WALSH FELLOWSHIPS PROGRAMME

TEAGASC WALSH FELLOWSHIP SEMINAR 2014

Teagasc, Johnstown Castle, Wexford | Friday, 5 December 2014

ABSTRACTS

Teagasc
Agriculture and Food Development Authority

INTRODUCTION

Professor Gerry Boyle, Director

This year marks the centenary of the birth of Dr Tom Walsh, whose vision and dynamism led to the development of An Foras Taluntais (predecessor of Teagasc) as a world-class research institute and which laid the foundation for the extraordinary success of Ireland's agri-food industry. Under his inspired leadership, a cohort of young scientists engaged in pioneering research which was not only published in the best international scientific journals, but which also found application right across all aspects of Irish farming and rural life. Dr Walsh had a global vision of agriculture, which was reflected in the schemes he put in place for the training of young Irish scientists in universities and research institutes in the US, New Zealand and the UK. Today, through its Walsh Fellowships Postgraduate Programme, Teagasc continues to honour this aspect of Dr Walsh's contribution to the development of generations of Irish scientists

As a way of marking this very special year in the history of Teagasc, and in recognition of Dr. Walsh's special connections with Johnstown Castle, we are holding the Annual Walsh Fellowships Seminar in the Castle and combining it with a centenary lecture.

The Fellowships Programme, named in honour of Dr Walsh, has grown in scale and significance since it was launched in Johnstown in 1995. Up to 2,000 postgraduate students have participated in the scheme over the past twenty 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 €4 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 continued 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 and the Agricultural Trust.

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 Teagasc 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 Programme 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.

Of course, one of the factors in the Programme's success over the years has been the emphasis on continuous change and renewal. Our commitment to change and improvement will continue into the future. In this regard, we are now committed to working more closely with our university partners to ensure that students can realise the full potential of the joint supervision model and also in ensuring that the real benefits of a Structured PhD programme can be realised in return for the very significant investment being made by Teagasc in PhD training.

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Nitrogen fertiliser formulation: the impact on yield and gaseous emissions

M. Harty[1,3], D. Krol[1], G. Lanigan[1], G. McNeill[2], K.L. McGeough[2], R.J. Laughlin[2], C.J. Watson [2], K.G. Richards[1] and P.J. Forrestal [1].

[1] Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Co. Wexford
[2] Agrifood and Biosciences Institute, Belfast, Northern Ireland.
[3] Queen's University Belfast, Northern Ireland

Agriculture was responsible for 31% of Ireland's Greenhouse Gas (GHG) emissions in 2012, with 39% of these emissions arising from chemical/organic fertilizers in the form of nitrous oxide (N_2O). Switching from calcium ammonium nitrate (CAN) to a urea-based fertiliser limits the soil residence period of nitrate, the major substrate for denitrification loss in the N_2O form. However, urea is susceptible to ammonia (NH_3) volatilisation, but this risk can be managed using urease inhibitors. The aim of this study was evaluating the effect of switching from CAN to urea, urea with the urease inhibitor N- (n-butyl) thiophosphoric triamide (trade name Agrotain®) and/or the nitrification inhibitor dicyandiamide (DCD) based on three criteria: impact on agronomic yield; impact on N_2O emissions; and impact on NH_3 emissions. The experiment is a two year study (commenced March 2013) at six permanent pasture sites located at Johnstown Castle, Moorepark and Hillsborough, covering a range of soil textures and drainage characteristics. The experiment simulated a grazing environment; annual fertiliser N was applied at different rates (0, 100, 200, 300, 400 or 500 kg N ha^{-1}) in five equal splits, with grass harvested prior to fertilizer application. Dry-matter yield and N offtake was measured over six harvests; daily N_2O and NH_3 emissions were measured using static chambers and wind tunnels, respectively and annual emission factors calculated. Switching from CAN to urea dramatically reduced N_2O emissions, but had little effect on dry-matter yield. However, there was evidence of pollution swapping of N_2O for NH_3. In the first year, two urea based formulations (urea with the urease inhibitor and urea with both inhibitors) resulted in the highest yield at two sites and successfully reduced both N_2O and NH_3 emissions at all sites. Fertiliser formulation strategy has the potential to be a win-win solution for agriculture enabling reduction of GHG emissions without sacrificing productivity.

High density genetic linkage maps of perennial ryegrass using genotyping by sequencing

J. Velmurugan[1, 2], D. Milbourne[1], C. Hackett[3], D. Marshall[4], C. Creevey[5,6], L. Milne[4], H. Meally[1], M. McCabe[5], B. Lynch[2], E.M.B. Mollison[1, 4] and S. Barth[1]

[1] *Teagasc Crops, Environment & Land-Use Research Centre, Oak Park, Carlow*
[2] *University College Dublin, School of Agriculture and Food Science, Dublin4*
[3] *BioSS, James Hutton Institute, Dundee*
[4] *ICS Group, James Hutton Institute, Errol Road, Invergowrie, Dundee,*
[5] *Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[6-present] *IInstitute of Biological, Environmental and Rural Sciences, Aberystwyth University, U.K*

Perennial ryegrass underpins pasture-based production of milk and meat in Ireland, and genetic improvement of the species is pivotal in increasing productivity of this system. In animal systems, biotechnology-based approaches such as genomic selection (GS) are revolutionising breeding, and developing and deploying GS-based approaches in grass breeding is a national priority. As a necessary precursor for this strategy, a next generation sequencing (NGS)-based approach for genome-wide surveying of single nucleotide polymorphisms (SNPs) originally developed in cereal species was adapted for perennial ryegrass. This approach, called genotyping by sequencing (GBS), can identify thousands of SNPs in large numbers of genotypes in a cost and time-efficient manner – a key prerequisite for applying GS in breeding. To illustrate the utility of the GBS approach we have developed high density SNP-based genetic linkage maps of *Lolium perenne* in F2 and F6 genetic mapping populations at a fraction of the cost and time than possible using previous methods. In total, 192 individuals from a F2 mapping population of *L. perenne* previously used at CELUP OakPark Research Centre and 49 individuals from a F6 population generated by intercrossing F2 were used to construct GBS libraries. The methylation sensitive restriction enzyme *PstI,* was used for F2 and a double enzyme digest 'Pst-Msp1' was used for the F6. Each sample was tagged with a unique 4-9 nucleotide barcode and sequenced on Illumina HiSeq 2000 platform. The sequencing resulted in 345 million reads with ~1.35 million reads per individual for F2 and 388 million reads with ~3.5 million reads per individual for F6. In total, 2019 SNPs, 7429 presence/absence variants for F2 and 7390 SNPs for F6 were identified using a bioinformatics pipeline. Two high density linkage maps were created using these markers. This dataset would be used to compare the power of mapping applications in both population types.

Investigating plant available nitrogen and phosphorus from composted wastes for use in Irish agriculture

A. Lee [1, 2], M. Prasad[3], J. Cassidy[1], M. Gaffney[2]

[1] Dublin Institute of Technology, Kevin St. Dublin 8
[2] Horticultural Development Department, Teagasc Food Research Centre, Ashtown, Dublin 15
[3] Compost Research and Advisory, Naas, Co. Kildare

Current EU legislation on waste management (2008/98/EC) has seen resurgence in compost research. Escalating fertiliser prices, increasing volumes of biodegradable waste and heightened environmental awareness have placed a greater emphasis on utilising these waste materials. Understanding plant available nitrogen (N) and phosphorus (P) from composted organic wastes is essential to ensure effective application, particularly as there are few practical studies observing release of both nutrients from the one source. Historically, this has led to ineffective application rates and poor crop quality. Composted wastes sourced both nationally and internationally were characterised in detail, chemically, biologically and spectrally with follow-on incubation and pot-based experiments to establish the N and P availability from these materials. Further investigations into the ability of different Irish soils to bind compost-derived P were also conducted. Pot-based growth experiments using a model plant (Cabbage) indicated that P availability was highest from composted manure (109% equivalent of SSP). Both composted green waste (96%) and biowaste (88%) also showed a high availability of P compared to SSP. N availability was greatest from composted animal manure (68% equivalent of CAN) with biowastes (39%) and green waste (38%) significantly less. Mineralisation of organic N was also observed in some compost amended soils after 16 months. Interactions between soil type and compost feedstock in relation to P availability was significant, suggesting that some compost feedstocks may partially overcome the P binding capacity of some Irish soils. Approximately 320,000 tonnes of biodegradable waste is available annually for composting. Given the high level of plant available P from biowastes, in combination with a high humic acid and organic matter content, application of these materials could contribute to maintaining good levels of soil health and P in agricultural soils and maintaining the sustainability of Irish agriculture.

Unsaturated time lag: correlating water quality changes with programs of measures

Sara E. Vero[1,2], Rachel Creamer[1], Tiernan Henry[3], Mark G. Healy[2],
Tristan Ibrahim[4], Karl Richards[1] and Owen Fenton[1]

[1] Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Wexford
[2] Civil Engineering, National University of Ireland, Galway
[3] Earth and Ocean Sciences, National University of Ireland, Galway
[4] Deptartment for Environment, Food and Rural Affairs, London

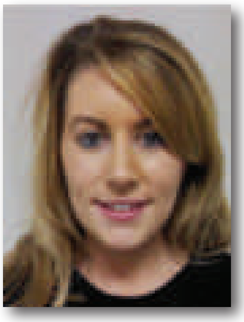
The European Union Water Framework Directive (EU WFD) aims to achieve at least "good" quality status in all water bodies by 2015, via programmes of measures such as the Nitrates Directive. One cannot correlate water quality with agricultural mitigation measures without first estimating the inherent delay or "time lag" of nutrients lost at surface level and now in transit along different pathways. To date, nobody has conducted such work in Ireland. Although the unsaturated zone is a critical control within the context of total time lag, it is often ignored or simplified, as the laboratory methods required for its assessment are arduous, of low resolution, expensive, and include a large element of uncertainty. In this project, the consequences of varied soil hydraulic and meteorological complexity on unsaturated zone time lag estimates were assessed using a numerical solute transport model in nine soil profiles. Results showed that low complexity, generic soil data is sufficient to inform the monitoring regimes imposed in agricultural catchments, but insufficiently reflect the full duration of unsaturated zone time lag (underestimation by up to 0.97 yrs). Consequently, high resolution soil data is essential to inform policy makers as to mitigation timescales. Furthermore, this project has updated the traditional laboratory methods to enable the rapid collection of high resolution equivalent data, providing the necessary inputs for the numerical model. In collaboration with the Irish Soil Information Survey and the Agricultural Catchments Program, unsaturated zone monitoring stations were installed in contrasting arable and grassland catchments, in which potassium bromide tracers will be applied. Results from this experiment are forthcoming and will allow validation of numerical simulations. The field, laboratory and computer techniques developed by this research form a toolkit to determine unsaturated time lag in soil profiles, and will contribute to a holistic appraisal of total catchment scale time lag.

Quantifying the effect pyramiding Potato Cyst Nematode *(Globodera pallida)* resistance QTLs in potato

Brian Rigney[12], Vivian Blok[3], Denis Griffin[1], Claire Cave[2], Dan Milbourne[1]

1* Teagasc Crops, Environment & Land-Use Research Centre, Oak Park, Carlow
2 School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4
3 James Hutton Institute, Cell and Molecular Sciences, Errol Road, Invergowrie, Dundee, DD2 5DA, UK

Globodera pallida is considered to be one of the most economically important nematode pests of potato causing yield losses in excess of €6 million in crop losses in the UK per year. Field populations of *Globodera pallida* are comprised of a mixed population of two pathotypes, Pa2 and Pa3, referred to as Pa2/3.Potato breeders are constantly seeking strong, durable and broad spectrum resistance towards *G.pallida*. The heterogeneous nature of the population has made it difficult to integrate resistance that address all three features. An earlier study at Teagasc demonstrated the pyramiding of two resistance QTLs, Gpa IV^{s}_{adg} and *Gpa V,* provides an increased resistance to *Globodera pallida Pa2/3 (Chavornay).* However, the study didn't address aspects related to the durability and broadness of effect resulting from having two resistance sources within the one genotype. The objectives of this study were to quantify the effect of the individual QTL and the breadth of resistance conferred by pyramiding the QTLs by testing their ability to resist a number of different *G. pallida* populations from the UK. A population was developed, segregating for both QTLs; using molecular markers we identified groups of individuals from the population that contained the QTLs in various combinations; No QTL, *Gpa* IV^{s}_{adg} only, *Gpa V* only, and *Gpa V* and *Gpa* IV^{s}_{adg} .The individuals were then assessed for their resistance across four *G. pallida* populations; Luffness, Lindley, Newton, and Farcet. The study showed the individuals containing both QTLs had a significant reduction in the number of females present on the roots ($P<0.001$) in comparison with the other groups containing either QTL separately, across all four nematode populations. We also detected a significant difference between the two *G. pallida* resistance sources ($P<0.001$) with Gpa IV^{s}_{adg} consistently less effective than *GpaV*. This study supports the pyramiding strategy for *Gpa V* and *Gpa*IV^{s}_{adg} as a strategy to develop new varieties with a strong and broad spectrum resistance to multiple PCN populations however durability of the resistance remains to be quantified.

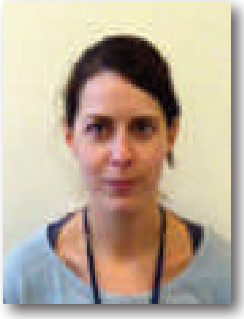


Influence of protein concentration on surface composition and rehydration properties of spray-dried milk protein concentrates

Grace M. Kelly[1, 2], James A. O'Mahony[2], Alan L. Kelly[2], Thom Huppertz[3] Deirdre Kennedy[1], and Donal J. O'Callaghan[1*]

[1] *Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork*
[2] *School of Food and Nutritional Sciences, University College Cork, Cork*
[3] *NIZO food research, Ede, PO Box 20, 6710 BA, The Netherlands*

Due to their high protein content, milk protein concentrate (MPC) powders are a popular choice of ingredient in clinical and nutritional beverages, protein bars, cheese, yogurt, ice cream and infant formula. Complete rehydration is normally a prerequisite for effective expression of a dried protein ingredient's underlying functionality. The objective of this study was to examine the effect of increasing protein content (35 to 90%) on the microstructure and rehydration properties of MPCs. The surface and microstructure of powders were examined using X-ray Photoelectron Spectroscopy (XPS) and Scanning Electron Microscopy (SEM). Water sorption properties of MPCs were measured by Dynamic Vapor Sorption (DVS). High-performance liquid chromatography (HPLC) was used to identify solubilized proteins after 30 min rehydration. XPS confirmed that powders with increasing protein content had greater amounts of protein and reduced amounts of lactose on the surface, which led to longer rehydration times. SEM images showed that lower protein powders (35, 50 and 60% protein) had a wrinkled surface with difference in morphology being evident as protein content increased. DVS results showed that high protein powders, compared to low protein powders, had higher water sorption at low RH (0-20%) and lower water sorption at maximum RH (90%). Only MPC35 exhibited lactose crystallization upon humidification. Monolayer moisture value (m_m), determined from sorption isotherms, increased with increasing protein content. HPLC results show that solubilizing high protein powders at increased temperatures (50 °C rather than 20 °C) significantly improves rehydration time. Overall results show that high protein MPCs have different surface composition to low protein MPCs causing reduced rehydration times which can be overcome by solubilizing at higher temperatures. They also have high resistance to humidity-induced changes which improves their storage stability.

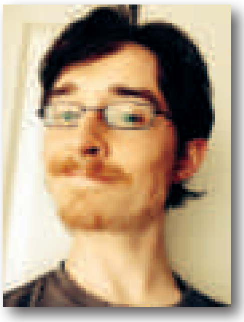


Investigation into the survival potential and inactivation of *Escherichia coli* O157:H7, *Listeria monocytogenes* and *Salmonella* in compost and anaerobic digestate derived from food waste

S. Murphy[1,2], D. Walsh[1], M. Gaffney[1], S. Fanning[2] and C. Burgess[1]

[1] *Teagasc Food Research Centre, Ashtown, Dublin 15*
[2] *School of Public Health, Physiotherapy & Population Science, UCD, Belfield, Dublin*

As part of the European Landfill Directive (1999/31/EC), it is essential to seek new strategies to enable greater recycling of biodegradable waste. Composting and anaerobic digestion are both methods of transforming this waste into value products such as soil amendments, but assurance is needed of their absolute safety. The survival potential of three human foodborne pathogens; *Escherichia coli* O157:H7; *Listeria monocytogenes* and *Salmonella*, in both composted waste (CW) and anaerobic digestate liquid (AD) has been demonstrated but not investigated in great detail. The objectives of this study are to assess the thermal inactivation of *E. coli* O157:H7, *L. monocytogenes* and *Salmonella* in CW and AD and to assess and compare the survival of each pathogen in CW and AD at a range of relevant temperatures. The thermal inactivation of each pathogen in both matrices, at 55°C and 60°C, was determined. Ten gram samples of CW and AD were inoculated with each pathogen at a concentration of $\log_{10}7$ CFU/ml. Samples were submerged in a water bath and removed at selected time points. Enumeration was carried out using the MPN method. For the survival study, CW and AD were spiked with a cocktail of streptomycin resistant *E. coli* O157:H7, *L. monocytogenes* or *Salmonella* at a concentration of $\log_{10}5$ CFU/ml. Survival was assessed at 10°C, 25°C and 37°C for all samples. Enumeration was again carried out using the most probable number (MPN) method, from initial inoculation until no counts could be recovered. Detection by enrichment was then carried out. The results from the inactivation study demonstrated that pasteurisation, if appropriately carried out, is effective in eliminating pathogens from both matrices. The survival study results demonstrated that *E. coli* O157:H7, *L. monocytogenes* and *Salmonella* all exhibit extended survival capabilities in both CW and AD at lower temperatures, suggesting that recontamination of CW and AD under storage conditions may pose a potential public health risk.

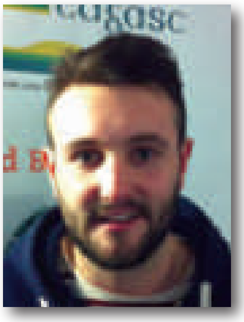


Expanding the possibility for biocontrol of *Listeria monocytogenes* with bacteriophages & disinfectants

Aidan Casey[1, 2], Olivia McAuliffe[1], Aidan Coffey[2] and Kieran Jordan[1]

[1] *Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork*
[2] *Dept. of Biological Sciences, Cork Institute of Technology, Cork*

Biocontrol of *Listeria monocytogenes* in the food processing environment has become of paramount importance to the issue of food safety, given the numerous high profile outbreaks that have occurred worldwide in recent years. This PhD adopts a multi-faceted approach to tackling the problem of *L. monocytogenes* persistence in this particular niche; two of which are discussed here. Firstly, the research involved studying the effects of a common disinfectant, benzethonium chloride (BZT), on a persistent strain of *L. monocytogenes* at the transcriptome level, using RNA-Seq. Subsequent gene expression analysis identified networks of genes which were highly differentially expressed. The results indicate that numerous genes from pathways involved in peptidoglycan biosynthesis, motility and carbohydrate metabolism exhibited significant upregulation in the presence of BZT, and that the cellular response of *L. monocytogenes* to sublethal BZT exposure is centred on cell wall reinforcement & motility. Secondly, we attempted to isolate lytic bacteriophages from environmental sources in order to further our knowledge in understanding their methods of host interaction and infection. To date, we have successfully isolated two bacteriophages which have been shown to be capable of infecting and killing a wide range of *L. monocytogenes* strains of the 4b serotype. The genomes of these phages were sent for commercial sequencing and results detailing their genetic composition, structural architecture and relatedness to other sequenced *Listeria*-specific phages are presented. This analysis indicates that both phages are tailed dsDNA members of the order Caudovirales, with genomes of approximately 38-42,000 bp in size. Other on-going research is centred on comparative genomic research of *L. monocytogenes* isolates from different environmental niches and represents another approach to identifying the underlying mechanisms employed by the bacteria in order to survive and proliferate in the processing environment, which, based on the results, appear to be more complex than previously thought.



The effect of supplementing a high fat diet with the dairy whey proteins, bovine serum albumin and lactoferrin, on the composition of the gut microbiota.

Peter Skuse[1], Bettina McManus[1], Kanishka Nilaweera[1], Gerald Fitzgerald[2,3] and Paul D. Cotter[1,3].

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

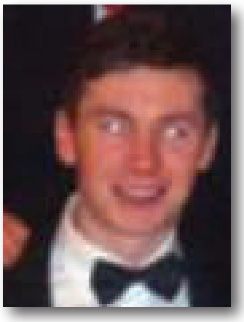
Overweight and obesity is now a global epidemic. By 2008, 1.5 billion people were overweight, of which 200 million men and nearly 300 million women were obese. Obesity is associated with a host of metabolic diseases, as well as leading to considerable economic cost. The primary cause of obesity is a positive energy balance. However, other factors, such as energy harvest and other activities by the trillions of bacteria which reside in our gut, are now thought to play an important role. Dairy whey proteins are known to confer beneficial health properties, many of which have been extensively investigated. However, their impact on the composition of the gut microbiota is relatively unknown. This study investigated the effect of supplementing a high fat diet with the whey proteins, bovine serum albumin (BSA) and lactoferrin, on the gut microbial composition of C56BL/6 mice. This analysis was carried out using high-throughput DNA sequencing which, in contrast to more traditional microbiology-based approaches, provides an accurate insight into gut microorganisms regardless of whether they can be grown in the lab or not. The results of DNA sequencing revealed differences in the gut microbial community of mice depending on whether they were fed a high or low fat diet. More specifically, there were significantly higher proportions of the phylum Firmicutes in animals fed the high fat diet, while significantly lower proportions of the phylum Bacteroidetes were observed in the low fat fed cohort, observations which are consistent with several previous studies. Notably, supplementation of a high fat diet with either BSA or lactoferrin reversed these high fat associated microbial changes, causing the bacterial gut profile to revert once more akin to that of animals fed a low fat diet as well as significantly increasing other health associated populations. In the case of BSA supplementation, these changes were consistent with reduced weight gain, and it is postulated that the beneficial consequences associated with consumption of this whey protein may be at least partly attributable to changes in the gut microbiota.

An assessment of the potential for online / electronic based teaching in agricultural training

Donna Deegan [1, 2], Padraig Wims [1] and Tony Pettit [2]

[1] *University College Dublin, Belfield, Dublin 4, Ireland*
[2] *Teagasc Kildalton Agricultural & Horticultural College, Kildalton, Piltown, Kilkenny*

With reduced staffing numbers in agricultural colleges, the potential to utilise the numerous advantages that are offered by the blended method of teaching is becoming an area of interest to an institution that historically has placed emphasis on the teacher's one way delivery of subject matter through traditional teaching. The key objective of this research was to compare traditional and blended methods of teaching in formal agricultural education. This involved the planning, developing and testing of online material in education. Classes were divided into two groups and the same academic content was delivered by either traditional or by blended (online supplemented with interpersonal) approach. The students were then assessed on their knowledge of the subject matter. The experimental design was replicated in two academic years (2012 and 2013) with a total of 260 students. No significant differences were found when comparing the traditional and blended methods when teaching practical skills. Academic material that was text-based became more interactive through blended learning. However, material that was already interactive in the traditional method of delivery led to students performing better through the traditional method of teaching. It was also found that academically weaker students performed equally well as academically strong students in the online environment. Key findings of this research have also highlighted the appropriateness of using blended learning technologies in agricultural education.



The use of local radio and podcasts in knowledge transfer

Owen Keogh[1], Pat Clarke[2], Monica Gorman[3]

[1] *Teagasc Advisory Office, Ballina, Co. Mayo*
[2] *Teagasc Animal & Grassland Research and Innovation Centre, Athenry, Co. Galway*
[3] *School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*

For farmers, information is now more accessible than ever, with which they need to act upon to remain competitive within an ever changing industry. Radio is listened to on average by 83% of Irish adults daily, with local radio holding its own in several regions across the country. Teagasc utilizes the medium of the radio in an adhoc manner in most regions, but in County Mayo there are short daily broadcasts by advisers that reach an audience of approximately 20,000 people. In this age of the internet, the power of the radio can be expanded through podcasts that make information available ‘on demand’. While traditional Advisory and Extension services have involved direct contact with the farmer, does the medium of radio and the podcast offer potential to reach a wider audience of farmers? The overall aim of this research is to document and evaluate the Mayo local radio experience in order to identify areas for continued growth and innovation in Mayo and to inform Teagasc on further development of local radio potential for knowledge transfer in other regions and counties. To that end, the methodology used was that of a mixed method approach while also adopting a method of triangulatiuon to co-ordinate the different streams of results with an end goal of addressing four study objectives. (1) To profile and analyse the listenership / audience of both the farming slots on Midwest Radio; (2) To establish and test a podcast system for the Teagasc website (3) To identify the key characteristics for effective agricultural radio broadcasting and use these to assess if and how any improvement can be made; (4) To create a country-wide map that shows existing agricultural-based radio slots (Teagasc or other) and that shows the most suitable local radio stations to target. Through a face to face survey of farmers (clients and non-clients), 71% of the respondents listen to the Farming Scene (daily), 62% of the respondents listen to the Farming Matters Wednesday evening show (weekly). More preliminary results have formed the conclusion that radio does play a vital role in the information gathering and can influence decision making of a farmer in the Mayo region.

Genetic control of cow fertility via energy status, uterine health and ovarian function

S.G. Moore[1,2], T. Fair[2] and S.T. Butler[1]

[1] Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2] School of Agriculture and Food Science, University College Dublin

Two groups of Holstein cows with similar genetic merit for milk production traits, but with either good (Fert+) or poor (Fert-) genetic merit for fertility were characterised to identify the physiological mechanisms under genetic control that contribute to differences in phenotypic reproductive performance. Greater dry matter intake and more favourable bioenergetic status in Fert+ cows was associated with reduced body condition mobilisation, superior uterine health and earlier resumption of ovarian cyclicity. Endometrial genes involved in immune response (*SAA3*, *SPP1*) and cellular energy sensing (*PRKAG3*) were differentially expressed between Fert+ and Fert- cows, indicating molecular mechanisms in the endometrium that underlie the differences in uterine health and metabolic status. Fert+ cows had a larger corpus luteum and greater circulating concentrations of progesterone, the essential hormone of pregnancy. Endometrial expression of genes involved in the synthesis and secretion of prostaglandin $F_{2\alpha}$(*PGFS2*, *ABCC4*) was greater in Fert- cows, possibly representing a key mechanism associated with the reduced size and steroidogenic capacity of the corpus luteum in Fert- cows. In addition, Fert- cows had reduced expression of the steroidogenic factor *NR5A1,* and a signature expression profile of genes associated with regression of the corpus luteum (*ADAMTS5*, *ATP2A1* – both up-regulated in Fert+ cows; *THBS1*, *TGFBI* – both down-regulated in Fert+ cows). Genome-wide association studies using data from Irish and Australian cattle identifed genomic variants associated with fertility. We have identified deep phenotypes, transcriptomic profiles and genomic variants that underlie differences in phenotypic fertility performance. The research will pave the way to increase the rate of genetic improvement in the national dairy herd.

A two year Irish national survey of mycotoxins in silages

C. McElhinney [1, 2, 3], M. Danaher [3], C. Elliott[2], P. O'Kiely [1]

[1] *Teagasc Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*
[2] *Institute for Global Food Security, Queen's University Belfast, Belfast, N. Ireland;* [3]*Teagasc Food Research Centre, Ashtown, Dublin 15*

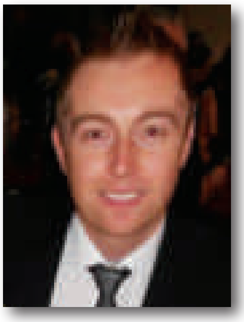
Fusarium and *Penicillium* have been previously identified in silages. These moulds are toxigenic and can produce secondary fungal metabolites, namely mycotoxins. Mycotoxins can induce a range of detrimental ailments in livestock. Monitoring feed for mycotoxins is requested by the European Food Safety Authority and this study includes all mycotoxins that are regulated in Commission Directive (EC) No. 32/2002 and recommendation (EC) No. 576/2006. The objective of this study was to identify the mycotoxin challenge present in silages produced throughout Ireland over a two year period. Three hundred farms were visited between December 2012 - March 2013 (n=150) and December 2013 - March 2014 (n=150). On each farm, two core samples of silage were removed from either pit grass silages (n=175), pit maize silages (n=10) or baled grass silages (n=115) using a motorised coring device. Mycotoxin analysis was conducted by validated liquid chromatography tandem mass spectrometry (LCMS-MS). This 16 minute analytical run can detect 20 mycotoxins (aflatoxins A1, B1, A2 and B2, deoxynivelenol, HT-2, mycophenolic acid, roquerfortines C and E, ochratoxin A, T-2, zearalenone, enniatins A, A, B and B1 and, fumonisins B1 and B2, anadrastin A and beauvericin), and includes all the regulated mycotoxins concerned with feed. Mycotoxin data were analysed by Fishers exact test and Binary Logistical Regression for year and silage type. Nine mycotoxins (roquefortine. C, enniatin A, A1, B and B1, anadrastin A, beauvericin, mycophenolic acid and zearalenone) were present within the silages. Although baled and pit silages had similar mycotoxin profiles, baled silages had a greater range of mycotoxin concentrations. The most abundant mycotoxin among the silages was mycophenolic acid (baled), detected at 4386 µg/kg DM in year 1. It is concluded that none of these mycotoxins exceeded EU legislation or recommendations.

Factors affecting grass growth, grazing season length and milk production on heavy wet soil

P. Tuohy[1, 2], O. Fenton[3], N.M. Holden[2] and J. Humphreys[1]

[1] *Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2] *UCD School of Biosystems Engineering, University College Dublin, Dublin 4*
[3] *Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Co. Wexford*

Pasture production, length of the grazing season and profitability of milk production are curtailed on heavy wet soils. The overall objective was to examine ways of improving productivity on such soils by lessening pugging/poaching damage and relieving soil wetness. In one study the impact of treading by both Holstein-Friesian (HF) cows (mean live-weight 570 kg) and Jersey × Holstein-Friesian (JX) (499 kg) was compared. Soil physical properties, soil surface deformation and herbage yield were measured and found to be unaffected by breed. Hoof-print depth was greater under HF (39 vs 37 mm, s.e. 0.5 mm). Surface loading pressure was the same for both breeds due to the relationship between live weight and hoof size. Using the lighter JX cow offered no advantage in terms of lowering the negative impact of treading on soil physical properties, poaching damage or herbage production compared with the heavier HF cow. A concurrent study examined the performance of mole drains and gravel mole drains on a clay-loam soil over 12 rainfall events. Treatments were: (A) un-drained control, (B) mole drainage installed in January 2011 (suboptimal), (C) mole drainage installed in July 2011 (optimal) and (D) gravel mole drainage installed in July 2011. Mole and gravel mole drainage were effective in removing excess water. Gravel mole drainage was more effective than mole drainage in this soil type. Mean total drain flow was greater ($P<0.05$, s.e. 0.56 mm) in treatment D (7.4 mm) than either treatment B (3.8 mm) or C (4.2 mm). Flow from the drainage treatments was seen to reduce with time due to the deterioration of soil macropores formed during moling in persistent wet weather. Mole drains were effective for approximately 2 years. Conventional mole drainage, repeated every 2 years could provide adequate drainage at low cost on this site.

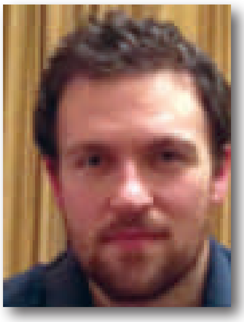


Biomethane production from grass silage

David M. Wall[1,2,3], Padraig O'Kiely[3], Jerry D. Murphy[1,2]

[1] *Bioenergy and Biofuels Research Group, Environmental Research Institute, University College Cork, Cork*
[2] *School of Engineering, University College Cork, Cork*
[3] *Teagasc Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath*

The Renewable Energy Directive (2009) requires that 10% of all energy in transport in Ireland must be renewable by 2020. Second-generation biofuels such as grass biomethane can be used to comply with such targets. Ireland has a temperate climate which can potentially achieve high annual yields of grass in a European context. Surplus grass, in excess of livestock requirements, could serve as an excellent feedstock for biomethane production. Batch digestion studies indicated that co-digestion of dairy slurry with grass silage quantities equivalent to 1.1% of grassland in Ireland, on a 50:50 volatile solids (VS) basis, would generate over 10% renewable energy supply in transport (RES-T). The industry proposed would equate to 170 digesters, each treating 10,000 t a^{-1} of grass silage and 40,000 t a^{-1} of dairy slurry. To highlight potential process limitations for the production of biomethane on Irish farms, a continuous digestion study of grass silage and co-digestion of grass silage with dairy slurry at different mix ratios was undertaken using six continuously-stirred tank reactors. The trial was run for a period of 70 weeks. The organic loading rate (OLR) was increased incrementally from 2.0 to 4.0 kg VS m^{-3} d^{-1} for all reactors. Optimum conditions were assessed for mono-digestion of grass silage at an OLR of 3.5 kg VS m^{-3} d^{-1} generating a specific methane yield (SMY) of 398 L CH_4 kg^{-1} VS. Increasing the OLR to 4.0 kg VS m^{-3} d^{-1} inhibited the SMY by 12%. Co-digestion with 20% dairy slurry was found to be optimal at an OLR of 4.0 kg VS m^{-3} d^{-1}, generating a SMY of 349 L CH_4 kg^{-1} VS. Supplementation of deficient trace elements, specifically cobalt, iron and nickel, was shown to increase the SMY for mono-digestion of grass silage and improve the volatile fatty acid profile of the reactor.



Animal demographic indicators of flock performance on Irish sheep farms

K. Kilcline[1,2], C. O'Donoghue[1], T. Hennessy[1], S. Hynes[2]

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

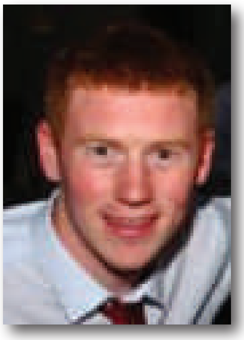
Successive CAP reforms have led to the expectation of a more market orientated outlook for livestock production systems in the EU. Given that Irish farmers are considered price takers in a globally traded market with little scope to affect meat prices, any strategies to improve margins necessarily focus on increasing output volume to increase output value or cost minimisation practices. In line with contemporary research and extension advice, farmers have two main strategies for increasing output; increased stocking rates through improved grassland management and or increased ewe output through targeted breeding. Our research findings indicate that despite the expected changes in producer priorities post decoupling, Irish sheep farms exhibit relatively low levels of technical performance and which have been deteriorating over time. To date, there has been no in-depth research conducted on the gap between farm-level performance and industry targets set out under Food Harvest 2020. Our research investigates the structure and characteristics of farms that are achieving various levels of financial and technical performance and position the performance of the national flock relative to the industry roadmap. Raw NFS data files not previously manipulated for research purposes are used to capture monthly animal data flows for the sample of NFS sheep farms for the three year period 2008 – 2010. Utilising this data we identify and analyse key herd performance indicators including stocking, reproduction, mortality, culling, and replacement rates. These "Livestock Demographic Parameters" are important indicators for estimating and modelling flock dynamics and production, combining two drivers of flock performance: the biological characteristics of the stock on the farm and the farmers' herd management practices. This information also provides important input parameters for a "Sheep Systems Bioeconomic Model**"** as part of the project's wider research objectives. Results indicate the potential of improved breeding and grassland management technology adoption to drive output per hectare and minimise costs which will be necessary in bridging the gap between actual performance on farms and the targets set out in the sheep sector roadmap under Food Harvest 2020.

Do formal family farm arrangements provide an environment which facilitates young farmer innovation more readily than the more conventional informal family farm arrangements?

J. McKillop[1, 2], K. Heanue[1], J.Kinsella[2]

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

This research examines whether formal farm arrangements such as farm partnerships and leasing agreements, provide an environment which facilitates young farmer innovation more readily than the more conventional informal family farm arrangements. A positive environment for innovation is hypothesised if the family farm arrangement generates autonomy in decision making for the young farmer, a situation which is likely to arise within a formal arrangement. A case study approach was used, consisting of semi-structured interviews with 12 young farmers from a variety of formal and informal family farm arrangements in Counties Galway and Wexford. Different levels of autonomy were identified between those working in formal farm arrangements versus those in informal family farm arrangements. For young farmers in the former, they were solely in charge of the technical or tactical management decisions, whereas strategic management decisions the young farmer and parent or both parents were involved. These farms were more innovative as measured by the number of key best practices implemented on the farm. For those young farmers in informal family farm arrangements, technical or tactical management decisions were taken jointly by the young farmer and his parent, while strategic management decisions were taken primarily by either one or both parents. These farms were less innovative. Common to the formal farm arrangements was a history of intra family communication about the future of the farm prior to the establishment of the formal arrangement. Such communication facilitated smoother intra family working relationships in general, which in turn created an environment more conducive to changing farm practices and trying out new ideas.



Drivers of consumer choice, perception and acceptance of new cheese products and reformulations

É.Heffernan[1,2], S.McCarthy[1], M. McCarthy[2]

[1]*Teagasc Food Research Centre, Ashtown, Dublin 15*
[2]*Department of Food Business and Development, University College Cork, Cork*

Food Harvest 2020 has set a 50% increase in milk production by 2020 from the 2007-2009 base figures. Cheese has been targeted as an important end product for this increased milk pool because of the high global consumption levels, its high end-use versatility and potential for added value. Consequently, Food Harvest 2020 calls for substantial growth in Irish cheese production, in both volume and specific varieties, over the next decade. The development of new value added products that meet consumer needs will maximise the return for cheese. As new product development (NPD) is a costly and high risk activity for firms, it is important to create a product that truly meets consumer needs. Involving the consumer in the early stages of the NPD process is critical to market success. Furthermore, involving the first buyers of new products in a specific domain can help refine a product. Thus, cheese innovators were identified, using the Domain Specific Innovativeness scale, and recruited for qualitative focus groups (6 participants * 5 groups with varying demographics) to identify the drivers of cheese consumption and test a set of concepts developed in line with market trends. Acceptance of concepts varied across life stage and depended on the perceived need and personal benefit of the product. Consumers were more willing to accept products where the benefit of added ingredient was familiar to them and already established in other food formats. Elaboration on potential benefits and effective clear communication were pivotal for potential acceptance of modified or value added cheese products. Using outputs from the marketing review and focus groups, a range of new cheese concepts with varying attributes will be assessed in a quantitative survey in Irish and UK adults. By means of conjoint analysis, the preferred combination of attributes for new cheese concepts will be identified.

POSTER ABSTRACTS

Predicting grain protein concentration in malting barley
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Investigation of the prebiotic potential of polysaccharide rich extracts from Irish seaweeds using an *in* vitro faecal fermentation model.
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POSTER ABSTRACTS *(continued)*

Haplotype-specific interleukin 8 production in Holstein-Friesian calves following an intravenous LPS challenge
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Development of a dynamic, mechanistic whole farm model for grass based dairy systems
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Supplementation of grazing lactating dairy cows – effects on production, nutrient use efficiency and milk quality
M. Reid

Investigating land-use in medieval Ireland
M. Corcoran

Predicting grain protein concentration in malting barley

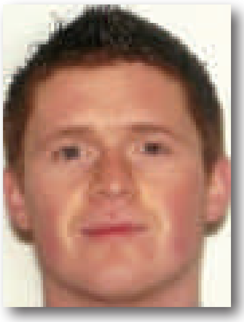
Eamon Nolan[1,3], Richie Hackett[1], Ian Bingham[2], John Spink[1] and Caroline Nichol[3].

[1] Teagasc Crops, Environment & Land-Use Research Centre, Oak Park, Co. Carlow.

[2] SRUC, Crop and Soil Systems, West Mains Road, Edinburgh, EH9 3JG.

[3] University of Edinburgh, Crew Building, The King's Buildings, West Mains Road, Edinburgh EH9 3JN.

Grain protein content of malting barley is a major quality criterion with restricted protein content of 9.5-11.5%. Grain protein concentration (GPC) is a product of grain nitrogen (N) concentration multiplied by a factor of 6.25. It is determined by grain yield and grain N accumulation per unit area. Predicting both parameters independently should facilitate accurate prediction of GPC. Two experiments of spring barley (cv. *SY Taberna*) were established in Oak Park, Co. Carlow and Knockbeg, Co. Laois in 2013. Treatments included six fertiliser N levels (0-210 kg N/ha – 30 kg N/ha applied at sowing with the remainder applied at mid-tillering) each with or without an additional 30 kg N/ha applied at anthesis. Anthesis N was applied to stimulate increased post anthesis N uptake. Anthesis measurements of canopy reflectance using a Crop Circle instrument and estimates of soil nitrogen availability were collected. Grain yield, GPC and grain N accumulation were determined at harvest. For the Oak Park trial, where fertiliser had been applied a significant relationship between Normalised Difference Vegetative Index (NDVI) measured at anthesis and grain yield, grain N accumulation and GPC was determined. However, for yield, the proportion of variation accounted for was low. For grain N accumulation and GPC, but not for yield, the relationship was affected by the application of N at anthesis. The 2013 season experienced uncharacteristic heat stress and drought during July. NDVI was not a strong indicator of final grain yield, which may be the result of restricted grain filling due to conditions that occurred subsequent to measurements. It would appear that NDVI cannot be used alone to predict GPC, given that the relationship between NDVI and GPC was influenced by variation in post-anthesis N uptake. Soil mineral N tests at anthesis may contribute to the improvement of the predictive power of this method.



Characterisation of the genetic basis of foliage and tuber blight resistance in the potato variety Setanta using the Infinium 8303 Potato Array

Joseph Mulhare,[1,2*] Dan Milbourne[1], Paul McCabe[2], Steven Kildea[1] Denis Griffin[1]

[1] *Teagasc Crops, Environment & Land-Use Research Centre, Oak Park, Carlow.*
[2] *College of Life Sciences, School of Biology and Environmental Science, UCD Science Centre, Belfield, Dublin 4.*

Upon release, the Teagasc-bred variety, Setanta, displayed high levels of resistance to potato late blight, caused by *Phytophthora infestans*, one of the most serious diseases in worldwide potato production. The arrival of new, aggressive strains, have defeated foliage resistance which was present in Setanta, although preliminary experiments suggested tuber blight resistance remains intact. Identifying quantitative trait loci (QTLs) underlying this tuber blight resistance would prove useful for marker-based breeding of tuber blight resistance in new varieties. A cross was made between Setanta and the blight-susceptible breeding clone C1992/42 and 185 F_1 genotypes were generated. A detached leaflet assay was performed on this population to determine foliage blight resistance using a historical genotype of late blight, to which Setanta is resistant. To determine the tuber resistance, field grown tubers of the population were inoculated with a mixture of new aggressive strains. As a basis for linkage map construction and QTL mapping, the population was analysed using the Illumina Infinium 8303 Potato Array. Preliminary analysis of the Infinium array yielded 1300 simplex SNP's that were suitable for initial linkage map construction. QTLs responsible for 35.2% of the variation in foliage blight were found across chromosomes IV, V and XI in 2013, and 35.5% in 2014. Tuber blight QTLs accounting for 21% of variation in tuber blight were found on chromosomes V and XII in 2013.The lack of major QTLs for tuber blight resistance suggests that this trait is under polygenic control. Both maturity independent QTLs associated with foliage blight, (chromosome IV and XI), were mapped in the regions of QTLs that were discovered in previous genetic mapping studies. Tissue specific phenotyping of tubers (periderm, cortical and medullary resistance assays), yielded significant differences in the population while also showing no correlation between each resistance mechanism, suggesting they act independently of each other._

Physiology of *Fagus sylvatica* and *Quercus robur* seedlings in response to shading

Ignacio Sevillano[1,2], Ian Short[1], Conor O'Reilly[2], Olga Grant[2], Jerry Campion[1]

[1]*Forestry Development Department, Teagasc Food Research Centre, Ashtown, Dublin 15*
[2]*UCD Forestry, School of Agriculture & Food Science, University College Dublin, Dublin 4*

There is a growing demand for research regarding the thinning of broadleaf forests in Ireland. Broadleaf planting has become important in recent years, with European beech (*Fagus sylvatica*) and pedunculate oak (*Quercus robur*) being two of the most popular species planted. Continuous cover forestry is increasing as an alternative to clearfelling and uses the control of light through thinning to produce stand benefits. To determine the effects of shade on physiology of beech and oak, seedlings were grown in the open or under shadehouses (providing 100%, 62%, 51% and 28% of incident photosynthetically active radiation) for two growing seasons (2013 and 2014) in a randomised block design experiment. Results showed different physiological responses in beech and oak under shade, whilst there was no difference between species at full sunlight during the first growing season. Oak seedlings generally showed greater values than beech for the gas exchange parameters (photosynthesis rate, stomatal conductance, water use efficiency) and fluorescence parameters (photosystem II efficiency, electron transport rate) under the different light conditions studied during the first growing season. In contrast, maximum photosynthetic rates were significantly higher in oak than in beech in the open and minor differences were found under shade in the second growing season. Beech seedlings showed greater physiological plasticity than oak seedlings during the first growing season, but the opposite occurred in 2014. Physiological responses during the second growing season are closer to what might be expected for shade tolerant beech and the more light-demanding oak. This simulated study suggests that beech and oak seedlings may require more than a full growing season before they can acclimate to different light conditions. Further work is required in order to gain a better understanding of the physiological adaptations of these broadleaf species to light availability.

Next Generation Sequencing of Mushroom Virus X reveals novel viral community

Greg Deakin[123], Edward Dobbs[2], Julie Bennett[2], Ian M Jones[3], Kerry Burton[2]
Helen Grogan[1]

[1] *Teagasc Food Research Centre, Ashtown, Dublin 15*
[2] *East Malling Research, East Malling, Kent ME19 6BJ*
[3] *Animal and Microbial Sciences, University of Reading, Reading*

Mushroom Virus X (MVX) disease has been associated with a complex of multiple RNA viruses infecting a single organism, the white button mushroom, *Agaricus bisporus*. Next generation sequencing of MVX-infected mushroom samples taken from industry has revealed a collection of at least 19 (16 novel) viruses and 10 RNA molecules of unknown function. All of the identified RNAs are unique and none of the samples contained identical viruses. We are investigating how this complex of viruses interacts with each other and how they may have originated. Seventy per cent (70%) of all described mycoviruses are double stranded RNA; surprisingly in this study all identified viruses have closest similarity to single stranded positive sense RNA viruses. Of these only four fit into existing genera. Fourteen viruses have homology to known viruses, but phylogenetic analysis places them into nine new clades in existing orders or families. Finally, based on our data, we are hypothesising two novel multipartite viruses. The first consists of replicase and capsid molecules which share a conserved 150 base 3’ UTR sequence and have correlated abundance. The second which has only distant homology to any described virus consists of a replicase divided across two RNA molecules. Data-mining of transcriptome and EST databases reveals homologs to both molecules in the same and across a diverse range of hosts. Phylogentics places this virus in a new family within the alpha-like RNA virus super group.

Integrating soil characteristics, land management and soil microbial communities

A. Richter,[1,2] E. Doyle,[2] N. Clipson,[2] R. Creamer,[1] and D. Ó hUallacháin[1]

[1] *Teagasc Crops, Environment and Land Use Research Centre, Johnstown Castle, Co. Wexford*
[2] *School of Biology and Environmental science, University College Dublin, Belfield, Dublin 4*

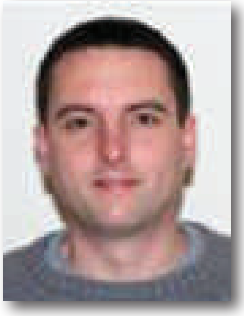
Microorganisms play a key role in soil ecosystem functioning. They are the drivers of nutrient cycling, in particular improving the ability of plants to absorb nutrients, but also protecting them from environmental stress and disease. Despite the vital role soil microbes play, we only understand a fraction of their ecosystem function in relation to improving plant growth and soil health. With increasing pressure on agricultural production there is a need to optimize soil fertility in a sustainable manner on the background of ever-limiting resources. In order to achieve this, a greater understanding of below-ground biodiversity, community structure and functioning is required. This project, in conjunction with the Irish Soil Information System project, identifies how microbial functionality, as well as community structure, depends on soil type, land use and geographical location in Ireland. Soil sampling for biological analysis, including surface and subsurface soils, was performed over two years at 240 different locations across Ireland. An array of different methods was used to analyse the functional, phenotypic and genetic microbial properties. Results were compared to physicochemical, land-use and soil-type parameters. Results for multiple substrate induced respiration across surface horizon soils suggest that abiotic properties such as total nitrogen, organic matter and pH significantly enhance the response of a microbial community to a range of soil carbon sources. Multivariate analysis of respiration profiles showed a significant effect of the drainage class, with poorly drained soils having an overall higher microbial biomass, but lower respiration per unit biomass. In regards to microbial community structures, similarities between geographically distinct soil horizons, as well as soil type profile patterns, could be identified, but were not consistent across all data analysed so far. All results showed that the combination of explanatory variables best describes shifts in soil microbial structure and function.

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

Stephanie Ellis,[1,2] Sean Tyrrel,[1] Karl Richards,[2] Bryan Griffiths,[3] and Karl Ritz[1,4]

[1] *Cranfield University, Cranfield, Bedfordshire, MK43 0AL*
[2] *Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Co. Wexford*
[3] *SRUC, King's Buildings, West Mains Road, Edinburgh, EH9 3JG*
[4] *University Nottingham, Sutton Bonington, Loughborough LE12 5RD*

Enteric pathogens pose a substantial risk to public health. They are shed in the faeces of infected individuals, resulting in their accumulation in sewage sludge. Once this sewage sludge is spread to land, surviving cells may contaminate both food and water. Hence understanding their fate in the soil environment is important. We hypothesised that supplementary nutrients added to 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 such biotic interactions. To test these theories, 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 yeast extract (a balanced source of nutrients) had little effect, but pathogen 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. Furthermore, the matrix to which the nutrients were added had no effect upon *E. coli* decline, implying that the matrix in which highly mobiles substrates are present is of no consequence.

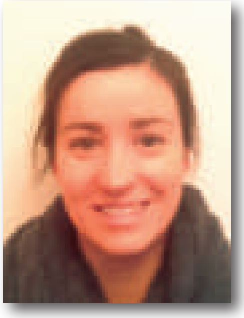


The identification of important areas of plant diversity in Ireland

Aidan Walsh[1, 3], John Finn[1], Matthew Jebb[2], Steve Waldren[3], Caroline Sullivan[4]

[1] *Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Wexford*
[2] *National Botanic Gardens of Ireland, Glasnevin, Dublin 9*
[3] *Department of Botany, Trinity College Dublin, College Green, Dublin 2*
[4] *Department of Environmental Science, Institute of Technology Sligo, Ash Lane, Sligo*

Limited resources necessitate the targeting of measures for the conservation of biodiversity, and such targeting is now a strong requirement of RDP measures and relevant agri-environment schemes. Quantitative methods are required to support such targeting. We investigated two methods to identify Important Areas of Plant Diversity (IAPD) in Co. Fermanagh and Co. Waterford at the tetrad scale (2km x 2km). Our scoring-based approach uses available sources of information on the status and distribution of species to characterise the landscape in terms of plant conservation value. The most valuable sites can then be identified as priority areas. This method is relatively easy to implement but does not consider how individual priority areas complement each other in terms of species representation (known as complementarity). We used two complementarity-based approaches, linear programming and Marxan, to identify sets of priority areas that are efficient at maximising species representation. Marxan identified spatial networks of IAPD that successfully targeted this goal but often failed to guarantee that all target species were represented. Linear programming identified the minimum number of tetrads required to guarantee species representation. The complementarity-based approaches proved more efficient at maximising species representation over fewer tetrads, but are more complex to use and do not characterise the entire landscape.



The effect of nitrogen source on nitrous oxide emissions in spring barley production

L. Roche[1,3], K.G Richards[1], P.J. Forrestal[1], G.J. Lanigan[1], L.J. Shaw[3], M. Gooding[3], R. Hackett[2], and D.P. Wall[1]

[1] *Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Co. Wexford*
[2] *Teagasc Crops, Environment & Land-Use Research Centre, Oak Park ,Co. Carlow*
[3] *University of Reading, UK*

Under the EU climate and energy package 2020, Ireland has to reduce greenhouse gas emissions to 20% below 2005 levels. For arable land, one of the main sources of greenhouse gas emissions is nitrous oxide (N_2O) loss from nitrogen (N) fertilisers. Calcium ammonium nitrate (CAN) is the dominant N fertiliser used and immediately contributes to the soil nitrate pool, increasing the risk of N loss as N_2O. The use of urea fertilisers could help to manage the soil nitrate pool and reduce N_2O emissions. However, urea could increase N loss through ammonia volatilisation and contribute to indirect N_2O emissions. The use of inhibitor technologies, in conjunction with urea, shows potential to manage the soil nitrate pool and reduce N_2O emissions. The objectives of this study were (1) to assess the effect of CAN and urea on N_2O emissions and (2) to evaluate the ability of inhibitors (nitrification inhibitor DCD and urease inhibitor n-BTPT) to mitigate N_2O emissions. Two sites with contrasting soil types and cropping history were used to measure N_2O emissions in 2013 and 2014. Site 1 is a long-term tillage site on free-drained loam and site 2 is a short-term tillage site on poorly drained clay loam which received organic manure until 2012. Nitrous oxide emissions were measured using the static chamber technique. Results for year 1 (2013 (April 2013-April 2014)) and for year 2 (2014 (April 2014 – July 2014)) show that overall emissions from spring barley were relatively small. There was no significant difference in cumulative emissions between CAN and urea. There was a trend for reduced emissions with the addition of DCD to urea, and this was significantly lower at the long-term tillage site (1) in 2014. Early results from this study indicate that the use of DCD in conjunction with urea has potential to mitigate N_2O losses from spring barley production.

The effect of heating temperate grassland on CO_2 emissions

A.B. Jansen-Willems[1,2], C. Mueller[1] and G.J. Lanigan[2]

[1] *Institute of Plant Ecology, JLU, Giessen, Germany*
[2] *Teagasc Crops, Environment & Land-Use Research Centre, Johnstown Castle, Co. Wexford*

In the past century, the earth's surface temperature increased by 0.6°C, and it has been predicted to rise 1.4-5.8°C by the end of this century (IPCC, 2001). Under the new draft Climate and Energy 2030 targets, carbon sequestration in grassland may be permissible for achieving national greenhouse gas targets. It is therefore important to quantify the carbon sink potential of grassland in relation to climate change. The goal of this study was to examine the effect of ecosystem warming on net ecosystem exchange of CO_2 and ecosystem respiration. Sixteen plots on a permanent temperate mixed grassland site were assigned one of the four treatments (+1°C above ambient (T_1), +2°C above ambient (T_2), +3°C above ambient (T_3) and a control ($T_{control}$)). The plots were heated using ceramic infrared heaters. Five years after the heating started, frequent CO_2 flux measurements were taken. Soil respiration was measured monthly, and net ecosystem exchange (NEE) during the months April, July and October. In total, 32,889 valid ecosystem respiration and 2,793 valid NEE measurements were taken. NEE was divided into ecosystem respiration and photosynthetic uptake by modelling the ecosystem respiration. Ecosystem respiration was significantly different under the different treatments ($p<0.001$). T_1 had the lowest respiration, while T_2 and T_3 had the highest ecosystem respiration. Similar patterns were observed for each month, with the lowest respiration observed in T_1, and the highest in T_2 and T_3. Photosynthetic uptake was similar across all treatments in the summer and autumn ($p>0.20$). In spring, the photosynthetic uptake was significantly higher for T_2 compared to any of the other treatments ($p=0.001$). The other treatments were not significantly different from each other. The result of shifting the proportion of photosynthesis/respiration may ultimately result in a lower C sink potential in grasslands with the continuing onset of climate change.

Is the rhizosphere priming effect an important mechanism for nitrogen mineralisation in soil?

Conor J Murphy [123], Elizabeth M Baggs[1], Nicholas Morley[1], David P Wall[2], Eric Paterson[3]

[1] University of Aberdeen, Cruickshank Building, St Machar Drive, AB24 3UU, Aberdeen, Scotland
[2] Teagasc; Environment, Soils & Land-Use Research Centre, Johnstown Castle, Wexford
[3] James Hutton Institute, Craigiebuckler, AB15 8QH, Aberdeenshire, Scotland

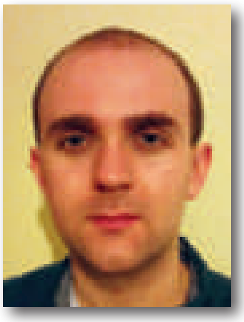
Currently, scientific techniques are inadequate for quantifying the soil's supply of nitrogen over a growing season. This is largely due to our poor understanding of the myriad of evolutionary mechanism developed to release nutrients from soil organic matter (SOM). One such mechanism is the priming effect (PE); this is where microbes utilize labile carbon from roots (root exudates or senescing plant material) for energy and subsequently mineralise SOM for nutrients, inevitably mobilising nutrients from SOM to plant available pools. However, the mechanism and regulators underpinning PE's are virtually unknown. We hypothesized that (1) addition of labile C would increase gross N mineralisation and plant N uptake, and this is soil specific (2) the stoichiometry of primed and basal mineralisation fluxes would be different, indicative of these processes being functionally distinct (3) the presence of fertilizer nitrogen and grazing would reduce priming and plant uptake of SOM derived N. To do this we coupled continuous steady-state ^{13}C labelling and ^{15}N isotope dilution to measure specific gross C and N fluxes from two contrasting soils. Addition of carbon increased gross C and N fluxes from SOM, but the effect was soil specific. The C-to-N ratio of the flux from 'primed' SOM was much lower than that of the basal flux indicating that the release of labile carbon from plant roots functions as a nutrient acquisition response, increasing mineralisation of SOM. Addition of N fertiliser resulted in negative priming of SOM, but overall, and in both soils, the plant accessed more organic-N. Grazing and priming were closely coupled, grazing increased SOM priming. Our results demonstrate that priming effects are an integral component of N mineralisation and should be incorporated into nitrogen management strategies.

Using sediment flux and provenance to target soil erosion management strategies

S.C. Sherriff[1,2], J.S. Rowan[2], P. Jordan[3], A.R. Melland[4], O. Fenton[1], and D. Ó hUallacháin[1]

[1]Teagasc Crops, Environment & Land Use Research Centre, Johnstown Castle, Wexford.
[2]School of the Environment, University of Dundee, Dundee, UK.
[2]School of Environmental Sciences, University of Ulster, Coleraine, Northern Ireland.
[4]National Centre for Engineering in Agriculture, University of Southern Queensland, Toowoomba, Australia.

As excessive sediment delivery from land to water can degrade freshwater habitat quality, this study aimed to quantify suspended sediment flux and identify sediment source areas in intensively managed agricultural catchments. Suspended sediment transport was quantified using calibrated, end-of-catchment turbidity sensors combined with hydrometric data in five catchments across a range of land-use types. Sediment fingerprinting was also used to investigate sediment sources in one catchment. Soils from potential sediment sources (fields, river channel and damaged road verges) and river sediments were analysed for a suite of mineral magnetics components; these ‘tracers’ were statistically analysed to differentiate sources. River sediments, assumed to be a mixture of sources, were statistically un-mixed to quantify the relative contribution of each source. Flux results over three to four years showed that average annual suspended sediment yield (SSY) ranged from 8-25 t/km^2/yr. Differences in SSY between catchments was attributed to soil permeability influencing dominant transport pathways, and land-use type influencing the availability of source material. Despite low to moderate annual average SSYs, high inter-annual variability (up to -83% to +196% of mean SSY) highlighted that the capacity exists, under certain conditions, for extreme sediment transport. Sediment fingerprinting results showed sediment contributions from channel banks, fields, and road verges, were on average 50% (range 17-71%), 33% (range 4-83%) and 17% (range 0-35%) respectively. Integrating sediment source and quantity data show that channel contributions during winter months were significant, and, therefore, mitigation measures should consider channel bank stabilisation in this catchment. These results improve the understanding of the extent and processes underlying soil erosion and sediment delivery in intensive agricultural catchments and can be used to target cost-effective management.

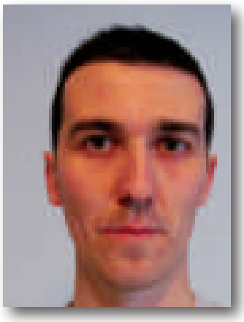


Investigation of the prebiotic potential of polysaccharide rich extracts from Irish seaweeds using an *in* vitro faecal fermentation model.

K. Collins[1,2], CR Strain[3], G. Fitzgerald[2], C. Stanton[1] and R. P. Ross[1,2]

[1] Teagasc Food Research Centre Moorepark, Fermoy Co. Cork
[2] Department of Microbiology, University College Cork,
[3] Northern Ireland Centre for Food & Health (NICHE), University of Ulster, Northern Ireland

Several seaweed polysaccharides (fucans and laminarins etc.) are resistant to degradation by human digestive enzymes and are recognised as dietary fibres. These polysaccharides pass through the GIT intact, until they reach the colon where they act as a source of fermentable substrates for the microbiota. This stimulates the production of SCFAs such as acetate, propionate and butyrate. Here, polysaccharide extracts from the Irish seaweeds *Fucus serratus* (FSE) and *Chondrus crispus* (CC) were investigated for prebiotic potential using an *in vitro* faecal fermentation model. It was found that total production of SCFAs was significantly increased (P <0.05) during the FSE fermentation after 5hrs (84%), 10hrs (65%), 24hrs (48%), 36hrs (44%) and 48hrs (45%) and during the CC fermentation after 10hrs (16%), 24hrs (14%) and 36hrs (18%). During the FSE fermentation, propionate production was significantly increased (p<0.05) after 5hrs (212%), 10hrs (163%), 24hrs (134%), 36hrs (130%) and 48hrs (130%) and acetate production was significantly increased after 5hrs (67%), 10hrs (47%), 24hrs (43%) and 36hrs (41%). In the CC fermentation, production of propionate was significantly increased (p<0.05) after 24hrs (41%) and 36hrs (42%) while acetate production was significantly increased after 10hrs (16%). 16s DNA sequencing was carried out to access the impact of the extracts on the *in vitro* microbiota. At the family level, the FSE extract gave rise to an significant (p-value <0.05) increase in levels of Proteobacteria, while at the genus level the CC extract significantly reduced levels of the pathogens *Pseudamonas* and *Enterobacter* and the opportunistic pathogen *Klebsiella*. SCFA are associated with several health benefits. Acetate is thought to play a role in controlling inflammation and pathogen invasion while propionate is positively associated with satiety and protection against obesity. The inclusion of seaweed polysaccharides in the diet may stimulate the activity of the microbiota and help improve colonic health.

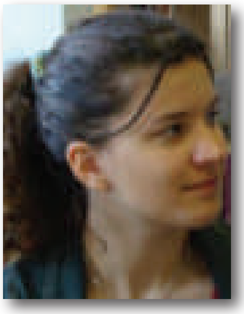


Haplotype-specific interleukin 8 production in Holstein-Friesian calves following an intravenous LPS challenge

B. Stojkovic[1,2], R. McLoughlin[2] and K. G Meade[1]

[1] *Teagasc Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath.*
[2] *Host Pathogen Interactions Group, School of Biochemistry and Immunology, Trinity Biomedical Sciences Institute, Trinity College, Dublin 2.*

Interleukin 8 (IL8) is a proinflammatory chemokine involved in neutrophil recruitment and activation. IL8 production is rapidly activated in response to microbial products and oxidative stress. Lipopolysacharide (LPS), also known as endotoxin, is a gram-negative bacterial cell wall component and it is a potent inducer of IL8 production. In addition, levels of IL8 are significantly increased in the milk and lymph nodes of cows with *E.coli*- or endotoxin-induced bovine mastitis. IL8 is encoded by a 3.7 kb long gene that contains 4 exons and 3 introns with 2.1 kb long upstream promoter region, which is characterised by 29 novel polymorphisms. It was also shown that these polymorphisms segregate into only two distinct haplotypes, which are different in their ability to activate *IL8* expression in bovine mammary epithelial and endometrial cells *in vitro*. In the present study, we aimed to investigate the haplotype-specific IL8 expression in response to LPS *in vivo*. Nine and eight Holstein-Friesian calves of IL8 haplotype 1 and 2, respectively, were challenged with the predetermined concentration of LPS and IL8 expression at both gene and protein level was measured at multiple time points. A linear mixed model, with the fixed effects of IL8 haplotype and time post-challenge and the interaction of IL8 haplotype and time, was fitted. Significant effects of the IL8 haplotype and time post-challenge were found. IL8 haplotype 2 showed significantly higher IL8 expression and this difference was observed at 6h, 12h, 24h, 48h, and 192h post-stimulation and at 2h and 24h post-stimulation for protein and gene expression, respectively. Observed difference in the capacity for IL8 production between the two haplotypes might have important consequences for the neutrophil migration post-infection which could lead to the differential ability to fight infection in cattle.

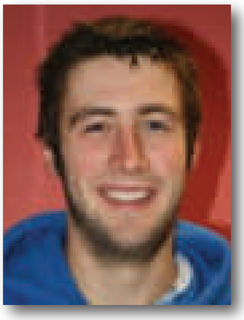


Development of a dynamic, mechanistic whole farm model for grass based dairy systems

E. Ruelle[1,2] L. Delaby[3], M. Wallace[2] and L. Shalloo[1]

[1] *Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork*
[2] *School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*
[3] *INRA-Agrocampus-Ouest, UMR 1348, Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'Elevage, Domaine de la Prise, 35590 Saint Gilles, France*

The removal of milk quotas in 2015 presents an opportunity to increase milk production on many farms for the first time in a generation. However, this policy change coincides with greater milk price fluctuation as the dynamic of global milk supply and demand interact. Models have the potential to allow the investigation of the effect of a policy change and the interaction of management change at farm level. The objective of this PhD was to develop a mechanistic, dynamic whole farm model of grazing-based dairy systems. Within this study, the Pasture Base Herd Dynamic Milk (PBHDM) model was developed which simulates each animal individually with a daily time step. Model outputs include daily milk production, intake, BCS, fertility, mortality and culling. The PBHDM model simulates grazing through simulating each individual animal in each paddock. Each paddock is characterised by its area, grass height and biomass. Intake of the animal at grazing is dependent on intake capacity of the animal but also pre- and post-grazing grass height. The model was evaluated by simulating grass-based experiments which were operated in Ireland and in France between the period of 2009 and 2011. Model outputs were compared to experimental outputs for milk yield per day, per lactation, body condition score and post grazing grass heights. The model outputs showed a relatively high level of accuracy for daily milk yield, with a relative prediction error of 11% and 12% for French and Irish experiments respectively. It is generally assumed that a relative prediction error between 10 and 20% indicates a relatively acceptable model prediction. The model was very accurate in predicting the pre and post-grazing height and body condition score. The model will be used to investigate the effects of various technical, institutional and policy change on the overall farm system.

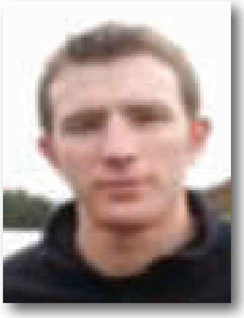


Productivity and persistency responses to simulated and animal grazing of perennial ryegrass genotypes

P.A. Cashman[1, 2], T.J. Gilliland[2, 3], M. O'Donovan[1], M. McEvoy[1].

[1] Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2] Institute for Global Food Security, School of Biological Sciences, Queen's University, Belfast, BT7 1NN, Northern Ireland
[3] Agri-Food and Biosciences Institute, Plant Testing Station, Crossnacreevy, Belfast, BT5 7QJ

The objective of this thesis was to investigate changes within perennial ryegrass cultivars over time. The effect of animal grazing on cultivar performance and the effect of cultivar on animal performance were also investigated. These factors were examined in a number of experiments. Large genetic diversity exists with perennial ryegrass cultivars, creating the potential for directional selection to occur within sown swards. Cultivars were managed under a number of sward conditions before plants were extracted and compared to the original seed lines. Directional selection within perennial ryegrass was detected; however, the occurrence and magnitude of this selection was influenced by both cultivar and sward management. Of the twelve cultivars tested in an Irish climate, directional selection was detected in 8 and 10 cultivars under simulated grazing and conservation, respectively. No such change was observed under sheep grazing management in a New Zealand climate. Phenotypic measurement from the Distinctness, Uniformity and Stability protocol proved to be affected by directional selection within cultivars under mechanical defoliation. When directional selection did occur, the plants that survived had a smaller mean phenotype in comparison to the original seed lines, suggesting plants with a lower yield potential survived. Simulated grazing was found to be a good predictor of the DM yield and digestibility of cultivars under animal grazing, supporting the reliability of information generated during recommended list trials to identify elite cultivars for utilisation by grazing animals. Sward chemical and structural attributes were found to influence animal performance of lactating dairy cows. A cultivar that produces large leaves, in conjunction with a low sheath height, and can maintain a high digestibility across the season, will likely optimise animal performance from grazed pasture. Cultivars that exhibit declining sward digestibility in the autumn period can significantly inhibit animal performance.



Supplementation of grazing lactating dairy cows – effects on production, nutrient use efficiency and milk quality

Michael Reid[1, 2], Eva Lewis[1], Chris Elliott[2]

[1]Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork
[2]Queen's University Belfast, University Road Belfast, BT7 1NN, Northern Ireland

The objective of this PhD was to investigate the effects of supplementary feeds on milk production, nitrogen utilization efficiency (NUE) and milk processability when offered in early or late lactation to grazing spring-calving dairy cows. Four studies were carried out, with perennial ryegrass as the primary feed. Two early lactation studies were completed. The diet consisted of 13 kg DM grass with 4 kg DM concentrate. In the first study, the concentrates differed in crude protein (CP) and phosphorus (P) concentration. Blood P was reduced to below acceptable with a low P concentrate. When a high CP concentrate was fed, milk urea nitrogen concentration was increased, milk heat stability at pH 6.8 was reduced and urinary nitrogen excretion was highest, all of which are undesirable. In the second study the difference among treatments was the concentrate energy source (fiber or starch) and rate of degradation (rapid or slow). A starch-based rapidly degradable concentrate decreased milk fat concentration and solids yield, and milk heat stability was negatively affected, which are all undesirable. Supplementing with a fiber-based, rapidly degradable concentrate increased milk true protein and casein concentration, which is positive from a processability perspective. Two studies were carried out in late lactation. The first used similar quantities of grass silage or concentrate as supplements. Offering no supplementation reduced milk yield, solids yield and true protein concentration. Offering concentrate increased milk yield and solids yield, and improved NUE, compared to no supplementation or supplementing with grass silage. The second study investigated the effect of using different quantities (3 or 6 kg DM) of grass silage or concentrate as supplementation. Milk yield and solids yield was increased to the greatest extent when 6 kg DM concentrate was used. Increasing the dietary supplement: concentrate ratio decreased milk true protein concentration, indicating that milk processability was negatively affected. Grass only treatments excreted the greatest amount of N suggesting that, in late lactation, supplementation improves NUE.

Investigating land-use in medieval Ireland

M. Corcoran[1,2], S. Green[2], T. O'Keeffe[1] & S. Davis[1]

[1] *School of Archaeology, University College Dublin, Belfield, Dublin 4, Ireland*
[2] *Teagasc Rural Economy & Development Programme, Ashtown, Dublin 15*

The objective of this research project is to more accurately chart & understand the nature of open-field agriculture and the process of enclosure from the medieval period up to that of peak corn production beginning in the 18th century. There are three study areas for this project, in the east, north-west and south of the country, to account for spatial variation in generalised agro-climatic and socio-political environments. Satellite imagery & LiDAR data are used in order to more accurately quantify & analyse the spatial extent and morphology of relevant archaeological landscape features. This is in conjunction with traditional desk-based research using primary records and historic mapping. Specific sites are also targeted for structural & environmental analysis to understand site-specific soil & drainage conditions and past vegetation growth. This is carried out through soil profiling, pollen & testate amoeba analysis and measurements of humification in peatland environments. Preliminary results are as follows: *(1) Settlement density*. A potential 534 new archaeological sites were identified using aerial imagery & LiDAR-derived visualisations, of which 117 are most likely of medieval origins. *(2) Land-use intensity*. Landscapes previously poorly understood or interpreted as isolated and/or associated with non-arable use have been reinterpreted on the basis of new structural information. Several examples of problematic site-types (e.g. moated sites) have been shown to have intensively-managed agricultural landscapes. *(3) Enclosure*. Evidence has been found of phases of landscape enclosure far pre-dating the assumed boom in enclosure at the end of the medieval period (c. 16th – 17th centuries AD). *(4) Drainage*. Analysis of relict agricultural ridges, drains and their associated field systems has enabled the creation of models of agricultural land-use. These, in-turn, have highlighted significant variation both across geographic space and within traditional archaeological landscape / site types.

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Contact Details:

Teagasc Head Office
Head Office, Oak Park, Carlow
Tel: +353 (0) 59 9170200
Fax: +353 (0) 59 9182097
Email: info@teagasc.ie

www.teagasc.ie

Teagasc
Agriculture and Food Development Authority