INTRODUCTION

Professor Gerry Boyle, Director

An Foras Talúntais (AFT, now Teagasc) was founded in 1958, and in the following year it's first Director, the late Dr Tom Walsh, instituted scholarship and university research grant schemes for postgraduates. These two initiatives helped to strengthen the scientific base of AFT in its formative years by linking the organisation's mainly applied research programme to the more basic research activity of the third-level sector.

In the first few decades up to ten grants and scholarships were awarded annually. The severe financial cutbacks, coinciding with the merger of AFT into Teagasc in 1988, resulted in the suspension of the postgraduate scholarships and a limitation of the research grants. However, improved finances from the mid-1990s, and in particular the availability of EU Structural Funds, facilitated a significant expansion of the scheme to its current level of around 200 on-going fellowships and a turnover of about 50 new fellowships each year.

More than 2,000 postgraduate students have participated in the scheme over the past fifty years. A number of these are now (or have been) Teagasc staff members and others are employed in the agri-food industry in Ireland and abroad. The annual budget is now well over €3 million, consisting of the basic student stipend and fees and other essential direct costs (travel, materials, consumables, etc.). This level of investment meant that for many years the Walsh Fellowships was the largest postgraduate scheme in Ireland, providing research opportunities for significant numbers of high calibre graduates.

Over the years, Teagasc has introduced a series of initiatives designed to ensure that the scheme continues to maintain and enhance a learner-centred postgraduate research environment that stimulates good research practice and further enhances Teagasc's research capacity. These new initiatives included the introduction of formal evaluation and selection mechanisms; the establishment of a Foresight Committee to identify new science areas; the introduction of formal training courses in research methods for students; and the initiation of the Annual Walsh Fellowship Seminar in association with the RDS.

More recently, the Authority approved a proposal to establish a formal link between the Walsh Fellowships and the Fulbright Fellowships Programme. The Fulbright Programme has been widely recognised, since its inception in 1957, as the premier USA/world scientific and educational exchange programme. The development of a linkage with this highly esteemed international programme has helped to further enhance the image and value of the Teagasc scheme.

Over the years, Teagasc has used the scheme to extended university linkages to colleges outside of Ireland and the scheme is now being positioned to ensure that the organisation can fully exploit opportunities opened up by the development of the Irish Fourth-Level sector. This most recent development will ensure that Teagasc continues to assist in producing our future knowledge leaders, help to strengthen the climate of innovation in the agri-food sector and ensure that that the sector plays its part in meeting the national policy objective of developing Ireland as a knowledge society and economy.

The scheme represents a cost-effective means of initiating new research in Teagasc, which otherwise could not be attempted. It is a flexible means of deploying staff to priority areas and benefits the three parties involved- Teagasc by getting more research done, students by providing them with financial support, and the universities in the number of graduate students whom they can register for higher degrees. It is a very effective means of generating and maintaining Teagasc/university co-operation. The scheme has been invaluable in developing new relationships with universities outside of Ireland in a number of key areas. All in all, students represent good value for money, and the Walsh Fellowships will remain as a vital and dynamic element of the Teagasc Research Programme.

ORAL ABSTRACTS

Maximising dairy calf health through colostrum management and early nutrition

M. Conneely[1,2], Emer Kennedy[1], Michael Doherty[2], Ingrid Lorenz[2]

[1]Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2]School of Veterinary Medicine, University College Dublin, Dublin 4

The calf mortality rate in Ireland is well above that currently reported in other European countries. The provision of high quality colostrum is necessary to provide calves with immunological protection and resistance to disease, and is vital to ensure their health and wellbeing. The aim of this project was to investigate strategies to maximise calf health in early life. This was achieved by i) determining the factors associated with colostrum quality, ii) ascertaining colostrum feeding strategies that ensure optimal transfer of immunity to the calf, and iii) establishing milk feeding regimes that ensure optimal growth and health. The colostral immunoglobulin G (IgG) concentration of cows in the study was 112 g/L; colostrum is classified as being of good quality if it has an IgG concentration of greater than 50 g/L. Colostrum of the highest quality was obtained from cows that were milked earliest post-calving, older parity cows, cows that produced a smaller quantity of colostrum and cows that calved earlier in spring or in autumn. Greatest levels of transfer of immunity were achieved when calves were fed 8.5% of birth bodyweight in colostrum, compared to calves fed 7% or 10%. Calves that were fed subsequent feeds of transition milk were less likely to exhibit signs indicating compromised health. Calves that were fed 15% instead of 10% of their birth bodyweight in milk were heavier at the beginning and end of the pre-weaning stage; feeding calves this higher volume of milk once a day or in two equally divided meals did not adversely affect calf performance or health. Good colostrum management is crucial to reduce calf mortality and morbidity; the results of this study suggest that this can be achieved by milking the cow as soon as possible post calving, and by feeding the neonatal calf 8.5% of birth bodyweight in colostrum within 2 hours of birth.

Genetics of dystocia and perinatal mortality within Irish cattle herds

D. Purfield[1,2], D.P. Berry[1], D.G. Bradley[2]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork
[2]Smurfit Institute of Genetics, Trinity College Dublin, Dublin 2

Dystocia (CD) and perinatal mortality (PM) are quantitative traits influenced by characteristics of both the dam (e.g. pelvic width) and neonate (e.g size). Evidence from monitoring of genomic evaluations for calving difficulty in Irish bulls suggests the existence of a major gene segregating in the Irish cattle population. The objective of this study was to quantify the contribution of genetics to dam and neonatal characteristics of calving performance and elucidate the genomic variation governing these traits. Moreover, recent Teagasc research highlighted that inbreeding increased the incidence of stillbirth. Inbreeding has been shown to impact on genomic regions, with long runs of genotype homozygosity being associated with recent inbreeding events; this phenomenon was investigated also in this thesis. The prevalence of both CD and PM was greater in primiparous, cows with dystocia (PM in parenthesis) prevalence of 4.29% (4.15%) in comparison to 2.61% (1.79%) in multiparous cows. All traits were lowly heritable, with the direct genetic effect of CD (i.e. genetic effects due to the neonate) being the most heritable trait in primiparous animals (0.21). Several genomic regions of homozygosity were detected and total genomic homozygosity length per animal strongly correlated (r=0.75) with inbreeding. The first genome-wide association study of this thesis used 54,001 DNA (i.e. SNP) markers on 1,970 Holstein-Friesian dairy sires to detect associations with calving performance using a Bayesian approach. Several SNPs on chromosomes 5, 6, 11, 12, 17,18 and 28 were strongly associated with these calving performance traits. Of particular interest were the genes Siglec-5 and HHIP for direct CD, accounting for 2.1% and 0.5% of the genetic variance and SLC26A7 for PM accounting for 0.03%. The second genome-wide association study comprised 3,962 dairy and beef bulls with 777,962 DNA markers and refined previously detected genomic regions harbouring likely causative mutations as detecting new putative regions of interest.

Response to *Teladorsagia circumcincta* infection in Scottish blackface lambs selected for divergent phenotypes for resistance

Kathryn M. McRae[1, 3*], Barbara Good[2], J P. Hanrahan[2], Torres Sweeney[4], Mary J. O'Connell[3], Orla M. Keane[1]

[1]*Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[2]*Teagasc, Animal & Grassland Research and Innovation Centre, Athenry, Co. Galway*
[3]*Dublin City University*
[4]*University College Dublin*

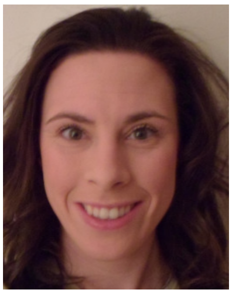
Infection with gastrointestinal nematodes (GIN) is one of the major constraints of sheep production worldwide. An increase in the incidence of anthelmintic resistance has led to a search for alternative options for GIN control, such as selective breeding for resistance or immunomodulatory treatment. The objective of this study was to identify lambs that differed in their response to natural GIN infection and characterise their response to a controlled challenge. Scottish Blackface lambs, grazed together from birth, were monitored for faecal egg count (FEC; 2 samples following each of 2 independent natural infections). These observations were used to develop a model to reliably identify resistant (low FEC) and susceptible (high FEC) animals. Selected high (n=10) and low (n=10) FEC lambs were challenged with 30,000 *Teladorsagia circumcincta* larvae (L3), and slaughtered at 7 or 14 days post infection (dpi). Samples were collected at slaughter for worm burden enumeration, haematology and gene expression analysis. Total RNA was extracted from abomasal lymph nodes and cDNA libraries generated and sequenced. Reads were aligned to the *Ovis aries* reference genome (Oarv3.1) using TopHat. Transcript abundances were normalised, and used to detect differentially expressed genes. Worm burden was not significantly different between High and Low FEC animals, consistent with previous studies, which showed the time taken for animals to activate a protective immune response and expel worms is greater than 14 days. Low FEC animals had a higher number of circulating basophils ($P < 0.05$); however all other haematology variables were not significantly different. A number of genes were differentially expressed ($FDR < 0.05$) between High and Low FEC animals at 7 or 14 dpe.

Dissecting the immune response associated with postpartum uterine disease

C. Foley[1,2], A. Chapwanya[3], F. Narciandi[2], J.J. Callanan[4], C. Creevey[1], R. Miranda[5], W. Meijer[5], D. Lynn[1], C. O'Farrelly[2], K.G. Meade[1]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co, Meath
[2]Comparative Immunology Group, School of Biochemistry and Immunology, Trinity College, Dublin 2
[3]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, Pretoria, South Africa
[4]UCD School of Veterinary Medicine, Dublin 4
[5]UCD School of Biomolecular & Biomed Science, Conway Institute, Belfield, Dublin 4

Postpartum uterine disease occurs in approximately 30% of cows and is associated with sub-fertility. Activation of local innate immune mechanisms by postpartum bacterial contamination of the uterus occurs in all cows. However, uterine disease involves persistent bacterial infection and inflammation. Mechanisms that control inflammation and achieve a physiologically functioning endometrium postpartum while avoiding disease have not been identified. The aim of this study was to define mechanisms differentiating cows with healthy and inflamed postpartum endometria locally and systemically. A multi-layered approach involved the analysis of histology, microbiology, mRNA-Seq global mRNA and microRNA gene expression, whole blood cell counts and blood proteins. A pilot study in healthy cows 15 days and 30 days postpartum (DPP) characterised global gene expression in endometrial biopsies using mRNA-Seq. A follow-on study defined functional differences between cows with sustained endometrial inflammation (Sub-clinically endometritic (SCE), n=6) and healthy cows (n=9) displaying relatively low endometrial inflammation 21DPP, defined using histology scoring of immune cell infiltrate. mRNA-Seq showed 182 genes 7DPP and 1219 genes 21DPP significantly (FDR <0.1) differentiated healthy and SCE cows enriching immune response pathways in SCE cows and calcium signalling pathways in healthy cows 21DPP. A significant ($P < 0.05$) shift in uterine microbial populations is a potential factor contributing to sustained inflammation in cows 21 DPP. Reduced expression of calcium signalling genes 21DPP and increased expression of miRNAs regulating cellular proliferation genes 7DPP in SCE cows are possible mechanisms influenced by local endometrial inflammation. This study revealed significant differences ($P < 0.05$) in systemic levels of serum amyloid A and haptoglobin 7DPP between healthy and SCE cows. Divergent local inflammatory and calcium signalling profiles and systemic acute phase proteins differentiate SCE from healthy cows and endometrial elevation of *IL-17* gene expression prior to and during subclinical endometritis are potential early biomarkers of subclinical endometritis.



Increasing the phosphorus fertiliser use efficiency in Irish grasslands

Timothy Sheil[1,4], Stan Lalor[1], Eva Lewis[2], David Wall[1], Deirdre Hennessy[2], Karen Daly[1], John Bailey[3], Chris Elliott[4]

[1]Teagasc, Crops, Environment and Land Use Research Programme, Johnstown Castle, Wexford
[2]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[3]Agri-Food and Bioscience Institute, New Forge Lane, Belfast
[4]Institute for Global Food Security, Queen's University Belfast

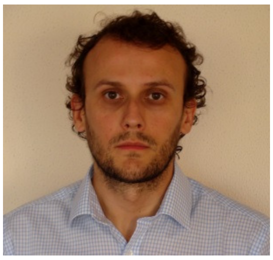
Phosphorus (P) is an essential element for grassland productivity, but P fertilisers are mined from finite resources of phosphate rock. As a result, there is growing interest in increasing the efficiency of P fertiliser use in agriculture to ensure the future sustainability of food production. Maintaining soil P fertility is critical if agriculture is to achieve the productivity targets set by Food Harvest 2020. This project was designed to increase our knowledge on the behaviour of, and requirements of P in grassland soils. Data from a long-term field experiment showed that a sustained annual application of 15 kg P ha^{-1} yr^{-1} was required for maximum herbage yield, whilst seasonal trend indicated that P concentration in herbage was lowest during summer months. Results from a short-term field experiment carried out on two sites with contrasting soil fertility levels found a comparable response to nitrogen and P on the herbage yield and soil P levels had a strong influence on herbage P concentration. A soil incubation experiment carried out on a range of different Irish soils showed that in this study lime plays an important role in increasing the availability of soil P and fertiliser P. In the same range of soils, the examination of soil P behaviour using P sorption isotherms and organic P speciation were investigated and the results highlight the variation that exists in P dynamics across Irish soils. Overall, the results from these experiments suggest that as the future availability of P fertiliser becomes uncertain, a greater emphasis on soil specific fertiliser P guidelines will be required to maximise P efficiency in grasslands. This project will underpin the rationale and provide an initial investigation for the future implementation of more soil specific P fertiliser guidelines in Ireland.

Unearthing the nutritional and phytochemical diversity of Irish grown potatoes

Jesus Valcarcel[1,2], Michael Gaffney[1], Kim Reilly [3], Nora O'Brien[2]

[1]Teagasc, Food Research Centre, Ashtown, Dublin 15
[2]School of Food and Nutritional Sciences, University College Cork
[3]Agrifood Scientific, 219 Tonlegee Rd, Dublin 5

Potatoes (*Solanum Tuberosum* L.) contain secondary metabolites that may have an impact on human health. The aim of this study was to assess the levels of some of these compounds in a wide range of varieties, including rare, heritage and commercial cultivars. Vitamin C, total carotenoids, phenolics flavonoids, antioxidant activity and glycoalkaloids were determined, using spectroscopy and chromatography, in the skin and flesh of tubers grown in field trials. Transcript levels of key synthetic enzymes were assessed by qPCR. Accumulation of selected metabolites was higher in the skin than in the flesh of tubers, except ascorbate, which was undetected in the skin. Differences were on average 2.5 to 3-fold for carotenoids, 6-fold for phenolics, 15 to 16-fold for flavonoids, 21-fold for glycoalkaloids and 9 to 10-fold for antioxidant activity. Higher contents of carotenoids were associated with yellow skin or flesh, and higher values of phenolics, flavonoids and antioxidant activity with blue flesh. Variety 'Burren' had maxima values of carotenoids in skin and flesh, variety 'Nicola' of ascorbate, variety 'Congo' of phenolics, flavonoids and antioxidant activity in both tissues, except antioxidant activity in the skin, which was higher in 'Edzell Blue'. Varieties 'May Queen' and 'International Kidney' had highest glycoalkaloid content in skin and flesh respectively. The effect of the environment was diverse: year of cultivation was significant for all metabolites, but site of cultivation was not for carotenoids and glycoalkaloids. Levels of expression of phenylalanine ammonia-lyase and chalcone synthase were higher in varieties accumulating high contents of phenolic compounds. However, levels of expression of phytoene synthase and L-galactono-1,4-lactone dehydrogenase were not different between varieties showing contrasting levels of carotenoids and ascorbate respectively. This work will help identify varieties that could be marketed as healthier and the most suitable varieties for extraction of high-value metabolites such as glycoalkaloids.



Slowing the increase of fungicide resistance – does rate or type of application matter?

Hilda Dooley[1,2], Steven Kildea[1], Michael W. Shaw[2], John Spink[1]

[1]*Teagasc, Crops, Environment and Land-Use Research Programme, Oak Park, Carlow*
[2]*School of Agriculture, Policy and Development, University of Reading, Whiteknights, Reading, RG6 6A, England*

Septoria tritici blotch (STB), caused by the fungal pathogen *Mycosphaerella graminicola* is the most destructive disease of winter wheat in Ireland. Triazole fungicides are the backbone of STB control for over a decade; however their efficacy has declined in recent years due to changes in the *M. graminicola* population. Consequently, control strategies must adapt in order to maintain control of this pathogen. To assess the impact alternating, mixing and reducing the recommended rates of different triazoles (epoxiconazole and metconazole) has upon the selection of resistant *M. graminicola* and STB control, field trials were conducted at six locations over two years. Disease severity was assessed and sensitivity to epoxiconazole and metconazole was determined for 3977 *M. graminicola* isolates obtained from across all treatments/locations. Data were analysed using ANOVA and REML with contrasts. Disease control was best achieved with the full rate mixture. Averaged over all strategies (solos, alternations and mixtures), the full rates provided better disease control than the half rates. Disease control was positively correlated with a reduction in sensitivity. Populations from all sites were less sensitive to epoxiconazole than metconazole. Contrary to the FRAC resistance management strategy, the half rate treatments reduced selection with the exception of the mixture. In this study, while there was no significant difference between alternating and mixing triazoles, or between alternating and using solo components on selection for resistance, the order in which the fungicides were applied in alternation did affect selection. Given the continuing challenges of STB control to the Irish tillage sector, the findings from these studies will be communicated to stakeholders with the intention of immediate implementation in the field.

Antibiotics and the infant gut microbiota

F. Fouhy[1,2], RP Ross [1,3], GF Fitzgerald [2,3], C Stanton [1,3], PD Cotter [1,3]

[1]*Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork*
[2]*Microbiology Department, University College Cork*
[3]*Alimentary Pharmabiotic Centre, Cork*

The negative impact of antibiotics on the gut microorganisms (microbiota) of infants, i.e. the collateral damage inflicted on commensal strains and the selection for antibiotic resistance, is a cause of considerable concern. By better understanding these impacts, one could minimise these effects through nutritional interventions. We have employed state-of-the-art high-throughput DNA sequencing to study the effects of aminoglycoside and ß-lactam antibiotics on the infant gut microbiota. This technology facilitates a detailed assessment of the microbiota (and contrasts with older approaches whereby only easily cultured gut microorganisms were assessed). The results demonstrated the undesirable increase in *Proteobacteria*, at the expense of generally beneficial *Bifidobacterium* species, following antibiotic therapy. To understand this increase in *Proteobacteria*, we employed a degenerate PCR-based approach to study the sources of aminoglycoside and ß-lactam resistance genes in the healthy gut. The findings highlighted that the gut is a rich source of such genes, particularly amongst members of the *Enterobacteriaceae* (a family within the phylum *Proteobacteria*). These findings explain the ability of *Proteobacteria* to become dominant following antibiotic treatment. To understand why the *Bifidobacterium* population was so dramatically affected by the use of a combination of aminoglycoside and ß-lactam antibiotics, we studied antibiotic resistance genes in the genomes of bifidobacteria. We noted the presence of resistance genes, but established that these protected against aminoglycosides only. These findings highlight the potential benefits of using certain species of *Bifidobacterium* as probiotics in advance of, and during aminoglycoside, therapy, to minimise the negative impacts on the host gut microbiota. Overall, our findings provide a comprehensive insight into the interactions between antibiotics and the human gut microbiota, and the resistance mechanisms which allow particular gut microbes to become dominant. Moreover, our results highlight the benefits of employing bifidobacteria as probiotics to limit the negative impact of aminoglycosides on the gut microbiota.

Organoleptic enhancement of a puffed corn snack using Irish apple pomace

N. O'Shea[1,2], E. Arendt[2], E. Gallagher[1]

[1]Teagasc, Food Research Centre, Ashtown, Dublin 15
[2]Department of Food and Nutritional Sciences, National University of Ireland, Cork

Apple pomace is a by-product of the drinks/beverage industry (e.g. juice and cider). It has been well-documented to contain high levels of fibre, low fat and a rich source of micronutrients such as calcium and magnesium. The Apple Farm (Co. Tipperary) collaborated with Teagasc on this project, donating their apple pomace. The aim of this study was to demonstrate how such a by-product could be utilised as a novel food ingredient in a puffed corn snack. This by-product is normally of little value to the producer. This study investigated the effects of two extrusion parameters (die head temperature and screw speed) and the addition of apple pomace (AP) on a corn-based extruded snack. A D-optimal response surface design was calculated; this generated 21 combinations of the parameters. Error was assessed based on five combinations repeated twice. Extrudate characteristics i.e. bulk density and porosity, textural and acoustic attributes and cooked starch characteristics were examined. Extruder screw speed had the most significant effect on the textural qualities of the extrudate ($p<0.001$). Both AP addition and screw speed impacted the expansion ratio of the product ($p<0.0001$). An acoustic detector was used to determine the crispy/crunchy properties of the snack as it was being deformed by the texture analyser. AP increased the 'crisp' properties of the snack compared to the control, which was found to be 'crunchier' ($p<0.001$). The optimised and validated formulation contained 7.7% AP; it was extruded at 150°C (die head temperature) and with a screw speed of 69 rpm. This study highlighted how "waste" streams from Irish food processing may be utilised in a novel, functional way.

A combination of chemical and ultrasonication treatment to reduce *campylobacter jejuni* on raw poultry

Leonard Koolman[1,2], Joseph Meade[2], Paul Whyte[2], James Lyng[2], Declan Bolton[1]

[1]Teagasc, Food Research Centre, Ashtown, Dublin 15
[2]University College Dublin, Belfield, Dublin 4

Campylobacter jejuni is the most common cause of bacterial gastroenteritis, with poultry regarded as the main vehicle for disease transmission. A recent European Food Safety Authority baseline survey established that approximately 98.3% of Irish broiler carcasses are contaminated with *Campylobacter*. The use of organic acids and other chemicals has been previously investigated as a means of reducing the levels of *Campylobacter* on broiler carcass. However, to our knowledge they have never been studied in combination. This study evaluated the effectiveness of 12% (w/v) trisodium phosphate (TSP), 2% (w/v) citric acid (CA) and 5% (w/v) capric acid (CP) in reducing the levels of *Campylobacter* present on artificially inoculated poultry drumsticks used individually and in combination with one another. The chemical treatments were also used in conjunction with ultrasonication to determine if this combination enhances the decontaminating effect. Total viable counts (TVC) and total *Enterobactericeae* counts (TEC) were also evaluated. Chemical combination treatments resulted in significantly lower counts of *Campylobacter* ($P<0.05$) when compared to control treatments, with reductions of 2 $\log_{10}$ cfu/cm^2 (TSP+CA), 2.1 $\log_{10}$ cfu/cm^2 (TSP+CP) and 3.3 $\log_{10}$ cfu/cm^2 (CA+CP), respectively. TSP combined with ultrasonication (2.7 $\log_{10}$ cfu/cm^2) and TSP+CP combined with ultrasonication (2.8 $\log_{10}$ cfu/cm^2) increased the decontaminating effect. This study further expands our knowledge of the potential use of chemicals as potential decontaminants during poultry slaughter and processing.

From fields to fermentations: characterisation & application of non-dairy cultures in dairy foods

D. Cavanagh[1, 2], K. Kilcawley[1], G. Fitzgerald[2], O. McAuliffe[1]

[1]*Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork*
[2]*Department of Microbiology, University College Cork*

Lactic acid bacteria (LAB) used in cheese manufacture play a pivotal role in the formation of cheese flavour. While the limited numbers of established dairy cultures in use have greatly reduced inconsistencies in cheese quality, it is often at the expense of flavour. LAB isolated from non-dairy environments often exhibit enhanced metabolic capabilities when compared to dairy cultures and have been shown to contribute to flavour diversification in cheese. The objective of this study was to characterise isolates of *Lactococcus* from various non-dairy niches and to evaluate the potential of these strains for use in cheese processing, in terms of flavour enhancement and bacteriophage resistance. In all, 7 *L. lactis* subsp. *cremoris* and 1 *L. lactis* subsp. *lactis* were isolated from various sources including grass, vegetable matter and the bovine rumen. Analysis of the volatile compounds produced when these cultures were grown in milk demonstrated the potential of certain non-dairy strains as flavour developers in cheese. Strains that grew well in milk were selected for further analysis as adjuncts in the production of mini Gouda-type cheeses. Compositional, proteolytic and sensory data highlighted that use of non-dairy lactococci impacted on the sensory character of cheeses, observed as a reduction in bitterness but an increase in production of off-flavours and off-aromas, but did not adversely impact on cheese composition. Isolates were also examined in terms of their bacteriophage susceptibility, and this led to the isolation and identification of a novel lactococcal phage. Phage ΦL47, isolated from sewage, is the largest sequenced lactococcal phage reported to date (128,546 bp) and possesses a long tail fiber not previously reported in phages of this species. Our results to date indicate the potential array of metabolic activities within these non-dairy strains which may be harnessed to produce diverse dairy products with potentially fewer production losses.

Grass utilisation as a driver of efficiency on European dairy farms

P. Gillespie[1,2], C. O'Donoghue[1], T. Hennessy[1], S. Hynes[2], F. Thorne[1]

[1]Teagasc, Rural Economy & Development Programme, Mellows Campus, Athenry, Co. Galway
[2]J.E. Cairnes School of Business and Economics, National University of Ireland, Galway

Agricultural policy reform in Europe has led to a more market orientated outlook for livestock production systems in the European Union. Research into effective and efficient management of grass swards suggests that improved grassland management practices may be a viable alternative to more intensive production strategies. We analyse the effect of grass utilisation in dairy systems on enterprise level efficiency, examining the hypothesis that the choice of a higher level of grass input results in a greater level of efficiency. Our analysis is conducted using panel data from the Farm Accountancy Data Network for a selection of countries showing a good variety of input systems, biogeographic zones and levels of intensity. We estimate panel frontier functions and predict the effect of increased grass utilisation on efficiency levels using the single step variant of the Stochastic Frontier model. We find that the sign and magnitude of increased grass utilisation varies across Member States. The type of efficiency measured, *i.e.* technical efficiency or cost efficiency, also has important implications for the magnitude of the grass measure's effect. This underscores the importance of behavioural assumptions underpinning the analysis. If our interest is in grass utilisation's effect on least cost modes of production, then the cost frontier model is more appropriate, but if we wish to describe how grass utilisation helps or hinders farmers in attaining their business goals efficiently, then we must stop at the production frontier model.

Supporting problem focused innovation: the creation of an innovation broker

C. Ryan[1,2], K. Heanue[1], F. Devitt[2]

[1]Teagasc, Rural Economy Research Centre, Mellows Campus, Athenry, Co. Galway
[2]Department of Design Innovation, National University of Ireland, Maynooth, Co. Kildare

Mastitis control on dairy farms is a substantial cost for the Irish dairy sector. The national mastitis control programme – CellCheck-undertakes ‘a new approach to tackling an old problem’ on the basis that knowledge on best practice in mastitis control exists; the challenge is bringing these practices into use. The activities of CellCheck at farm level centre on multidisciplinary service providers working together to disseminate clear consistent information on best practices in mastitis control. The activities of service providers to address the challenge of mastitis control in the dairy sector can be viewed as a problem focused innovation system. To promote interaction and networking among stakeholders, CellCheck established seven regional coordinators identifiable as innovation brokers. Drawing on the innovation brokering literature, the study undertakes a longitudinal analysis of the activities of newly appointed innovation brokers in CellCheck to contribute new theoretical knowledge on the creation of an innovation broker and inform CellCheck activities to support the network of innovation brokers. A case study approach is employed using semi-structured interviews, observations and secondary data analysis. Findings show the fulfillment of functions required of an innovation broker is a process of trial and error. The diffusion of innovation brokering practices occurs through interaction with peers and industry stakeholders. Furthermore, the approaches undertaken by the innovation brokers differ, reflecting the specific characteristics of the dairy regions in which they operate. The findings support the value in establishing a peer networking group to provide a platform for newly appointed innovation brokers to share and reflect on experiences and facilitate learning. In addition, prior analysis of the context is needed to guide provision of appropriate support to help an incoming innovation broker address context specific challenges to the fulfillment of innovation brokering functions.

POSTER ABSTRACTS

The relationship between nitrogen isotopic fractionation and nitrogen-use efficiency in parent and progeny pairs

N.M. Wheadon[1,2], R.J. Dewhurst[1], G.R. Edwards[2]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath
[2]Faculty of Agriculture and Life Sciences, P.O. Box 84, Lincoln University, New Zealand

In this study we evaluated the suitability of nitrogen (N) isotope fractionation ($\delta^{15}N$) as an indicator of nitrogen-use efficiency (NUE; Milk N g/d / Feed N g/d) and the heritability of these measurements in parent and progeny pairs. Feed intake of 17 mother and daughter Holstein-Friesian and Holstein-Friesian × Jersey cross pairs were recorded for 5 consecutive days by offering access to cut herbage *ad lib* daily for a 5 hour period. Samples of milk, urine, faeces, blood and pasture were collected for composition and metabolite analysis and isotope ratio mass spectrometry to determine the ratio of isotopes N^{-14} to N^{-15}. Linear regression and ANOVA were used to analyse the relationship between NUE and $\delta^{15}N$ and the influence of genetic and animal factors and differences between mothers and daughters. Pearson correlations were used to measure heritability coefficients (h^2) for various efficiency and production traits ($h^2 = r_{obs}/r_{exp}$; expected r = 0.5). Live weight, dry matter intake and milk yield averaged 440 (kg), 11.72 (kg/d) and 13.21 (kg/d) and average NUE was 0.28 (g/g). Average $\delta^{15}N$ milk, plasma, urine and herbage were 5.28 ‰, 5.12 ‰, -1.30 ‰ and 2.38 ‰ respectively, resulting in the enrichment ($\Delta^{15}N$; milk or plasma $\delta^{15}N$ - herbage $\delta^{15}N$) of body tissues by 2.90-3.00‰ units. There was a significant negative relationship between NUE and milk, plasma, urine $\delta^{15}N$ and $\Delta^{15}N$. Within groups NUE had a weak relationship with milk urea N (mmol/d), plasma urea N (mmol/l) and urine metabolites including purine derivatives. There was a significant group effect and there were significant differences between pairs of animals, however between mothers and daughters there was no significant difference between isotope or metabolite measurements. Heritability coefficients between mothers and daughters were high for some traits but there was a large range within traits and inconsistency between sample days and groups. N isotopes may be useful as general indicators of NUE, however both the efficiency trait and predictors are influenced by a number of animal (genetic) and environmental factors which causes high variation between animals. Heredity relationships need further investigation with a larger sample size.

Body composition, carcass traits and visceral organ weights of bulls differing in residual feed intake

C. Fitzsimons[1,2], D.A. Kenny[1], A.G. Fahey[2], M. McGee[1]

[1]*Teagasc, Animal and Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[2]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*

Residual feed intake (RFI) is a feed efficiency trait with potential to reduce feed costs, however, relatively little is known about factors contributing to variation in RFI. The objective of this study was to characterise body composition, carcass traits and visceral organ weights of beef bulls differing in phenotypic RFI offered concentrates *ad libitum* for 105 days pre-slaughter. Individual dry matter intake (DMI) and growth were measured in a total of 67 Simmental bulls [mean initial live weight 431 kg (SD=63.7)] over three years. Beginning and end of trial ultrasonic muscle and fat depth were determined. After slaughter, carcasses and perinephric and retroperitoneal fat were weighed, carcasses were graded for conformation and fat score and weight of non-carcass organs were determined. Individual RFI was computed as actual minus expected DMI, with bulls assigned to high (inefficient), medium or low groupings. High RFI bulls consumed 7% and 14% more than medium and low RFI bulls, respectively ($P < 0.001$). Ultrasonic muscle and fat depth, slaughter weight, carcass weight, perinephric and retroperitoneal fat weight, carcass conformation and fat score, and kill out proportion did not differ ($P > 0.05$) between high and low RFI groups. No differences ($P > 0.05$) between RFI groups were detected for weight of non-carcass organs except for reticulo-rumen empty ($P = 0.05$), which was 8% lighter for low compared to high RFI bulls. Given its large metabolic activity, the lighter reticulo-rumen may be reducing maintenance energy requirements in the low RFI bulls.

Perennial ryegrass digestibility

Marion Beecher[1,2],Eva Lewis[1], Tommy Boland[2], René Baumont[3], Michael O'Donovan[2]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co Cork
[2]School of Agriculture and Food Science, UCD, Belfield, Dublin 4
[3]INRA, UMR1213 Herbivores, F-63122 Saint Genès Champanelle, France

Grazed grass and grass utilisation are key components of profitability in Irish ruminant production systems. The production and utilisation of high quality grass is essential to achieve the 50% increase in milk production targeted by Food Harvest 2020. This research focused on increasing our knowledge of perennial ryegrass digestibility in dairy cows. A study investigating different dairy cow genotypes found that Jersey cows have a greater capability to digest perennial ryegrass compared with Holstein Friesian cows. The differences in digestibility are driven by differences in feeding behaviour, rumen capacity and rumen microbial populations between the genotypes. Another study investigated the change in proportion and chemical composition of plant components throughout a grazing season. The different components of grass vary in their digestibility and are ranked in the following order: leaf > pseudostem > true stem > dead. Leaf is the dominant component of the sward, but the true stem increases in May/June and the dead material increases in February, at the expense of leaf content. Focusing on increasing the leaf proportion in the sward can lead to higher sward digestibility. An investigation into the effect of pre-grazing herbage mass on digestibility using the total collection method found that pre-grazing herbage mass swards of 1000 kg DM/ha gave rise to higher intakes and higher digestibility than swards with a pre-grazing herbage mass of 3000 kg DM/ha, reflecting the premise that low pre-grazing herbage mass swards contain more leaf and less stem and can lead to increased production in dairy cows. Therefore choice of cow breed coupled with a greater focus on grassland management techniques to maintain low pre-grazing herbage mass swards with high leaf proportion can help achieve the increased milk production targeted by Food Harvest 2020.

The effect of post-grazing sward height on dairy cow performance and sward characteristics

Elodie Ganche[1,2], E. Kennedy[1], T. Boland[2], M O'Donovan[1], L.Delaby[3]

[1] *Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2] *University College Dublin, Belfield, Dublin 4*
[3] *Institut National de Recherche Agronomique, 35590 St Gilles, France*

The objective of this study was to investigate the immediate and carryover effects of post-grazing sward height (PGSH) as a grassland management tool on dairy cow performance and sward characteristics. This was achieved by imposing three PGSH (2.7, 3.5 and 4.2 cm) for 10-weeks directly post-calving in early spring. A PGSH of 2.7 cm maximised grass utilisation but reduced subsequent pasture dry matter (DM) production when compared to all other treatments. Cows grazing to 2.7 cm in early spring had reduced milk yield and component concentrations and greater bodyweight loss. Increasing PGSH from 3.5 to 4.2 cm did not increase the 10-week cumulative milk yield but reduced grass utilisation over this period. Early spring treatment had no carryover effect on subsequent (April – November) milk production, indicating that the dairy cow can recover from a short-term nutrient deficit in early lactation. Cows grazing to 2.7 cm in early spring, however, had significantly lower cumulative lactation milk solids yield when compared to cows grazing to 3.5 or 4.2 cm. Following spring, cows were re-randomised within treatment and grazed to either 3.8 or 4.8 cm until the end of the grazing season (November). A PGSH of 3.8 cm increased sward leaf content but reduced pasture DM production. Cows grazing to 4.8 cm achieved a higher energy intake and therefore greater milk and milk solids yields. The results indicate that a PGSH of 3.5 cm in early spring should be targeted to achieve the best compromise between animal performance and grass utilisation. From mid-season onwards, PGSH should be increased to approximately 4.8 cm to maximise milk production per cow while maintaining high pasture productivity and nutritive value. Ultimately this work delivers grazing management guidelines to Irish farmers that will help achieve the 50% increase in milk production outlined in the Food Harvest 2020 Report.

Bioeconomic modelling of pasture based dairy calf-to-beef production systems in Ireland

A. Ashfield[1,2], P. Crosson[1], M. Wallace[2]

[1]*Teagasc, Animal and Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[2]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*

With the abolition of EU milk quotas in 2015, the Irish dairy sector is positioning itself for substantial expansion which will also result in an increase in calves from the dairy herd becoming available for beef production. A wide range of beef systems are possible for these extra calves reflecting differences in breed, gender and finishing age. The Grange Dairy Beef Systems Model (GDBSM) was developed and used to simulate beef production from male and female calves born to Holstein-Friesian dairy cows bred to late maturing, early maturing and Holstein-Friesian sires and finished at different ages. The model is a whole-farm, static, single-year deterministic model and operates with a monthly time-step. There are four sub models; farm systems, animal nutrition, feed supply and economics. Scenario analysis was conducted involving the economic assessment of production systems finishing: 1) Holstein-Friesian progeny as steers at 24 and 28 months of age and bulls at 16 and 19 months of age; 2) late maturing progeny as steers at 24 and 28 months of age; bulls at 16 months of age and heifers at 21 months of age and 3) early maturing progeny as steers at 20, 22 and 28 months of age and heifers at 19 months of age. The most profitable system was finishing steers at 28 months of age because of the high percentage of live weight gain from grass. The least profitable system was finishing male animals as bulls at 16 months of age due to the high requirement for concentrate feeding. All systems were sensitive to beef, calf and concentrate price variations. The main drivers of profitability were found to be maximising the proportion of grazed grass in the diet and percentage of live weight gain from grass while also maintaining a high carcass output per hectare.

Effect of feed restriction and compensatory growth on the somatotropic axis in Holstein Friesian bulls

K. Keogh[1,2], D.A. Kenny[1], A.K. Kelly[2], A.R.G. Wylie[3], S.M. Waters[1]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath
[2]School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4
[3]Agri-Food and Biosciences Institute, 18a Newforge Lane, Belfast, BT9 5PX

Compensatory growth is the ability of an animal to undergo accelerated growth after a period of restricted feeding. The objective of this study was to characterise the effect of feed restriction and a period of compensatory growth on the somatotropic axis. 60 Holstein Friesian bulls were blocked into one of two groups: (i) restricted feed allowance for 125 days (Period 1) (RES; n=30) followed by *ad libitum* feeding for 55 days (Period 2) or (ii) *ad libitum* access to feed throughout (ADLIB; n=30). On day 89 of Period 1 and 35 of Period 2, a growth hormone releasing hormone (GHRH) challenge was performed. At the end of each period, 15 animals from each treatment were slaughtered and hepatic tissue collected. Total RNA was extracted from hepatic tissue, with the expression of component genes of the somatotropic axis and reference genes then measured using qRT-PCR. Data were statistically analysed using the mixed procedure of SAS, with terms for treatment, period and their interaction included in the model. Average daily gain (ADG) for Period 1 was 0.6 kg/d for RES and 1.9 kg/d for ADLIB. During Period 2, ADG was 2.5 and 1.4 kg/d for RES and ADLIB respectively. There was no difference ($P>0.05$) between treatment groups in growth hormone response following GHRH challenge, however, IGF-1 response was greater in ADLIB animals in Period 1 ($P<0.05$). Treatment x period interactions ($P<0.05$) were evident for *IGF-1, IGFBP2*, and *GHR1A*, with higher expression of *IGFBP2* and lower expression of *IGF-1* and *GHR1A* observed in RES compared with ADLIB during Period 1. The documented difference in IGF-1 response to GHRH challenge given no difference in growth hormone response indicate uncoupling of the somatotropic axis following feed restriction, which may potentially be mediated through a reduction in the expression of *GHR1A* in the liver.

Heterogeneity in mammalian cell adherence and invasion among mastitis-associated S. aureus

Kathleen E. Budd [1,3], Jennifer Mitchell [3], Finola McCoy[2], Orla M. Keane[1]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath
[2]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[3]School of Veterinary Medicine, University College Dublin, Belfield, Dublin

Staphylococcus aureus is an important pathogen associated with veterinary disease and is a common cause of bovine mastitis. S. *aureus* expresses a number of surface proteins which facilitate adherence to host tissues and mediate internalisation in non-professional phagocytes and the subsequent ability to evade host defence mechanisms and antibiotic therapy. S. *aureus* isolates (n=137) were recovered from milk samples collected over a one year period from cattle displaying symptoms of clinical mastitis. The genetic diversity of the isolates was characterised by Multi Locus Sequence Typing (MLST) analysis which identified 55 different sequence types (ST), of which 46 were novel, demonstrating a large array of genetic diversity. Groups of related genotypes were identified using the eBURST algorithm with five CCs identified - CC5, CC1, CC151, CC97 and ST71. Some isolates did not cluster including those belonging to Sequence Type 136 and a small number of singletons. The ability of the isolates to adhere to and invade bovine mammary epithelial cells (Mac-T) was determined by flow cytometric analysis. Mac-T cells stained with DAPI were infected with Calcein AM stained S. *aureus* at a Multiplicity of Infection of 10:1 for 3 hours. Externally adherent S. *aureus* were stained and analysed on the Attune cytometer. Between 4-10% of the initial S. *aureus* inoculum, adhered to the mammalian cells while between 0.1 and 4% internalised within the cells. Despite the relatedness of isolates within a clonal complex at the core genome level, phenotypic differences between isolates within a CC were observed in mammalian cell adherence and internalisation. Differences in the variable genome of these isolates may be responsible for these phenotypic differences.

Effect of grass white clover swards on dairy cow feeding behaviour, rumen function and milk production

D. Enríquez-Hidalgo[1,2], T.J. Gilliland[3], M. O'Donovan[1], C. Elliott[2], D. Hennessy[1]

[1]*Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2]*Queen's University Belfast*
[3]*AFBI, Plant Testing Station, Crossnacreevy, Belfast*

Grass-white clover (GWc) swards will become more common due to price increases of and environmental concerns regarding N fertiliser application. The effect of grass-only (GO) and GWc swards on dairy cow feeding behaviour, rumen function, methane (CH_4) emissions and milk production was investigated. Thirty cows were allocated to GWc or GO swards (n=15 per treatment) from April to October. Milk (MY) and milk solids (MSY) yields were measured. Eight rumen-cannulated cows were arranged into four 2 (treatment) × 2 (14-d periods) Latin Squares and allocated to each treatment in May, July and September. Feeding behaviour, rumen volatile fatty acids (VFA) and pH were measured. In September, five additional cows were added to each treatment (n=20) to estimate CH_4 emissions. Annual GWc sward clover content was 20% (7.5, 8.8 and 30.9% in May, July and September). Cows had similar MY (19.4 kg/d) and MSY (1.49 kg/d). In May and September cows had similar grazing times (9.8 h/d). In July GWc cows tended to graze 0.9 h/d less than GO cows (11.2 h/d; $P=0.07$). In September, GWc cows spent less time ruminating than GO cows (7.7 and 6.6 h/d, respectively; $P<0.01$). Cows had similar VFA (128 mmol/l). In September rumen pH was higher for GWc (6.16) than GO cows (6.00; $P<0.05$). Absolute CH_4 emissions were similar (357 g CH_4/d), but GWc cows had lower CH_4 emissions yield than the GO cows (21.5 and 24.5g CH_4/kg of DMI, respectively; $P<0.05$). GWc swards did not affect MY and MSY compared to GO swards and only resulted in a small CH_4 yield reduction. GWc swards influenced cow feeding behaviour and rumen characteristics with increased effect as the season progressed.

Management of dictyocaulus viviparus, ostertagia ostertagi and fasciola hepatica on Irish dairy herds

Yris Bloemhoff[1,4], Andrew Forbes[5], Martin Danaher[2], Barbara Good[3], Eric Morgan[6,] Grace Mulcahy[4], Ríona Sayers[1]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2]Teagasc, Food Research Centre, Ashtown, Dublin 15
[3]Teagasc, Animal & Grassland Research and Innovation Centre, Athenry, Co.Galway
[4]University College Dublin, School of Veterinary Medicine, Belfield, Dublin 4
[5]Merial, 29 Avenue Tony Garnier, 69007 Lyon, France
[6]School of Biological Sciences, University of Bristol, Woodland Road, Bristol, BS8 1UG, UK

Parasites such as *Dictyocaulus viviparus*, *Ostertagia ostertagi* (nematodes) and *Fasciola hepatica* (trematode) negatively impact on productivity and health of dairy animals. *F. hepatica* alone is estimated to cost Irish farmers €90M annually. Currently, prevalence and management data relating to these parasites in Irish dairy cows is limited. The objective of this study, therefore, was to address this deficit. In 2009, management data (questionnaire) and four quarterly bulk milk samples were collected from 305 dairy farms. Samples were tested by ELISA for antibodies against *D. viviparus* (Fiedor et al., 2009), *O. ostertagi* (Svanova) and *F. hepatica* (UCD). The overall apparent prevalence of *D. viviparus* (64.1%), *O. ostertagi* (99.0%) and *F. hepatica* (74.7%) was higher than previously reported in an Irish cull cow study. Effective control measures in dairy cows are therefore essential, but were not found to be optimal. Univariate and multivariate regression analysis (PROC GENMOD, SAS) identified demographic and management risk factors for increased prevalence of parasitic infestation. While 58.7% and 64.8% of dairy herds were treated for nematodes and *F. hepatica*, respectively, a third of farmers used products ‘unsuitable for purpose’ for control of nematodes. Ivermectin (48.6%) and triclabendazole (40.2%) (prior to flukicide restrictions) were the most popular treatments for nematodes and *F. hepatica* respectively. Albendazole was more likely to be used by herds in southern regions for both nematodes (p=0.0003) and *F. hepatica* (p=0.0129) compared to western and eastern regions. Pasture management has evolved considerably in Ireland, but parasitic pasture systems have not kept pace with over 80% using traditional sub-optimal dose and move systems. Research updates, such as the study outlined here, are vital in continuously monitoring farming practices relating to parasite management, to arm farmers and their service providers with current data to inform optimal control.

Identification and ranking of microRNA binding sites of seven cattle breeds for gene association studies

Martin Braud[1,2], Dermot Morris[1], David MacHugh[3], Tad Sonstegard[4], Charles Spillane[2]

[1] Teagasc, Animal & Grassland Research and Innovation Centre, Athenry, Co. Galway
[2]Genetics & Biotechnology Lab, Plant & AgriBiosciences Research Centre (PABC), School of Natural Sciences, National University of Ireland, Galway
[3]Animal Genomics Laboratory, School of Agriculture, University College Dublin
[4]Bovine Functional Genomics Laboratory, USDA-ARS, Beltsville, USA

MicroRNAs (miRNA) are small non-coding RNAs which have strong regulatory effects on targeted genes. In mammals, miRNAs predominantly target miRNA binding sites located within the 3'UTR of messenger RNA. miRNA targeting of miRNA binding sites can lead to mRNA degradation and/or inhibition of protein synthesis. Where genetic variation in either miRNA genes or miRNA binding sites exists between individual cattle or cattle breeds there is potential for such variation to be associated with economic traits in cattle. The identification of Single Nucleotide Polymorphisms (SNP) in miRNA genes (or in the miRNA binding sites in the 3'UTR of targeted genes) could facilitate improvements in cattle breed selection where such SNPs are associated with economically important traits in cattle. We used SNP data provided by USDA which was obtained from resequencing of 45 cattle genomes from seven different breeds (dairy: Holstein, Jersey; beef: Angus, Romagnola, Limousin; dual-purpose: Fleckvieh, N'Dama). By comparing the SNP variation across all 3'UTRs, we identified 3401 SNPs located in a total of 1747 3'UTRs. Using Targetscan software we identified the miRNA binding sites within each polymorphic 3'UTR. This revealed that 576 cattle genes contain polymorphic miRNA binding sites in their 3'UTRs. For each miRNA predicted to bind to a given 3'UTR, TargetScan provided a quality score. We used a combination of these scores to devise an overall score for each gene, which allowed the development of an objective ranking system to identify which genes contain 3'UTRs which have undergone the most significant changes in terms of miRNA binding site polymorphism. The top-ranked miRNA binding sites in cattle will be used for genomic selection via gene association studies across 1000s of dairy and beef cattle. This will determine the extent by which miRNA variation subjected to artificial selection contributes to economic traits in beef and dairy cattle.

Hepatic miRNAome profile of the early postpartum dairy cow and effects of severe negative energy balance

Attia Fatima[1,3], David Lynn[2], Padraig O'Boyle[1], Sinead Waters[2], Cathal Seoighe[3], Dermot Morris[2]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Mellows Campus, Athenry, Co. Galway
[2]Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Co Meath
[3]School of Mathematics, Statistics and Applied Mathematics, National University of Ireland, Galway

For many years it was thought that only around 2 percent of the genome was functional or coding while 98 percent of the genome or non-coding region was considered as non-functional. The discovery in the last decade that microRNAs (miRNAs), a class of small non-coding RNAs, are key regulators of gene expression together and recent miRNA expression-profiling studies in domestic livestock have revealed their tissue specific and temporal expression pattern. In addition, single nucleotide polymorphisms (SNPs) in either the miRNA or in the target mRNA binding sites have revealed associations with traits of economic importance and their potential importance in future genomic selection programmes. Increased energy demands to support lactation, coupled with lowered feed intake results in negative energy balance (NEB) in the early postpartum cow. In previous studies we have shown that severe NEB (SNEB) has pleiotropic effects on gene expression in the liver, spleen and uterus of the early postpartum dairy cow. The objectives of this study was to examine the liver miRNAome of the dairy cow in the early postpartum and to investigate how changes in liver gene expression as a result of SNEB are mediated by changes in miRNAs. The liver miRNAome was found to express a total of 53 annotated miRNAs and dominated by miR-122 that accounted for 78% of all the expressed miRNAs. One miRNA was down-regulated while five were up-regulated as a result of SNEB. Their putative target genes differentially expressed under SNEB are associated with important metabolic pathways including glucose, amino acid and lipid metabolism and homeostasis. *FADS2*, a critical lipogenic enzyme down-regulated under SNEB is a putative target of miR-2885. This novel study provides the first miRNA profile of the dairy cow liver under SNEB and a possible link between differentially expressed miRNAs and important metabolic genes differentially expressed during NEB.

Presence of *Salmonella*, *N. caninum* and *L. hardjo* in Irish dairy herds

E. O' Doherty [1,2], D.P. Berry[1], L. O' Grady[2], R. Sayers[1]

[1]*Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2]*School of Veterinary Medicine, UCD Veterinary Sciences Centre, University College Dublin, Belfield, Dublin 4*

The clinical and sub-clinical manifestations of infections due to *Salmonella*, *Neospora caninum* and *Leptospira interrogans* serovar *hardjo* (*L. hardjo*) on dairy farms can result in serious economic losses. Bulk milk analysis and questionnaire surveys were, therefore, used in 2009 to document exposure to these pathogens and provide data on management factors, including vaccination status, for risk factor analysis using logistic regression. Associations between bulk milk antibody levels and performance parameters were also quantified. The prevalence of *Salmonella, N. caninum*, and *L. hardjo*, were 49%, 19%, and 86%, respectively. Contact with animals both between and within herds was associated with a greater likelihood of testing positive for exposure to both *Salmonella* and *L. hardjo*. Access to watercourses that passed through other farms was associated with testing positive for exposure to *Salmonella*. Year-round calving, earlier housing of cows, and the presence of non-secure farm boundaries were associated with a greater likelihood of testing positive for exposure to *N. caninum*. Herds that tested positive for exposure to both *N. caninum* and *L. hardjo* had compromised reproductive performance. Relative to cows in herds negative for exposure to *Salmonella*, cows in positive herds, irrespective of parity, had lower milk production. A greater prevalence of young-calf mortality and mortality amongst animals over 12 months of age was evident in herds bulk milk positive for exposure to *Salmonella* and *N. caninum*, respectively.

The results highlight that the implementation of biosecurity measures and management practices relating to these pathogens are sub-optimal on Irish dairy herds. The results also highlight that exposure to these pathogens resulted in sub-optimal performance in Irish dairy herds. The information from this study will therefore prove to be of enormous benefit in designing appropriate control programmes for these pathogens leading to optimisation of herd health and performance in Irish dairy farms.

Lameness prevalence in replacement gilts and sows and the effect of gilt nutrition as a mitigation measure

A.J. Quinn[1, 2], L.E.Green[2], P.G. Lawlor[1], L.A. Boyle[1]

[1]*Teagasc Pig Development Department, Animal & Grassland Research & Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2]*Life Sciences, University of Warwick, Coventry, CV4 7AL, England*

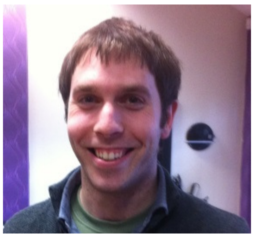
Lameness in pigs is a major health and welfare concern and a cause of poor longevity and productivity. Inappropriate nutrition of replacement gilts is a major risk factor. This project firstly aimed to determine the prevalence of lameness in replacement gilts and sows by conducting a cross-sectional survey of 69 Irish pig farms. It was determined that 39% of replacement gilts and 48% of loose housed sows were lame. This project also evaluated the effect of feeding a diet specially formulated for replacement gilts (i.e. a developer diet=D) with a gestating sow (G) and a finisher (F) diet on several indicators of limb health: locomotory ability, claw lesions, limb lesions, joint lesions, bone mineral density and pig behaviour. Indicators were firstly compared in individually-housed limit fed gilts (Study 1) followed by group housed gilts which were *ad libitum* fed (Study 2). In Study 1, D gilts had a lower risk of lameness, uneven claw size and joint cartilage lesions than F and G gilts. In Study 2, D gilts had a lower risk of lameness than F and G gilts and D gilts had a lower risk of claw lesions and uneven claw size than G gilts. There was no effect of treatment on bone mineral density or behaviour. This project illustrated that lameness is highly prevalent and that feeding a diet specifically formulated to take the nutritional requirements of gilt development into account can lead to reduced levels of lameness and improved joint and claw health when compared to diets that are formulated for gestating sows and finisher pigs. This could reduce current lameness levels and ultimately improve sow longevity to help overcome current high culling rates on Irish pig farms.

Closing the farm nitrogen balance at Solohead research farm

W. Burchill[2, 3], D. Li[4], G. Lanigan[1], M. Williams[3] and J. Humphreys[2]

[1]Teagasc, Crops, Environment and Land Use Research Centre, Johnstown Castle, Wexford
[2]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[3]Trinity College Dublin
[4]Institute of Subtropical Agriculture

Irish grass-based systems are highly reliant on the input of fertiliser N and tend to have relatively high farm-gate N surpluses (N imports minus N exports passing though the farm gate). Despite high N surpluses, losses of nitrate-N to water are not particularly high from Irish grass-based dairy systems. Where substantial N surpluses do not lead to high nitrate-N losses to water, it raises the question: what happens to the remaining surplus N? The objective of this study was to quantify all N flows on a white clover based system of dairy production at Solohead Research farm from January 2011 to December 2012 and to account for surplus N. The system was rotationally grazed by Holstein-Friesian cows at a stocking density of 2.35 cows ha^{-1} and received annual fertiliser N input of 112 kg ha^{-1}. Biological N fixation (BNF) was quantified using two ^{15}N isotope techniques. A ^{15}N gas flux and static chamber method were used to quantify N_2 and N_2O emissions, respectively. Inputs (fertiliser N, BNF, feed and rainfall deposition) and outputs (Milk and livestock sales) of N (kg ha^{-1}) from the system were 274 and 80 respectively, with a farm-gate surplus of 194 kg ha^{-1} in 2011. Total measured N losses (kg ha^{-1}) were 246 including 19, 43, 25, and 159 as N lost to water, NH_3, N_2O and N_2, respectively. These N losses were increased by the release of N from soil organic matter (N mineralisation) which resulted in total measured N losses being higher than the farm-gate N surplus in 2011. Although there are high N surpluses associated with Irish dairy farms, the results of the present study indicate that a large proportion of these surpluses are returned to the atmosphere as environmentally benign N_2 gas.



MicroRNAs are amplifiers of monocyte inflammatory networks and repressors of metabolism

Nathan Lawless[1, 2], Timothy A. Reinhardt[3], Kenneth Bryan[1], Mike Baker[4], Bruce Pesch[3], Duane Zimmerman[3], Kurt Zuelke[3, 5], Tad Sonstegard[6], Cliona O'Farrelly[2], John D. Lippolis[3], David J. Lynn [1]

[1]*Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[2]*School of Biochemistry & Immunology, Trinity College, Dublin 2*
[3]*USDA-ARS, National Animal Disease Center, Ames, IA, 50010 USA*
[4]*Iowa State University, DNA Facility, Molecular Biology Building, Ames, IA, 50010 USA*
[5]*Australian Animal Health Laboratory, CSIRO, 5 Portarlington Rd, East Geelong VIC 3219, Australia*
[6]*USDA-ARS, 10300 Baltimore Avenue, Bldg 200 BARC-East, Beltsville, MD, 20705-1350, USA*

Bovine mastitis is an infectious disease of the mammary gland costing the global dairy industry several billion dollars per annum. Here, we report an integrative multi-omic approach to profile mRNA and miRNA transcriptional change at 0, 12, 24, 36, & 48 hours in milk and blood CD14+ monocytes from Holstein-Friesians infected in vivo with *Streptococcus uberis*. Hierarchal clustering of genes from milk isolated monocytes (MIMs) revealed that the control and infected animals clearly separated at 36 and 48hpi. In MIMs, 2,056 and 1,721 genes were up- and down-regulated, respectively, at a minimum of one of the time-points following S. *uberis* infection. In blood isolated monocytes (BIMs), however, we also observed a subtle but significant response to infection. 83 genes were up-regulated in BIMs by 48hpi. Pathway analysis revealed that up-regulated genes in MIMs were significantly enriched for roles in inflammatory and other innate immune pathways (e.g. TLR, NLR and RIG-I signalling), while down-regulated genes were significantly associated with metabolic pathways. InnateDB network analysis of differentially expressed (DE) genes revealed that contextual hubs were highly enriched for roles in innate immunity (FDR $< 1.16E^{-12}$). The majority of the top 20 contextual hubs were well known transcriptional regulators of innate immunity (e.g. CREBBP, EP300, IRF1, IRF9, JUN, NFKB1, REL, RELA, STAT1, STAT3). Genes up-regulated in BIMs showed a significant association with interferon and chemokine signalling. Twenty-six miRNAs were DE in response to infection in milk monocytes, with 4 miRNAs found to be DE in BIMs. Pathway analysis revealed that predicted targets of down-regulated miRNAs were highly enriched for roles in innate immunity (FDR $< 3.4E^{-8}$) in particular TLR signalling, while up-regulated miRNAs preferentially targeted genes involved in metabolism. We conclude that during S. *uberis* infection miRNAs are key amplifiers of monocyte inflammatory response networks and repressors of metabolism.

Identifying sources of genetic resistance to M. graminicola in wheat

Aoife O' Driscoll[1], John Spink[1], Fiona Doohan[2], Ewen Mullins[1]

[1]*Teagasc, Crops, Environment and Land-Use Programme, Oak Park, Carlow*
[2]*School of Biology and Environmental Science, UCD, Dublin*

Septoria tritici blotch (anamorph: *Mycosphaerella graminicola*) is the most important disease of winter wheat in Ireland with farmers heavily reliant on fungicides to preserve yields. The problem is further compounded by the emergence of fungicide-resistant isolates, and thus a severe lack of efficacy exists for these products. In light of this, we are conducting a gene discovery programme in wheat, with the goal of isolating genes that could provide effective resistance to *M. graminicola*. Transcript abundances in the *M. graminicola* inoculated and mock-inoculated wheat cultivars Stigg (resistant) and Gallant (susceptible) were analysed at 0, 1, 4, 8, 12 and 14 days after inoculation (dai) using the Affymetrix^{TM} 61k Wheat Gene Chip Array. Preliminary analyses indicate that up to 1,762 transcripts were differentially expressed. Higher levels of gene activity occurred in Gallant in comparison to Stigg across all time points, with peak expression occurring at 12 dai. An early, mostly basal defence response occurred at both 1 and 4 dai. By 8 dai, the level of *M. graminicola* responsive induced genes increased 2-fold for Stigg and 25-fold for Gallant. This response lasted for ca. 5 days due to *M. graminicola* infecting and degrading the plant RNA, indicated by the number of *M. graminicola* genes expressed in the plant tissue at 14 dai. Thus, evidence exists for the presence of a temporal defence reaction against *M. graminicola* in wheat. RT-PCR will be carried out for specific gene sets across varieties and time points, allowing us to trace possible defence mechanisms and associated genes. Specific genes of interest include OPI10, LOX6 and members of the ERF family which were found to be differentially expressed in both cultivars upon pathogen infection. This research, combined with phenotypic studies in field and glasshouse environments will help not only to understand changes in the wheat transcriptome during *M. graminicola* infection, but also to identify potential targets for development of disease control strategies.

Impact of agronomic practices of an intensive dairy farm on nitrogen concentrations in a karst aquifer in Ireland

M. Huebsch[1,4*], B. Horan[1], P. Blum[4], K.G. Richards[2], J. Grant[3], O. Fenton[2]

[1]Teagasc, Moorepark, Fermoy, Co. Cork
[2]Teagasc, Environmental Research Centre, Johnstown Castle, Co. Wexford
[3]Teagasc, Kinsealy Research Centre, Dublin
[4]Karlsruhe Institute of Technology (KIT), Institute for Applied Geosciences (AGW), Kaiserstr. 12, 76131 Karlsruhe, Germany
**Corresponding author: manuela.huebsch@kit.edu*mailto: *(+49 721 60845017)*

Correlation of nitrate (NO_3^-) occurrence in groundwater with nitrogen (N) applications resulting from intensive agriculture sited on thin free draining soils and karstified limestone are often difficult and therefore avoided. This is unfortunate as groundwater NO_3^- concentrations in these environments react quickest to farm management changes, thereby offering farm managers and policy makers a tool to test the success of legislation implementation. The objective of the current study was to evaluate local weather conditions, (hydro-)geological site characteristics and detailed agronomic N-loadings with groundwater NO_3^- occurrence using a statistical tool. During the study period (2002–2011) NO_3^- concentrations in 11 wells were monitored as well as paddock-specific farm management practices. The statistical analysis involved a multiple linear regression with automatic variable selection. Four scenarios were created to compare paddock specific changes to groundwater wells while using topographic and hydrogeological assumptions of a tracer test and a geoelectric survey. In addition, a time lag from source to groundwater of up to 3 years was considered. Results indicated that site specific characteristics such as soil and unsaturated zone thickness, hydrogeological connections of wells, local weather conditions such as rainfall, sunshine, soil moisture deficit and improved best management practices all influenced NO_3^- occurrence in groundwater. In particular, results suggested that agronomic practices became more important after a time lag of 1 to 2 years and agronomic practices such as: reductions in inorganic fertiliser application, changes of timing of slurry application, the relocation of a dairy soiled water irrigator to a less karstified area and the implementation of minimum cultivation reseeding instead of ploughing, led to reduced NO_3^- occurrence in the aquifer. The present approach is a suitable tool to elucidate the consequences of agronomic practices on groundwater quality and can be used in vulnerable areas for the assessment of present and future legislation implementation.

An assessment of sitka spruce growth phenology on provenances used in Ireland

N. O Neill[1,2], N. Farrelly[1], C. O' Reilly[2], O. Grant[2]

[1]Teagasc, Forestry Development Department, Mellows Campus, Athenry, Co. Galway
[2]University College Dublin, Agriculture and Food Science Centre, Belfield, Dublin 4

Sitka spruce (Picea sitchensis (Bong.) Carr.) is the most dominant species in Irish forestry. It represents up to 60% of the current planting programme and occupies 90% of the total harvested volume in Ireland each year. The potential of increasing productivity through provenance selection is becoming more of an issue for the forest sector and could become a factor for future forest planning. This study was initiated to test the performance of existing and new provenances of Sitka spruce planting stock; Queen Charlotte Islands (Improved), Washington (Danish Seed Orchard), Washington (Cuttings), Washington (Standard) and Oregon (Standard) on typical farmland sites in Ireland. The research will contribute to our understanding of provenance adaption to site specific variables such as soil type, climatic influences and elevation. Four experimental trials were established at Teagasc owned locations in Carlow, Cavan, Galway and Wexford representing typical farmland planting sites, at under 150m elevation. Each site underwent a randomised block design to eliminate the influence of any extraneous factors, with a minimum of six replications of each provenance for scientific analysis. Parameters assessed include budburst or “flushing”, periodic height, root collar diameter, cessation, cold hardiness and destructive sampling (biomass potential). A preliminary analysis of flushing and cold hardiness results indicate that there is no significant variation between flushing times at each site given the geographical and meteorological differences. More variation occurred within each provenance than between selected provenances. These results support the findings of previous research carried out on a similar analysis. Tentative findings from cold hardiness assessment data show that all provenances are substantially affected by frost levels of minus six degrees celsius for early October. The results seem to suggest that autumn frost risk is uniform across all provenances tested. Further research will be carried out in future analysis.

The effect of supplementary nutrients upon enteric pathogens in soil, co-introduced with sewage sludge

Stephanie Ellis[1,2], Sean Tyrrel[2], Karl Richards[1], Bryan Griffiths[3], Emma Moynihan[1], Karl Ritz[2]

[1]Teagasc, Crops, Environment & Land Use Research Programme, Johnstown Castle, Co. Wexford
[2]Cranfield University, Cranfield, Bedfordshire, MK43 0AL, UK
[3]SRUC, King's Buildings, West Mains Road, Edinburgh, EH9 3JG, UK

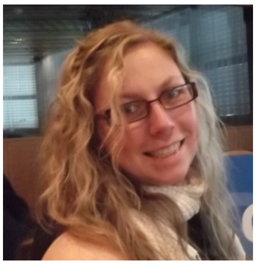
Enteric pathogens are shed in the faeces of infected individuals, resulting in their potential accumulation in sewage sludge. When sewage sludge is spread to land, there is a potential risk that the pathogens could be transferred to humans. Hence, understanding their fate in the natural environment is important. We hypothesised that nutrients in sewage sludge could encourage enhanced activity of the native microbial community and accelerate a decline in pathogens. It was also proposed that the interface between the two matrices may significantly influence the extent of these biotic interactions. To test this hypothesis, a microcosm-based study was carried out where glucose or yeast extract were added to soil, sewage sludge, or both phases, with microbial activity and *E. coli* numbers quantified periodically. Results showed that the matrix to which the nutrients were added had no effect upon *E. coli* decline, implying that the matrix in which such substrate is added is of no consequence. Yeast extract (a balanced source of nutrients) had little effect, but decline in systems containing glucose (purely C-based) was accelerated. This could be related to competition for nutrients induced by glucose, which being a simple C-based energy source would place competitive pressure on acquisition of such nutrients by the microbial communities. Subsequent experiments will investigate repeated substrate amendment and the impact of sustained competition on the survival of *E. coli*.

Sudden internal lake P loading events: results from high frequency monitoring

L. Crockford[1,2], P. Jordan[3], A. Melland[1], G. Shortle[1], D. Taylor[4]

[1]*Teagasc, Agricultural Catchments Programme, Johnstown Castle, Wexford*
[2]*Geography, Trinity College Dublin, Dublin*
[3]*School of Environmental Science, University of Ulster, Coleraine, Northern Ireland*
[4]*Department of Geography, National University of Singapore, Singapore*

Hypolimnia (deep water) in temperate lakes may become anoxic during summer thermal stratification leading to reduced redox potential. Alternative electron acceptors such as Fe^{3+} may be employed in the decomposition of organic matter, a process which consequently releases iron-coupled bioavailable phosphate (P) into overlying waters (internal loading). As summer progresses, these P-rich waters remain in the hypolimnion, excluded from epilimnetic (surface) waters where conditions (light and heat) are conducive for algal growth; until the ambient conditions cool the lake surface and incur lake-mixing in early autumn. However, at this time the light availability has reduced and the temperature no longer promotes algal growth. Lough Namachree (a small inter-drumlin temperate lake in Co. Monaghan) has been instrumented with equipment to monitor dissolved oxygen, temperature, pH, redox potential, turbidity, chlorophyll a, and conductivity at a high frequency (once per hour). In addition, P contribution from the catchment was monitored by a bankside analyser operated by the Agricultural Catchments Programme in a nearby catchment. Data from two water years show lake thermal stratification in spring in water year one and throughout both summers. In late spring of water year one weather conditions prevailed such that the lake completely mixed and reintroduced P-rich hypolimnetic waters to the epilimnion providing a nutrient boost to otherwise P starved phytoplankton. This reintroduced 4.8 kg of P to surface waters, three times higher than total spring catchment loading at 1.7kg. In mid-summer water year two, thermal stratification unexpectedly broke down providing 4.1kg of P to surface waters. In comparison with catchment loading (9.4kg), internal P loading was much lower but occurred at a crucial time for algal growth and in one individual event. Sediment-derived P loading may therefore stall the remediation efforts employed in the catchment to improve water quality.



Herbivore hitchhikers: an investigation of defoliating beetles on biomass crop in Ireland

P. D. Fanning[1, 2], J-R. Baars[2], M.T. Gaffney[1]

[1]*Teagasc, Food Research Centre, Ashtown, Dublin 15*
[2]*School of Biology and Environmental Science, Science Centre (West), University College Dublin, Belfield, Dublin 4*

There has been an increasing interest in the potential of biomass as an alternative to fossil fuels, for electrical generation through co-firing and use in combined heat and power plants. These practices will help meet targets stipulated in the European renewable energy directive (2009/28/EC). A number of biomass crops have shown potential including short rotation coppice willow (SCRW) and short rotation forestry (SRF) of Eucalyptus. Expected yields from SRCW and SRF of Eucalyptus range from 7-12 ODT ha^{-1} $year^{-1}$ (oven dried tonnes) and 10-12 ODT ha^{-1} $year^{-1}$, respectively. However, a major threat to these yields are losses due to defoliating insect pests. Leaf beetles, including the brown willow beetle, *Galerucella lineola*, and the recently introduced chrysomeline, *Paropsisterna selmani*, pose a significant risk. The aim of this study was to investigate the interactions between *G. lineola* and current commercially available willow varieties and clones of the native Irish variety *S. viminalis*. A comprehensive study of the biology and the effect of temperature on *P. selmani* were conducted to determine its pest status, in Ireland, and potential status for other European countries. The effects of *G. lineola* on SRCW could be reduced significantly through the selection of resistant varieties. Resistant varieties were shown to reduce the fecundity of females, and deter feeding by the beetle in choice and no choice trails. Investigations into the feed preference of *G. lineola*, indicate a wide range of resistance to damage within native varieties, thus highlighting the potential for breeding and selection of willows for greater resistance to damage in the future. Studies on *P. selmani* have indicated that the species, which is native to Tasmania, Australia, is suited to temperate conditions (<27°C) to the climate found in Atlantic Europe. *P. selmani* has been shown to do considerable damage to Eucalyptus varieties, eating flush growth and disbudding stems.

Grain number m-2 in barley – how much is too much?

Shane Kennedy[1,2], John Spink[1], Ian J. Bingham[2]

[1]Teagasc, Crops, Environment & Land Use Research Programme, Oak Park, Carlow
[2]Crop & Soil Systems Research Group, SRUC, West Mains Road, Edinburgh, UK

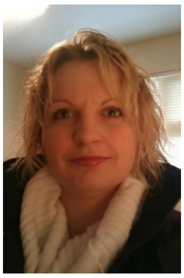
Yield of a grain crop can be expressed as a product of the number of grains per unit area and mean grain weight. Monitoring of growth and development of spring barley crops (cv. Quench) at three Irish sites across three seasons (2011-2013) has shown that grain number and yield in barley are correlated suggesting that further increases in yield can be achieved through increasing grain number m-2 either through improved crop management or improved germplasm. But data has shown that at anthesis crop canopies are already intercepting all available light and as such any increase in grain number would result in less light intercepted per grain and less potential assimilate per grain. Furthermore, the literature identifies a two week cell division period early post-anthesis that can largely determine final grain storage capacity and unfavourable growth or competition for resources during this period may as such set a limit on final grain weight. So is breeding or managing for higher grain numbers a good idea? A series of targeted field experiments at Oak Park, Carlow designed to artificially modify assimilate availability per grain during this two week period through increasing radiation (manipulation of canopy architecture), decreasing radiation (shading) and manipulating grain number (seed rate) aims to test the hypothesis that final grain weight in crops of high grain number is limited by assimilatory capacity early post-anthesis. Treatments applied during this period have not had a significant effect on final grain weight indicating that grain storage capacity is not sensitive to growth conditions early post-anthesis. This may be due to the buffering effect of stem reserves supplementing reduced photosynthesis during the treatment period. Evidence points towards an apparent excess of assimilate for grain filling indicating that the crop can support more grains m-2 than is currently achieved.

Greenhouse gas and ammonia emissions from animal housing and manure storage

N.M. Rochford[1,2], S.T.J. Lalor[1], G.J. Lanigan[1], K.A. Byrne[2]

[1]Teagasc, Crops, Environment & Land Use Research Programme, Johnstown Castle, Wexford
[2]Department of Life Sciences, University of Limerick

Livestock production contributes to emissions of ammonia and greenhouse gases (GHG). The objective of this study was to investigate GHG and ammonia emissions from bovine housing and slurry storage using a combination of controlled environment experiments and on-farm measurements. The study also investigated the methane production potential (B_o) of bovine slurries relative to current Intergovernmental Panel on Climate Change (IPCC) default values. Controlled environment experiments were conducted to evaluate the effect of storage temperature, diet and animal type on emissions, followed by an experiment comparing a range of amendments which can be mixed with slurry during storage to mitigate these gaseous emissions. Increasing temperature above 15°C had a significant effect on methane (CH_4) emissions, with all three factors affecting ammonia (NH_3) emissions. In the amendment trial, there was a significant difference between the two slurry types, with nBPT and dilution having higher CH_4 emissions than the other treatments. Emissions of NH_3 were highest from the nBPT and no dilution treatment. A laboratory incubation experiment measuring B_o from a range of manures showed that the IPCC default value may be overestimated for Irish bovine slurries. On-farm measurements from animal housing and manure storage were conducted on four farms with contrasting animal housing and slurry management. Results showed emissions of CH_4 and NH_3 to be highly variable across all farms with mean daily NH_3 fluxes ranging between 4.5 and 33.1 g NH_3-N 500 kg LW^{-1} d^{-1} and mean daily CH_4 fluxes ranging from 44 to 300 g CH_4-C 500 kg LW^{-1} d^{-1}. From this study, it can be concluded that emissions from bovine slurry can potentially be reduced by using slat mats with valves in housing, the use of chemical amendments in slurry during storage, and/or by diluting slurry during storage. It is also concluded that IPCC default B_o values should be investigated further and potentially revised for some animal categories.



The production of staphylococcal enterotoxin cbovine in milk

Karen Hunt[1,2], Kieran Jordan[1,] Francis Butler[2]

[1]Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork
[2]Biosystems Engineering, UCD School of Agriculture, Food Science and Veterinary Medicine, Belfield, Dublin 4

Staphylococcus aureus can produce Staphylococcal Enterotoxin type C (SEC), one of the protein toxins that can cause foodborne illness when consumed. *S. aureus* strains are capable of producing 6 sub types of SEC, including SEC_{bovine}. The aim of this study was to determine the factors affecting the SEC_{bovine} production in milk by 2 strains isolated from unpasteurised milk and associated cheese. To determine their toxin producing capability in milk, the strains were first grown in pasteurised and unpasteurised milk at temperatures from 20 to 30 ° C for 3 days. In sterile skimmed milk, a full factorial experiment was designed, with combinations of 4 different temperatures and 4 different controlled pH values. Temperature conditions were set at 25, 30, 37 and 40 ° C, and pH values were controlled at 5.5, 6.0, 6.5 and 7 where samples were taken at 5 timepoints for 66 hours. Samples were enumerated for *S. aureus* and quantified for SEC using Baird Parker agar and a sandwich ELISA assay, respectively. Results showed that at 30°C the SEC_{bovine} strains only produced toxin in broth and sterile skimmed milk, but not in pasteurised or unpasteurised milk. In sterile skimmed milk the optimum controlled conditions for SEC_{bovine} production were 37°C/pH6.5. The toxin production in milk was not coupled to *S. aureus* growth as SEC_{bovine} was only produced in the stationary phase. These data will form part of a risk assessment of enterotoxins production in unpasteurised milk and unpasteurised milk products.

Detection of covalently-bound residues of 5-nitroimidazoles: metronidazole

Margaluz Arias[1,2], Martin Danaher[1], Paul Stevensson[2], Christopher Elliott[2*]

[1]Teagasc, Food Research Centre, Ashtown, Dublin 15
[2]Institute for Global Food Security, Queen's University, Belfast

The 5-Nitroimidazole compounds, Metronidazole, Ronidazole and Dimetridazole have been banned for use in the treatment of food-producing animals since residues of the parent compounds and related metabolites are suspected of having genotoxic and carcinogenic properties. In addition, the reductive metabolism of 5-Nitroimidazoles leads to the formation metabolites covalently-bound to tissue macromolecules. Covalently-bound metabolites remain in tissues for longer but as yet unknown periods of time, their toxic properties have not been further assessed, neither is there an analytical method for their detection and quantification. Therefore the aim of this project is to develop an analytical method to detect the covalently-bound 5-nitroimidazole metabolites in edible animal tissues. Due to the nature of the covalent bond between the protein and the metabolites, the intact molecule cannot be released from the protein adduct without employing harsh conditions, conditions that in turn could destroy the bound metabolite itself. Therefore the strategy followed to develop the analytical method was based on the cleavage of the bound metabolite to release a marker compound related to covalently-bound 5-Nitroimidazoles 2-N (Hydroxyethyl) Oxamic acid has been selected as a potential marker compound of covalently-bound metabolites of Metronidazole. Proteins recovered from incubations of liver microsomes treated with Metronidazole and muscle samples from Metronidazole medicated pigs were successively washed with different polar and non-polar solvents. Then, the protein pellets were submitted to mild basic hydrolysis. Extracts of the reaction media were analysed with UHPLC-ESI-MS/MS and 2-N (Hydroxyethyl) Oxamic acid was detected in both types of Metronidazole-treated samples.

Assessing the role of feed as a risk factor for Salmonella in pig production

A.M. Burns[1, 2, 3]*, P.G. Lawlor[2], G.E. Gardiner[3], G. Duffy[1]

[1]*Teagasc Food Research Centre, Ashtown, Dublin 15*
[2]*Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[3]*Department of Chemical & Life Sciences, Waterford Institute of Technology, Waterford*

Contaminated feed represents a potential source of *Salmonella* introduction to fattening pig herds and may cause human infections via consumption of contaminated pork. In a 'Farm to Fork' food safety concept, safe feed is therefore the first step in ensuring safe food. The objective of this study was to carry out an in-depth study on 10 commercial pig farms having a historically high *Salmonella* seroprevalence to firstly identify which production stages are the principal harbours of *Salmonella* infection in pigs. Secondly, to assess the occurrence of *Salmonella* in pig feed throughout the different production stages on these farms and thereby assess potential risks as well as epidemiological relationships. A total of 1545 samples consisting of faecal (n=458), feed (n=321) and environmental (n=749) samples were taken across all production stages and analysed for the presence of *Salmonella*. Isolates were further characterised by serotyping and antibiotic resistance profiling. The pathogen was detected in pigs on 9/10 farms, in (12.7%) faecal samples, with a high prevalence among gilts, weaners and finishers and (5.9%) environmental samples. Only (2%) of feed samples were *Salmonella*-positive, with four farms having at least one *Salmonella*-positive feed sample. Several isolates were multi-resistant to four or more antibiotics. The *Salmonella* 4,12:i:- variant that predominated in the pigs and feed is a monophasic variant of the serovar Typhimurium, that have been emerging in Europe and are of increasing food safety concern. Genetic subtyping using pulsed field gel electrophoresis (PFGE) and multiple locus VNTR analysis (MLVA) is needed to ascertain if the *Salmonella* contamination originated from the purchased feed or if on-farm contamination occurred. Assurance of food safety underpins the goals set out in Food Harvest 2020; results from this study will contribute to the implementation of novel control measures to enhance pork safety from farm to fork.

Evidence of innate immune proteins in milk – development of a bacterial sequestration technique to detect and monitor complement bioavailability

S. Maye[1,2], C. Stanton[1], G. Fitzgerald[2], P.M. Kelly[1]

[1]Teagasc, Food Research Centre, Moorepark, Fermoy, Co.Cork
[2]University College Cork

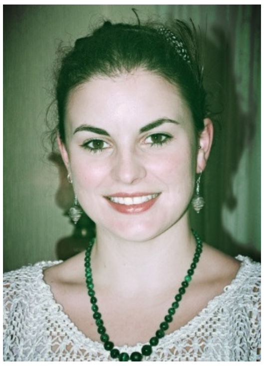
The natural emulsifying layer in bovine and human milks is largely due to the phospholipid-rich milk fat globule membrane (MFGM) to which other biologically active compounds appear to be attached. It is speculated that Complement proteins which form part of the innate immune system may also be associated with MFGM. Complement proteins have been shown to be active in sequestering target pathogens in human breast milk (HBM). As there is increasing emphasis on the 'humanisation' of bovine milk for use as infant feed formula, it is important to deepen our understanding of both bovine and HBM Complement systems, so that detected bioactivity in freshly secreted milk may be characterised and protected in the course of dairy manufacturing processes. In this study, a bactericidal sequestration assay was adapted to detect and characterise Complement activity in fresh bovine milk, complement-inactivated milk samples and processed (pasteurised/homogenised) milks. The Complement sensitive strain was genetically modified by incorporation of a fluorescent p16Slux plasmid. This allowed direct measurement of the antimicrobial activity of the samples. During the studies that followed, the antimicrobial activity of fresh bovine milk was found to be comparable with HBM samples, but that the antimicrobial effect as evidenced by the escalating ineffectiveness at reducing microbial numbers of the target microorganism was diminished with increasing heat treatment (40°C, 50°C and 60°C). Thus, it became clearer that Complement proteins in bovine milk are heat labile and easily inactivated by milk heat treatment >52°C. The processed milk samples showed some residual Complement activity but at substantially reduced levels compared to the untreated milk samples. The results of this study suggest that Complement proteins in untreated bovine milk possess comparable activity with HBM against a targeted pathogenic *E. coli* strain. However, this bioactivity would appear to be easily lost during conventional milk processing, and suggests that alternative milder thermal processes may be needed in order to protect these heat labile biologically interesting innate immune proteins.

Asymmetric synthesis of polyacetylene natural product falcarinol

Eimíle Sheehy[1,2], Juan Valverde[1], Dilip K. Rai[1], Nigel Brunton[1], Paul Evans[2]

[1]Teagasc, Food Research Centre, Ashtown, Dublin 1
[2]UCD Centre for Synthesis and Chemical Biology, School of Chemistry and Chemical Biology, University College Dublin, Belfield, Dublin 4

Falcarinol is a highly unsaturated 17-carbon compound, with a single stereogenic centre in the 3-position, and a *Z*-alkene in the 9-position. Found in plants, in particular the families *Apiaceae* (e.g. carrot and parsnip) and *Araliaceae* (e.g. ginseng and ivy) the elucidation of the stereochemistry at the 3-position has caused some confusion, partly because both enantiomers have been isolated from different sources. These compounds are known to have significant biological activity, and studies have revealed falcarinol to have anti-inflammatory, anti-bacterial, anti-fungal effects and show cytotoxicity against some cancer cell lines. We have carried out a short, convenient synthesis of (±)-falcarinol to access both enantiomers of the compound, augmenting the natural supply and facilitating isolation. Additionally, an asymmetric adaptation of our synthesis of (+)- and (−)-falcarinol has also been executed using a dinuclear zinc ProPhenol system developed by Trost and co-workers. These studies, along with ongoing efforts to resolve regioselectivity issues will be presented.



Streptozotocin induced type-1-diabetes alters the intestinal microbiota and decreases diversity over time with disease progression

Elaine Patterson[1,2,3], Tatiana M. Marques[1,2,3], Orla O'Sullivan[1,2], Pat Fitzgerald[2], Gerald Fitzgerald[2,3], Paul D. Cotter[1,2], R. Paul Ross[1,2], Catherine Stanton[1,2], Timothy G. Dinan[2] John F. Cryan[2]

[1]*Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork*
[2]*Alimentary Pharmabiotic Centre, Biosciences Institute, Co. Cork*
[3]*Department of Microbiology, University College Cork, Co. Cork*

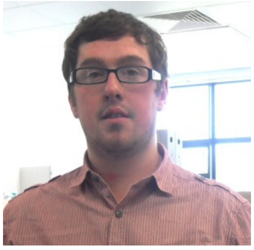
The intestinal microbiota has become a controversial environmental factor involved in various disease states, particularly within developed countries. Previous studies which have begun to look at the intestinal microbiota as an environmental factor involved in the development of type 1 diabetes (T1D) are often limited due to the models used (genetically pre-disposed animals and humans that develop T1D), making it difficult to determine whether the observed correlations had any causative role or resulted from disease development itself. The aim of this study was to look at the impact a streptozotocin (STZ) induced T1D model had on the intestinal microbiota of one group of otherwise healthy Sprague-Dawley rats and compare this profile to that of healthy control animals over time. The intestinal microbiota profiles between the groups were similar at week 0, before STZ injection in one of the groups. Subsequent time-points at 1, 2, 4 and 5 weeks after STZ injection in the T1D animals revealed a dramatic impact of disease development and progression on the intestinal microbiota profile. Most notably, T1D was associated with a shift in the Bacteroidetes: Firmicutes ratio ($P < 0.05$), while at the genus level, increases in the lactate producing bacteria such as *Lactobacillus* and *Bifidobacterium* were associated with the later stages of diabetes progression ($P < 0.05$). T1D significantly reduced the intestinal microbiota diversity profile over time following diabetes induction ($P < 0.05$) and principle coordinates analysis (PCoA) demonstrated temporal clustering in both groups over time with separation of the T1D clusters at each time point from the healthy control animals. The results provide a comprehensive account of how T1D alters and reduces diversity of the intestinal microbiota over time with disease progression.

Whey protein effects on body weight, food intake and insulin signalling are dependent on dietary challenge duration in low fat diet fed C57BL/6J mice

Liam McAllan[1,2], John F. Cryan[3,4], Kanishka N. Nilaweera[1]

[1]Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork
[2]Department of Pharmacology and Therapeutics, University College Cork
[3]Department of Anatomy and Neuroscience, University College Cork
[4]Alimentary Pharmabiotic Centre, University College Cork

Our group previously found that whey protein isolate (WPI) intake partially suppressed high-fat (45% kcal) diet (HFD) induced obesity. However, possible WPI effects may have masked due to the fact that high dietary fat intake could overwhelm energy balance regulatory mechanisms. Therefore, to further identify the mechanisms of WPI action, here we investigated how WPI intake in a low fat (10% kcal) diet (LFD) background affects energy balance. C57BL/6J mice were fed a LFD with either casein or WPI for 7 or 15 weeks. At 7 weeks, there was no significant effect of WPI on body weight gain, daily and cumulative energy intake, energy expenditure, substrate metabolism, and plasma levels of triacylglycerol and glucose, but plasma insulin levels did show a trend towards an increase ($P = 0.07$), which was accompanied by decreased epididymal adipose tissue mRNA expressions of insulin substrate-1 and glucose transporter 4 in WPI fed mice ($P < 0.05$). In contrast, at 15 weeks, weight gain and daily and cumulative energy intake were significantly reduced in WPI fed mice ($P < 0.05$), while there was no significant changes in energy expenditure, plasma insulin levels or epididymal adipose expression of insulin-related genes. In conclusion, the results here show that the decreased body weight gain associated with prolonged WPI intake in a low-fat background was primarily driven by a suppression of energy intake, while acute effects of WPI on insulin and its associated signalling mechanism were lost with prolonged intake of the dietary protein, presumably driven by the suppression of energy intake.



Fermented milks for infant health and nutrition

S.M. Mackey[1, 2], R P Ross[1], P J Simpson[1], K Nilaweera[1], G F Fitzgerald[2], C Stanton[1]

[1]Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork
[2]Department of Microbiology, University College Cork

Bifidobacteria are present at high levels in the gastrointestinal tract of breast fed infants, and a dietary regime that would beneficially alter the colonic microflora towards higher levels of bifidobacteria is desirable. Two reconstituted skimmed milk (RSM) fermentates, produced using Lactobacillus acidophilus and Lactobacillus helveticus were shown to promote the growth of 4 bifidobacterial strains in vitro in comparison to an unfermented RSM and a prebiotic control (FOS). Faecal fermentations, using 1% w/v of the fermentates were performed over 48hrs, with colony forming units of lactobacilli and bifidobacteria recorded every 8hrs, for 48hrs. Bifidobacterial counts in the mixed culture faecal fermentation model were significantly higher at 16hrs, in the presence of Lactobacillus helveticus and acidophilus fermentates (6x108 and 8 x 108 CFU/ml, respectively) compared with unfermented RSM and FOS controls (1x108and 2x108 CFU/ml, respectively). Subsequently, an animal study was undertaken in which mice (C57) were fed a standard diet and 30mg of each of the RSM fermentates daily. Bifidobacteria and lactobacilli counts in the faecal pellets, and weight gain were monitored weekly and compared to control mice on a standard diet with a commercial prebiotic and unfermented RSM (30mg/day). The RSM fermentate-fed groups exhibited enhanced weight gain compared with controls during the trial, and faecal bifidobacteria and lactobacilli numbers were elevated in the former, compared with the latter groups. The data indicated that the RSM fermentates tested in this study have potential as ingredients for enhancing gut heath, when included into foods such as infant formula, yoghurt and dairy beverages.

Influence of somatic cell count in heifers on lifetime milk yield and disease management

Simon C. Archer[1,2], Finola McCoy[3], Wendela Wapenaar[2], Martin J. Green[2]

[1]Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2]University of Nottingham, School of Veterinary Medicine and Science, Sutton Bonington, UK
[3]Animal Health Ireland, Carrick-on-Shannon, Co. Leitrim, Ireland

Expansion of dairy herds can occur through increasing the number of heifers, and maximising their longevity. In Ireland, this trend may lead to overstocking and increased risk of environmental mastitis if investment in improved facilities for optimal management cannot be justified. Mastitis has been highlighted as a common problem for heifers in early lactation that is economically important through its impact on first lactation productivity. However many heifers do not survive beyond the first lactation, and therefore fail to at least break-even on rearing costs. The aim of this research was to assess the impact of milk somatic cell count (SCC) early in the first lactation on the lifetime productivity of heifers, and therefore estimate potential savings through implementing control measures; this represents scope for investment to control disease. Test day milk recordings were available from 7,423 Irish dairy herds with 233,176 heifers that calved in 2005, and had a record of SCC between 5 and 30 days in milk during parity 1 (SCC1). 'Lifetime milk yield' was determined up to July 25, 2012. The economic impact of specific interventions to control heifer mastitis was simulated and used to determine budgets for their implementation in different circumstances. Increase in SCC1 from 50,000 cells/mL to 400,000 cells/mL was associated with a median decrease in lifetime milk yield of 1,700 kg. Budgets were highly dependent on the willingness of decision makers to pay. Approximately 50% of Irish dairy herds have potential to make savings through reducing the prevalence of heifers with high SCC1 which could involve implementing mastitis control measures during the *pre-* and *peri-partum* period. This research supports decisions around the cost effectiveness of interventions. Factors affecting the willingness of decision makers to pay for control require further investigation.