profile designed for high oil yields can cause stronger temperatures up to 100°C. These temperatures are high enough to inactivate the myrosinase activity. When the temperature is lower, the proteins solubility in KOH remains close to the solubility of the oilseed rape seeds.

Another alternative is double pressing, concerning oil mills with medium capacity (60 – 200 t/day). The first step is cold pressing at high flow rate resulting in a press cake containing about 20% of oil. The second step is a thermal treatment where the cake is cooked at about 100°C. The last step is a secondary pressing with higher pressure resulting in cakes having oil content of 8-10% of oil. Protein solubility is decreased in relation with the cooking temperature with values as low as 50% in KOH. Full press processing is a processing where seeds are flaked followed by cooking at relatively high temperature and subsequent single pressing resulting in meals with similar characteristics as the cakes from double pressing. It is generally observed in large feed-mill where the production of oil is not the main objective. Compared to double pressing, this process gives oils of a lower grade.

Ethanol extraction is a new process that is not yet observed in the industry but is regarded as an interesting alternative to hexane. Ethanol is allowed in the processing of "organic" feedstuffs, widely available and cheap. Its weakness is a low power of oil solubilisation but this drawback could be turned in advantage since ethanol could also extract phenolic compounds and carbohydrates to obtain meals with higher proteins content and bland taste. A recent study on the economic feasibility of this process shows that processing cost could be offset by the gain in meal and oil values. Combined with dehulling, this new process could lead to a rapeseed meal able to compete with non-GMO soybean meal.

Gas-Assisted-Mechanical Extraction (GAME) is based on the fact that at 100 bar, the supercritical CO_2 remains a poor solvent of oils but becomes rather soluble in the oils. It is therefore possible to solubilize up to 30% of CO_2 in the oil under this pressure, which is attainable in screw presses. When the pressure decreases, the CO_2 change of state and generate a gas pressure inside the cake which propels oil with the liquid phase out of the press cage. The HF company in association with Crowns Iron Works have developed a prototype press (HIPLEX). Although the results at this stage were not sufficient to generate the adoption of the process by the industry, further improvement of the technique like CO_2 recovery and longer diffusion time at 100 bar could significantly improve oil extraction efficiency. The main advantage of supercritical CO_2 extraction would be the low temperature of extraction and solvent removal, which could result in a combination of low oil residues and no protein denaturation. However, this technique remains expensive because pressure required for a good oil extraction is about 500 bar, which is not feasible in continuous mode.

Conclusion Mechanical extraction, both in cold press mode or with moderated thermal treatment is an available alternative to hexane extraction that gives rapeseed cakes having better protein quality. In the future, ethanol extraction in association with dehulling could bring to the market new meals with high protein content and preserved quality.

Precision agriculture meets the genomics revolution

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Introduction   The advent and application of genomics to livestock breeding populations has revolutionised breeding programmes through many avenues including increased precision of animal selection, as well as the greater opportunity to select on complex traits such as animal resilience and efficiency. At the same time, there has been a rapid expansion in the use of on-farm technology to monitor animals, the so-called precision livestock farming boom. This offers the possibility to phenotype an expanding range of traits, in increasing detail, and in large populations. The objective of this presentation is to explore the complementarities, and the synergies, between these two fast-growing sectors.

Opportunities and limitations from the genomics perspective   As the cost of genomic sequencing decreases and the required computing power and associated bioinformatics and statistical tools improve, genomic technologies can be applied to predict a wider range of traits than have traditionally been used in breeding programmes, such as resilience and efficiency. This is due to the increasingly fine-grained description of individual genomes that allows the genetic determinism of the myriad components of complex traits to be characterized from relatively limited numbers of animals (thousands rather than the hundreds of thousands traditionally needed). Such a fine-grained description can be used to determine key genes, and the molecular products they encode, and thereby identify new candidate biomarkers for key physiological mechanisms of, for example, resilience and efficiency. Although there are significant challenges to identifying such biomarkers (disentangling correlated effects from causal genes, variation between breeds in genomic associations, etc), this is one avenue where genomics will contribute to the development of precision monitoring tools. Another opportunity provided by genomics is for precision mating. As the cost of genomic sequencing drops it will become worthwhile to genotype females that are to be bred. This will allow the choice of males to be made on the basis of achieving a better genomic match, i.e. reducing unwanted recessive genes and increasing favourable gene combinations, especially where artificial insemination is being used. With respect to the present topic, the major limitation for genomics is in the precision of phenotyping of reference populations for these complex traits.

Opportunities and limitations from the precision farming perspective   Precision livestock technologies have, to date, largely been deployed for the detection of specific health events such as onset of disease or for detecting reproductive events such as heat. As such they have overwhelmingly been used for monitoring with almost no attention paid to their possible use for phenotyping, which is a major limitation of the current precision farming approach. Another limitation is relative lack of integration of information coming from different monitoring technologies, which tend to each focus on one type of event. However, these technologies can be used for precision phenotyping, requiring only a different treatment of the data being generated. This offers a huge opportunity for future research into complex traits, and also for future breeding and management strategies. The key feature of such technologies lies in their providing high-frequency automated measures. High-frequency measures mean that instead of having occasional snapshots of an animals status, e.g. when examined by the vet or farmer, we have access to the whole "movie", to the evolving time-series of an animal's status (for the given measure). In a monitoring context, this allows the animal to act as its own control. In a precision phenotyping context, this allows quantification of growth, production, and other life function trajectories. These life function trajectories, thus, contain important information about an animal's robustness. For example, is it an animal that builds up appropriate body reserves and then makes good use of them during nutritionally demanding periods? Is it an animal whose life function trajectories give rise to a high feed efficiency early in its productive life but at the expense of a higher frequency of disease events? These are questions that until very recently were difficult to answer with any degree of precision outside of research farms. Now the data to address these questions is becoming readily available from far greater numbers of animals, on commercial farms in widely varying environments.

Potential synergies and concluding remarks   It is clear that considerable synergy can be expected from aligning and then combining precision livestock and genomic approaches. Developing the use of data from on-farm technologies for precision phenotyping will bring these two sectors into alignment with substantial benefits to both. In research terms this alignment will lead to improved operational definitions of traits such as efficiency and resilience, and thus open up for quantifying the relative importance of these two traits in differing production environments. Achieving this will then provide a platform for combining information on the animals' genetic make-up with time-series information on how it has been shaped by prior conditions to predict its future robustness and production. Ranking animals on these predicted criteria will open up for on-farm breeding and management strategies that are tailored to the local production environment.

Genomics of feed efficiency and related traits in cattle

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Application Feed efficiency is a key trait governing the economic sustainability of beef cattle production systems. This review aims to discuss current knowledge on the molecular control of feed efficiency in beef cattle, as well as future opportunities for progress.

Introduction On-going global population growth concomitant with strict environmental legislation has placed an increased pressure on livestock production systems to supply growing requirements for meat in an efficient and sustainable manner. However, one of the greatest impediments to a successful economically efficient beef production system is the ever increasing input costs. For example, provision of feed represents the single largest direct cost incurred by beef producers, accounting for between 70 to 80% of the total costs of production (Finneran *et al*., 2010) and is therefore a major factor in determining competitiveness and profitability. Consequently, there is currently significant worldwide interest in improving the feed efficiency potential of beef cattle as a method of augmenting both the economic and environmental sustainability of beef production systems. Published studies have evaluated aspects of the molecular control of feed efficiency in beef cattle, using animal models based on either inherent variation in the trait or management regimen to evoke greater efficiency of feed utilisation. Many studies aimed at examining inter animal differences in feed efficiency potential at either genotype or phenotype level have ranked animals using the concept of residual feed intake (RFI), where feed efficient animals are those consuming less feed than expected based on their weight and expected growth rate. Imposed feed efficiency approaches include those associated with exploiting compensatory (or catch-up) growth or 'backgrounding'. Compensatory growth is a physiological process whereby an animal has the potential, upon re-alimentation, to exhibit accelerated growth following a period of undernutrition (Hornick *et al*., 2000). However, the challenge facing beef production systems is to reliably and cost-effectively identify animals with the inherent potential to utilise feed efficiently for carcass growth within the context of a structured breeding programme. Due to the logistical difficulty and considerable expense associated with measuring the feed efficiency potential of individual animals, greater knowledge of the molecular mechanisms regulating feed efficiency in cattle and the subsequent development of biomarkers to assist genetic selection for the trait hold promise as an alternative to direct phenotypic measurement. To date our own work, as well as that of others, has clearly shown that feed efficiency is a complex multifaceted trait, under the control of many biological processes (Fitzsimons *et al*., 2017). These include variation in feeding behaviour, digestion, absorption, nutrient partitioning, cellular energetics and turnover, physiological stress response as well as the composition and function of the ruminal microbiome. However, data generated to-date are not always consistent across studies, which may be due to variance in management practices as well as the breed, gender and physiological status of the animals employed. Indeed, data have shown that ranking of individual beef cattle for feed efficiency is not consistent when animals are successively offered diets of differing chemical composition (Coyle *et al*., 2016). Thus, due to the many factors contributing to divergence in feed efficiency status, a multi-faceted research approach is required to fundamentally understand the biochemical mechanisms regulating the trait at a cellular level. To this end recent research efforts have sought to exploit systems biology approaches such as gene co-expression network analyses (Kong *et al*., 2016, Weber *et al*., 2016). Co-expression network analysis is a systems biology method for describing correlation patterns of genes across datasets, resulting in the formation of networks or clusters of highly correlated genes which may contribute to the expression of a particular trait. These analyses provide a more holistic evaluation through the integration of gene expression data from multiple datasets as well as through incorporation of associated phenotypic data. This is achieved through examining all expressed genes as opposed to those detected as differentially expressed, allowing for a more equitable comparison across diverse study designs. Moreover, from networks of co-expressed genes, the most inter-connected genes, also known as hub genes, may be identified. Hub genes are genes that are important in regulating the expression of several other genes within a network and may be potential biomarkers for the selection of a trait. Thus, any future effort to identify and develop molecular biomarkers for the selection of beef cattle with improved feed efficiency potential must employ a more integrated analytical approach in order to identify biomarkers that are robust across the potential confounding influences of differential management regimen and environment.

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The adaptations of the gastrointestinal tract of the young calf: From pre to post-weaning

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Introduction The gastrointestinal tract (GIT) plays an important role in supporting the absorption and metabolism of nutrients for growth and production, while protecting the host from luminal contents and pathogens. The health of the GIT is most critical as the calf undergoes major transformations in early life that make it the most susceptible to gastrointestinal disease and disorders compared to all herd-mates.

Neonatal One of the most critical management factors in calf survival and health is feeding a sufficient amount of high-quality colostrum in order to improve passive transfer. However, further benefits to GIT function and health are now also being recognized. It has recently been shown that a delay in colostrum feeding of only six or twelve hours after birth can impact not only passive transfer but also the colonization of healthy bacteria (*Bifidobacterium*) in the small intestine of newborn calves. In addition, the heat treatment of colostrum has been shown to increase the colonization of *Bifidobacterium* and decrease the colonization of *Escherichia coli* in the small intestine of calves during the first 12 hours of life. New research is showcasing how the transition from colostrum to milk in the first days of life is critical to GIT development. For example, calves that transition directly to milk after the first meal of colostrum have less overall GIT mass and small intestinal villi development compared to calves fed a transition milk or colostrum at three days of life. Based on these preliminary findings, there is a need to consider other bioactive components in colostrum and transition milk that impact GIT development in order to provide the calf with the best chance to combat GIT ailments later.

Pre-weaning The amount of milk to be fed to calves has been a hot topic in the past decade, as it directly impacts pre-weaning average daily gain which may be associated with lifetime production. However, most dairy calves are only fed two meals per day and it is thought that increasing meal sizes to anything greater than 2.5 litres may cause milk overflow into the rumen, resulting in digestive upsets and hyperglycemia. What recent research has shown however is that the GIT of the calf has a certain degree of plasticity and can adapt to meal sizes as large at 4 litres in the first weeks of life by altering abomasal emptying as a means of controlling nutrient delivery to the intestine, thereby stabilizing blood metabolites such as glucose. This research suggests that we have been underestimating how much milk calves can consume and thus overlooking the advantages of feeding more milk.

Weaning Research has historically focused on the transition during weaning and characterizing ruminal papillae development using microscopy. Through the use of molecular-based approaches we have recently shown that delaying the age of weaning and providing a step-down weaning protocol is associated with a more gradual shift in ruminal microbiota to a post-weaned state. In addition to ruminal adaptations during weaning, nutrient flow to the lower gut changes dramatically during weaning, coinciding with a wide array of structural and microbiological changes. A study examining structural and gene expression changes suggests that the lower gut of the dairy calf undergoes alterations that may reduce barrier function when solid feeds are consumed. Additionally, a recent *in vivo* calf study revealed that the weaning transition increases the calf's total gut permeability. Interestingly, some evidence suggests that the upper and lower gut are able to communicate with the forestomach, meaning that a nutrient can be sensed in the lower gut and cause subsequent adaptations in the forestomach.

Conclusion An improved understanding of how diet, microbiota, and functional ingredients interact to impact growth and barrier function of the calf's GIT would greatly benefit the industry. A mechanistic understanding of such adaptations would also aid in the formulation of specific management regimens and the provision of functional ingredients required to support or enhance gut function in young calves.

The gut microbiome of the broiler chicken

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The role of the gut microbiome of all animal species is crucial to the health and well-being of all animal species. The broiler or meat-producing chicken is no exception to this, indeed its microbiome in central to its gut health, increased productivity and carriage of foodborne bacterial pathogens such as *Campylobacter jejuni*. Manipulation of the microbiome through feed additives including prebiotics and probiotics and competitive exclusion products are frequently used to improve feed conversion and reduce the likelihood of pathogen carriage. However, the development and application of such products has been largely empirical in nature with limited understanding of the composition of the microbiome, its variation in the developing bird and limited description of any mechanism of action of such products.

Commercial chicken production differs greatly from traditional backyard or extensive/pastoralist chicken production systems. Two crucial features are the use of modern hybrid breeds that have been selected on the ability to convert feed and gain breast muscle mass and secondly chicks are hatched in large modern hatcheries with no maternal contact. The consequence of this is that the early or 'pioneer' microbiome is not derived from a maternal microbiome. Indeed, it may be more 'human' than avian. What is clear is that modern broilers can suffer from poor gut health leading to problems such as necrotic enteritis, dybacteriosis and wet litter. Experimental infection studies also suggest that the intestinal immune response and its regulation may be defective contributing to problems including pathogen carriage and gut inflammation.

In our work, we have begun to explore the chicken microbiome, its development and role it plays in immune development and homoestasis. We have also begun to explore both how currently applied interventions work and develop new interventions including the potential of faecal transplantation.

It is clear the gut microbiome of the chicken is highly dynamic and these changes may well contribute to key factors such as immune development in the gut and susceptibility to infection. The post-hatch microbiome has poor diversity and is made up of only a few species of opportunistic environmental bacteria such as *Escherichia coli* and *Enterococcus* spp. Divergence between the caecum and ileal microbiomes occurs between 0 and 3 days post hatch with the caecum rapidly establishing a community of *Firmicutes* and *Bacteroides,* with some *Actinobacteria* and *Bacillus*, which stabilises at around 14 to 21 days post hatch. The ileal microbiome undergoes successive waves of colonisation by different taxa starting with *Candidatus Arthromitus* followed by *Lactobacillus* before a stable microbiome is established at between 28 and 42 days post hatch consisting of a mix of *Lactobacillus, Escherichia coli, Turicibacter* and *Romboutsia.* Furthemore, although broadly similar, co-housed broilers of differing genotypes have significant differences in their microbiome that could underlie some variance in disease susceptibility.

One of our main aims is to seek ways to 'improve' the microbiome of developing chicks to both enhance development and reduce *C. jejunu*. The use of single probiotic species such as *Bacillus amyloliquifaciens* have relatively little impact on reducing levels of *Salmonella* and C*ampylobacter* in the gut, but appear to reduce spread from the intestinal tract and lead to a better regulated inflammatory response.

Using a 'seeder bird' infection model challenged at 21 days of age, we have shown that the use of a commercial competitive exclusion production slows transmission of *C. jejuni* within the group but has no impact on levels of the bacterium in the caeca (the main site of colonisation) by slaughter age (36 days). However, by transferring caecal content from 'clean' 8-week old Ross 308 broilers to newly hatched Ross 308 chicks both greatly reduces transmission and final numbers in the gut by $5Log_{10}$, a level beyond that achieved by any experimental vaccine system. The effect is reproducible and the caecal contest of a single bird can produce several hundred thousand doses. We are currently analysing how this modifies the microbiome and gut development, though the transferred material has an exclusion effect, at least *in vitro*. The observation that transplanted birds are healthy and thrive but gain weight around 10% more slowly is intriguing and suggests that resources usually utilised in gaining muscle mass may be diverted elsewhere that could improve bird health and welfare. Better understanding of these processes will allow us to develop a more defined and rational approach to improving gut health.

Supporting the symbiotic relationship between mucosal morphology, immunity and the gut microbiome in the pig

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The mammalian gastrointestinal tract (GIT) is a dynamic environment, where a symbiotic relationship exists between the digestive system, the immune system and the resident microbiota. The GIT is the first organ to develop during embryonic development, which is marked by the onset of gastrulation beginning on day 8 of an approximately 115-day gestation period in the pig. Immune cells can be detected in the GIT within the first trimester of pregnancy, with the immune system undergoing dramatic maturation following the intake of colostrum as well as the colonization of the GIT with microbiota after birth. The establishment of the pig intestinal microbiota is a complex process that involves an initial colonizing phase during which the intestine of the new-born is rapidly invaded by bacteria, followed by different successional steps where diverse groups become predominant. The early establishment of the mucosal-microbiome relationship is fundamental to the development and long-term maintenance of gut homeostasis. In fact, unfavorable alterations in the composition of the microbiota, known as dysbiosis, in conjunction with damage to the mucosal architecture are implicated in many conditions. The weaning period of the piglet under modern husbandry conditions is very prone to dysbiosis in the gastrointestinal tract, resulting in a period of post-weaning diarrhoea. It involves complex dietary, social and environmental stresses that interfere with gut development, and is characterized by a reduction in feed intake and growth, atrophy of small intestine architecture, up-regulation of intestinal inflammatory cytokines, alterations in GIT microflora, diarrhea, and heightened susceptibility to infection. The overall aim of our research program is to provide dietary support to ensure an appropriate level of immune reactivity in the gut to accommodate the presence of beneficial and dietary microorganisms, while allowing effective immune/inflammatory responses to clear pathogens. A variety of natural sustainable bioactives have been identified that target different components of the gastrointestinal tract environment. Modes of action vary from commensal microbial stimulants, targeted antimicrobial activity, gut barrier repair, mucosal structure (villous architecture, absorptive capacity, nutrient transporters) and mucosal anti-inflammatory activity.

Understanding the role of the rumen microbiome in animal phenotype

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The rumen microbiome is diverse, containing bacteria, protozoa, fungi, methanogens and bacteriophages, which interact and govern nitrogen (N) use efficiency, methane (CH_4) emissions and the fatty acid content of meat and milk. Estimates suggest that through the action of the methanogens, livestock are responsible approx. 37% of the anthropogenic CH_4, which is a major environmental issue and a concern for animal production as 6-12% of the animals' energy is lost through CH_4 production (St-Pierre *et al.*, 2015). Ruminant N use efficiency also needs improving as ~70% of ingested nitrogen is excreted to the environment, with only ~30% utilised for protein conversion. A major limitation for N use is the largely recalcitrant nature of the plant cell wall which impedes microbial plant degradation (Mayorga *et al.*, 2016). Alongside these challenges, red meat and milk are often defined as being 'unhealthy' due to their high levels of saturated fatty acids (SFA) (Scollan *et al.*, 2017). Nonetheless, ruminant diets are high in human health beneficial polyunsaturated fatty acids (PUFA), yet these are toxic to the rumen bacteria which remove the double bonds, through a process called biohydrogenation, resulting in products which are low in PUFA and high in SFA (Scollan *et al.*, 2017). Technologies to improve upon animal production, reduce environmental impact, whilst ensuring the delivery of healthy products have previously consisted of dietary interventions (Kinston-Smith *et al.*, 2010) and more latterly, the potential to breed highly efficient ruminants with low environmental impact has shown potential (Roehe *et al.*, 2016). In summary, the rumen microbiome is complex making manipulation challenging and as such future approaches will require a much greater understanding of the rumen microbiome to develop long term innovative technologies for improving ruminant production, reduction environmental impact and ensuring that meat and milk are safe and nutritious for the consumer. This paper will discuss recent advances in the field and potential future developments to manipulate the rumen microbiome overcome these agricultural challenges.

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The challenges of appropriate trace element nutrition in sheep production systems

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Application   Trace elements in grazing sheep can be problematic, the risk of problems should be identified before appropriate supplementation strategies or changes in management are implemented. Consider the use of check strategies.

Introduction   Feeding sheep is relatively simple when they are actually physically feed. However, the best sheep systems make the best utilisation of the grazing and the idea is to actually physically feed sheep as little as possible. Supplementing sheep to ensure adequate trace elements is relatively simple when we are feeding a complete diet, such as TMRs fed to some housed sheep, when variable dietary components can be analysed (forage) and consistent components can use book values to formulate an intake to match requirements. When feeding concentrates to sheep, whether at grass or housed with free access to forage (hay/silage) then the concentrate can easily be used as a mineral carrier. The potential issue here can be over-supplementation, which can be especially an issue with inducement of copper toxicity in housed sheep. Grazed sheep where there is no additional feeding is where the largest risks occur and where solutions can be tricky.

Material and methods   Feeding trace elements when not required will, at best, cost money and decrease margins and at worse can induce toxicities and result in sheep losses. Therefore we need to be able to determine the risk of a sheep having a trace element imbalance issue. This is multifactorial and depends on many factors including grazing type, sheep type, soil pH and even the weather. To determine risk then we need to check some things: have we actually got a production issue? Is there enough dry matter intake, and is the intake of suitable energy and protein content? Is there an adequate source of clean potable water? Are there animal health or parasitism issues which could be causing the problem? Once these points have been addressed then mineral imbalance risk can be assessed. If there is no identified issue then there is little risk and then supplementation is not required and the saving will be on NOT buying supplements. To determine mineral imbalance risk then what happened over previous years can be indicative of what is likely to happen this year, especially in terms of seasonality and the sheep calendar. Sampling of grass and animals are also be indicative, remember grass samples are what is about to be consumed, whereas animal samples will give a much more historical perspective. Remember fields will be different as will be the sheep that graze them. The recommended sample numbers for animals diagnostic purposes for nutritional monitoring are 4 per group, with different physiological animals in the same area (e.g. ewes and lambs) counting as different groups (Kendall *et al*., 2015). Recent work has shown a huge seasonal variation in grazing concentrations of some elements, cobalt for example is high in early spring and late autumn and is decreased (often to levels unable to fulfil the increased demands from rapid growing lambs) mid-season (Kendall *et al*., 2017). Weather can affect status, the dry spring of 2015 had a lower grass cobalt concentration than that for the wet spring of 2016. The seasonality of cobalt emphases another problem, where peri-tupping a low cobalt status is identified and supplementation is started. However, in trials we have found the control group to have no issue on follow up samples due to the seasonal increase in cobalt concentration in the grazing. Although this might suggest that the supplement is not needed, it could be argued using the history that supplementation was required but much earlier to cover the low risk in the summer and to include the peri-tupping period.

Results   Once the risk of imbalance has been determined then there is the need to match the supplementation strategy to the risk, situation and duration. This does not necessarily need to be the administration of a supplement, sometimes clever management to utlise variation between different grazing can be utilised, e.g. high clover pastures have a higher cobalt concentration than straight grass swards. It is very important that supplements actually do what they claim, for example if copper is required for 4 months pre-housing in the autumn it is important for it to last four months to cover the grazing risk, but not to last longer and increase the risk of copper toxicity when the sheep are housed, fed concentrates and removed from significant soil consumption. Some supplements do not actually supply what is claimed in an utilisable form and will fail.
Consider the use of sentinel groups and on farm trials to check risk and supplement responses.

Conclusion   To effectively manage trace element nutrition we need to be able to accurately determine risk and have strategies available to counter the determined risk, which might or might not include supplementation.

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The role of small ruminant production systems in feeding a growing global population

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With the global human population predicted to reach 9.7 billion by 2050, and potentially 11.2 billion by the end of the 21st century (UN, 2015) the drive for sustainable food production systems to meet the increasing global demand has never been more significant. Further, demand for animal food products is predicted to increase by 70% to 2050 (Alexandratos and Bruinsma, 2012) placing increased pressure on livestock production systems to mitigate and reduce the potential impact of such systems on greenhouse gas emissions, water quality and biodiversity. Meat represents an energy-dense source of high quality protein, and is enriched in micronutrients such as thiamine, niacin, vitamin B12, calcium, iron, zinc, potassium and phosphorus (Wyness *et al*., 2011). Milk and dairy products are also an important source of protein and make major contributions to human requirements for calcium, phosphorus, iron, vitamin A and riboflavin (Kliem and Givens, 2011).

Small ruminant productions systems provide a range of products and services. In the developed world their major contributions include provision of meat, milk, wool, skin and pharmaceutical by-products. However, in developing regions of the world additional outputs include offal for food consumption, manure for fertiliser and biogas production. In particular, these animals provide an entry point into animal keeping and generation and accumulation of capital thus underpinning the rural economy. Currently there are approximately 1.17 billion sheep and 1 billion goats in the world, representing population increases of 11% and 34% respectively over the preceding five years. Between 1997/99 and 2030, annual meat consumption in developing countries is projected to increase from 25.5 to 37 kg per person, compared with an increase from 88 to 100 kg in industrial countries. Consumption of milk and dairy products is projected to rise from 45 kg per person annually to 66 kg in developing countries, and from 212 to 221 kg in industrial countries (FAO, 2002). In particular, ovine meat production is expected to increase by 33% by 2030 to meet this increased demand.

Small ruminant production systems are characterised by their ability to produce nutrient dense meat and milk from the consumption of forages, forage by-products and waste streams from cereal grain processing. Furthermore, their grazing behaviour and agility allows small ruminants to graze/consume feed resources that are not suitable to other grazing livestock species, and open up the possibility of producing food from land that would otherwise be entirely unsuited to food production. In the future this ability must be capitalised on to enhance the sustainability of, and output from small ruminant production systems (van Zanten *et al*., 2016). In intensive temperate grazing systems as much as 95% of the energy requirements of sheep can be met by forages offered either as grazed grass or conserved forage (Davies and Penning, 1996). For example, Earle *et al*. (2017) reported that up to 91% of lambs could be finished from a perennial ryegrass pasture without any requirement for supplementation.

The production of small ruminant products, however, similar to all foods generates unwanted environmental side effects such as greenhouse gas and nitrates emissions, which policymakers and consumers are increasingly concerned about and which potentially lead to irreversible environmental damage as production grows. In developing countries small ruminant production system represent one of the most efficient animal production systems producing 24.4 kg of edible protein for each kg of edible protein consumed (Makkar, 2016). Notwithstanding this, in developed countries, food-related environmental impact and resource use of sheep farms can be further improved by increasing meat production from grazed grass within area-based regulatory limits on nitrogen and phosphorous (O'Brien at al., 2016).

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Resilient pasture-based dairy production systems

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Worldwide demand for dairy products has been increasing rapidly as a result of projected population growth, urbanisation, and increases in per capita disposable income (Delgado, 2005). Commensurate with the increased global food demand, increased competition for land, water, and energy resources necessitates that global agricultural production becomes more productive based on systems that are also more environmentally and socially sustainable.

There is an increasing international awareness of the multifunctional benefits of pasture based farming (O'Mara, 2012) due to its capability for high farm productivity and profitability (Dillon *et al*., 2008; McCarthy *et al*., 2013), and more recently also, for the environmental (O'Brien *et al*., 2012), animal welfare (Arnott *et al*., 2016) and product quality (O'Callaghan *et al*., 2016) benefits it confers to livestock production. Indeed, both Taube *et al*. (2013) and Baumont *et al*. (2014) have recently suggested that systemic improvements in pasture-based food production efficiency can be ascertained by increasing pasture utilisation and placing less emphasis on external supplementary feed and fertilizer inputs. In comparison with mechanically harvested or purchased feeds, grazed pasture provides a relatively inexpensive and uniquely nutritious feed source for milk production. Consequently, the profitability of milk production on Irish farms is closely related to the amount of pasture consumed (tonnes DM/ha) each year. Research studies continue to highlight the significant potential for additional productivity gains where best practices grazing management is implemented. On that basis, pasture-based food producers must refocus on this uniquely cost free potential within their farms and continue to refine their grazing management practices to release this additional performance from grazed grass over the coming years.

The overall strategy for resilient pasture-based milk production requires a 'fit for purpose' system that will provide a consistent level of production and profit, within the general averages of climate, input prices and availability, and milk price uncertainty. The fundamental tenet of pasture-based farming involves utilising a genetically appropriate cow to harvest the majority of the pasture grown, thereby minimising the requirement for, and use of machinery and confinement accommodation, and maximising the proportion of the cow's diet that is grazed pasture. The cost of milk production declines as the contribution of grazed pasture to the diet of the dairy cow increases (Dillon *et al*., 2008; Ramsbottom *et al*., 2015), thereby representing a production system that is more able to withstand the troughs of commodity price cycles. Moreover, the exponential relationship between grazed pasture proportion and operating expenses also indicates that the overall reduction in operating expenses is greater within systems which are highly reliant on grazed pasture and consequently, minimise overhead costs associated with animal confinement to a greater extent. In New Zealand, Australia, many parts of Western Europe, Southern Africa, and South America, pasture can be the sole feed for the herd for long periods of pthe lactation. This is achieved by manipulating feed supply and demand to achieve approximately coincidental profiles. From a systems perspective, stocking rate and calving date are the most important strategic levers influencing pasture harvest per hectare within grazing systems. The balance between feed supply and demand, as influenced by stocking rate, and to a lesser extent by calving date, is critical because an imbalance will result in either underfeeding of the herd or poor utilisation of available feed (McCarthy *et al*., 2013). Efficient pasture-based systems time the start of calving for about 60 days before pasture growth rates equals herd feed demand, thereby matching peak intake with peak pasture provision. Calving is compact, with 50% of cows calved in two weeks, 40% in a further four weeks, and the remainder shortly thereafter. Surplus pasture is harvested based on weekly pasture measurement and feed budgeting and offered to cows during periods of feed deficit or during winter. In most systems, grain- or co-product-based concentrate feeds are offered during early and late lactation; but, operating costs of milk production are heavily influenced by the proportion of the diet that is grazed pasture vs. these other feeds. In general, pasture utilisation, a key determinant of net profit per hectare and return on assets, declines with increasing use of non-pasture feeds. Resilient systems, therefore, limit the importation of supplements to less than 500 kg DM/cow over the lactation. On an implementation basis, grazing systems that incorporate greater amounts of supplemental feeds require careful management and high stocking rates to ensure pasture utilisation does not decline. In future, further improvements in the productivity and profitability of pasture systems will be derived from management changes which result in further increases in pasture, production, quality and utilisation efficiency.

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The development of a high-output grass-based spring milk production system

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Application In regions where it is possible to grow and graze large quantities of highly digestible perennial ryegrass it is favourable to produce as much milk as possible from this low-cost feed source. However, grazing systems that have been developed to utilise large quantities of grazed grass have been based on low-output per cow. In this scenario, high levels of profitability are possible through avid cost control and comparatively high stocking rates. There are now reasons to consider the development of grazing systems that are based on high-output per cow. These reasons include (i) concerns about increasing dairy cow numbers and environmental emissions, (ii) facilitating farm expansion post EU-milk quota removal for land limited and fragmented farms, (iii) increased requirement for dairy product for export, (iv) lack of available skilled labour on farms to deal with expanding animal numbers.

Introduction The aim of this project was to report the animal and grassland performance for a grazing system based on high-output per cow and the resultant system profitability. It was decided that the system targets would include a whole-farm stocking rate of 2.4 cows per ha, a stocking rate on the milking platform of 3.4 cows per ha, a concentrate feeding level of 1.5 t (as fed) per cow per year, the rest of the diet to comprise of the maximum amount of grazed grass and approximately 1.5 t of grass silage DM. Target animal performance was the production of 625 kg of milk solids per cow per lactation (7750 kg of milk) a 75% six-week in-calf rate for the herd and an empty rate of 10% or less following 12 weeks of AI.

Material and methods A total of 60 dairy cows were used to create a herd with a high overall EBI (Economic Breeding Index) that was within the top 1% nationally. The intended genetic profile of the herd was to have a balanced milk and fertility sub-index ratio initially, and a positive figure for milk kg. The swards were predominantly perennial ryegrass with some containing white clover. Herbage supply was measured weekly using a rising platemeter (diameter 355 mm and 3.2 kg/m²; Jenquip, Fielding, New Zealand). Herbage availability (herbage mass; kg DM/ha; above 4 cm) was determined prior to and after each grazing event for each paddock by taking 3 quadrat (0.25 m² quadrat) cuts and harvesting to 4 cm (above ground level). Fifty compressed sward height (CSH) measurements were recorded before and after grazing of each paddock using a rising platemeter. Milk samples were taken at both a.m. and p.m. milking's on two days every second week during the lactation. Daily milk yields were recorded using the Weighall milk meter system (Dairymaster, Causeway, Kerry, IE). Cows were scanned at 30 and 50 days after AI and again at least 60 days following the last AI of each breeding season that lasted 12 and 13 weeks in 2016 and 2017.

Results Preliminary data for forage production and utilisation, milk yield and fertility are presented in Table 1. The herd comprised 22.4 and 23.3% first lactation cows in 2016 and 2017 respectively. The feed budgets that were realised were 2.9 t of grazed grass DM, 1.85 t of grass silage DM and 1.5 t of concentrate (as fed) in 2016 and 3.0 t of grazed grass DM, 1.5 t of grass silage DM and 1.5 t of concentrate (as fed) in 2017. In the first two years of the study submission rates of 91% (2016) and 90% (2017) were recorded and first service conception rates of 43% and 50% were confirmed in 2016 and 2017.

Table 1 Preliminary forage production and utilisation (t DM/ha), milk yield (kg/cow/lactation) and fertility parameters (%) for UCD Lyons Farm high-output grazing herd

Year	Grass grown	Grass utilised	Grazed grass utilised	Milk yield	Milk fat and protein	Six week in-calf rate	Empty rate
2016	13.06	11.4	9.7	7407	588	59	9
2017	14.00	12.2	10.2	7466	595	54	15

Conclusion High levels of milk and milk solids output per cow and per ha are achievable from moderate concentrate feed input in a grazing system. These high levels of output are possible from cows that score highly on a selection index that has had a significant fertility component for some time. High levels of grass utilisation can be achieved in higher output grazing systems. It remains to be demonstrated that high levels of fertility and high levels of output can be achieved simultaneously in grazing dairy cows. Preliminary financial simulations of this system compare favourably to other relevant systems.

Trends among alternative dairy production systems in the United States

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Application This presentation is intended to provide a glimpse of the dairy industry in the US with emphasis on how alternative production and marketing strategies provide options other than the dominant confinement production system.

Introduction Dairy systems in the US are dominated by confinement facilities in which lactating cows do not have access to pasture as a source of nutrients. In contrast, there are many types of alternative dairy systems that range from organic production with a pasture requirement, grass-fed only farms, hybrid systems that include pasture as a small-to-moderate portion of rations, as well as farms producing specialty products usually for a local market. The latter includes on-farm fluid milk processors, farmstead and artisan cheese makers, A2 milk, as well as direct marketing of raw milk to consumers.

Material and methods Data for this report are from various sources including the USDA National Agricultural Statistics Service (NASS), various published studies, dairy magazine articles, and extension reports, as well as observations and personal communications of the author/presenter with dairy industry professionals.

Results Numbers of US dairy farms selling milk declined from 116, 874 in 1997 to 59,130 in 2007 and down to 41,809 farms in 2016 with 9.238 million cows (~221 cows/farm). Farms produced 96.56 billion kg of milk in 2016 and about 97.93 billion kg in 2017, an increase of 1.4%. For many years, farm milk prices have fluctuated widely from year to year with prices influenced by domestic supply as well as world markets. With loss of farms, numbers of cows on remaining or new farms have increased and there has been more consolidation of dairy cooperatives and support industries. Large confinement dairy farms with 400 or more cows that are fed total mixed rations (TMR) account for about 70% of the total US milk supply. Such farms typically produce at least a tanker load (~30,000 litres) of milk in 2 days or less. By 2009, 30% of dairy cows in the US were on farms of 2,000 cows or more. Though not likely to happen, it would only require only 1,747 herds of 5,000 cows producing 12,000 kg milk each to yield a total of 104.8 billion kg milk (7% above 2017).

Over the past 30 years, many "last-generation" farms have exited the dairy business and that trend continues. However, many small and moderate-sized farm owners have explored alternative production and marketing strategies rather than expansion *per se* in order to maintain economic viability. Organic dairy production began on a very small scale and has grown steadily for many years. By 2016, a total of 2,258 certified organic dairy farms (~107 cows/farm) achieved a market share of about 5.2% of total fluid milk sales. Though costs of producing organic milk are more, higher and more stable milk prices via supply management strategies have made organic production economically attractive for some producers. Within the organic market there seems to be growing interest in grass-fed only milk and that trend is expected to continue. Herd sizes are smaller on average but some organic dairy farms have more than 1,000 cows. Meeting USDA organic requirements for pasture in such larger herds can be difficult. Concurrent with the emergence of organic production, there was renewed interest among some producers to incorporate more use of pasture in an effort to reduce costs and keep a higher percentage of the milk cheque. Such systems spanned a wide range from nearly exclusive use of pasture with seasonal calving to use of pasture as a supplemental feed to cows primarily fed a TMR. Because supplemental feedstuffs are generally readily available, most farms fed at least some supplemental concentrate and/or stored forages. A challenge in such systems is to be efficient in using pasture forage and to avoid using costly supplements to offset inadequate pasture management. Another challenge was that for most producers in various locations in the US, perennial ryegrass could not be used as the primary forage species as in New Zealand and Ireland or other pastoral dairy regions. Multiple forage species, variable climates including hot summers and cold winters, lack of infrastructure support, as well as dairy cooperative concerns about seasonal fluctuations in milk supply were further challenges faced by US dairy graziers. After some initial momentum through the 1990's and into the 2000's leading to more pasture-based systems in some areas, new entrants or conversions have slowed in recent years. Some historically successful graziers have moved to organic production as organic demand has continued to grow. Other areas of growth in the past 20 years are dairy farms seeking to capture local niche markets by use of on-farm processing of fluid milk products and specialty cheeses. This adds complexity to the farm business and is certainly not a strategy that all dairy producers can adopt because added management responsibilities for processing and marketing may mean different skill sets from production alone. There is growing interest in A2 (beta casein variant) milk across many segments of the dairy industry but only a few producers are currently using that for marketing purposes. Raw milk sales directly to consumers are legal in many states but potential down side risks are of concern.

Conclusion Concentration of the US dairy industry is expected to continue with increasing proportions of total milk supply coming from larger dairy farms of more than 500 cows. Close margins and fluctuating milk prices make it more difficult for herds under 500 cows to compete long term unless risk management strategies are incorporated and/or alternative production and marketing strategies are adopted. Those alternatives may include organic, pasture-based, and on-farm processing among other approaches.

The genetics of (feed) efficiency in ruminants

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Application There are many strategies to achieve making more (higher quality and safe) human-edible animal-derived food from less, one of which, but only one, is selection for daily feed efficiency or environmental efficiency.

Introduction Interest is mounting, particularly in recent years, on (daily) feed intake and efficiency in ruminants. These studies, and associated commentary, have almost exclusively focused (often unknowingly) around daily feed intake and efficiency while often remaining ignorant to the other, often lower hanging fruits, that contribute to overall efficiency. It is often proclaimed in studies and presentations that moderate heritability estimates exist for such daily efficiency traits despite the fact that heritability is not actually a good indicator of the evolvability potential of a trait.

The real efficiency System efficiency, irrespective of the trait which is flavour of the day (e.g., energy intake, methane emissions, protein intake), can be defined as

$$\text{Efficiency} = \frac{n_{Mature} \cdot VALUE_{Mature} + n_{Cull} \cdot VALUE_{Cull} + n_{Off} \cdot VALUE_{Off}}{n_{Mature} \cdot I_{Mature} + n_{Cull} \cdot I_{Cull} + n_{Off} \cdot I_{Off}}$$

where $VALUE_{Mature}$, $VALUE_{Cull}$, and $VALUE_{off}$ is the (nutritive) value of the output from the mature animals, culls and (surplus) offspring, I_{Mature}, $I_{Replace}$ and I_{Off} is the total intake (or output in the case of environmental parameters) of the mature animals, replacements and other offspring, respectively, and n_{mature}, n_{Cull}, $n_{Replace}$ and n_{Off} is the total number of mature animals, replacements and other offspring, respectively. Key here is that the total intake (or output in the case of environmental parameters) is in the denominator, not daily values which are often used.

Therefore, factors which affect system efficiency, in for example a dairy enterprise, include, but are not limited to, milk production per cow, fertility and survival, animal health, age at slaughter, and of course daily feed intake. For example, extending the number of lactations per cow from the current mean of four in Ireland to an optimum of 5.5 will increase milk output per cow by, on average, 40% without a pro-rata increase in the denominator. Similarly, improving the number of calves per beef cow from the current mean of 0.79 will also improve the numerator, without necessarily resulting in a *pro rata* increase in the denominator. Significant exploitable genetic variability exists in all these factors.

Although data do exist in many populations for feed intake, the individual datasets are typically small and often historical, and therefore the achieved reliability, and thus genetic gain, is low. Data, however, are already plentiful for routinely measured traits like milk output, carcass yield, fertility, survival and age at slaughter, and high accuracy of selection can be achieved for these traits as well as genomic evaluations to help reduce the generation interval. Although large coefficients of variation, which is a truer measure of evolvability (i.e., ability to evolve), are documented for such traits, such statistics can be deceptive since they do not consider the genetic correlations with other breeding goal traits. Antagonistic genetic correlations can deplete the exploitable genetic variation and cited genetic parameters in studies should reflect this.

Future priorities? Research funding currently appears to favour the more interesting and less traditional phenotypes. No breeding goal however explicitly selects for product quality. Product quality can affect 1) the processing characteristics and thus the efficiency of converting the harvested product into usable products, and 2) the nutritive value and product portfolio. For examples, predictions of milk quality parameters from routinely available mid-infrared spectroscopy analysis of all milk samples taken from individual cows are already available. Few breeding goals directly select for lactation efficiency which can be one strategy to increase milk output without necessarily intensifying the metabolic stress on the female. Survival is a complex trait and therefore influenced by many traits – at the extreme, it includes culling and mortality. Not only is survival likely to suffer from genotype-by-environment interactions but also genotype-by-age interaction; the genetic predisposition to culling may be more governed by lameness in older cows but temperament in younger cows. Only France undertake a genetic evaluation for age at slaughter in cattle; such a trait is in fact often used in sheep. The phenotypic standard deviation in age at slaughter to a common carcass weight and fat score is 44 days (Berry *et al*., 2017) which is under moderate genetic control. Relative to the mean, the 20% earliest slaughtered animals eat and excrete/eructate for, on average, 62 fewer days. Additionally, a proportion of the "improvement" in fertility observed in cattle, for example, can actually be due to a shortening in maternal genetic merit for gestation length though this may not be the most optimal approach.

Conclusions There is more than one way to skin a cat – sometimes the perceived less interesting approaches may reap most benefit in breeding programs and do so more quickly with less investment given their extent in usable genetic variability.

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Impact on horse welfare

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Application To provide evidence and recommendations to policy makers when considering the UK and EU's approach to equine welfare post-Brexit

Introduction With the UK about to exit the EU there is still widespread uncertainty about what this will mean in practice. One thing is certain: it will present both opportunities and threats. As such, everyone involved in the horse industry - particularly those responsible for overseeing welfare and disease surveillance - must look ahead to the future and ask themselves what changes might affect horses, and ultimately the industry as a whole, either positively or negatively.

Material and methods World Horse Welfare has conducted desktop research, including a review of horse movements and current legislation, as well as collating anecdotal evidence from policy makers and the equine industry and undertaken field investigations to inform its understanding of the potential impacts of Brexit on horse welfare.

Results When considering the horse's role in international trade, it is tempting to focus solely on the trade in high-value performance horses. However, the UK also has a significant trade in other horses and an often-overlooked trade in horse meat and by-products (European Commission 2018). Much of the trade in these 'other' horses appears to be with the EU (although horses may travel beyond the EU's borders), including a known indirect trade in horses for slaughter. In 2016, 3,300 horses were slaughtered for human consumption in the UK (Food Standards Agency 2017). Many horses in the UK are currently ineligible to enter the human food chain because they have received certain veterinary medications, have been voluntarily signed out or their background and/or identity cannot be verified. There is the potential that the UK may agree a trade deal with the EU that allows for a six-month withdrawal period to be instigated as a requirement for trading horse meat with the EU (similar to the Comprehensive and Economic Trade Agreement with Canada). Alternatively, the UK may choose to diverge from the EU on lifetime exclusion without a trade deal, instead focusing on international markets. Could these scenarios lead to stockpiling of horses in the UK? Additionally, if the UK is less stringent than the EU on its entry requirements for equines what does this mean - could it lead to an increased market in horses going to slaughter, particularly if combined with changes to lifetime exclusion requirements? If this happens could our slaughterhouses cope as currently only five are licensed to take equines? If the UK chooses to go down this route then this will have the potential to impact all equines, not just those going to slaughter, as it could increase the UK's susceptibility to disease incursion and potentially be a barrier to movement from the UK to the EU, particularly for non-competition horses with increased checks for equines at EU Border Inspection Posts. The UK will also have the opportunity to place more stringent entry requirements on equines from the EU and non-EU countries. While this would improve the UK's biosecurity it could lead to additional checks on equines as they enter into the country. Increased checks (either upon entry into the UK or the EU) could be a contributing factor to delays at the border and it is unclear whether ports have the facilities required to hold equines if they are denied entry. There is strong scientific evidence to show that journey times over 12 hours are detrimental to equine welfare (Marlin *et al*. 2001, Stull *et al*. 2004). Any policy decision / agreement between the UK and EU that increases queues at the border – which cannot be adequately mitigated by increased resources – should be avoided. What impact to equine welfare will there be if, as the UK has committed during Phase 1 of talks, there is no hard border on the island of Ireland? Could it be used as a backdoor into or out of the UK for the non-compliant movement of equines?

Conclusion Considering questions such as these will help the industry and policymakers to maximise and exploit any opportunities presented, and identify potential threats so that mitigating measures can be put in place. It is World Horse Welfare's view that all equines should be fully traceable across the UK and EU and this would address many of the concerns and opportunities around Brexit, including the need for enhanced checks at borders and non-compliant movement of horses via Ireland. If the UK and the EU implement robust equine identification and traceability systems, which are compatible with each other and user friendly for equine owners, all equines would be identifiable and traceable in the UK and across the EU.

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The labelling of feed and supplements

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The aim of the presentation is to explain how to correctly label animal Feed and Supplements, with a particular focus on the labelling of equine feeds. The presentation will include explaining the legal framework in the EU of placing animal feeds on the market. This will include discussing feed labelling regulations, specific labelling requirements and compliance at a local level. The presentation will cover the legal definitions of feed and explains the differences between feed types as appropriate.

The presentation will focus on Regulation (EC) 767/2009 - Marketing and use of animal feed and will cover its focus, scope and definitions and requirements. This will provide the foundation to look more closely at labelling itself and will look at specific examples of correct and incorrect labelling of equine products. The presentation will go further to discuss dietetic feed (feeds for a particular nutritional purpose) and will focus on those dietetic feeds approved for equine species and will explain the conditions on labelling such feeds and placing them on the market.

In terms of labelling, we will look at what constituents a label and packaging, what mandatory information must be included and claims which can be made on products. We will loom at feed additive categories and calculating maximum limits of additives and will look at additives specifically authorized for equine species and why.

I hope that Equine FBOs will find the presentation useful with a view to ensuring the compliance of their labelling for placing on the market in the European Union.

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Regulation (EC) 178/2002 - General food law
Regulation (EC) 767/2009 - Marketing and use of animal feed
Regulation (EC) 1831/2003 - Additives for use in animal nutrition
Regulation (EC) 1829/2003 - GM food and feed
Directive 2002/32/EC - Undesirable substances

Research and industry collaborations

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Application   There are many benefits obtained by research and industry collaborating. Engaging with industry is a key focus for many research institutions and this paper outlines the various ways in which this collaboration may take place**.**

Introduction   Universities play a key role in society by educating the population and generating knowledge. However, more recently universities have increased their focus on fostering links with knowledge users and facilitating knowledge transfer and impact.

Types of collaboration   There are many ways that a research institution and industry can work together. A research collaboration and strategic partnership provides the opportunity to collaborate on a research project that is of mutual interest. Such collaboration can lend itself to attracting external funding and most institutions will have a business development team who can guide on what funding is available and provide support with the application process. Most research institutions can also undertake contract research, whereby research is generally based on the company's intellectual property and carried out to their specification. Researchers can also provide consultancy services for industry; this consultancy work could include expert advice and opinion, expert witness, customised training and strategic planning. Student projects and industrial studentships are also an excellent way of a research institution engaging with industry. In this instance, the company can access new ideas, expertise and capability via the student and the academic supervisor. This can be a company supporting an undergraduate project or a master's dissertation or sponsoring a PhD. This type of arrangement has the added benefit of facilitating the student and the company to consider future employment opportunities. Knowledge transfer partnerships (KTPs) enable companies to work with Universities promoting sharing of knowledge and expertise. A KTP associate is recruited to work specifically on managing the KTP project, apply their own knowledge, and ensure that the University's expertise is shared with the company. Companies can also benefit for a University's commercial licencing arrangements.

Benefits of engaging with industry   The benefits of working with industry is that it allows research institutions to ensure that the research they are conducting is of relevance beyond a community of scholars and that it has practical implications and real-world benefits. It can facilitate a greater understanding of the needs of a particular sector that the University wishes to engage with, it can be rewarding to see research make a different to society, and it facilitates and virtuous circle whereby research informs practice and practice informs research.   Industry partners can become a valuable source of research questions, allow researchers to apply and evaluate their research, and reduce the likelihood of researchers making incorrect assumptions about practical applications. Collaborating with industry, allows universities to experience a different perspective, which may lead to new research opportunities. The knowledge exchange that takes place when a university works with industry is extremely beneficial for evidencing the impact of research. There is great emphasis placed on impact in research assessment exercises and many funding bodies require evidence of a university working with industry; for example, having PhD students that are industry funded.   Knowledge exchange and transfer is also a key priority for government policy on higher education research to help develop a thriving economy. The industry partner may be more receptive to research findings or be more willing to disseminate and advocate research based on their experience of working with the university; thus influencing others to adopt or adapt their practices in light of research findings.

Challenges of engaging with industry   One of the main challenges of working with industry is the different timescales for research to be concluded. Therefore, it is important that both partners agree on timescales at the outset. Managing the collaboration is also important; ideally both partners contributions should be equal and valued. It is also imperative to ensure that intellectual property rights are clearly defined from the outset. Being clear on who owns what (for example, data) at the start of the project is imperative as well as discussing the potential outputs (publications, new technologies) and who these belong to. Negotiating this contract can be time consuming and often underestimated; however, this process can be quicker if both parties are clear and agree on the inputs, outputs and benefits.

Conclusion   There are great benefits gained by research and industry collaborating with each other, and although there are some challenges that need to be navigated, the knowledge exchange and outcomes that arise can be invaluable.

Communication of science to industry

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Application Scenario planning is a participatory tool to promote effective and trusted communication with stakeholders at the animal health science-policy-industry interface.

Introduction The veterinary and scientific knowledge-base for animal health is evolving rapidly, with improving technologies and faster access to better data. In parallel, there is an increasing public demand for rapid translation of knowledge into transparent, robust, future-proofed evidence-based health policies which will have a beneficial impact for industry stakeholders (Boden *et al.* 2015). Creating effective channels of communication between science, policy and industry is an essential foundational step in this process to ensure mutual understanding and public trust. We propose that scenario-based stakeholder engagement is an effective method in which scientists can forge relationships with stakeholders through involvement in the scientific process and create a meaningful dialogue about the complexities and uncertainties inherent in any evidence-based decision-making.

Material and methods EPIC, a Scottish Government-funded Centre of Expertise on Animal Disease Outbreaks employs a myriad of approaches to engage with industry stakeholders in Scotland. The Centre seeks to foster a synergistic environment in which scientists from a broad range of disciplines can work with Government veterinarians and policy officials as well as industry stakeholders and the public to share knowledge and expertise to improve disease preparedness and respond robustly to animal disease outbreak emergencies. This presentation explores in detail the use of one participatory approach: scenario planning (Boden *et al.* 2017), as a tool to communicate scientific risk and uncertainties and incorporate stakeholder values and (perhaps conflicting) preferences to inform a robust scientific evidence-base for policy-makers.

Results EPIC scenario planning workshops (in addition to other EPIC industry interface opportunities) have offered a structured robust approach by which EPIC scientists can develop strategic partnerships with stakeholders by sharing experiences, exchanging knowledge and finding common ground through understanding one another's constraints (Boden *et al.* 2015). Workshops have created opportunities for scientists, industry stakeholders and policy-makers to participate in a dialogue about the importance and impact of different societal, economic, environmental, technological, legal and political drivers on the explicitly uncertain long-term future of animal health in Scotland (Boden *et al.* 2017). In addition, scenario planning workshops have enabled a degree of social learning, "not least through the creation of new relationships, the development of understanding built on trustworthiness, and an appreciation of other legitimate viewpoints" (Duckett *et al.* 2017). With regard to research outcomes, workshop participants have also increased the knowledge base available to EPIC, and provided useful inputs which have contributed to new networks and collaborations and "more realistic epidemiological models being developed" to improve disease contingency planning (Duckett *et al.* 2017).

Conclusion Communication between scientists, policy-makers and stakeholders is critical to successful uptake and compliance with animal health policy decisions and interventions in "peace-time" and in animal disease emergencies. Trusted and established relationships with stakeholders are essential to underpin effective communication channels. Scenario planning is a useful participatory tool which can create opportunities to develop solidarity at the science-policy-industry interface.

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Breeding the ideal ewe of the future

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Application The key characteristics and strategies required for the development of the ideal ewe of the future are outlined. This allows for the development of a holistic breeding goal that will accelerate genetic gain and take us closer to breeding the ideal ewe of the future.

Introduction In a well-structured breeding programme genetics can account for up to half the production changes in animal performance. Although evidence of genetic progress is evident in many livestock sectors including dairy, pigs and poultry, the level of genetic gain achieved in sheep remains relatively slow and country dependent (Santos *et al.*, 2015). However most traits investigated to date for sheep display genetic variation (Safari *et al.*, 2005) indicating that genetic gain is achievable within a structured breeding programme. Since no single trait dictates flock productivity, selection on a single trait can have a detrimental effect on genetic progress; therefore a multi-trait holistic breeding goal is required. This paper outlines the ewe characteristics that must be considered and also the long term strategy to breeding the future ideal ewe.

Defining the ideal ewe Breeding is a long term strategy therefore characteristics of the ideal ewes should consider the (likely) ewes characteristics of the future not the ewe of today. Although the characteristics of the ideal ewe differ between production systems (i.e. upland versus lowland systems), a number of key characteristics are required across all systems. These include: *Low input* – an "easy-care" ewe is one of the key demands of all sheep producers. With approximately 20% of total farm labour required at lambing, traits such as lambing difficulty, lamb vigour and ewe mothering ability play a key role in identifying a low input or low labour requirement ewe; *High reproductive performance* – the prolificacy potential of a ewe has been highlighted as one of the key determinants of profitability, high reproductive performance must be achieved by the ideal ewe not just within parity but across her lifetime; *High output* - direct and maternal (i.e., milk yield) weight traits are the two output traits that are often included in international breeding goals, but other output traits such as carcass traits should also be considered; *Healthy* – reduced flock health not only has a knock on effect on overall farm profitability in terms of reduced performance and treatment costs but also has a knock on effect on consumers perception of sheep systems. Lameness, worm burden and mastitis are often highlighted as the key health traits in sheep but are generally not included in international breeding goals due to lack of data; *Longevity* – the age profile of the flock has a large knock on effect on flock productivity, with greater lamb growth rates, lower lamb mortality and lambing difficulty associated with older ewes; *Low environmental hoofprint* – the environmental load is an area of increasing importance for all livestock sectors and can be linked to traits such as feed intake, output and longevity. The use of new technology such as the portable accumulation chambers allows the measurement of gaseous emissions on large numbers of animals in a commercial environment and will allow for selection of environmental friendly ewes in the future; *Resilient to change* – with greater revenue returns from livestock sectors such as dairy, sheep are likely to be farmed in greater numbers in marginal areas, therefore identifying ewes that can adapt and perform in varying climatic changes is of increasing importance.

Strategies for breeding the ideal ewe Genomic selection has led to a paradigm shift in dairy breeding goals, it not allows for the generation of more accurate data at a younger age, but in the case of sheep can reduce labour requirements around lambing and mating through the use of mob mating and DNA parentage. However access to large quantities of accurately recorded data will remain essential now and into the future. One potential method of generating such data is the use of phenotyping flocks whereby farmers are incentivised to record a range of routine (i.e., lambing and weight) and novel traits (i.e. feed intake, methane emissions); such systems are already operated internationally. In addition the sharing of germplasm is common practice across neighbouring countries therefore the sharing of phenotypic, genetic or genomic data could enhance the breeding goals in participating countries – the development of INTERSHEEP therefore warrants serious consideration. Finally the use of new technology such as EID readers, automatic scales and thermal cameras will continue to reduce the labour burden associated with recording of data in the future.

Conclusion Identifying the key characteristics of the ideal ewe is the first step in breeding the ewe of the future. Strategies in the recording of the phenotypic data around these traits as well as knowledge of the genetic (co) variance between the traits will allow for the development of the holistic breeding goal that will accelerate genetic gain and allow the ideal ewe of the future to be identified.

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Use of AI in beef herds

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Application Currently, a small number of beef farms routinely use artificial insemination (AI) to increase genetic gain and productivity. The implementation of AI programs in beef herds based on estrus detection is hampered mainly by postpartum anestrous and estrus detection failure. Timed artificial insemination (TAI) - which eliminates the need for estrous detection - deserves to be highlighted for facilitating management and by improving reproductive efficiency of the herds.

Introduction The correct use of biotechnologies in beef farms plays a critical role on productivity. Artificial insemination promotes genetic and economic gains through the use of superior genetic bulls. Despite the technological advances of AI programs, the implementation of AI in beef herds based on estrus detection is hampered mainly by postpartum anestrous and estrus detection failure. To avoid the problems associated with estrus detection, several research groups have developed different strategies to inseminate bovine females at an appointed time, eliminating the need for estrus detection. A number of protocols were designed to control both luteal and follicular function, which permit timed AI (TAI) with satisfactory pregnancy per AI (P/AI). Currently, TAI programs are applied routinely in beef herds providing a systematic approach to the use of AI, facilitating management and improving reproductive efficiency and genetic gain of the herds.

Material and methods We designed two experiments to compare the performance of different reproductive programs that used natural service (NS), AI upon ED and TAI within a 90-day breeding season. In experiment 1, 594 suckled beef cows between 55 to 70 days postpartum were randomly allocated to one of four groups according the strategy of breeding. Cows in the TAI + NS group (n = 150) were synchronized with an E2 plus progestin-based TAI protocol. Bulls were placed with cows 10 days after the TAI and remained together until end of the BS. Cows in the TAI + ED + NS (n = 148) received TAI, then AI based on estrus detection for the next 45 days, and then NS for the last 45 days of the BS. Cows in the ED + NS (n = 147) were artificially inseminated based on twice daily estrus detections during the first 45 days of the BS and then exposed to NS for the last 45 days of the BS. Cows in the NS (n=149) were bred by NS for the entire 90 days BS. In experiment 2, 507 suckled beef cows between 30 and 60 days postpartum were assigned randomly to one of two groups at the onset of the BS. The NS group (n = 255) received only NS during the entire BS and TAI + NS group (n = 252) received TAI at the onset of the BS followed by NS until the end of a 90-day BS.

Results In Experiment 1, cows in the ED + NS or NS groups had decreased (P < 0.001) hazard of pregnancy compared to cows in either groups that received TAI at the onset of BS. Furthermore, cows receiving TAI had higher (P < 0.01) pregnancy rates at the end of the BS compared to cows that did not receive TAI. In Experiment 2, cows in the TAI + NS group had 63% higher hazard of pregnancy (P < 0.001) compared to cows in the NS group. This change in rate of pregnancy reduced the median days to pregnancy by 44 days (11 *vs.* 55 days).

Conclusion Timed AI programs achieved a satisfactory stage of technological development; advances in reproductive management of insemination are widely available and routinely in use on commercial farms worldwide. Currently, beef cattle operations are incorporating TAI programs to increase the productive and reproductive performance. The TAI allows the producers to reach different market opportunities, such as enhance the use of AI on large scale, synchronize the parturition to the better seasons of the year for calf trade and improve the number of calves from bulls with high genetic merit. In addition, the calf production may become more consistent and predictable with the use of large scale TAI programs in commercial herds.

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Why synchronization programs are now referred to as fertility programs for dairy cows: an update

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Introduction The decrease in fertility from nulliparous to primi- and multiparous dairy cattle continues to be a critical problem limiting profitability and sustainability of dairy farms. Reproductive performance of lactating dairy cows is dependent upon service rate (or estrus detection rate), fertility of the service sire, and maternal fertility. Service rate can be controlled utilizing Ovsynch based technologies. The majority of dairy producers in the U.S. regulate time to 1st and subsequent artificial inseminations (AI) with Ovsynch (Pursley *et al*., 1995) technologies. High fertility sires in the U.S. can be chosen utilizing the USDA-ARS sire conception rate summaries. Yet, maternal fertility, defined as the mother's ability to ovulate a competent oocyte and provide an oviductal and uterine environment capable of fertilization and complete embryonic and fetal development, continues to be the key limiting factor for profitable reproductive performance in lactating dairy cows. Conception rates of lactating cows are approximately 30% compared to 60% in virgin dairy heifers when inseminated following a detected estrus (Sartori *et al*., 2004). Increasing conception rates of lactating cows to that of heifers would allow producers to employ the most profitable calving interval strategies for cows with different production levels to increase profit. Aspects of maternal fertility that are limiting to conception and embryonic/fetal development, and methods whereby Ovsynch can be modified to enhance maternal fertility while continuing to control service rate, are becoming well defined. Key phenotypic differences in nulliparous heifers and lactating cows that relate to their fertility differences have been utilized to develop fertility programs. They are: circulating concentrations of 1) progesterone and 2) estradiol-17b during ovulatory follicle development, and 3) the cycling status at time of synchronization. A significant change in circulating concentrations of steroid hormones takes place following the transition from heifer to lactating cow (Sartori *et al*., 2002). Concentrations of progesterone drop to nearly half the levels in lactating cows compared to nulliparous heifers (Sartori *et al*., 2004). This difference in P4 appears to influence follicle growth by prolonging the age of the ovulatory follicle via reduced negative feedback of progesterone on pulses of luteinizing hormone. Allowing more LH pulses to occur may drive the growth of a dominant follicle similarly, but likely not to the extreme, to a persistent follicle (Roche and Ireland, 1981) and cause a reduction in the fertility potential of the follicle. When the persistent DF is allowed to ovulate, fertility is decreased in comparison to younger ovulatory follicles (Mihm *et al*., 1994). The ovulatory follicle is greater in diameter in lactating cows compared to heifers, but lactating cows only have about ½ of the circulating concentrations of estradiol compared to heifers just prior to the LH surge. There is clearly a positive relationship in circulating levels of estradiol and fertility. Cows that are anovular at the start of a fertility program are less likely to become pregnant compared to cycling cows. These three concepts will be discussed in this presentation. Further information including calendars of the 1st AI fertility programs described in the presentation may be found at www.dairycattlereproduction.com.

Conclusion This presentation will lay the groundwork for the development of synchronization programs in the U.S. The combined use of GnRH and PG can be utilized to manipulate ovarian function and control the timing of ovulation in a precise period to allow for timed-AI. Further manipulation assures the control of the antral age of the ovulatory follicle at time ovulation and the hormonal environment during antral development. It appears that manipulating ovarian development can provide a hormonal environment in lactating cows similar to that of nulliparous heifers and increase fertility.

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Host genetics of bovine tuberculosis resistance: the route to gene identity and marker assisted selection

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Application SNP markers have been associated with bovine tuberculosis (bTB) resistance and identified genetic loci in order to enhance breeding strategies for greater resistance to bTB and improve basic understanding of bTB pathogenesis

Introduction *M. bovis* infection, the causal pathogen of bTB, affects ruminant, wildlife and human health worldwide. Despite statutory testing, it persists in the UK and Ireland. HF dairy cattle vary in their genetic liability for infection with this pathogen. Thus selection for more resistant animals has the potential to contribute to its eradication. A novel genetic index "TB Advantage" can now assist farmers and breeders to breed dairy cows with better resistance to bTB (Agriculture and Horticulture Development Board Dairy; Banos *et al*, 2016). SNP markers associated with bTB resistance will improve the accuracy of predictors (Tsairidou *et al*, 2014) and identify genomic regions for bTB resistance in cattle. We have identified a number of loci and candidate genes in three genome wide association (GWA) studies for bTB resistance (Bermingham *et al*, 2014; Raphaka *et al*, 2017; Wilkinson *et al*, 2017). We have now whole genome sequenced 88 HF sires with known estimated breeding values (EBV) for bTB resistance in order to provide novel information that could enhance accuracy of genomic predictors as well as identifying novel SNPs closer to the causal loci for bTB resistance in cattle.

Material and methods The case-control GWA consisted of female HF cattle from bTB high prevalence herds in Northern Ireland. Cases were: (1) infected and positive for the single intradermal comparative cervical tuberculin test (SICCT) with visible lesions ("VL"); (2) infected cattle SICCT positive with no visible lesions, but positive predictive values (PPV) for *M. bovis* infection ≥ 0.90 ("NVL"). Control were: herd and age matched healthy SICCT negative tested on multiple occasions before, during and after a herd breakdown ("C"). Following quality control 607 VLs, 800 NVLs and 559 Cs were genotyped with 538,231 autosomal SNPs (BovineHD chip). Analyses included a single SNP genome-wide association (GWA) and regional heritability mapping (RH) with several SNP window sizes. After Bonferroni correction, likelihood ratio tests (LRT) were calculated. 88 sires with an average reliability > 0.9 for "TB Advantage" have been genome sequenced by Illumina HiSeq X. The DRAGEN BIO-IT platform was used as a pipeline for genome analysis and the GATK pipeline for variant discovery.

Results RH mapping identified both distinct and overlapping loci for VLs and NVLs. with one locus on BTA 13 with suggestive significance for VLs only and three loci on BTA 17, 22 and 23 for NVLs only, of which the first two reached the suggestive threshold, and one on BTA23 was above genome-wide significance. The locus identified on BTA23 contains genes that are part of the bovine Major Histocompatibility Complex (BoLA) class IIb region and are associated with immune variation.
Whole genome sequencing of sires with varying EBVs for bTB resistance resulted in an average read coverage of 52X with between 88.96% - 95.06% reads mapped to the UMD3.1 bovine genome assembly. Each sire had > 8 million variants and preliminary analysis has identified over 1.5 million unique SNPs in the 20 lowest risk and 20 highest risk sires. Functional annotation and greater exploration of the data is ongoing.

Conclusion Host genetics of bTB is complex with many loci of small effect. Our data suggest that variation in pathological outcome is partly controlled by distinct genes. Novel loci not on the bovine HD SNP chip that are associated with bTB resistance may be discovered through whole genome sequencing

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Are microbiomes important to mammary gland health in dairy cows?

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Application A large, prospective longitudinal study was used to study whether the mammary gland microbiome was an important aspect of dairy cow health.

Introduction Mastitis, the most economically important endemic disease of dairy cattle, is caused by a wide range of bacterial pathogens. It is now clear that a microbiome inhabits the bovine mammary gland (MG) and the relationship between these microbial communities and their hosts is critical to understanding and managing mastitis.

Material and methods Milk samples were collected from ~200 cows from two UK dairy farms from drying off to 28 days post-partum (11 samples in total per quarter; 10 samples for heifers). Somatic Cell Counts (SCC) were taken for all samples and 45 animals from one farm were selected for microbiome analysis based on a analysing a variety of SCC dynamics within the quarters over time. DNA was extracted from ~1,600 quarter samples, model microbiomes and milking parlour and extraction controls. Bacterial load in the samples were determined by bacterial 16S rRNA gene-targeted qPCR and the microbiome analysed by PCR amplification and deep sequencing of the bacterial 16S rRNA gene. Sequences were processed and analysed using USearch8.1 and high-quality sequence reads were clustered into operational taxonomic units (OTUs) at 97% (~ species level) and the closest related species was identified if possible. SCC and microbiome data were analysed using statistical modelling and machine learning approaches.

Results SCC, a measure of the immune response of the host in the mammary gland varied over time in the sampled quarters although there was a general trend for SCC to fall with time after parturition. Bacterial load sequencing data indicated that the size and diversity of the microbiomes in individual quarter samples was very variable over time. The relationship between SCC and bacterial load in each quarter sample was analysed taking into account both the parity of the animal and days-in-milk. Statistical and machine learning analyses highlighted relationships between SCC, bacterial load and individual OTUs.

Conclusion It was clear that all samples contained a microbial community and that the host responded to that community with increasing somatic cell counts in its mammary gland quarters. These data and analyses allow us to consider the role of the mammary gland microbiome in dairy cow health and of the nature of microbiomes in general.

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Is multistrain infection with *Dichelobacter nodosus* important in the severity of footrot and management of disease?

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Application We hypothesise that both load and the community of strains of *D. nodosus* are key to understanding flock managements that could provide resilience to disease.

Introduction Footrot, caused by the anaerobe *Dichelobacter nodosus*, has a major impact on the UK sheep industry. More than 3 million sheep are lame with footrot per annum in the UK, costing > £80 million in 2006 alone (Wassink *et al.*, 2010). *D. nodosus* has several virulence factors, currently AprV2 / B2 differentiates a protease that is associated with virulent and benign disease respectively.

Material and methods
Study 1 Twenty-four flocks of sheep that were distributed throughout England and had >5% prevalence of lameness were visited on three occasions. At each visit fifteen sheep were examined, their feet scored for presence and severity of footrot (Moore *et al.*, 2005) and then swabbed. Swabs were stored in media immediately and frozen at -20°C until analysed. Swabs were pooled for analysis by one of 10 disease states within visit within farm. DNA was extracted from pooled samples and *Dichelobacter nodosus* load was estimated using rpoD qPCR, virulence was investigated using AprV2/B2 qPCR. Serogroups were investigated using PCR.
Study 2 Data from a previous study (Witcomb *et al.*, 2014) were used to develop a simple mechanistic model of the development of footrot using *Dichelobacter nodosus* load and lesion severity (Moore *et al.*, 2005; Kaler *et al.*, 2011). Climate was added to the model to investigate which environmental factors influenced transmission of *D. nodosus*.

Results
Study 1 There were 394 pooled samples. All 24 flocks were positive for *D. nodosus* but not all were positive for AprB2. The load of *D. nodosus* was higher in interdigital dermatitis and severe footrot lesions than in healthy feet. The load of AprV2 was correlated to total load and therefore also higher in diseased feet. The load of AprB2 was not correlated with disease. The number of serogroups varied between flocks but there was no clear link with footrot severity.
Study 2 It was possible to construct a model using disease severity and load of *D. nodosus* that fitted the data used to develop the model and other datasets (Atia *et al.*, 2017). Rainfall influenced disease spread in a flock of sheep in Bristol UK. The model appears robust at predicting disease in climates other than the UK.

Conclusion *Dichelobacter nodosus* strain types and load were linked to severity of footrot in both mathematical models and laboratory analysis of pooled isolates. The AprB2 strain was not associated with expression of footrot whilst AprV2 strain was associated with severity of footrot and load was higher with increasing severity.

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Gene edited pigs are resistant to PRRSV infection whilst maintaining biological function of the editing target gene CD163

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Porcine Reproductive and Respiratory Syndrome (PRRS) is a panzootic infectious disease of pigs, causing major economic losses to the world-wide pig industry. PRRS manifests in pigs of all ages but primarily causes late-term abortions and stillbirths in sows and respiratory disease in piglets. The causative agent of the disease is the positive-strand RNA PRRS virus (PRRSV). There are two different species of PRRSV with distinct geographic distribution, PRRSV-1 is found primarily in Europe and Asia, overlapping the range of PRRSV-2, which is found in Asia and the Americas.

PRRSV has a narrow host cell tropism, limited to cells of the monocyte/macrophage lineage. CD163 has been described as a fusion receptor for PRRSV, whereby the scavenger receptor cysteine-rich domain 5 (SRCR5) region was shown to be an interaction site for the virus *in vitro*. CD163 is expressed at high levels on the surface of macrophages, particularly in the respiratory system.

We have used CRISPR/Cas9 editing in pig zygotes, resulting in the generation of pigs with a deletion of Exon 7 of the CD163 gene, encoding SRCR5. Deletion of SRCR5 showed no adverse effects in pigs maintained under standard husbandry conditions with normal growth rates and complete blood counts observed. Macrophages isolated from the animals show the characteristic differentiation and cell surface marker expression of macrophages of the respective origin. Expression and correct folding of the SRCR5 deletion CD163 on the surface of macrophages and biological activity of the protein as hemoglobin-haptoglobin scavenger was confirmed. *In vitro* challenge of macrophages with PRRSV-1, subtypes 1, 2, and 3 and PMMs with PRRSV-2 showed complete resistance to viral infections assessed by replication. *In vivo* infection analysis with a PRRSV-1 subtype 2 strain showed complete resistance in the pig as well and further confirmed biological function of the CD163 SRCR5 deletion variant by expression of the protein in its soluble form in the serum of these animals.

The creation of ΔSRCR5 pigs holds tremendous opportunity for the pork industry worldwide to improve both animal welfare and productivity at the same time. PRRSV infection has immunomodulatory outcomes and plays an important role in polymicrobial disease, such as the porcine respiratory disease complex. As such PRRSV-resistant animals could benefit general health and decrease the need for antimicrobial use at the same time. However, for the implementation of the next generation breeding / genome editing techniques in animal production, both consumer acceptance and the legislative framework need to be in place.

Perspectives on bovine respiratory disease: new technologies open new avenues

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Respiratory disease in cattle has been a significant economic issue for decades. In the U.S., it is the number one cause of mortality and has an estimated $23.60 impact per treated calf, with total cost to the industry exceeding one billion dollars annually. Additionally, it is by far the main reason for the medicinal use of antibiotics in beef production. Despite over 40 years of research addressing the problem, the incidence of respiratory disease in U.S. cattle has not been substantially reduced. In large part, the intractability of the problem can be ascribed to the multifactorial etiology of Bovine Respiratory Disease Complex (BRDC), which can be initiated by a number of potentiating pathogens and complicated by a variety of opportunistic secondary infective agents. Further complications arise from the contributions of environmental stressors compromising host immunity, and the interactions of management factors with host genetics and pathogen exposure. The reductionist approach to investigation of BRDC has identified many of the microorganisms involved, and led to development of a variety of vaccines targeting specific organisms, and yet overall management to effectively reduce incidence has been elusive.

The advent of a variety of "Omics" technologies, particularly high-throughput sequencing platforms, has expanded the available toolbox and provided new pathways to studying the occurrence of respiratory disease. The development of high-density genotyping arrays, based on single nucleotide polymorphism markers, has enabled the application of genome-wide association studies (GWAS), that do not necessarily require high quality pedigree information, to identify genetic variation in cattle populations that contribute to disease susceptibility. To date, the GWAS approach has met with limited success, in part because fully controlled experimental populations are generally too small to have power to detect variation of modest effect, in part because the use of single pathogen challenge experiments do not adequately represent the course of natural infection, and in part because accurate classification of phenotypes upon which GWAS depends is challenging. Other Omics technologies may help to overcome these limitations, by providing alternative, higher-resolution, objective phenotypes. Examples include sub-classification of disease through the use of biomarkers, cell-free DNA screens, or immune repertoire profiles.

At the U.S. Meat Animal Research Center in Nebraska, part of the USDA Agricultural Research Service, we have developed a strategy to investigate the biology underlying the occurrence of BRDC that takes a broad approach to the problem. Various populations are being studied to identify microbiome, immune repertoire, vaccine responsiveness, cell-free DNA/RNA, and biomarker components related to emergence of disease. Various preliminary results and a general discussion of the approach will be presented in the context of describing the emerging opportunities to address this complex problem.

Economic and environmental sustainability of suckler calf to beef systems

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Application Large improvements in productivity and efficiency are possible on commercial suckler beef farms leading to much greater economic performance and lower greenhouse gas (GHG) emissions per unit of beef carcass.

Introduction The profitability of suckler beef production systems is low. However, when compared to bio-economic models based on research farm performance, there is scope for commercial suckler beef farms to increase productivity and economic performance. Additionally, the environmental footprint, particularly GHG emissions, of beef production is of concern. The objective of this study was, using data from suckler calf-to-beef farms participating in a farm improvement programme, to investigate the importance of key performance indicators on physical and economic performance and GHG emissions.

Material and methods Data from commercial suckler calf-to-beef farms participating in a farm improvement programme, the Teagasc/Farmers Journal BETTER farm beef programme (Taylor *et al.*, 2018), were obtained, analysed and used to parameterise an existing bioeconomic model of sucker beef production systems (Crosson *et al.*, 2006). Data pertained to 19 suckler calf-to-beef finishing farms who participated in the programme from 2010-2014 (65 farm by year observations). Physical data, including fertiliser and feed inputs, suckler cow reproductive performance, progeny pre-weaning growth performance and slaughter characteristics were recorded on farm and by abattoirs. The dataset generated included a measure of variation (standard deviation) for key performance indicators which permitted the economic implications of these indicators to be quantified. The importance of variation in these performance indicators on GHG emissions was assessed using the BEEF systems Greenhouse gas Emissions Model (BEEFGEM) (Foley *et al.*, 2011).

Results Key results relating to feed inputs, and physical, financial and GHG emissions performance are presented in Table 1. Stocking rate ranged from 1.88 LU/ha (EF) to 2.64 LU/ha (LF). Forage consumption (grazed grass and grass silage) was greatest on LF relative to the BASE (+32%). HIGH and LCR had the highest and lowest net margin (+89% and -32%, respectively). GHG emissions per kg carcass were lowest for the HIGH scenario and highest for the LOW scenario.

Table 1 Physical, economic and GHG emissions results of suckler beef steer-heifer systems

Scenario[1]	BASE	HCR	LCR	HADG	LADG	EF	LF	HIGH	LOW
Stocking rate	2.05	2.16	1.94	2.05	2.05	1.88	2.64	1.97	2.46
Conc. fed per LU (kg DM)	374	394	352	428	347	274	216	453	153
Herbage utilised (t DM/ha)	7.6	8.1	7.2	8.1	7.2	7.2	10.1	8.0	8.7
Live weight gain (g/d)	845	845	845	911	781	894	807	1029	729
Net margin	264	346	180	309	203	323	253	498	180
GHG (kg CO_2e/kg carcass)	19.5	19.2	19.9	19.4	20.3	18.9	21.2	18.5	22.1

[1] BASE=level of technical efficiency on commercial farms, HCR= high calving rate scenario, LCR=low calving rate scenario, HADG=high average daily gain scenario, LADG=low average daily gain scenario, EF =earlier finishing scenario, LF=later finishing scenario, HIGH=BASE scenario with high technical efficiency (HCR, ECD, HADG and EF), LOW = BASE scenario with low technical efficiency (LCR, LCD, LADG and LF). Land area = 61 hectares, Cows calving = 73.

Conclusion Calving rate had the greatest effect on economic performance, and age at slaughter had the greatest impact on GHG emissions per kg output. Combining the highest level of performance of the individual traits in a single system (HIGH) yielded the greatest profitability and lowest GHG emissions per kg output.

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Feed efficiency of beef cows: a way to improve their feeding allowances through the quantification of non-productive functions

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Application In the revised INRA feeding system for ruminants (INRA, 2018), it is now possible to take into account bodyweight variation for rationing beef cows.

Introduction Maintenance requirements of beef cows account for at least 70% of total energy requirements (Ferrell and Jenkins, 1984), compared to 40 to 50% for dairy cows. Energy for maintenance corresponds to the energy required to ensure the integrity of life functions, to maintain muscle tone, renal excretion, secretion of enzymes and hormones. Traditionally, maintenance requirements were defined as the minimum energy required for body weight gain or body energy balance equal to zero, but this is difficult to estimate directly. Estimates reported in literature are highly variable (91 to 180 kcal/kg$^{0.75}$, Ortigues *et al.*, 1993), due to the measurement methodologies used and factors linked to the animal (breed, level of production, body composition) and its environment (especially the feeding level). In the context of improvement of efficiency and robustness of beef production, a better knowledge of energy use, and in particular the partition of energy intake and its variation to physiological expenditure components, is needed.

Material and methods Beef cows were submitted to a nutritional challenge in order to measure their ability to cope with nutritional changes through the partition of available energy between productive and non-productive (NP) functions. From a systemic approach, the cow is considered as a dynamic system that takes up energy from the environment to maintain its function over a productive cycle. Changes in energy partition are known to be modulated by the stage of lactation and other various metabolic pathways (e.g. protein accretion and mobilisation or/and lipogenesis/lipolysis). The energy balance can be estimated over the duration of the nutritional challenge and summarises the partition of energy fluxes. Energy changes expressed in net energy for lactation (UFL; INRA, 2018) is: UFLreq = UFLreq_MY + UFLreq_ΔBR + UFLreq_gest + UFLreq_NP, where UFLreq is the total net energy requirements, UFLreq_MY is the energy requirements for milk production, UFLreq_ΔBR is the net energy equivalent to body reserves changes, UFLreq_gest is the energy requirements for pregnancy and UFLreq_NP is the net energy required to NP functions; all the terms are expressed in UFL/day. By definition, when body weight (BW) change is null, ΔBR is null and UFLreq_NP corresponds to maintenance requirements. The relative importance of UFLreq_NP was determined by quantitative analysis of the INRA "Beef Cows" database. It included 33 INRA challenge trials (from 1975 to 2014) on late-maturing 'continental' beef cows with simultaneous measurements of diet intake, BW, BW changes corrected for variations in DMI, body reserves changes (ΔBR) assessed by adipose cell measurements, milk yield assessed by the weigh-suckle-weigh method. Within this database, the energy equivalents were expressed in UFL (INRA, 2018) using the metabolic efficiency coefficients (kpf, kg and kls for protein and fat deposition, gestation and lactation, respectively). Feed (ingredient) intake was also expressed in UFL calculated according to INRA (2018). The database included 101 treatments differentiated by the production stage and the parity of cows: 54 treatments related to lactating multiparous cows, 26 to lactating primiparous cows, and 21 to dry or pregnant multiparous cows. Special attention was paid to the energy of NP functions linked to the lipid and protein composition of BW change.

Results From the quantitative analysis of the database, it was shown that: i) energy intake or mobilized from BR was mainly allocated to milk production whatever the level of feeding, ii) net energy equivalent of BW change was on average 2.4 UFL/kg BW (38 % lipids) in multiparous cows and 1.8 UFL/kg BW (21 % lipids) in primiparous cows, iii) NP functions can be expressed as the sum of maintenance requirements and energy to support BR changes. The net energy required for maintenance amounted to 0.043 and 0.049 UFL/kg BW$^{0.75}$/d in dry pregnant and in lactating cows, respectively. These values must be increased by 10 and 20 % in free-stalls and pasture environments, respectively.

Conclusion With this work, we have upgraded the beef cows' energy requirements for the revised feeding system, using a larger number of observed data. The improved knowledge about chemical composition of body reserves changes help to provide a more detailed and original model of energy partitioning. Although the model was derived using late-maturing 'continental' breeds, this approach can be used generically and adapted to other breeds.

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A review of New Zealand equine research

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The New Zealand equine industry consists of approximately 100,000 horses, which economically can be separated into two main sectors – Racing (Thoroughbred and Standardbred) and the sport horse sector (showjumping, eventing and dressage). The Racing industry has received the most attention from equine researchers, in part due to high level of reporting within the industry and the large export focus with ~40% of all Thoroughbred foals born in New Zealand being exported either as yearlings, or racehorses. Another unique feature of the New Zealand industry is a reliance on pasture as the primary source of nutrition for breeding, youngstock and sport horses. This pasture based industry in association with the export focus has seen research focus on "equine production"; optimising of growth and development while minimising wastage and loss throughout the production and sport process.

Reproduction research has focused on stud or industry level data. The export focus and therefore a drive for foals born as close to August 1 (Southern hemisphere official birthdate) results in a short commercial breeding season. Mares bred early in the season have longer gestation lengths which may be related to nutritional status and environmental stimuli within a pasture based management system.

Pasture intake and the relative digestibility of pasture and the macro nutrients for both the mare and youngstock has been a primary focus of nutrition research. The high nutritive value and intake of pasture available within commercial farms is capable of meeting most of the nutritional requirements mares and youngstock. The efficient utilisation of pasture by breeding stock and grazing management systems has been a focus of much on-farm research.

The growth and development of the Thoroughbred in New Zealand has been well documented. The pasture based management influences the onset of puberty and the growth curve of the Thoroughbred. A focus on pasture management may optimise early exercise and a resultant increase in the development of the musculoskeletal system. Increased development of the musculoskeletal systems primes the horse for a future life as an equine athlete.

The competitive life of both Thoroughbred and sport horses within New Zealand is similar to those reported for other countries. In racing, epidemiological studies have identified a low race day failure to finish rate and low catastrophic fracture rate. Analysis of the pattern of racing and the race track conditions indicates a consistent pattern of racing and of the racing surface across tracks and seasons.

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Update of equine research in Michigan

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The primary focus of the horse research program in the Department of Animal Science at Michigan State University has been to evaluate the role nutrition, exercise, and management play in improving the growth and development of the equine athlete, with special attention given to prevention of musculoskeletal injuries. Research is commonly done with horses, but cattle and dogs have been used as models, as will soon be poultry. Of particular note are studies evaluating housing management on bone development in young horses, which has led to collaborative work in horse behavior and welfare. Nutritional studies are frequent, particularly in the area of mineral nutrition. Special dietary needs of growing horses have been studied in order to improve growth and prevent developmental orthopedic disorders. Additionally, the effects of ergogenic agents on performance have been examined.

Work to commence shortly: While the element silicon (Si) is widely present in the environment, it is found in a form not readily absorbable. Research by the PI has previously shown benefits of supplementation with a bioavailable form of Si including decreased injuries to racehorses and alterations in bone markers suggesting enhanced bone turnover. However, that form of Si was unpalatable and contained large amounts of aluminum (Al) – which would seemingly be undesirable. An alternative source of bioavailable Si does not contain Al and our lab has previously shown it to positively enhance mineral absorption and retention. The objective of our research is to evaluate the influence it has on bone, cartilage, and collagen in horses and to assess its ability to enhance skeletal integrity in broilers. The results from this study should prove beneficial to animals as a novel means to improve skeletal health - improving their welfare and reducing economic losses.

Work in progress: First, a study using calves as a model for horses is currently examining the number of short, high intensity exercise bouts needed to stimulate bone formation and increase bone strength. Previous work showed five 50-m sprints per week resulted in increased bone strength and greater cortical area compared to that in calves not exercised. In addition to no exercise and five bouts per week, the current study includes treatments of one and three sprints per week in an attempt to determine the minimum number of sprinting episodes needed to optimize bone strength. Another on-going study is examining short-term furosemide usage. Previous research has documented that furosemide negatively impacts calcium balance for three days. This study seeks to answer if calcium balance returns to normal within seven days, as well as how the horse's body responds to an initial dose of furosemide by tracking biomarkers of bone metabolism and calcium regulation. By measuring short-term impacts of furosemide on these parameters, we hope to learn if caution is needed before administering furosemide frequently over the course of a horse's career.

Work recently completed: There has been little research conducted on cobalt (Co) requirements of horses. Preliminary research suggested increasing dietary Co concentrations above NRC (2007) requirements increased fiber digestion in growing horses. A study was conducted to determine if the addition of varying concentrations of Co increased fiber digestion. It was also designed to evaluate the Co requirement and to compare serum Co against dietary Co concentrations with potential implications associated with alleged performance-enhancing effects and welfare implications of providing Co in quantities beyond what would be done through normal dietary means. In a 4x4 Latin square design, varying concentrations of Co were provided using treatment tablets formulated to deliver 0.0, 5.6, 16.8, or 28.0 mg of Co daily. There was no effect of Co supplementation on the digestibility of fiber. Surprisingly, there was an inverse linear relationship between supplemental Co concentration and serum cobalamin levels (P=0.003). Additionally, serum Co differed (P <0.01) with a mean of 4.7 μg/mL for the high treatment and 0.8 μg/mL for the control treatment. This study suggests normal dietary supplementation with Co, even when provided substantially above the 2007 NRC requirement, will not result in Co concentrations resulting in health concerns or serum concentrations near the thresholds established by some racing jurisdictions.

Emerging anecdotal evidence on vibrating platforms and their success with healing injuries and improving performance in horses prompted a study hypothesizing that varying lamenesses would be improved with vibration therapy. Aged horses with known lamenesses were striated according to age, gender, total lameness scores, and stride lengths and then were pair-matched and randomly assigned to either vibration therapy (30 min at 50 Hz, five days per week, for 3 weeks) or control (standing on a platform for an identical time but with it not turned on). Evaluations were done by veterinarians and researchers, blinded to treatment, before and after the initial treatment and at the end of the study. No differences were seen with any measurement associated with improvement suggesting such vibration therapy is not affective in healing after either a single treatment session or after treatment for three weeks.

Artificially extended photoperiod administered to *pre-partum* mares via blue light to a single eye: observations on gestation length, foal birth weight and foal hair coat at birth

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Application Administration of extended photoperiod to *pre-partum* mares may improve breeding efficiency in terms of shorter gestation lengths and higher foal birth weights. This application is particularly relevant to breeders operating within the confines of an artificial, imposed early breeding season for certain breed registries.

Introduction In seasonally breeding animals, photoperiod perception is crucial for timing of important physiological events. In the horse, long day photoperiod influences the onset of ovulation and cyclicity, shedding of the heavier winter coat and the timing of parturition. In this compilation of three studies, conducted across three breeding seasons and two countries, the impact of artificially extended day length was investigated on gestation length, foal birth weight and foal hair coat at birth.

Material and methods For Study 1, 15 pregnant Thoroughbred mares (*Equus caballus*) (age range 5 to 18 years), with a history of prolonged gestation lengths (mean gestation length of 350 days for previous gestations) were used in a study conducted from Dec 1, 2011 through May, 2012 on a breeding farm located in Kildare, Ireland. Mares were maintained at pasture by day and in individual stalls at night and fed appropriate for body weight and stage of gestation. Beginning on Dec 1, Group 1 (n=6) received individual light therapy from head worn masks (Equilume® Light Masks, Equilume Ltd., Kildare, Ireland) that provided 50 lux of blue light (468 nm) to the right eye. The light turned on at 16:30 each day and turned off at 23:00 nightly, providing an initial 14.5 h day, gradually increasing to a maximum day length of 16 h 15 min as the natural hours of daylight advanced. Group 2 (n=9) were maintained under lighting conditions that reflected the natural photoperiod. For Study 2, 29 pregnant light breed mares, (age range 5 to 18 years) and their subsequent offspring were used in a study conducted from Dec 1, 2012 through April 30, 2013 on a single institutional research farm in KY, USA. All mares were previously inseminated with mixed semen collected from two Quarter Horse stallions. The mares were divided into two groups and blocked for age, parity, body condition score (BCS) and bodyweight. Beginning Dec 1, Group 1 (n=15) received an artificially extended photoperiod using Equilume® Light Masks. Group 2 (n=14) were maintained under natural photoperiod. Gestation length was calculated as the number of days from insemination to parturition. FBW in kg was measured within 24 h of birth using a freestanding animal weighbridge (HorseWeigh®, Kentucky, USA). Paternity testing was conducted on all foals following birth using a commercial Equine Parentage Test based on hair follicle DNA typing. For Study 3, 46 pregnant Thoroughbred mares (age range 5 to 23 years) and subsequent offspring were used for a study conducted from Nov 2014 through April 2015 on a commercial stud farm in Kildare, Ireland. Group 1 mares (n=19) were fitted with Equilume® Light Masks on Nov 24th. Group 2 (n=27) were matched for age and expected foaling dates and were maintained under natural photoperiod. Hair samples, complete with hair follicles, were pulled from the shoulder area of all foals within 48 h of birth, measured and weighed. Data for all studies were analysed using a Mixed Model in Graph Pad Prism Version 7.01 for Windows (Graph Pad Software, San Diego, CA, USA). In the Mixed Model, parity, age of mare, mare body weight, BCS of mare and sex of foal were considered as fixed effects and mare within treatment was considered a random effect.

Results In Study 1, reductions in gestation lengths were observed in Group 1 (124.8 ± 15.11 days) compared to Group 2 (P < 0.05; 339.7 ± 9.56 days vs 350.6 ±9.13). Study 2 revealed that *pre-partum* exposure to artificially extended day length (104.6 ± 9.89 days) increased foal birth weight in Group 1 compared to Group 2 (47.13 ± 2.93 kg vs 43.51 ± 6.14 kg; P < 0.05). In Study 3, artificially extended day length (87.53 ± 19.6 days) affected the coat condition of foals from Group 1 with respect to hair weight (P < 0.0001) and hair length (P < 0.0001) at birth compared to Group 2 (0.34 ± 0.20 μg vs 0.59 ± 0.12 μg and 1.93 ± 0.56 cm vs 2.56 ± 0.32 cm, respectively).

Conclusion Collectively, these studies serve to highlight the influential role of the circa-annual changes in photoperiod length on the *pre-partum* mare for normal foetal development during the natural breeding season. It also emphasizes the potential that exists to improve breeding efficiency parameters by artificially simulating this important environmental cue in the latter stages of gestation against the backdrop of an economically driven early breeding season.

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Update on the identification of risk factors and prediction of injuries in racehorses

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Application   Progress toward being able to better identify racehorses at greater risk of (fatal) injury is being made. Interventions based on individual risk profiles for horses entering races need to be considered by regulators and racing veterinarians.

Introduction   There have been many studies that have identified multiple risk factors for (fatal) injury in racehorses across the globe in the last 20 years. In recent years the focus of our effort has been to take this work from the identification of risk factors to the identification of the at risk horse. At the forefront of this work has been our collaboration with The Jockey Club in North America. Since 2008 the Equine Injury Database (EID) has been used to collate injury data for more than 95% of all Thoroughbred race starts in the USA and Canada. The more than 5,000 fatal injuries recorded in more than 3 million race starts, accompanied by significant improvements in computing power and statistical analyses, provides unparalleled ability to identify modifiable risk factors and test the predictive ability of the models produced.

Material and methods   Multivariable logistic regression models are built and updated on an annual basis, as each new year of data becomes available. An automated stepwise logistic regression selection process, to adjust for potential confounding, is used to arrive at final multivariable logistic regression models. A forward bidirectional elimination approach using Akaike's Information Criterion (AIC) is utilised for the stepwise selection. The outcome variables are fatalities occurring (most often euthanasia) within three days of an equine injury sustained during racing and more specific injury types (fatal or not) occurring during a race. Model fit is assessed by using the Hosmer-Lemeshow goodness of fit test (Hosmer & Lemeshow, 2000). The predictive ability of models is assessed by calculating the area under the receiver operating characteristic curve and the top 5% of fitted scores from the models are used to assess the ability of the models to identify a population of starts with higher prevalence of (fatal) injury than the average.

Results   We have identified numerous horse-, race-, track- and trainer-related risk factors during the course of our analyses. For example, the occurrence and number of previous EID recorded injuries and appearances on the 'vet-list' are both associated with an increased risk of fatal injury. Older horses at first start are associated with an increased risk of fatal injury as are horses dropping in claim price since their previous race. Race distance, surface and condition of the surface are all associated with different outcomes and the longer a horse spends with the same trainer, so the risk of injury decreases. Models generally have areas under the curve in the region of 65% and horse starts in the top 5% of most 'at risk' horses are at about 3-fold greater risk of (fatal) injury than the 'average' horse start.

Conclusion   Given the ability of data scientists and modellers, combined with significant computing power, it is now possible to run models based on very large datasets that identify very many risk factors, some of which are modifiable. Importantly such analyses provide the best opportunity for us to develop reliable predictions and risk profiles on which pre-race decision making can be based. These comprehensive analyses also indicate which aspects of the predictive models still contain 'untapped' variation, directing us to new areas which should be the focus of further data gathering likely to improve predictions in the future.

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Going 'cage free' by 2025 – welfare consequences for laying hens

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The commitment of the UK's (remaining) major supermarkets to only provide eggs from non-caged birds from 2025 will have a significant impact on the lives of millions of hens. Another paper (Gittins 2018, this volume) has detailed estimates of bird numbers going to alternative systems, but what does that mean for hen welfare? This paper considers welfare consequences for hens moving into barn, free-range or organic housing, using the Five Freedoms as a framework.

Thirst, hunger and malnutrition In all systems, these are generally prevented, as a thirsty, hungry or malnourished hen will not lay many eggs! However competition can still occur. Linear feed troughs must provide 10 cm/hen or more, but the width of a standard brown hen has been estimated at as much as 18 cm so not all birds can feed together. Subordinate birds are more likely to be displaced from feed troughs than dominant birds and displacements are greater at low feed space allowances (Widowski *et al*, 2017).

Pain, injury and disease Non-cage systems have a greater chance of causing pain, injury and disease compared to cage systems. Keel bone damage is higher in non-cage systems than cages, which is likely to be painful, and has been associated with perches and the height to which birds can ascend to. However, improved perch design reduces the chance of injury, and the provision of ramps in multi-tier systems to allow birds to execute controlled descents has been shown to reduce falls and collisions (Stratmann *et al*. 2015). Most barn and free-range hens are routinely beak trimmed by infra-red, but organic flocks are not. This method causes short-term pain in laying chicks; however the benefit is that the dulled beak tip helps reduce damage caused by injurious pecking, should it occur. Mortality rates are generally higher in non-cage systems than in enriched cages. Disease risks are higher where birds are housed on the floor compared to enriched cages where birds are separated from their faeces. Where birds have access to outdoor runs, there is greater exposure to bacterial, viral, parasitic or fungal pathogens, including avian influenza, Newcastle's disease and mycoplasma. Red mite infestations are also reported to be worse in free range systems. Air quality is typically lower in some non-cage systems where manure is not removed but collects beneath slats, and/or because the house is naturally ventilated, causing high ammonia levels. This can lead to respiratory damage and greater risk of respiratory diseases.

Thermal and physical discomfort There are greater thermal choices in non-cage systems, because birds can move around a greater footprint but also vertically. Especially where outdoor access is given, birds can choose to move in and out of different temperature zones, and other climate effects (wind, rain, sun, etc.). All systems provide nest boxes and perches, although interpretation around what these look like vary, but non-cage systems have the advantage over enriched cages of providing litter, which contributes to bird comfort, as long as it is dry and friable.

Fear and distress A more diverse environment, as is found with non-cage systems compared to cages, can make hens less reactive to novelty and thus less fearful, however birds in non-cage housing systems are more likely to smother when they do show a fear reaction.

Performing natural behaviours Non-cage systems allow hens to express a greater suite of motivated behaviours than enriched cages: they provide more space per hen, and free range and organic systems also provide outdoor runs. Perches can provide a refuge for hens seeking to escape unwanted attention of feather peckers or dominant hens, while also allowing perching and roosting behaviour, especially at night. Perches increase leg bone strength but the proportion of birds with keel bone damage increases in non-cage housing and with the height that birds can ascend to, suggesting that the freedom of movement comes with risk of injury. Feather pecking is a problem in all types of hen housing systems, but tends to be worse in non-cage systems. Feather pecking is closely related to foraging motivation, and studies show that if hens are provided with, and use, outdoor runs this can reduce the risk of feather pecking and cannibalism. Hens are highly motivated to show nesting behaviour. All systems in the UK provide nest boxes of some description, allowing birds to seek a secluded area in which to lay their eggs. Nest boxes are particularly crowded during peak laying times, and favoured nest boxes in non-cage housing (where hens have a choice of multiple nest boxes) can lead to smothering. Dustbathing behaviour can be expressed in non-cage housing, either in the floor litter or in dirt on the outdoor run. Dustbathing serves to remove stale preen oil from feathers, which keeps the plumulaceous (downy) part of feathers fluffy and thus aids with insulation.

In summary, non-cage housing comes with greater risks to hen welfare, but the scope for greater behavioural freedom is higher also. Decisions on how risks are balanced against bird preferences are somewhat subjective: which bird has the life worth living? Implementing suitable management strategies can reduce risks associated with non-cage housing, such as injurious pecking (Lambton *et al*. 2013). Therefore, while risks are higher there is also great scope for improvement.

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A bird's eye view of lighting in poultry housing – the science of poultry vision

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We like to think of ourselves as top of some evolutionary ladder don't we? Humans are more advanced that other mammals, and certainly more than birds – this helps us rationalise the fact that we kill billons of chickens each year to eat. And vision-wise we seem to be on a good footing – we see in three different colours – red green and blue, apart from those with red-green colour blindness that is- while all sub-primate mammals see only in two colours. But truth be told all birds are a good step above us in their visual perception. They can see in four colours; red, green blue and ultraviolet. Now quite what difference that means behaviourally to a bird is unclear apart from the fact that at dawn and dusk there is a greater level of UV than other elements of the electromagnetic spectrum so bird vision at these times is better than ours. Another key difference is that while we perceive a flickering light to be a constant illumination at a relatively low rate of flicker (the flicker fusion frequency FFF) birds still perceive a flickering at a significantly higher FFF. And while this difference is substantial at wavelengths in the visible spectrum (as far as humans are concerned), when we look at FFF in the UV range the value for birds is even higher, well above the flicker rate for the lighting normally available in broiler houses for instance. The question though is not primary a physiological one but rather a welfare one –does a flickering illumination impact on a bird's welfare as has been shown in humans experiencing migraines when working with computer screens where increasing the flicker rate of screen renewal has been shown to lessen headaches? Should we look at increasing the flicker rate of illumination in poultry housing? And how might we know if we had been successful in reducing deleterious effects on poultry? Having considered the chicken eye we should move to discussing recent developments in lighting technology. From an industry that depended on incandescent or fluorescent lighting we are now moving to light emitting diodes. These are much more energy efficient and thus cheaper but also can be tuned to specific light wavelength. We know that behaviourally red light increases aggression and feather pecking and that green lighting yields calmer behaviour. Being able to define much more precisely exactly what lighting regime we are providing for poultry will allow a more welfare-friendly environment to be created, especially important given how central vision is to these birds.