

Research

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RLS: another disease for
barley to contend with

SPECIAL FEATURE:
INTERNATIONAL YEAR
OF PLANT HEALTH

FACTORS AFFECTING
PREGNANCY PROTEINS

MILKEV

MANAGING MANURE

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Prioritising plant health to preserve food production and quality

The Food and Agriculture Organization of the United Nations (FAO) estimates that we need to increase agricultural production by 60 % to meet the world's projected population growth by 2050. This is a formidable challenge, made even more sobering by the fact that each year we as a global community lose 40% of our food crops due to pests and disease damage. Within Ireland and the broader EU, farmers mitigate such potential losses with the use of plant protection products (PPPs) and other agronomic practices. However, at the heart of Europe's Green Deal 'Farm to Fork' Strategy is the need to decrease the environmental footprint of food production by reducing the overall use and risk of chemical pesticides by 50 % by 2030. Achieving this will require an integrated, whole-systems approach that must exploit all available technologies to promote food quality and protect harvests against pests and pathogens, which are continuously evolving to overcome crop management practices placed in their way. Increasing temperatures and milder winter periods compound the issue by promoting the over-wintering of insects, when typically pest populations are knocked back before the next growing season commences. To raise awareness of the socio-economic importance of protecting plant health, the UN has designated 2020 as the International Year of Plant Health (IYPH2020). Protecting plants from pests and diseases is far more cost effective than dealing with full-blown plant health emergencies, as our history so aptly reminds us. While 'epidemiology' has become a familiar word to all due to Covid-19, the principles of health management remain the same, irrespective of the disease and its host. Key to ensuring plant health is accurately quantifying the incidence and distribution of a pathogen/pest and investigating those control factors that can impede its progress. In this issue of *TResearch*, we highlight some of the exciting research across Teagasc to identify control strategies against important diseases of mushrooms, barley, potato and laurel. Each respective crop has significant challenges, but increasing the resilience and efficiency of plant varieties as part of an integrated management approach is key to maintaining plant health and supporting sectoral-level sustainability.



Ewen Mullins

Head of Crop Science Department
Teagasc, Oak Park, Carlow

Tosaíocht a thabhairt do shláinte phlandaí chun táirgeadh agus cáilíocht bia a chaomhnú

Measann Eagraíocht Bia agus Talmhaíochta na Náisiún Aontaithe (FAO) gur gá táirgeadh talmhaíochta a mhéadú le 60 % chun freastal ar fhás réamh-mheasta daonra an domhain faoi 2050. Dúshlán mór atá ann, go háirithe i bhfianaise go gcaillimid mar phobal domhanda 40 % dár mbarra bia gach bliain mar gheall ar lotnaidí agus ar dhamáiste ó ghalair. In Éirinn agus san AE i gcoitinne, maolaíonn feirmeoirí cailteanais fhéideartha den chineál sin trí úsáid a bhaint as táirgí cosanta plandaí (PPPanna) agus as cleachtais agranamaíocha eile. Mar sin féin, i gcoilár Straitéis 'Ón bhfeirm go dtí an Forc' Chomhaontú Glas na hEorpa tá an gá le lorg comhshaoil táirgeachta bia a laghdú, trí úsáid agus riosca foriomlán lotnaidicídí ceimiceacha a laghdú le 50 % faoi 2030. Chun é seo a bhaint amach, beidh gá le cur chuige comhtháite córas iomlán a chur i bhfeidhm. Leis sin, ní mór na teicneolaíochtaí go léir atá ar fáil a úsáid chun cáilíocht bia a chur chun cinn agus chun fómhair a chosaint ar lotnaidí agus pataiginí, atá ag teacht chun cinn go leanúnach chun cleachtais bhainistíochta barr a chuirtear ar a mbealach a shárú. Déanann teochtaí méadaithe agus tréimhsí níos séimhe an gheimhridh an scéal níos measa trí ró-gheimhriú feithidí a chur chun cinn, nuair a dhéantar daonraí lotnaidí a bhualadh siar de ghnáth sula dtosaíonn an chéad séasúr fáis eile. Chun feasacht a mhúscailt faoin tábhacht shocheacnamaíoch a bhaineann le sláinte phlandaí a chosaint, tá 2020 ainmnithe ag na Náisiún Aontaithe mar Bhliain Idirnáisiúnta na Sláinte Plandaí (IYPH2020). Tá sé i bhfad níos éifeachtaí ó thaobh costais de plandaí a chosaint ar lotnaidí agus galair ná déileáil le héigeandálaí sláinte plandaí lánfhorbartha, mar a mheabhraíonn ár stair dúinn go hiomchuí. Cé go bhfuil 'eipidéimeolaíocht' ina fhocal aitheanta do gach duine mar gheall ar COVID-19, tá prionsabail na bainistíochta sláinte mar an gcéanna fós, beag beann ar an ngalar agus a óstach. Tá minicíocht agus dáileadh pataigine/lotnaide a chainníochtú go cruinn agus imscrúdú a dhéanamh ar na tosca rialaithe sin a d'fhéadfadh bac a chur ar a dhul chun cinn ina gcodanna rithábhachtacha maidir le sláinte phlandaí a áirithiú. San eagrán seo de *TResearch*, tarraingímid aird ar chuid den taighde iontach ar fud Teagasc chun straitéisí rialaithe a aithint i gcoinne galar tábhachtach muisiriún, eorna, labhrais agus práta. Tá dúshlán shuntasacha roimh gach earnáil faoi seach ach tá athléimneacht agus éifeachtúlacht cineálacha plandaí a mhéadú mar chuid de chur chuige bainistíochta comhtháite rithábhachtach chun sláinte phlandaí a chothabháil agus chun tacú le hinbhuanaitheacht ar leibhéal na feirme.



Ewen Mullins

Ceann na Roinne Eolaíochta Barra
Teagasc, Páirc na Darach, Ceatharlach

Teagasc events move online

Due to the ongoing uncertainty around Covid-19 and public events, Teagasc has moved many of its events online for the foreseeable future. Teagasc's Rural Economy and Development Programme and Food Industry Development Department are hosting a series of webinars. In addition, Teagasc's tillage researchers and advisors hosted a series of virtual crops walks.

The Signpost Series, 'Pointing the way to a low emissions agriculture', is organised through the Teagasc ConnectEd service, with the support of the National Rural Network, Dairy Sustainability Ireland and Food Drink Ireland Skillnet.

'Building a Sustainable Irish Beef Sector' is the theme for Teagasc's virtual beef week this July, which will involve two webinars each weekday. This will be accompanied by a continuous stream of content through social media platforms. 'Talking Timber' – our popular annual timber marketing event – is also back, this time virtually, in July. A number of 'Let's Talk' twice-monthly webinar series are taking place covering the following topics: dairy, cattle and sheep, equine, pigs and poultry.

Keep an eye on the Teagasc website and social media for updates on all our online events – www.teagasc.ie/webinars.

Tracking microorganisms through the dairy production process

Microorganisms from the environment can enter the dairy supply chain at multiple stages, including production, milk collection, and processing, with potential implications for quality and safety. The ability to track these microorganisms can be greatly enhanced by the use of high-throughput DNA sequencing (HTS), say Teagasc and UCC researchers, who recently published a paper in the peer-reviewed journal *mSystems* on 'Tracking the Dairy Microbiota from Farm Bulk Tank to Skimmed Milk Powder'.

According to lead author, Teagasc Walsh Scholar Aoife McHugh: "Microorganisms can enter and persist in dairy production at several stages of the processing chain. Detection of microorganisms within dairy food processing is currently a time-consuming and often inaccurate process. This study provides evidence that high-throughput sequencing can be used as an effective tool to accurately identify microorganisms along the processing chain". In addition, says Aoife, it demonstrates that the populations of microbes change from raw milk to the end product. Routine implementation of high-throughput sequencing would elucidate the factors that influence population dynamics. "This will enable a manufacturer to adopt control measures specific to each stage of processing and respond in an effective manner, which would ultimately lead to increased food safety and quality," explains McHugh.

Senior author, Head of Food Biosciences at Teagasc Paul Cotter, noted that: "This study has very important implications for the food industry in terms of tracking how spoilage and disease-causing microorganisms can enter into the food chain. It is of particular note that it was carried out through testing of real-world milk samples collected from over 50 farms and at the various steps along the process until the resultant skim milk powder product was made". This study also inspired the EU-funded MASTER project, led by Paul, whereby this approach will be further developed through testing across 100 food processing companies around Europe. These initiatives parallel similar applications of HTS around the globe to track the movement of microorganisms in other facilities, including hospitals.

Irish Coronavirus Sequencing Consortium

Teagasc researchers have received funding to track the genetics of the Covid-19 virus in Ireland. The virus that causes Covid-19, SARS-CoV-2, contains genetic information that can change over time. If we can 'read' those changes, we will have a better map of how the virus spreads across regions. Being able to determine the genetic make-up of the viruses circulating in Ireland will support efforts to respond to clusters of infection as they arise, and minimise the spread of the virus. Collecting the sequences of the viruses in Ireland will also mean that we can pick up on important new changes that could affect the ability of the virus to cause disease or to evade treatments or vaccines. Science Foundation Ireland is to fund a National Coronavirus Sequencing Consortium to read and analyse the genetic make-up of the SARS-CoV-2 virus in patient samples in Ireland. The data about the genetic sequences of the viruses will be freely available, allowing epidemiologists to monitor trends in Ireland and internationally, and to watch for changes in the virus that could have an impact on the development and delivery of treatments and vaccines.

The virus that causes Covid-19 contains RNA that can change slightly over time. Unless we track those changes comprehensively in Ireland, we won't have a clear picture of how strains of the virus are spreading, nor will we be able to spot changes in the virus that could affect how it causes disease, or how we could develop treatments or vaccines. The consortium is led by the Teagasc/APC Microbiome Ireland Sequencing Centre at Moorepark, with partners University College Cork, Cork University Hospital, the National Virus Reference Laboratory, University College Dublin, Beaumont Hospital, Genomics Medicine Ireland, Trinity College Dublin/St James's Hospital, University of Limerick (UL)/University Hospital Limerick, the National University of Ireland, Galway, and Maynooth University. The consortium will 'read' the RNA sequence of viruses isolated from samples of patients who have lab-confirmed infections of Covid-19 and make the sequence information freely available for analysis. This information will allow experts to monitor genetic changes in the virus and quickly spot developments that could affect human health and treatment or vaccination.

Integrated Pest Management (IPM) approach to mitigate BYDV of cereals

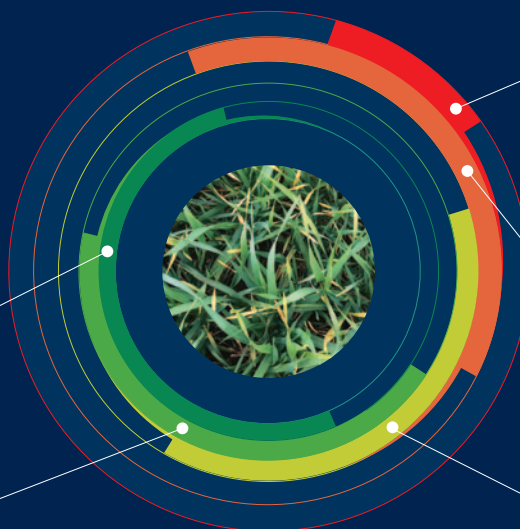
Barley yellow dwarf virus (BYDV) is transmitted from plant-to-plant by aphids. Primary crops susceptible to BYDV include barley, wheat and oats with infected plants visible due to yellowing of the leaves (central image). Working out from the centre, five layers of measures are described to assist in BYDV management

ROTATION AND CROP CHOICE

INCREASED DIVERSITY OF CROPS IN ROTATION MINIMISES RISK. MINIMISE AREA OF SUSCEPTIBLE VARIETIES. SELECT VARIETIES WITH RESISTANCE/ TOLERANCE TO BYDV

TIME OF PLANTING

PLANT LATER FOR WINTER CROPS
PLANT EARLIER FOR SPRING CROPS



PPP

ONLY USE WHERE NECESSARY
PROTECT NON-TARGET SPECIES

MONITORING/EVALUATION

USE FORECASTING/MONITORING TOOLS
COUNT/MONITOR NUMBERS POST PLANTING
MONITOR FOR CONTROL FAILURES

BIOLOGICAL CONTROL

ENCOURAGE NATURAL ENEMIES, BUFFER ZONES,
AND EFAS. DECREASE PESTS BY REMOVING FOOD SOURCES
PREVENT 'GREEN BRIDGE'

Teagasc games and experiments for children at home



Teagasc has developed a range of engaging STEM (science, technology, engineering and maths) activities and fun games for children currently at home due to the Covid-19 pandemic.

Teagasc has developed a range of engaging STEM (science, technology, engineering and maths) activities and fun games for children currently at home due to the Covid-19 pandemic. Ever wondered about how to make instant ice, water rainbows or extract DNA from a strawberry? Then this online content is for you. Catriona Boyle, Teagasc's Science Communications and Outreach Officer, said: "We have been developing games and activities and a YouTube playlist with experiments for families to carry out at home. We hope children and parents alike enjoy doing these activities and experiments at home and no special equipment is needed. We have been developing them over recent months and plan to add more experiments over time. Our aim is to deliver content that is both entertaining and educational".

As part of the initiative to keep pupils learning in a fun and innovative way, Teagasc has started a YouTube series called 'Science Experiments at Home', where Teagasc researchers show children different experiments they can do from home with materials that are found in every house. In a very entertaining episode that explores the science of DNA extraction, instant ice and also other experiments, Horticultural Technologist Brian McGuinness enlists the help of his children Maisie and Conn to show how simple and fun these experiments can be.

The Covid-19 pandemic is a great opportunity to teach your children why they should be washing their hands, and an insightful experiment by Teagasc researcher Shauna Holden does a remarkable job at that. Teagasc Walsh Scholar Siobhan McCarthy shows us what happens when you mix an acid and a base, Katie Hetherington looks at surface tension in milk, Cristina Botinestean shows how to make Irish flag bread and Luis Lopez-Sangil makes soil shakes. Ben Murray, Science Communications and Outreach Marketing Executive at Teagasc, said: "I'm working to ensure we provide resources for children to enjoy until we are at a point where we can return to normal and learn science in the classroom. I am constantly working on new resources for children and I am updating them weekly to take pressure off parents, who are already trying to work from home and keep children engaged with education".

See the Teagasc website for more details – www.teagasc.ie/STEM4kids – or www.teagasc.ie/fun4kids. Keep an eye on Teagasc's social media for newly updated content.

EU PiG Ambassador

Two Teagasc initiatives are among the winners of the 2020 EU PiG Innovation Group (EU PiG) Grand Prix. The Grand Prix is an annual competition that aims to identify and share innovative best practices in pig production throughout the European network of pig producers, and beyond.

Under the Health theme, the dashboard system developed by Teagasc to improve pig herd health using slaughter and farm data was selected. Under the precision theme, the 5S Lean programme to improve work efficiency in pig farms was awarded the prize.

Ciaran Carroll, Head of Knowledge Transfer in Teagasc's Pig Development Department, said: "Ireland has had four awards in the four years of the project and it's great to see best practice here being acknowledged across Europe through this network. We also gain insight into best practice in other countries from the other award winners and submissions to the EU PiG Grand Prix competition; thus, the objectives of the project are being met whereby the Irish and European pig farmer has ready access to a platform that identifies and shares innovative practices in pig production to ensure a more efficient and competitive industry". Ciaran and Edgar Garcia Manzanilla, Head of the Pig Development Department, are involved in this initiative, along with pig farmers Pat O'Keeffe, Cork (Lean 5S), and Patrick Ryan, Limerick (Use of Slaughter Data).

For more information see: www.eupig.eu.



Award-winning research at Teagasc is contributing to innovative practices in pig production to ensure a more efficient and competitive industry.

Researcher profile

Sheila graduated from the University of Algarve with a degree in biotechnology engineering in 2002 and completed a doctorate in chemistry at the University of Lisbon in 2010. She joined Teagasc in 2012 as a Research Officer, looking at the metal content in Irish produce and remediation strategies to reduce metal uptake in crops. She commenced her current role as Research Officer in



Teagasc Oak Park in 2017, where she develops and leads the new research programme on minor and new crops and new end markets, in collaboration with colleagues. Since then the focus of her research has been the agronomy of protein crops, namely faba beans and peas. Sheila is co-founder and co-leader of the Irish Grain Legumes Group, created under the auspices of the H2020 project Legumes Translated (2018). This informal group meets several times a year and comprises stakeholders from private and public institutions

aiming to increase the national production of protein legume crops by identifying constraints and influencing national policies. She led research that developed the national strategy for cadmium minimisation, and was first author of the document 'Final Report on the Progress with the Implementation of the Commission Recommendation of 4 April 2014 on the Reduction of the Presence of Cadmium in Foodstuffs' prepared by Teagasc, the Food Safety Authority of Ireland and the Department of Agriculture, Food and the Marine, and

submitted to the European Commission in 2018. Sheila is currently supervising five doctoral students and two research masters, and collaborates in two European and three national funded projects. She is a reviewer for a number of scientific journals, and participates in several public outreach activities, including the annual Teagasc Oak Park Open Day, the National Tillage Conference, tillage seminars for farmers and crop advisors, and dissemination of the National Cadmium Minimisation Strategy.

Shiela Alves

Catherine Stanton receives ADSA Distinguished Service Award



Catherine Stanton has been selected as the 2020 recipient of The American Dairy Science Association (ADSA) Distinguished Service Award. The Award was announced recently at the ADSA annual (virtual) meeting. The Award is in recognition of unusually outstanding and consistent contributions to the welfare of the dairy industry and is based upon a broad

contribution over Catherine's career.

Catherine is Senior Principal Research Officer at Teagasc Moorepark Food Research Centre, founding member and Principal Investigator in the APC Microbiome Ireland and VISTAMILK SFI Research Centres, and Research Professor at University College Cork. She has published over 300 research papers and was awarded a DSc by the National University of Ireland in recognition of her published work in 2009. Her research focuses on the development of innovative dairy foods that influence human health and the developing gut microbiota in early life. She was named a 'Highly Cited Researcher' from the Web of Science group in 2017, 2018 and 2019, which recognises researchers whose

citation records position them in the very highest strata of research influence and impact. She is ranked in the top 1 % by citations in the field of Agricultural Science (Clarivate Analytics, 2017, 2018 and 2019). She is member of the Royal Irish Academy and previously received the 'IDF Elie Mechnikoff Award'.

Catherine graduated from University College Cork with BSc and MSc degrees in Nutrition and Food Chemistry, and has a PhD in Biochemistry from Bournemouth University, UK. In her early career she carried out research with Johnson & Johnson UK, and was a postdoctoral fellow in the Department of Medicine, Wake Forest University Medical Center NC, USA. She joined Teagasc in 1994 and is based in the Food Research Programme in Moorepark, Fermoy, Co. Cork.

Congratulating Catherine on her award, Head of the Teagasc Research Directorate, Frank O'Mara, said: "Catherine is an outstanding research scientist, who has nurtured and led a team of people in Teagasc and the APC to achieve outstanding results. Her research on the nutritional aspects of dairy foods and functional foods, particularly showing the health benefits of probiotic cultures, has been a significant contribution".

Don't cry over fermented milk: specific kefir improve behaviours in mice

Fermented foods have become very popular because of the growing awareness of the importance of gut health. While fermentation is one of the oldest forms of food preservation, much has still to be learned about the specific health benefits of fermented foods for our physical and mental health.

Now researchers at APC Microbiome Ireland SFI Research Centre at University College Cork and Teagasc have shown that two varieties of kefir had similar effects on the gut microbiome of mice, yet had different effects on their immune systems and behaviour. Recently, a number of studies have suggested that the consumption of fermented foods, such as kefir, are associated with an improvement in mood in humans, but the reasons for this benefit were not clear. One way in which fermented foods could alter our behaviour is by changing the community of bacteria in our gut. It has become clear that these bacteria can communicate with our brain by producing chemicals called neurotransmitters, and this communication is referred to as the 'gut-brain axis'.

"In our experiment, we wanted to see if a kefir could affect the gut-brain axis," said the co-first author, Aaron Walsh, who was a member of Paul Cotter's team at APC Microbiome Ireland. Kefir is a fermented milk drink that is produced when a kefir 'grain', which contains a community of microorganisms, is added to milk to initiate natural fermentation. The grains ferment the milk, incorporating some of their friendly organisms to create the cultured product. Fermentation makes food easier to digest, less allergenic and

can release bioactive molecules that have health benefits in their own right. Consuming fermented foods can potentially deliver large numbers of beneficial microbes, and the substances that they produce (metabolites), to the gut, encouraging a healthy microbiome.

"We have previously used DNA-based technologies to determine the specific microbes present in kefir and how they might contribute to kefir's health-promoting properties," said Paul Cotter, Teagasc. Some positive effects of kefir have already been described and research has previously shown that consumption of specific kefir, or kefir microorganisms, can reduce weight gain or beneficially impact the immune system in rodents. However, it was previously unknown if different kefir have different effects when consumed, and if kefir consumption can alter behaviour.

"This research shows that these two different kefir had a similar effect on the gut microbiome and increased its capacity to produce the neurotransmitter GABA in mice," said Marcel van de Wouw, a former PhD student at APC Microbiome Ireland and co-first author on the research publication. "Interestingly, both kefir had different and positive effects on the immune system and various behaviours." John Cryan, leader of the research, said: "This research shows that kefir can impact the microbiota-gut-brain axis and mouse behaviour in different ways under different conditions. More research needs to be performed to identify why different kefir have different effects when consumed, and more research is needed to investigate the impact of kefir on humans".

Spot the difference on laurel leaves

Researchers from **TEAGASC** and UCD are investigating disease issues in cherry laurel, an important species for the Irish cut foliage sector.

Ireland's cut foliage industry supplies leafy stems of various tree and shrub species, such as eucalyptus and cherry laurel (*Prunus laurocerasus*), into the lucrative €2.5 billion European cut flower trade. High quality blemish-free foliage stems are required for a discerning market. Cherry laurel is the most important species, and foliage growers plant three different cultivars: 'Etna'; 'Caucasica'; and, 'Novita'. The cultivar 'Rotundifolia' is the main one used for hedging and is propagated in nurseries, largely for export. Research conducted by Teagasc and UCD has addressed disease issues of this important crop. In its native habitat, *P. laurocerasus* grows in the forest understorey but for foliage production it is grown in the open, in managed plantations that are harvested annually; thus, the plants are more exposed and remain relatively small (main image).

Shot hole

One of the most noticeable diseases to affect cherry laurel is shot hole disease, which is caused by the bacterial pathogen *Pseudomonas syringae* pv *syringae* (*Pss*). There are no antibacterial pesticides to control it apart from copper, which can be toxic to the soil and plants if applied on a regular basis. Growers are increasingly asked to follow sustainable production guidelines, similar to food crops, with minimum input of pesticides and increased implementation of integrated pest management (IPM) principles. This raises challenges for the sector, especially as the temperate climate, ideal for growing lush green foliage, also facilitates diseases and pests that can cause unsightly damage. However, as the industry is relatively new, little is known of the factors affecting shot hole development and spread within managed cut foliage

plantations. To address this, Teagasc's Brian McGuinness and Danielle Boland undertook a survey of cherry laurel plantations and nurseries to collect information on the main pathogens affecting the crop, and UCD's Leighton Smith and Angela Feechan looked at the epidemiology of *Pss* on cherry laurel.



Survey

Eleven commercial cherry laurel plantations and seven nurseries were visited and surveyed in a systematic manner to obtain diseased material, and to identify the pathogens associated with shot hole symptoms and other blemishes. In 2017, the predominant organism associated with disease symptoms was the *Pss* bacterium, with 28 % of samples testing positive for the diagnostic syringomycin B gene (n = 320). Shot hole symptoms can vary from distinct shot holes to leaf-edge necrosis, making the recognition of symptoms more challenging (**Figure 1**). A total of 6 % of samples were associated with a fungus identified as a *Neofabraea* sp., the first time this has been recorded on *P. laurocerasus* (**Figure 1**), while the known *P. laurocerasus* fungal pathogen *Eupropolella britannica* was isolated from just two samples. Many samples yielded no pathogen, most likely because once shot holes have formed, the pathogen has been excised from the plant and is no longer present. Other bacteria and fungi that were isolated from diseased samples were used to re-infect healthy leaves but none was able to do so. Separately, a new bacterial pathogen of *P. laurocerasus* Rotundifolia was isolated from an infected cherry laurel hedgerow and identified as *Micrococcus alovera* (**Figure 2**) (Smith *et al.*, 2020). Thus, not all shot hole symptoms are caused by the same organism – they may be a generalised response to infection, although this hypothesis needs further work.

Epidemiology

The epidemiology studies of *Pss* on cherry laurel at UCD found that the cultivar Caucasica was the least susceptible to shot hole disease, followed by Etna, while Novita and Rotundifolia (**Figure 3**) displayed the most severe symptoms. Abiotic factors such as wounding, exposed sites and mild temperatures were all found to promote shot hole disease and may account for why the disease can be prolific in cut foliage plantations. Thus, to sustainably reduce the occurrence of shot hole, growers may need to consider providing more shade for cherry laurel (e.g., interplanting with taller species), or counteracting 'wounding' effects by increasing the interval between harvests.



FIGURE 1: Disease symptoms on cherry laurel cultivars. Pss on Etna (left and middle); *Neofabraea* sp. on Etna (right).



FIGURE 2: Shot hole symptoms on a *P. laurocerasus* Rotundifolia hedge associated with *Micrococcus aloeverae*.

Xanthomonas arboricola pv. *pruni*

Xanthomonas arboricola pv. *pruni* (*Xap*) is a destructive pathogen of stone-fruit *Prunus* species worldwide, such as peaches, apricots and plums, and is also known to infect cherry laurel (Figure 4). It can cause a bacterial shot hole symptom so there could be confusion and misidentification were it to occur on cherry laurel in Ireland. Currently *Xap* is absent from the UK, which has 'Protected Zone' status, meaning that the UK restricts imports of *Prunus* plants to countries that also have Protected Zone status. In Ireland, the Department of Agriculture, Food and the Marine is seeking Protected Zone status for *Xap* in Ireland, which would be a distinct advantage for the sector, facilitating the growth of exports of *P. laurocerasus* cultivars for hedging.

Conclusion

From a plant health perspective, most shot hole symptoms on cherry laurel in cut foliage plantations and nurseries are caused by *Pseudomonas syringae* pv. *syringae* but other bacteria can cause similar damage. Ireland is well placed to embrace sustainable *P. laurocerasus* production for both cut foliage and hedging.

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FIGURE 3: Pss symptoms on (from left): Rotundifolia, Novita, Etna and Causcasica.

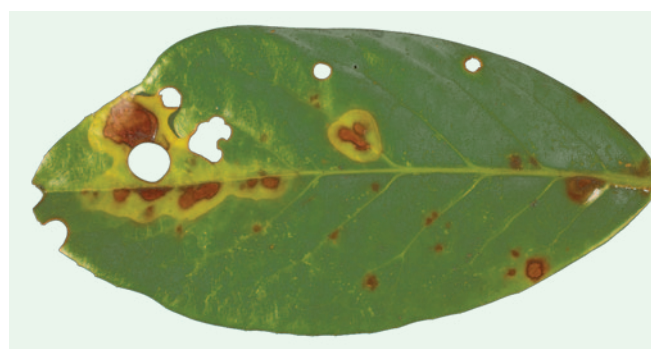


FIGURE 4: *Xanthomonas arboricola* pv. *pruni* on *P. laurocerasus*. (Image: UK Crown Copyright – courtesy of Fera.)

Reference

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RLS: another disease for barley to contend with

Photo credit: Catriona Boyle

TEAGASC research is investigating the conditions under which ramularia leaf spot develops in barley crops.

As barley crops bask in the sun during early summer they convert the sun's energy to carbohydrates that are subsequently stored in the grains. At some stage further down the line we will eventually utilise this energy, either directly or indirectly. However, we are not the only species aiming to exploit barley's ability to create carbohydrates from the sun's energy. Fungal pathogens are extremely efficient at doing this also, and in our wet climate well-known barley diseases such as mildew, net blotch and Rhynchosporium have been exploiting barley for centuries. In the late 1990s another disease was unfortunately added to this list of barley foes, and while the pathogen *Ramularia collo-cygni* had been identified over 100 years previously, its impact on barley was not fully understood. However since the late 1990s ramularia leaf spot (RLS) caused by *R. collo-cygni* has become potentially the most economically destructive disease of winter and spring barley throughout north-western Europe, New Zealand and parts of South America.

Impact of RLS

Unfortunately, RLS often only manifests itself late in the season during the growth stage known as grain filling. It is at this stage that the crop is capturing sunlight and converting it into sugars through the process of photosynthesis, and translocating excess sugars to the developing grains. As a critical period in the crop's life, any reduction in the capacity to do so will adversely impact yield, both in terms of quality and quantity. By producing necrotic lesions on the leaves, awns and stems of barley

(Figure 1), RLS can significantly and rapidly reduce the leaf area available to the barley plant for photosynthesis. If this occurs early during grain filling significant yield losses can occur, with over 1 tonne/ha losses often recorded in field trials where the disease has been allowed to develop unchecked (without fungicide).



Screening seed stocks for RLS

While we may understand how the disease impacts the growing crop and, subsequently, grain yield, our understanding of the conditions that initiate disease development is incomplete. For instance, although the disease is recognised as a barley disease, it can infect a multitude of species, including wheat. This in itself can make the dissection of the disease cycle that bit more difficult as initial inoculum sources could be the seed itself, the previous crop or even the surrounding non-cropping environment. As seed is regarded as a major source of Irish winter and spring barley, seed stocks for the growing seasons 2016-2018 were screened using a qPCR assay for *R. collo-cygni* DNA. As expected, a high proportion of the stocks had detectable levels of the pathogen (Figure 2). However, no discernible patterns, other than season and crop type (winter or spring), were identified as contributing to the levels detected. This collection also provides a unique snapshot of the Irish *R. collo-cygni* population that will be exploited further to dissect the dynamics of this unique pathogen.

Environmental conditions

In the absence of a sole inoculum source our attention turned to dissecting the environmental conditions that promote infection and disease development. Undoubtedly RLS is a wet weather disease as is evident from the regions of the world where it is a significant threat. However, as it only manifests later in the season it is difficult to know what the risk of disease is prior to its development. The potential role of leaf wetness around the period of crop extension was first proposed by researchers from Scotland's Rural College (SRUC). To test whether such conditions could be used to predict disease development under Irish conditions, trials were conducted during the 2016-2018 seasons, with varying treatments included to reflect potential risks, including varieties believed to vary in their ability to resist the disease. Although



FIGURE 1: *Ramularia* leaf spot on spring barley caused by the fungal pathogen *Ramularia collo-cygni*.

the risk predicted in 2016 and 2017 was a good indicator of the levels of disease experienced later in the season, the initial risk predicted in 2018 was high during stem extension, but as the season progressed little or no disease developed due to the drought experienced in June of that year. Furthermore, the levels of disease experienced across the trials over the three seasons did not reflect the perceived varietal resistances, further demonstrating the difficulties experienced with understanding this disease.

Further challenges

As highlighted above, the difficulties with understanding and predicting RLS present serious obstacles to controlling the disease and, as such, have resulted in fungicides being relied upon for control. As the ability to predict its development is as yet unreliable, farmers will generally err on the side of caution and apply fungicides. Unfortunately, *R. collo-cygni* is very closely related to the wheat pathogen *Zymoseptoria tritici*, and like *Z. tritici* it has an exceptional capacity to adapt to stressful environments such as those imposed by fungicides.

As such, *R. collo-cygni* has developed resistance to most of the major fungicide families once used for its control. Since its emergence as a serious threat in the late 1990s these fungicides have routinely included the multisite chlorothalonil. However, following review under Regulation 1107/2009, the use of chlorothalonil within the EU is no longer permitted. In the short to medium term this presents a serious risk to the production of barley in high-risk regions such as Ireland. Trials in 2019 suggest that careful consideration of fungicide programmes, including fungicide choice and timings, will alleviate some of the pressures of RLS; however, Irish barley crops are likely to be subjected to disease pressure from this fungus for some time to come.

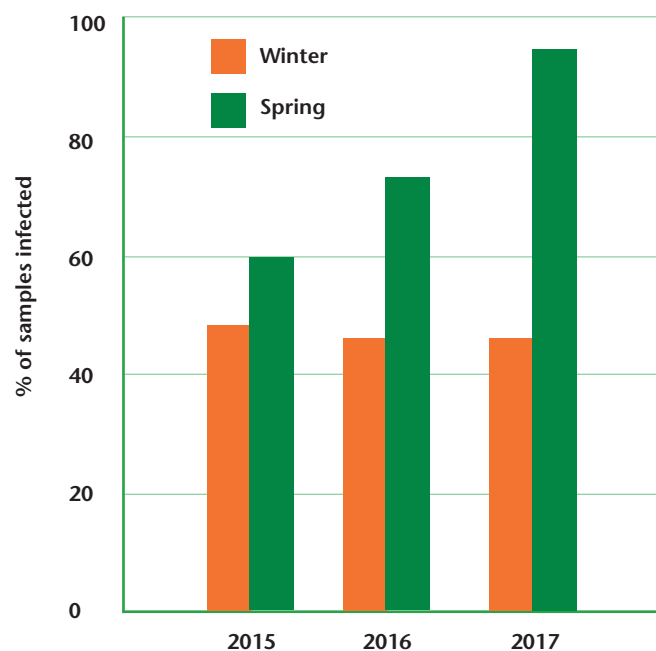


FIGURE 2: Percentage of barley seed samples with detectable levels of *Ramularia collo-cygni* harvested in the seasons 2015-2017.

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Management of insect pests in a changing world

TEAGASC researchers are involved in a number of projects to reduce insect damage in Irish crops.

As 2020 is the International Year of Plant Health, it is important to evaluate how we will manage plant health into the future, a future where we will have to contend with a changing climate, and attempt to manage pests with a greater emphasis on non-pesticide approaches, in order to adhere to increasing consumer pressure to decrease the impact of agriculture on biodiversity and ecosystem services. New regulations, such as the Sustainable Use of Pesticides Directive and the 'Green Deal', will significantly impact on how we manage our crops in the decades ahead, almost certainly with fewer pesticides and a need to increase our knowledge of pest behaviour and strategies to minimise their impact. In particular, the use of insecticidal products has received significant focus in the last decade and the number of available insecticidal active ingredients has fallen sharply, with few new ingredients coming to market. It is in this context that Teagasc is working to adopt, adapt and develop a number of new integrated pest management (IPM) strategies to reduce insect damage in Irish crops.

Barley yellow dwarf virus

Barley yellow dwarf virus (BYDV) is an insect-vector RNA virus that causes stunting of cereal crops worldwide. Once obtained from an infected plant, BYDV can persist in the aphid vector for its whole lifetime, but does not replicate within the aphid. The virus is transmitted from plant to plant through the saliva of feeding aphids. The time taken for the aphid to acquire the virus from an infected plant and inoculate a new plant with the virus varies from hours to days. In Ireland, there are three main aphid vectors of BYDV: the grain aphid (*Sitobion avenae*); the bird cherry-oat aphid (*Rhopalosiphum padi*); and, the rose grain aphid

(*Metopolophium dirhodum*). The most common serotype of this virus to occur in Ireland, BYDV-MAV, usually causes visually mild symptoms of yellowing and stunting in crops, while the less common serotype, BYDV-PAV, can cause extremely severe symptoms. However, both can cause economically significant levels of crop

damage, particularly if infection occurs in the early crop growth stages. The management of BYDV has largely relied on the use of pyrethroid-based insecticides in combination with sowing date, with a preferred sowing date of October and a pre-Christmas insecticide application time for autumn cereals. For spring cereals, an earlier sowing date is preferred, with an insecticide application at GS14 if required. These rules were largely developed to reduce the exposure of the crop to migrating aphids, thus reducing their exposure to BYDV. Indeed, in some years an aphicide is not required, depending on the weather conditions post planting. However, several factors have changed, which may alter this approach. There has been an emergence of partial resistance to pyrethroids in one dominant clone of the grain aphid (*S. avenae*), which is now relatively common in tillage crops (Walsh *et al.*, 2020b). We have also had the first report of pyrethroid tolerance in an Irish population of the bird cherry-oat aphid (Walsh *et al.*, 2020a). This coincided with the withdrawal of several insecticide active ingredients, leaving only two available for BYDV management (McNamara *et al.*, 2020). This scenario led to the development of the CAPTURE project, which will look to gain a better understanding of BYDV transmission and epidemiology in Irish tillage crops and, in combination with the construction of three 12.2 m high insect suction towers at Carlow, Cork and Dublin (Figure 1), will allow researchers to monitor and recover long-distance aphid migrants and potentially analyse them for both insecticide resistance genes and BYDV. It is envisaged that this work will build on our knowledge of BYDV dynamics and lead to a greater understanding of when and if crops require insecticide applications.

Managing other pests

While some pest damage, such as BYDV, can be unpredictable in severity, other pests are extremely predictable in their occurrence and severity, although this does not necessarily make them easier to manage. Root-feeding diptera (fly) pests of brassicas and carrots cause significant damage, leading to high levels of crop loss and rejection. Through the FLYIPM project (CIPM ERA-NET), the use of entomopathogenic (insect-





FIGURE 1: A 12.2m high insect suction tower, which passively samples the passing air for flying insects such as aphids.

killing) nematodes to control the larvae of the cabbage root fly (*Delia radicum*), was investigated. Entomopathogenic nematodes carry a symbiotic bacteria within their gut. Once the nematode enters the insect body, it voids the bacteria from the gut and the bacteria proliferates, leading to the death of the insect. The bacteria then serve as a food source for the subsequent generations of nematodes, until the resources within the insect are exhausted and the nematodes within the insect form a second cuticle, allowing them to survive outside of the insect. These nematodes then leave the insect to search for a new host. The use of entomopathogenic nematodes is common in protected horticulture and is the main control approach for weevil pests in soft fruit and sciarid fly larvae in mushroom production. However, their use in outdoor field production, particularly in soil as opposed to a growth medium, is less common. The entomopathogenic nematode *Steinernema feltiae* displayed good affinity for infecting and killing the larvae of *Delia radicum* (Figure 2) in laboratory assays across a range of relevant ambient temperatures (9 °C to 18 °C), with mortality usually occurring within five days. Field evaluations were conducted to determine their efficacy against *D. radicum* larvae. The entomopathogenic nematodes were applied as a soil drench around the plant root system, as an injection directly into the plant growing module, or as a combination of both methods. Overall, an application rate of 70,000 infective juveniles applied as a drench per plant was found to give some statistical differences in plant evaluation, such as visual root damage score and plant count, when compared to the untreated control. While not directly comparable to current insecticide control levels, when used in combination with additional control strategies such as trap crops and physical barriers, this approach may contribute to reducing pest populations and their damage to economically acceptable levels.

Conclusion

It is clear that there is a strong legislative and consumer demand for the development of pest management strategies that are less dependent on pesticides; however, it is also clear that replacement solutions and strategies are not yet available for many important pests. Therefore, while replacement strategies are being developed, particularly in the development of biopesticides and breeding for crop resistance, the use of increased monitoring and forecasting, such as insect sampling towers, will be required to improve our knowledge of pest behaviour.



FIGURE 2: A larva of the cabbage root fly *Delia radicum* infected with the entomopathogenic nematode *Steinernema feltiae*. The nematodes are visible as white threads through the insect cuticle.

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Test! Test! Test! Tracking potato viruses

TEAGASC research is looking at how we can use new technologies to gain a greater understanding of potato virus Y diversity in Ireland, and to monitor outbreaks.

Plant viruses are causal agents of diseases and represent a significant threat to many cultivated crops. Potatoes are particularly prone to viral infections because of their vegetative propagation, which supports the transmission of viruses over successive generations. To date, more than 50 virus and viroid (smallest known pathogens) species have been reported to infect global potato production, resulting in losses of up to 80 % if not managed. The main source of virus is from the planting of virus-infected seed tubers. This means that the sanitary selection and certification of the seed tubers plays a crucial role in controlling the spread of viruses in potato crops. To achieve this, the availability of a sensitive and reproducible diagnostics system is essential.

PVY – a major concern for potato production

Potato virus Y (PVY) is one of the world's most studied plant viruses and is considered the most economically harmful virus to cultivated potatoes (**Figure 1**). PVY is present in potato production areas all over the world and exists in nature as a complex of strains and variants. PVY^o used to be the predominant strain in potatoes, but in recent years recombinant virus strains have been increasingly detected in potato crops and now represent the majority of the PVY population in many countries. Recombinant viruses result from the combining of genomes from more than one virus infecting a plant cell. Recently emerged PVY recombinants are challenging the sanitary selection and certification of potato propagation material because they only induce mild or transient foliar symptoms in many potato cultivars, making it very difficult to detect PVY during visual field inspections of seed tuber crops. Currently, in addition to five non-recombinant genotypes, 36 unique recombinant structures have been reported globally.



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To make matters worse, PVY recombinants are also able to induce necrotic ringspot-like symptoms on tubers of susceptible potato cultivars, making them unmarketable.

Given the impressive genetic diversity of PVY and its impact on potato production systems, accurate detection and characterisation of the PVY isolates circulating in Ireland is essential to deliver efficient integrated pest management (IPM) strategies and support the planned expansion of the seed potato sector with a robust sanitary certification scheme. However, despite Ireland being one of the five High Grade Seed Potato Production Areas recognised by the European Union (2004/3/EC), there is still a lack of detailed information on the genetic diversity of Irish PVY isolates and their relative incidence.

The virome of a plant

Conventional serological (e.g., ELISA) and molecular (e.g., PCR based) assays for the detection of plant viruses are target specific (you only get what you look for), meaning that multiple assays need



FIGURE 1: Potato leaves showing no obvious (a) and severe (b) PVY symptoms.

to be performed to detect multiple viruses. Direct sequencing of target nucleic acids is now being increasingly exploited in plant virology research for diagnostic purposes, primarily because the cost of sequencing has fallen dramatically in the last decade (as an example, the cost of sequencing the human genome reduced from more than €100,000 in 2009 to circa €1,000 in 2019). The non-targeted nature of sequencing allows us to potentially detect any virus in a single assay, making it an increasingly important tool in plant virology, in order to study the total collection of viruses that a plant harbours (virome). New portable sequencing technologies are also offering enormous opportunities to rapidly identify viruses infecting plants in one assay.

New findings to improve PVY control

At Oak Park we have exploited these developments to investigate and characterise PVY isolates in Ireland. This involved detailed comparisons between ELISA, PCR, standard sequencing and portable sequencing platforms to investigate the suitability of recent sequencing advances to study the virome of potato plants that may/may not be showing symptoms.

We collected material from 200 plants showing severe or mild symptoms ascribable to viral infections from a diverse potato germplasm collection and from commercial seed tuber crops in the primary potato regions of Ireland to assess the genetic make-up of Irish PVY populations. Through serological and molecular analyses we found that more than 90 % of the PVY infections detected were sustained by recombinant strains of the virus. These results indicate that PVY recombinant strains not only are present, but are prevalent in Irish potato crops. In parallel, we have also established methodologies to support the use of portable DNA sequencing devices (MinION sequencer; **Figure 2**) to detect and characterise viruses infecting potatoes, with the complete genome sequences of sequenced isolates deposited in public databases as a community resource. Using these techniques we also detected additional potato viruses including PVX, PVS and PLRV, with their full genome sequences characterised, confirming the potential for the non-target detection of plant viruses (Della Bartola *et al.*, 2020). Our ability to reconstruct the genomes of PVY and other potato



FIGURE 2: The portable MinION sequencer, connected to a laptop.

viruses using simple and portable MinION sequencing is significant and indicates the technology's potential for virus detection in potato production systems. This study has provided important information to improve the control of PVY in support of expanding the potato seed trade sector, and also further adds to the global understanding of PVY genetic diversity.

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Mushroom viruses and *Agaricus* genomics

TEAGASC researchers have been examining how mushroom strains respond to virus infections, guiding efforts to develop new cultures that are either tolerant of or resistant to infection.

The commercial mushroom, *Agaricus bisporus*, is susceptible to a disease caused by a complex of viruses known collectively as mushroom virus X (MVX). Symptoms of MVX include poor-quality mushrooms and mushroom cap discolouration (browning), which are correlated with *A. bisporus* virus 16 (AbV16). Another virus, AbV6, is also associated with virus outbreaks but has not been directly correlated with distinct symptoms. Most modern-day commercial varieties of *A. bisporus* are mid-range hybrids, and are almost genetically identical, having been derived from a hybrid cross between two strains in the 1980s. One major disadvantage of this lack of genetic diversity is the universal susceptibility of mushroom crops worldwide to the same pathogens, including viruses. At the moment, control measures rely entirely on good crop hygiene to prevent cross-contamination and transmission of the viruses between crops.

A virus breaker

In the past, another *Agaricus* species, *A. bitorquis* was used as a 'virus breaker' strain as it was vegetatively incompatible with commercial *A. bisporus* strains and so virus transmission was halted when this species was grown. These days, *A. bitorquis* is not commercially acceptable; however, an *A. bisporus* culture that is incompatible with current commercial strains, and is commercially acceptable, could potentially work as a new virus breaker strain. There is a lack of knowledge of how *A. bisporus* responds to virus infection at a genomic and proteomic level, and so the main aim of this project was to characterise the vegetative interactions between a variety of genetically different strains, as well as their responses to viral infection. A modern mid-range hybrid, Strain D, and four others (Strains A, B, C and E) with different levels of vegetative incompatibility with Strain D, were used. At the same time a fluorescence *in situ* hybridisation (FISH) method was evaluated to visualise where viruses are located within the fungal mycelium to enhance our understanding of virus dynamics within the host.



FIGURE 1: Hyphal fusions between two compatible strains.

Interactions, compatibility and virus transmission

Fungi grow by means of fine filaments of cells called hyphae, which radiate outward, looking for substrate and nutrition. When the hyphae from two compatible cultures come into close contact with each other, they can fuse together by a phenomenon known as hyphal anastomosis. In our studies, such hyphal fusions occurred regularly between compatible cultures (Figure 1) but they were also shown to occur between incompatible strains, although at a lower level (O'Connor *et al.*, 2020a). This low level of hyphal anastomosis allowed transmission of the AbV16 virus from virus-infected culture MVX-1153 into the mycelium of all the other strains tested; thus, an *A. bisporus* virus breaker strain may be a challenge to develop. Virus transmission was also evident under cropping conditions where AbV16 was detected in all strains (Figure 2). However, only a few mushrooms of the less-compatible Strains A, B, C and E tested positive, indicating that although hyphal fusion and virus transmission had occurred, it was less effective than for Strain D (Figure 2). Proteomic analysis indicated that Strains C and E responded to virus infection differently, compared to the high stress response of Strain D, thus opening avenues to identify antiviral characteristics and defence responses among genetically different *A. bisporus* strains.

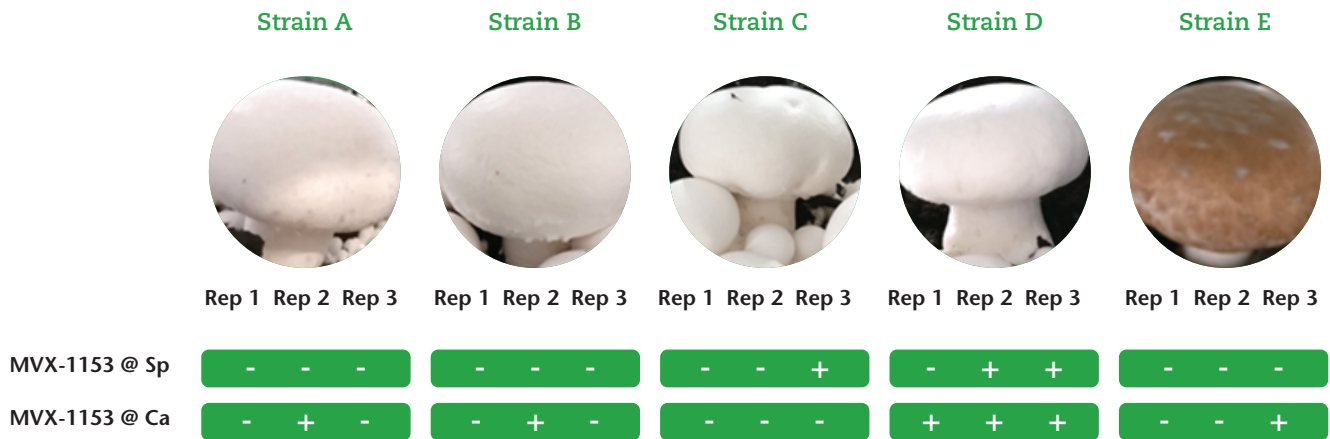


FIGURE 2: Detection of AbV16 (-/+) in crops following infection at spawning (@ Sp) or at casing (@ Ca).

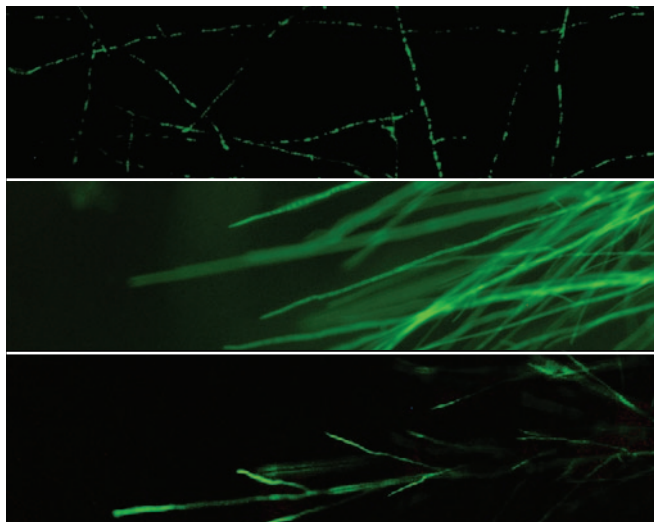


FIGURE 3: AbV16 virus detected in internal fungal hyphae (top); AbV6 virus in peripheral hyphae (middle); and, hyphal tips (bottom).

Virus visualisation

The FISH technique was used with excellent results to visualise where two viruses, AbV16 and AbV6, were located within the mycelium of infected cultures (O'Connor *et al.*, 2020b). Fluorescently labelled AbV16 showed high intensity and a compartmentalised distribution within the hyphal network, while the AbV6 virus was located more at the periphery of the culture and at hyphal tips (Figure 3), reinforcing the idea that virus transmission is likely during anastomosis events, even if only a small number occur.

Conclusion

These new insights into the different responses of *A. bisporus* strains to each other, and to virus infection, will enhance our understanding of potential barriers to viral transmission through vegetative incompatibility, as well as through antiviral activity, guiding future strain-breeding programmes.

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Finding farming in our placenames

TEAGASC researchers have used Irish placenames to find evidence of past farming activity.

Photo credit: Catriona Boyle

Mapping historic land use can be a challenge where spatially explicit data are limited. Yet we know of significant changes to the Irish agricultural landscape from archaeological and historical records. A useful source for former land use is toponyms (or placenames). Our countryside is replete with specific names that recall physical, cultural, historical, or functional characteristics for a location. Often different characteristics are coded into a single name. Frequently, placenames include a reference to agricultural use. Placenames were standardised by the Ordnance Survey in the 19th century, but many are of far greater antiquity. Frequently, they are simply Irish names spelt phonetically. This has preserved many names and pronunciations, even where the original meaning of a word has been lost. Placenames are an invaluable cultural inheritance, not least because they provide a window to how our ancestors viewed and conceptualised their landscape.

Mapping farming references in placenames

In a recent Teagasc Map of the Month, an initiative by the Agri-Food Business and Spatial Analysis Department, Jesko Zimmermann and Rob O'Hara used townland placenames to map certain references to arable farming. We have now expanded this map to include a greater number of terms, for specific arable crops, land measures, land use, and references to pasture and livestock farming (**Figure 1**). Our sources for this map were P.W. Joyce's *The Origin and History of Irish Names of Places* (1869), as well as the current online placename database (<http://www.logainm.ie>).

A map of current townlands was obtained from Ordnance Survey

Ireland in a geographic information system- (GIS) ready format, which included a record of the Irish names (not present in all cases). The list of Irish townland names was cross-referenced with our list of agricultural terms. The current agricultural landscape was based on information in the Irish Land Parcel Identification System (LPIS), where dominant land use (grassland, cropland or other, between 2000 and 2016) was identified and proportionally mapped onto a 2.5 km x 2.5 km grid to ensure anonymity. In the accompanying map, points represent previous agricultural use based on the placenames, and the underlying grid shows current agriculture. The points are colour coded by reference type, while the grid colour represents the ratio of cropland to grassland. The transparency of each grid square visualises the total prevalence of agricultural land use reported in the LPIS.

Placenames are an invaluable cultural inheritance, not least because they provide a window to how our ancestors viewed and conceptualised their landscape.



Burial mount on a tilled field at Newgrange.

Findings

This, of course, is a very rough proxy for former land use but can still provide insights. The map shows evidence for the mixed farming practices that were more common in previous centuries, with placenames relating to arable farming (blue points) intermingled with pastoral placenames and found far outside the current extent of arable farming. References to types of arable field are quite common, whereas names recording specific crop types are comparatively rare. Pasture and meadows are abundant in the north midlands and Galway-Mayo. Areas of extensive bog or mountain have fewer agricultural names, but they are not completely absent. Summer pasture (booleying) would have been common in these areas. There are several places that are quite specific types in describing livestock (e.g., calves, cows, heifers or bulls), reflecting the deep intrinsic nature of pastoral farming as a status symbol within ancient Irish culture. Both specific and generic terms for farming are found all over the country.

Mapping former land use in this way is an interesting exercise, but it has limits. Agriculture was ubiquitous in the pre-industrial era, so an absence of specific farming-related references does not mean that agriculture was not being practised. Rather, there were other characteristics at a location that were considered more important when naming the place. The densest concentration of agricultural references is in the mid-west region, while in Munster and Leinster there are fewer original placenames relating to farming. References to cropland in the eastern part of the country are uncommon, an area where cropland is now very prevalent.

Original placenames may also not have survived or their meaning has been lost. There are historical reasons why this is the case; a succession of wars in the 17th century left the country depopulated so former placenames may have been forgotten or were renamed by new settlers. There was even an attempt in that century to legislate against “barbarous and uncouth” Irish placenames being used but this, thankfully, was largely ignored. New placenames were adopted over time, reflecting new ownership, or where new agricultural or industrial practices developed.

As such, the information found in placenames, while useful, only represents one part in the complex puzzle that is agricultural history in Ireland.

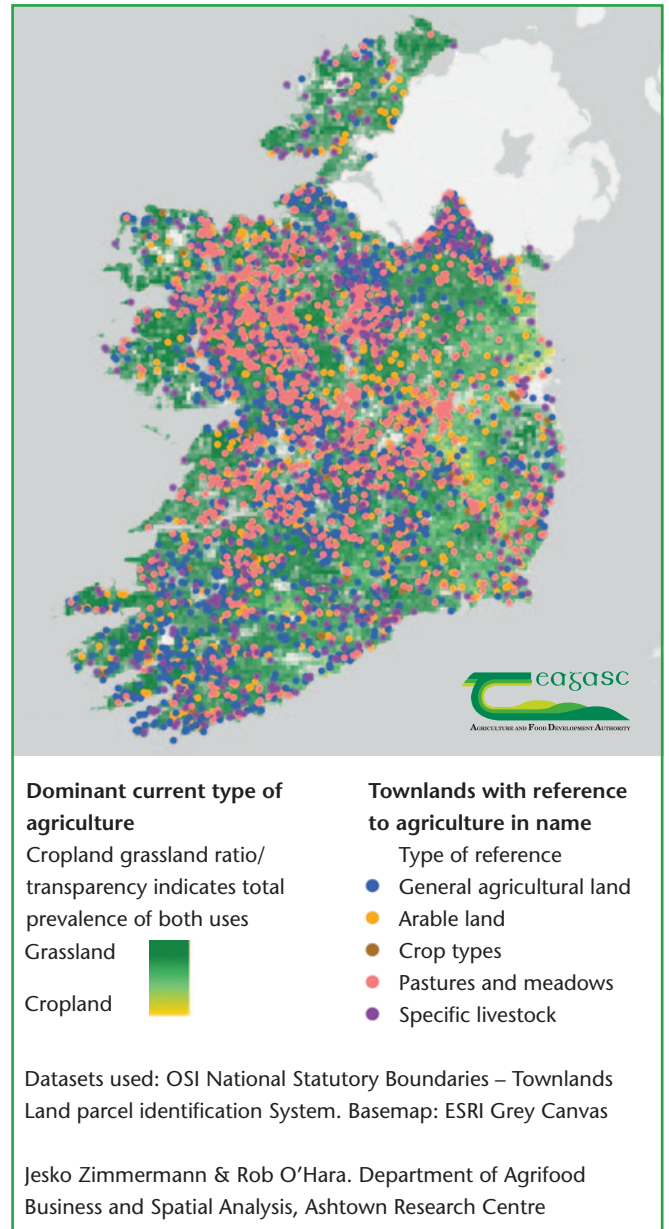


FIGURE 1: Map showing specific arable crops, land measures, land use, and references to pasture and livestock farming in placenames.

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Factors affecting pregnancy proteins

TEAGASC researchers investigated factors influencing pregnancy-associated glycoproteins in seasonal calving, pasture-based dairy cows.

In seasonal-calving systems of milk production, early pregnancy detection is a useful management tool to improve herd fertility performance. Pregnancy-associated glycoproteins (PAG) are proteins secreted by binucleate cells from the trophoblast of the developing embryo and are detectable in blood and milk four weeks after pregnancy establishment. The current gold standard for pregnancy diagnosis in cattle is based on transrectal ultrasound to visualise a viable embryo. PAG assays can be used as an alternative method to determine pregnancy status and embryo mortality. The PAG assay uses a plate reader to measure absorbance in both samples (S) with unknown PAG concentrations and negative controls (N) with no PAG present (i.e., a blank). The S-N absorbance value is used to indicate the presence or absence of pregnancy. Hereafter the PAG S-N value is referred to simply as PAG.

Pregnant dams have a well characterised PAG profile in blood and milk, with an initial peak at weeks four to six in pregnancy, followed by a decline to nadir between weeks seven and 10, and a recovery thereafter. The objective of this study was to investigate factors that influence PAG in seasonal-calving, pasture-based dairy cows. Spring-calving dairy cows (n = 499) located in three Teagasc research farms were enrolled in the study. Weekly milk samples were collected from each animal enrolled from weeks five to 21 after artificial insemination (AI) to determine PAG.

Dam and sire characteristics

There was a trend for declining milk PAG with increasing parity number (Figure 1). An interaction between parity and week post insemination was observed, whereby older cows (parity 3+) tended to have lesser PAG

values at the initial peak and nadir compared to parity 1 and 2 cows. Cows with the greatest fertility sub-index had greater PAG at weeks 5 and 6 post insemination compared with cows with the least or intermediate fertility sub-indexes, but differences were not detected thereafter (Figure 2). Sires of the gestating embryo with the greatest daughter fertility sub-index had greater nadir PAG than sires with intermediate and least fertility sub-index values (1.46, 1.34 and 1.31, respectively), and reached nadir PAG later (weeks 10, 8 and 9, respectively). A significant effect of sire (Figure 3) was observed on initial peak PAG (range 1.4-2.2), nadir PAG (range 0.5-1.2) and post-nadir recovery peak PAG (range 2.0-3.0). An interaction between milk yield and week post insemination was observed, whereby PAG decreased as milk yield increased.

Calf characteristics

Pregnancies with female offspring had greater initial peak PAG (1.83) and lesser PAG values at post-nadir recovery (2.50) versus pregnancies with male offspring (1.67 and 2.56, respectively). Pregnancies that subsequently resulted in low birth weight calves (< 30 kg) had greater initial peak PAG (1.84) than pregnancies with medium (30-38 kg = 1.73) and large (> 38 kg = 1.69) birth weight calves (Figure 4).

Conclusion

The overall temporal pattern of variation in milk PAG values in seasonal-calving pasture-based cows is consistent with previous reports from high-yielding cows fed a total mixed ration. The majority of the variation observed in milk PAG profiles occurred before week 12 post

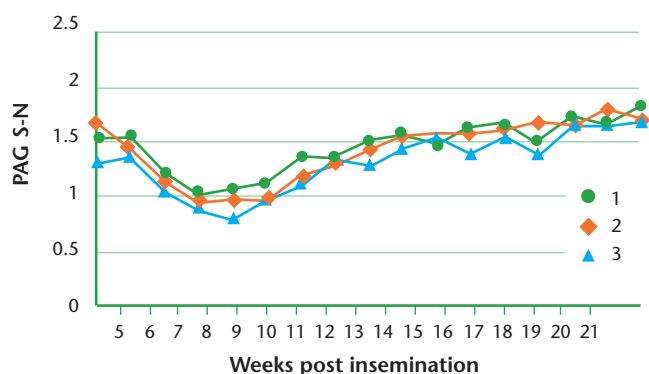


FIGURE 1: Pregnancy-associated glycoprotein profiles from five to 21 weeks post AI for parity 1 (●), 2 (◆), and 3+ (▲) lactating dairy cows.

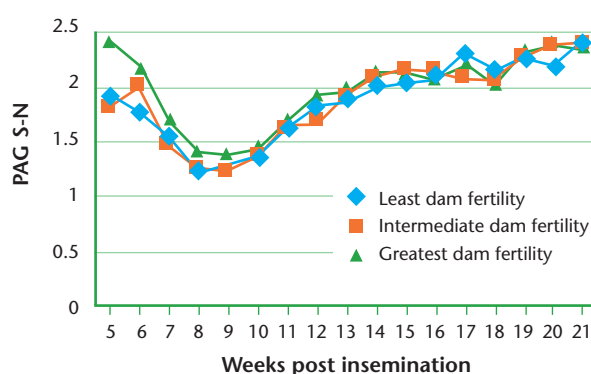


FIGURE 2: Weekly pregnancy-associated glycoprotein profiles in milk from five to 21 weeks post AI for cows with different dam fertility sub-index categories: least (< € 85); intermediate (€ 85-€ 120); and, greatest (> € 120).

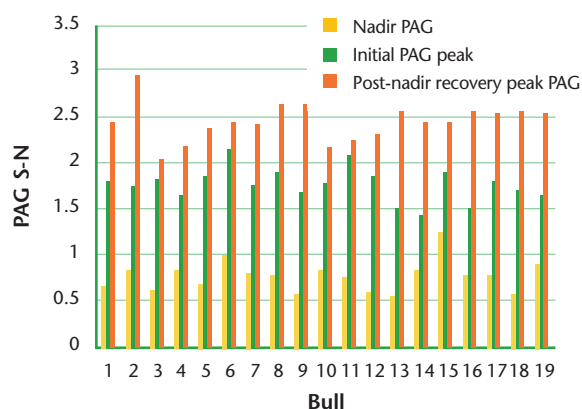


FIGURE 3: Variation between sires (n = 19) of the developing foetus on mean values for initial peak PAG, nadir PAG and post-nadir recovery peak PAG in milk.

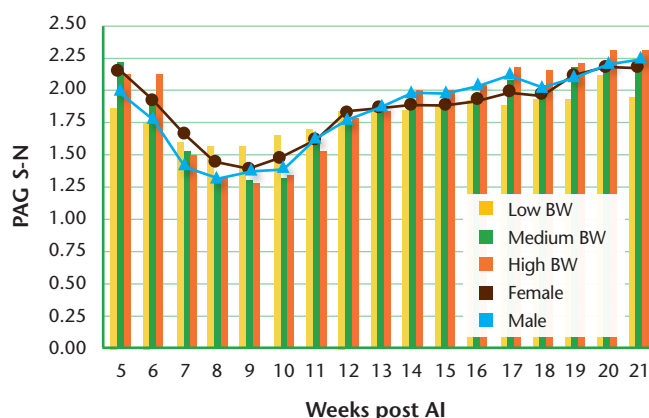


FIGURE 4: Weekly pregnancy-associated glycoprotein profiles in milk from cows with male or female calves (lines), or those with low (< 30 kg), medium (30-38 kg) or high (> 38 kg) birth weight (solid bars).

insemination. Our findings indicate that calf sex, calf weight, parity, dam and sire fertility sub-index, milk yield, and sire are all associated with milk PAG values observed from weeks five to 21 post AI. The use of a milk sample to diagnose pregnancy is a convenient method for pregnancy diagnosis, especially for farmers participating in milk recording, due to the low technical inputs required. The ability to determine pregnancy status through milk PAG may be useful to improve reproductive management in dairy herds.

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Heteropaternal superfecundation in sheep

TEAGASC research is using genotyping technology to detect heteropaternal superfecundation in sheep, and thus help explain some quirks in genetic evaluations of lambs.

What is it?

Superfecundation is where separate copulatory events occur, leading to the fertilisation and implantation of two or more eggs during the same oestrus/menstrual cycle, and resulting in the birth of two or more siblings. Heteropaternal superfecundation is where the multiple births originate from different fathers. Heteropaternal superfecundation is therefore more likely to occur in species that commonly ovulate more than one egg and are also mob mated (i.e., more than one male runs concurrently with the females). Sheep are a great example of such a population, as they often bear multiple lambs and are also often mob mated.

Commentary on superfecundation dates back to Leda from Greek mythology, who was the wife of Tyndareus, King of Sparta. Both Zeus and Tyndareus were said to have impregnated Leda, resulting in Pollux and Helen being fathered by Zeus, and Castor and Clytemnestra being fathered by Tyndareus; Helen was later to be better known as Helen of Troy. Also from Greek mythology, Heracles (and his brother Iphicles) were thought to have been born as a result of heteropaternal superfecundation, with clear distinctions cited between them supporting the hypothesis. Heracles was depicted as fair-haired, whereas Iphicles was dark haired; Heracles was also characterised as being strong and courageous, with the opposite being true of Iphicles.

Heteropaternal superfecundation in Irish sheep

Heteropaternal superfecundation in sheep can (sometimes) be detected if only one ram of each breed was present within the mating mob, and if these breeds were distinctly different; for example, a Texel ram with a white head and a Suffolk ram with a black head will each produce distinctly different lambs. DNA information on the lambs provides more concrete proof of heteropaternal superfecundation and is one of the only ways to determine its occurrence when multiple rams from the one breed make up the mob mating team. Quantification of the frequency of heteropaternal superfecundation in Irish sheep is enabled by the rapid growth in genotyping; this exercise has never been undertaken previously in any global sheep population. The data used in this study consisted of 685 multiple birth litters where DNA information on the sire, dam and all lambs were available; all dams were mob mated. Of the 539 pairs of twins included in the analysis, 160 (i.e., 30 %) were sired by two different rams. Of the 137 sets of triplets included in the analysis, 73 (i.e., 53 %) were sired by more than one ram. Of the nine sets of quadruplets, eight were sired by two rams, with the remaining litter being mono-paternal (i.e., all sired by the same ram). Therefore, the overall incidence of heteropaternal



Using DNA information is valuable to build confidence in genetic evaluation.

superfecundation among litters was 35 %. Given that the incidence of multiple births in these flocks was 65 %, heteropaternal superfecundation is expected to be relatively common in sheep; this is especially true since all but two of the litter mates were polyzygotic, meaning that the litter originated from separate eggs. Of the genotyped triplets and quadruplets, all originated from separate eggs, with the exception of one set of triplets where two of the lambs born had almost identical genotypes, suggesting that they originated from a split embryo. This in itself indicates that the extent of genetically identical full-sibling litters is extremely low. An equation was derived to deterministically calculate the probability of a litter (P) being sired by more than one ram (Figure 1), where N is the number of rams in the mating mob and L is the number of lambs born in the litter. For example, the likelihood that a set of triplets born to a ewe mated by two rams are sired by both rams is 75 %. This equation, however, assumes no differential in fertilisation capacity among the different rams, nor any difference in intrauterine embryo/foetal survival. Fertilisation capacity includes the semen quality of the ejaculate but also the receptiveness of the egg to the sperm of a given ram; differences in semen quality parameters among rams are known to exist. Differences in intrauterine survival of a zygote, embryo or foetus from particular rams could be due to a number of factors, not least the genetic relationships of the ram with the ewe (i.e., resulting in inbreeding) or whether both parents are carriers of lethal genetic mutations (also more likely with inbreeding).

Practical implications

Breeders and farmers alike are often concerned about how closely the predicted genetic merit of an individual reflects its true genetic merit. Genetic merit of sheep in Ireland is depicted in their 'star ratings', analogous to the star ratings of hotels. Disillusionment can often ensue among breeders and farmers when the star rating of a newborn lamb changes (significantly) once the lamb is genotyped. This can occur because, in the absence of any information on the animal itself (i.e., either lambing performance or genomic information), the estimated

genetic merit of a litter of lambs is assumed to be identical; this is simply the average genetic merit of the parents. This assumption ignores the random inheritance of the DNA of each parent. Our study revealed that the level of genetically identical litter mates (i.e., the same DNA is inherited) is extremely low. Dizygotic (i.e., non-identical) full siblings are assumed to have a genetic relationship of a half; if the twins are born from dual paternity (i.e., heteropaternal superfecundation), then the genetic relationship between siblings is expected to be one-quarter (i.e., half-siblings), assuming both sires are unrelated and the dam is non-inbred. Hence, where heteropaternal superfecundation occurs, the extent to which the star ratings of lambs from the same litter can diverge may be large. Notwithstanding this, being able to demonstrate, using DNA information, why the genetic ranking of the animal changed once genotyped will be invaluable in securing confidence in the genetic evaluation system and also the benefit of genotyping.

$$P=1-N(1/N)^L$$

FIGURE 1: Equation to deterministically calculate the probability of a litter being sired by more than one ram (P) where N = number of rams in the mating mob and L = number of lambs born in the litter.

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MilkEV

TEAGASC research is examining extracellular vesicles in milk and how they can be incorporated into infant formula.

The 'Milking extracellular vesicles for improved infant formula' (MilkEV) project is a new collaboration between Teagasc Moorepark and Trinity College Dublin, which aims to quantify and characterise extracellular vesicles in Irish cow's milk.

Extracellular vesicles

Extracellular vesicles (EVs) are small cellular particles composed of a lipid membrane encasing proteins and nucleic acids. They are released from cells and can be found in all body fluids (blood, milk, sperm). Initially scientists viewed them as cell debris or as playing a sinister role in cancer. We now know that EVs are secreted in every physiological condition and are a form of cell-to-cell communication. This communication can be a health benefit; for example, milk EVs carry immune signals from mother to baby.

Research question

We will track EVs during milk processing and the production of infant milk formula. The project will also seek to answer the following questions:

- what is the composition of milk EVs?;
- can EVs survive processing?;
- can EVs survive digestion?; and,
- are they transported across the gut barrier?

To understand the effect of processing on EVs, commercial first-stage infant milk formula has been produced at pilot plant scale.

Studies in Teagasc and Trinity College Dublin

Bulk milk from the current Irish dairy herd, as well as colostrum, first milk and mature milk from individual cows (representing the next-generation dairy herd) was collected from Teagasc dairy farms from February to December 2019. In total, 159 milk samples have been collected and EV extraction is currently underway using ultracentrifugation density gradients. In short, EVs are purified and collected from milk according to their density (1.1-1.2 g/mL), following the International Society of Extracellular Vesicles guidelines (Théry *et al.*, 2018).

To understand the effect of processing, commercial first-stage infant milk formula has been produced at pilot plant scale using two different processing methods: standard thermal processing; and, membrane cascade processing. The membrane



This research aims to create a next-generation infant formula enriched with EVs.

cascade process incorporates low heat, so we will be able to understand if reducing the thermal load during processing protects EVs, and ensures the presence of intact, bioactive EVs in the final product.

Teagasc scientists are global leaders in modelling food digestion in the laboratory. Using the INFOGEST protocol, infant milk formula has been subjected to semi-dynamic gastrointestinal digestion. We are currently attempting to extract EVs from both gastric and intestinal samples. The effect of EVs on the health of the intestinal barrier is estimated by monitoring transepithelial electrical resistance, and quantifying tight junction proteins (i.e., occludin and claudin-1) in 21-day-old Caco2-HT29MTX cell monolayers. Cellular bioassays have been developed in house to test the benefits of consumed EVs for immune cells based on THP-1 macrophages treated with bioavailable milk digesta.

Benefits of milk EVs

This project will be of benefit to the Irish dairy industry as it determines the quantity and composition of EVs present in Irish milk over the lactation curve. It will help infant formula manufacturers by tracking the fate of EVs during processing. Whether or not bovine EVs can play a positive role in maturing the gut barrier and boosting the immune system will also be investigated.

New knowledge gained

This collaboration brings together experts in EVs, gastrointestinal digestion and dairy processing. Ultimately this research activity aims to create a next-generation infant formula enriched with EVs.

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A new approach for monitoring the fate of agricultural herbicides

Weed management is an essential part of good agricultural management and yet the fate of herbicides following application, beyond weed control, is not fully understood. **TEAGASC** research developed a multi-dimensional monitoring approach to address this knowledge gap and applied it in two Irish river catchments.

This research was part of the EU Horizon 2020-funded WaterProtect project, with partners in seven member states and undertaken in two of the Teagasc Agricultural Catchments Programme sites in Co. Wexford – Ballycanew and Castledockrell. Following application, and beyond their action on weed plants, herbicides are designed to degrade in soils. However, before this can fully occur, herbicides and metabolites associated with partial degradation can be lost from soil surfaces during rainfall. This can be in water that moves across the land surface (as runoff) to rivers, or into groundwater (by leaching). If this river or groundwater is subsequently used as a drinking water source, it may present a health issue if concentrations exceed a limit as regulated by the EU Drinking Water Directive. These limits are 100 ng/L for a single pesticide or 500 ng/L for the sum of all pesticides (i.e., herbicides, insecticides, fungicides). Herbicide degradation, runoff and leaching is influenced by the physical and chemical characteristics of soil, subsoil, bedrock, land use, management practices, timing of pesticide application and prevailing environmental conditions.

This means that monitoring for herbicides only a few times per year in rivers or groundwater (as is normally done in Ireland) may not provide useful enough data to assess environmental or human health risks.

WaterProtect

The WaterProtect research developed a new monitoring approach that addressed all of these factors by monitoring multiple herbicides in rivers using passive samplers that captured all flow conditions over a one-year period, and in 95 groundwater wells. This was undertaken in grassland and arable land use settings in the two Wexford catchments and so, overall, can be considered a multidimensional approach. Of the 18 herbicides screened by the passive samplers, MCPA, fluroxypyr, mecoprop, 2,4-D and triclopyr were detected in variable concentrations

throughout the monitoring period in the two catchment rivers. Time-weighted average concentrations of individual herbicides ranged from below the limit of quantification (LQ) to 262.9 ng/L in the Ballycanew catchment and from below the LQ to 127 ng/L in the Castledockrell catchment (**Figure 1**).

The total herbicide concentrations ranged from 8.9 to 472.6 ng/L in Ballycanew and 0.9 to 169.1 ng/L in Castledockrell. In both catchments herbicides were present in the streams throughout the year, and there were large seasonal and temporal variations in their types and concentrations (**Figure 1**). In winter, losses of herbicides were likely to be from legacy soil stores that were mobilised during high rainfall conditions, indicating imperfect degradation. Herbicide concentrations were low during this period, but mass loads were high (concentration multiplied by river discharge). Occasionally, concentrations of MCPA, triclopyr, fluroxypyr, clopyralid and mecoprop were in excess of the EU regulatory limit, mainly in the Ballycanew catchment. High concentrations of herbicides in summer were associated with incidental losses (rainfall following application) and lack of dilution during low flow. This highlights the importance of physical conditions in the catchments where contrasting controls on flow paths were instrumental in controlling such losses to rivers. Herbicides were also detected in 38 % of samples of groundwater wells across the catchments (**Figure 2**). The concentrations of all herbicides in different areas were highly variable and comparatively low concentrations were detected in Castledockrell. In Ballycanew there were high detections of clopyralid (619 ng/L) and triclopyr (650 ng/L), highlighting a large variability in these herbicides and sometimes exceeding the regulatory limit.

Implications for practice

These results fill gaps in our understanding of herbicide transfer to water that are important for developing collaborative mitigation

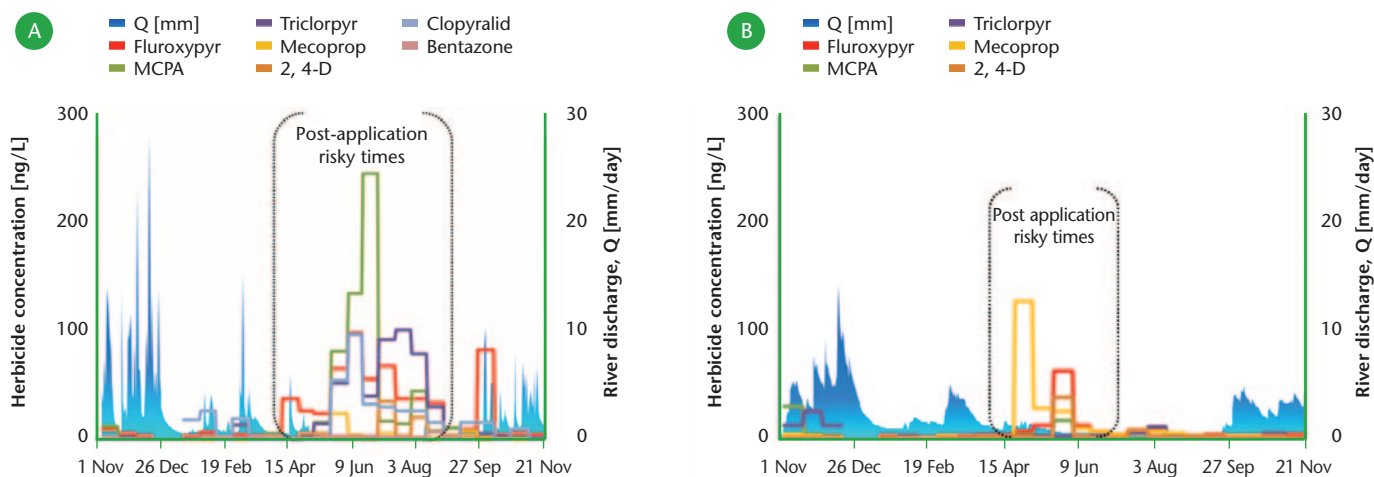


FIGURE 1: Herbicide concentrations (ng/L) in river and river flow (mm/day) in: a) Ballycanew catchment; and, b) Castledockrell catchment during the monitored period November 2018 to November 2019.

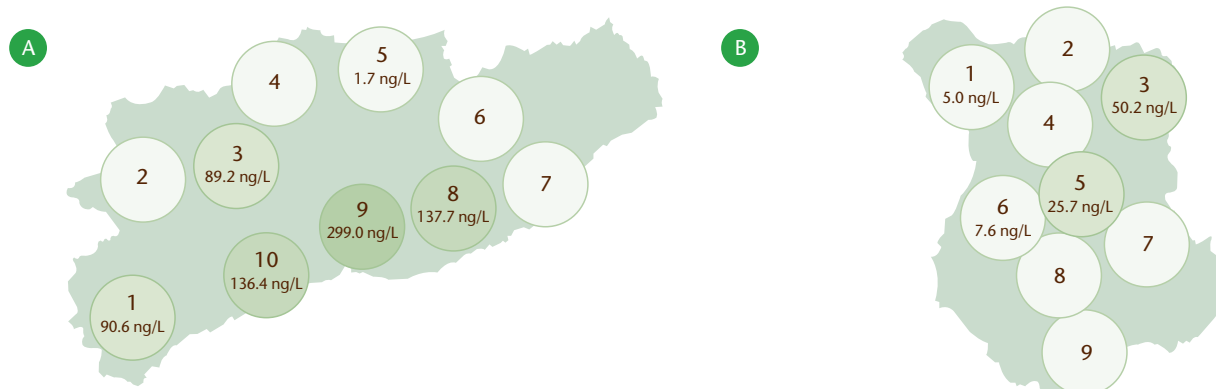


FIGURE 2: Herbicide concentrations (ng/L) in drinking water wells in: a) Ballycanew catchment; and, b) Castledockrell catchment. Values in individual circles represent average sums of detected herbicides in different areas across the two catchments.

strategies. Such strategies need to consider risky areas and risky times for the application of herbicides (and all pesticides) to avoid both incidental losses and build-up in soils. Such areas and times vary with different physical settings and land use, and efficient measures could be associated with changes in the handling and application of herbicides. This multidimensional and whole catchment approach provides the most detailed assessment of herbicide fate on agricultural land. The method can be used wherever pesticides are an unintended pollution problem and the datasets can be used as important knowledge exchange resources.

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Growing issues for the tillage sector



At the TEAGASC National Tillage Conference in January, live input from growers through a smartphone app helped to highlight the pressing issues in the sector.

Ireland's cropping systems underpin agri-food enterprises through the provision of high-quality, traceable livestock feed, and material for processing into food and drink products. The strategic importance of the crop sector is further supported by its potential to contribute significantly to the environmental sustainability of Irish food production systems. Ireland's tillage systems emit the lowest average greenhouse gases (GHGs) (~ 0.3-0.6 kg/kg finished product), in contrast to dairy (~ 1 kg/kg milk), and cattle (~ 13-18 kg/kg meat). The tillage sector is also the most resource efficient in regard to nitrogen (N) (> 60 %) and phosphorous (P) (> 80 %). Yet, while this carbon-efficient sector delivers quality traceable product that underpins much of our agricultural output, key profitability and sustainability challenges remain.

Live stakeholder poll

The 2020 National Tillage Conference gave us an opportunity to engage the 550 attendees on these sustainability issues, using the interactive Slido audience platform. This smartphone app allowed us to poll the audience in real time with nine questions, capturing a valuable perspective on stakeholder opinions, with results highlighting sectoral awareness of current and future challenges.

Main challenges

When asked to identify the main challenges to their enterprises (Figure 1), 91 % of respondents identified the continuous loss of plant-protection chemistry as the primary challenge, because of increasing resistance development in pathogens, weeds and insects, and product registration restrictions. This was followed by a lack of available varieties with increased stress resilience (47 % of respondents). This indicates the sector's acute awareness of these issues and the necessary route that must be taken at the research, and ultimately at grower level, to deal with the challenge.

Soil protection

The importance of protecting soil quality was a consistent topic throughout the Conference, with almost half of respondents acknowledging that from a soil perspective, additional measures were needed to promote soil health (Figure 2). On this, the incorporation of cover crops in rotations was seen as a key measure needed to protect and improve soil quality. While non-inversion tillage techniques were noted as an important step in improving soil structure, over 60 % replied that grass weed control was the main challenge restricting them from adopting non-inversion systems (Figure 3). Some 70 % of respondents noted that the potential loss of glyphosate in 2022 added further to the uncertainty around the viability of non-inversion systems, due to the lack of adequate weed control measures. Taken together, these results present a considerable challenge, for our current climate impacts on the relative benefits and challenges of non-inversion crop establishment systems, in terms of GHG emissions, crop establishment and grass weed control.

Opportunities for the future

Looking ahead, there was a strong consensus (72 %) among attendees that growing higher-value crops for specific markets is the primary opportunity for producers into the future, while also providing more protein crops to meet growing market demands (Figure 4). The need to exploit the use of organic manures from other enterprises was strongly supported. When asked about competitiveness, the need for high production standards, robust traceability, and research/agronomy support was identified, as well as the importance of accurate cost control on inputs. Throughout the Conference, the real-time poll delivered valuable stakeholder insights to support panel discussion on the day. Overall, the exercise provided an important insight into the awareness

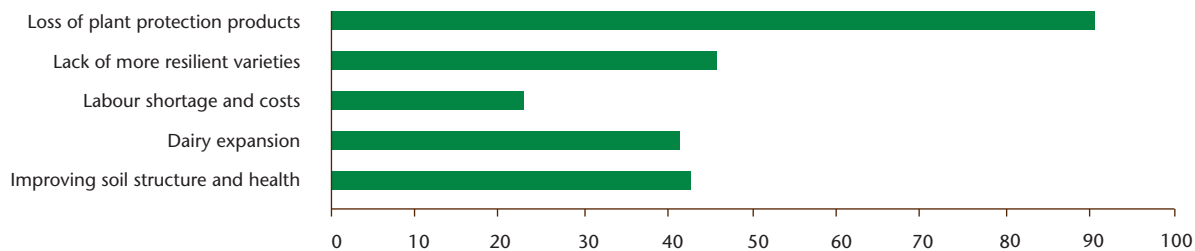


FIGURE 1: What are the main challenges facing the tillage sector?

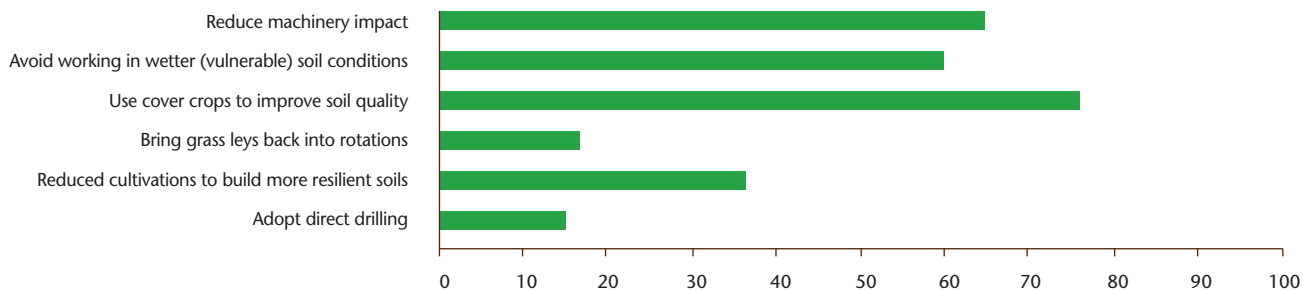


FIGURE 2: How can we protect our soils in continuous tillage

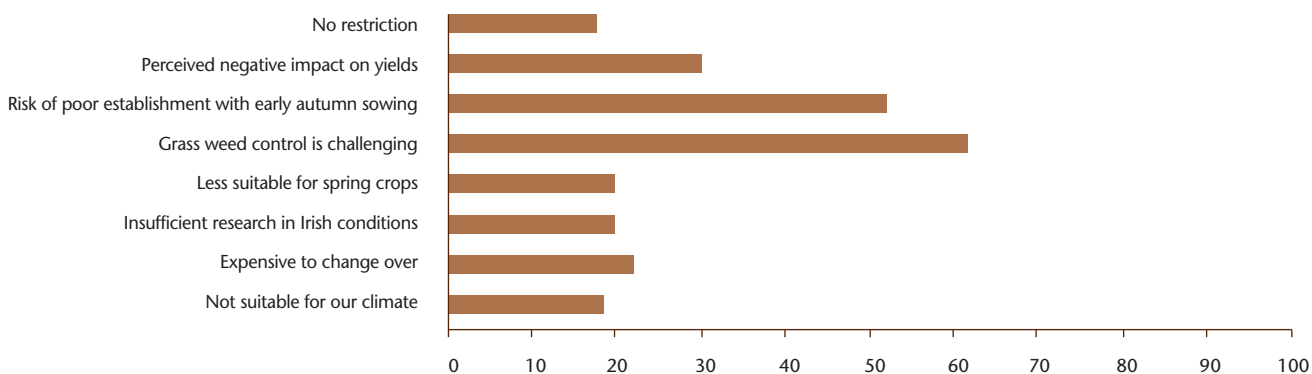


FIGURE 3: What currently restricts you from adopting non-plough tillage?

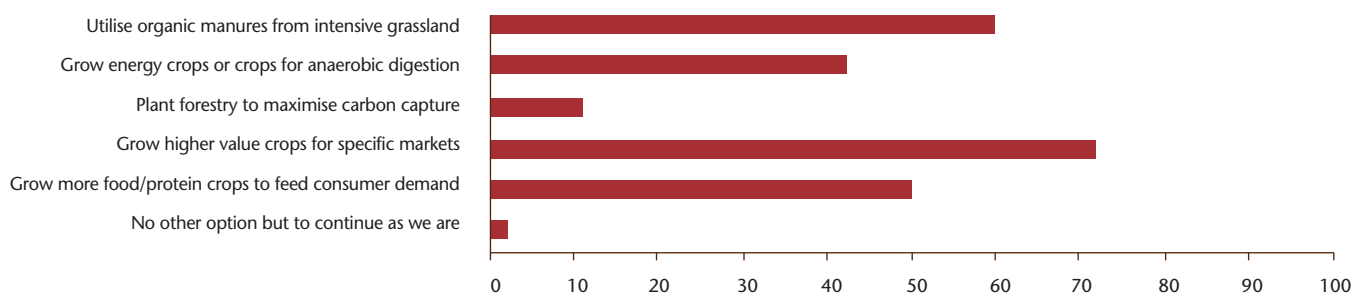


FIGURE 4: What will be the main opportunities for crop producers in the future?

of tillage stakeholders of the diversity of challenges that face the sector. Most importantly, it has identified the need for a continual industry response, at all levels, to ensure the future sustainability of the sector and the continued delivery of quality, traceable product.

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Corona lockdown: a time to cook!

TEAGASC research has found that our cooking and shopping habits have changed during the Covid-19 lockdown.

Time scarcity is frequently cited as a barrier to healthy eating and cooking meals from scratch at home. A recent survey of adults in Ireland conducted by Teagasc, University College Cork and the University of Antwerp, examining shopping and cooking behaviours before and during Covid-19 lockdown restrictions, has shown that most people had more time available for activities during lockdown compared to life before. So has this impacted on their food-related behaviour? Some answers are provided below based on approximately 400 consumers who responded to an online survey during April 2020, when full lockdown restrictions were in place. Most of the respondents (two-thirds) shop for themselves, with one-quarter having shopping done by a partner. Most indicated that they had been working before and during lockdown, with most working from home during the lockdown.

Getting food to the table

Positive food-related behaviours can be seen during lockdown, with significant increases in meal planning, use of shopping lists, using up leftovers and trying to make healthier choices. Food label and nutritional information usage, however, did not change during lockdown. While physically going to the shop has been commonplace before and during lockdown, there has been a small increase in online shopping practices since lockdown. There was also some evidence of stockpiling: the top five foods consumers indicated that they stockpiled when shopping were pasta/rice, followed by eggs, flour, vegetables (fresh and frozen) and milk. Interestingly, toilet roll was ranked in 15th place out of a list of 23 grocery items. In general, consumers increased purchasing of all foods to some degree relative to their purchasing behaviours prior to

lockdown. Cooking and shopping experiences are outlined in **Figure 1** and it is noteworthy that shopping has become increasingly stressful, frustrating and time consuming, as well as less enjoyable than previously.

Despite limited access to certain ingredients during lockdown, consumers have reported an improvement in their cooking skills, which was reflected in a significant increase in baking bread, pies and main meals from scratch, as a direct result of more time availability to engage in these behaviours. Consequently, people have experienced increased levels of satisfaction and enjoyment when preparing and cooking foods during lockdown.

Food consumption patterns have also changed during the lockdown period, with many consumers reporting that they consume certain foods with increased frequency, most notably alcohol and sugar-sweetened beverages followed by white bread/pasta, milk and dairy products.

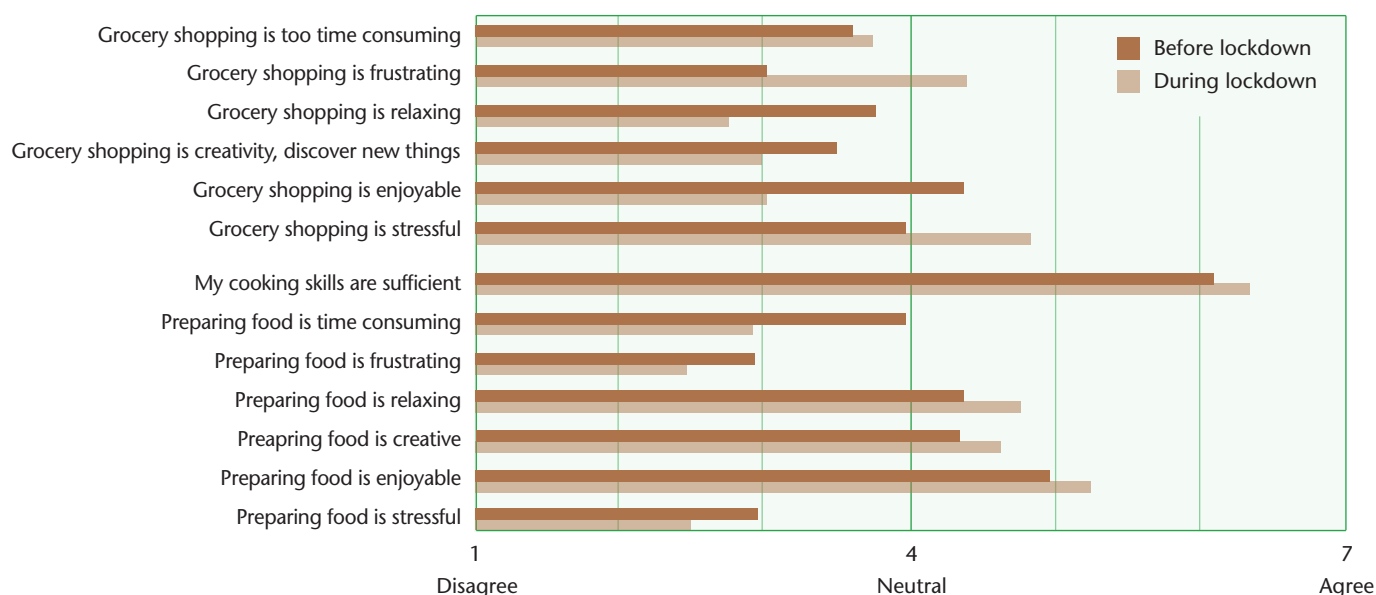


FIGURE 1: Adults' cooking and shopping experiences during the Covid-19 lockdown in Ireland.

What gets to the table?

Food consumption patterns have also changed during the lockdown period, with many consumers reporting that they consume certain foods with increased frequency, most notably alcohol and sugar-sweetened beverages followed by white bread/pasta, milk and dairy products. Increased frequency of consumption was also reported for sugary and savoury snacks. These are also the foods that were more likely to be stockpiled. Foods such as legumes/pulses, nuts, processed meats and fish were reported to be consumed less frequently during lockdown compared to before lockdown.

Living well in lockdown

Food-related behaviours from planning to shopping, preparation and subsequent consumption have changed in Ireland as a result of the lockdown. While some of the behaviours have a positive impact in terms of more cooking of meals from scratch and increased enjoyment in preparing foods, other behaviours have been less health oriented. Sustained higher frequencies of consumption of products such as alcohol, sugar-sweetened beverages and snacks could give rise to concern if the restrictions are to be in place for a longer time period. As most countries, including Ireland, start to ease restrictions, it would be useful to encourage consumers to maintain the healthy food and lifestyle habits developed during lockdown and to tackle the less healthy ones. Given the forecasts and the fears associated with future waves of the virus in the absence of a vaccine, the potential for future lockdowns remains high. Hence we need to continue to promote the healthy choice, ensuring that it is available, and encourage healthy lockdown behaviours, in the absence of time barriers. The improvement in cooking and baking skills provides a foundation upon which to build initiatives for healthy eating behaviours.

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Managing manure

TEAGASC research has tracked changes in manure management practice across Irish farms.

Agriculture accounts for 33 % of greenhouse gas (GHG) emissions and 99 % of ammonia emissions in Ireland (Duffy *et al.*, 2020; EPA, 2019). The manure management elements of agricultural production account for 10 % of agricultural-based GHG emissions and 77 % of ammonia emissions. Bovine animals account for the majority of these manure management-based emissions – 66 % in the case of GHGs and 81 % for ammonia. Hence, management of this component will play an important role in meeting Ireland's national emissions reduction targets in the future. Teagasc recently published a report on manure management practices covering the 2016-2018 period using results from the Teagasc National Farm Survey (NFS). The Teagasc NFS has been adapted in recent years to collect a wider suite of management data relevant to the environment. The last major comparative survey of manure management practices was conducted by Teagasc in 2003 (Hyde *et al.*, 2008). Results from this latest report are compared with those from 2003 to explore changes in farm-level manure management practices over the intervening period.

Methodology

The recently published report (Buckley *et al.*, 2020) is based on analysis of farms with bovine animals over the 2016 to 2018 period, using data collected by the Teagasc NFS. The sample size is 876 farms, representing circa 90,000 farms nationally. The report provides detail on: the duration of bovine animal housing periods; the prevalence of different types of slurry and farmyard manure storage facilities; the proportion of manures generated by different animal types; the extent of seasonality of manure application; and, the extent to which various slurry application and manure storage methods are employed.

Results

Table 1 presents results from the recent report and compares them with results from the 2003 survey. However, it should be noted that different sampling frames were employed for the two surveys.

Compared to the 2003 results, the new report indicates that some categories of animals were winter housed for longer (suckler cows, heifers, cattle 0-1, cattle 1-2 and cattle > 2 years) and some for shorter periods (dairy cows and bulls).

Across all bovine categories (except cattle 0-1 years), the recent report indicates that a greater proportion of manure is stored in slurry form compared to what prevailed in 2003. This is to be expected, as there has been significant investment in storage facilities in the intervening period. The aforementioned investment in facilities is also reflected in changes in manure management storage method, where results from the recent report indicate that 87 % of slurry is now stored under a roofed slatted tank compared to 71 % in 2003.

Estimates from the new report indicate a higher level of early season application of slurry (44 % of total) compared to the situation in the 2003 report (35 %). Conversely, there were higher levels of summer and autumn slurry application in 2003 (44 % and 16 %, respectively) compared to the recent report (40 % and 13 %, respectively). Finally, the 2003 report indicated that at that time, 98 % of slurry was applied by the splash plate method and only 1 % by a band spreader. Results from the recent report confirm that farmers have started to transition towards low-emission slurry spreading methods (trailing shoe, trailing hose and injection), with these methods accounting for 4 % of aggregate slurry applied over the 2016-2018 period. This is very important in that as farmers implement farm management practice change, such as adoption of low-emission slurry spreading, it is important that we are able to capture this change and reflect this activity in the GHG and ammonia national inventory accounting systems in the future.

Conclusion

Comparing results from the recent Teagasc report on manure management practices with the last major survey on this topic in 2003 indicates that there has been a substantial move towards more manure storage in slurry form as well as slurry storage under a roofed

Table 1: Results of manure management practices surveys – 2003 versus 2016 to 2018.

	Teagasc 2003 report	Teagasc 2016-2018 report
Days housed		
Dairy cows	129*	121
Suckler cows	129*	150
Heifers in calf	135*	149
Cattle 0 to 1 years	138*	147
Cattle 1 to 2 years	141*	149
Cattle > 2 years	144*	148
Bulls	141*	121
Proportion of manure stored as slurry		
Dairy cows	94 %	94 %
Suckler cows	73 %	82 %
Cattle 0 to 1 years	68 %	56 %
Cattle 1 to 2 years	80 %	87 %
Cattle > 2 years	59 %	85 %
Bulls	30 %	81 %
Method of slurry storage		
Under a roofed slatted tank	71 %	87 %
Covered over ground tank	4 %	3 %
Unroofed underground tank	16 %	5 %
Uncovered over ground tank	6 %	4 %
Lined lagoon	1 %	1 %
Unlined lagoon	2 %	0 %
Time of slurry spreading		
January-April	35 %**	44 %
May-July	44 %**	40 %
August-September	16 %**	13 %
October-December	6 %**	3 %
Slurry application method		
Splash plate	98 %	84 %
Injection	-	1 %
Low-emission slurry spreading	1 %	3 %
Umbilical	-	10 %
Other	1 %	2 %

*Reported in months (30 days is assumed here)

**This was reported as spring, summer, autumn and winter

slatted tank. Additionally, more slurry is now applied in early season and by low-emission slurry-spreading methods. Through the methods documented in this new report, the framework is now in place to capture changes in farm-level manure management activity data collected by the NFS. This development has the potential to be used in the national inventory accounting framework going forward.

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App value

Have smartphones become a valued piece of farm machinery? Research in the EU H2020 NIVA project explored farmers' views on smartphones and agricultural apps.



Background

Farmers take great pride, enjoyment and value from purchasing, owning and using farm machinery – tractors, trailers, mowers, loaders, fertiliser spreaders, the list goes on. A relatively new addition to that list is the smartphone. Increasingly, we see smartphones, and their lifeblood – ‘apps’, playing a role in farm management practices. In recent years, we have seen an exponential growth in digital technologies in agriculture: the so-called phenomenon of ‘smart farming’, which has captured the attention of scientists, technology developers, investors and policy-makers. Smart farming refers to the increasing development and update of a wide range of digital technologies including, for example, digital and connected farm machinery (e.g., tractors, drones and robotics), and sensors in fields, on animals and on crops. For many of these connected digital technologies, smartphones operate as the user interface between the technology and the farmer.

Smartphones have become increasingly popular in agriculture, due to their ability to create new opportunities for farmers to enhance farm productivity and keep up to date with agricultural information. Smartphones offer farmers a chance to efficiently communicate with one another, to gather, process, and share data accordingly, and to make use of a multitude of installable mobile apps according to their needs. Decision support tools accessed through smartphone apps offer an opportunity to interpret past and predict future farm trends, and allow farmers to make more time-efficient and accurate on-farm decisions.

Despite the benefits that smartphone technology can contribute to agricultural practice, research on farmer ownership and usage of smartphones is scarce, with only a limited number of studies available. Furthermore, what is missing in the studies conducted to date is an in-depth examination of farmers' views of smartphone technology, and their perceived utility and value for the farm. Given

this, our study aimed to explore: (i) factors that impact Irish farmers' engagement with smartphone use and new smartphone apps; and, (ii) supports required by farmers to successfully engage with smartphone apps for agriculture use.

Research approach

A qualitative research approach was used. A total of 41 farmers, consisting of 37 males and four females, represented the study sample. Data were collected through focus groups (n = 7) conducted across four regions in Ireland between October and December 2019. Purposive and convenience sampling techniques based on geographical location, age and farm type (dairy, beef, sheep, pig) were employed to recruit the target population. Each focus group was reasonably homogeneous in nature; groups consisted of full-time or part-time farmers, from the same farming sector and of similar age, in order to facilitate a comfortable setting that was conducive to open conversation. Data were thematically analysed, an approach that facilitates the identification and grouping of similar patterns and themes across focus group discussions.

Results

Results showed that the majority of farmers in our study did not use new farming technologies (in particular smartphones) for the purposes of work, largely due to perceived lack of capability and confidence to engage with new technologies. Some farmers, however, perceived benefits of smartphone technology, such as their ability to enhance quality of life (QoL) and sense of social cohesion. Younger farmers were particularly open to adopting smartphone technology and associated agricultural apps for work, due to an expressed greater sense of personal confidence and ability in operating such technologies. Barriers to using smartphones were

	Smartphone users	Smartphone non-users	
User persona	Currently using smartphones and agricultural apps	Open to using smartphones and agricultural apps	Unwilling to use smartphones and agricultural apps
Barriers (-) and motivators (+)	Positive about all technology in farming (+) Enhances farm work and QoL (+) Reduces labour costs (+)	Open to learning (+) Appreciate benefits (+) Currently lacking in technological self-efficacy (-)	No access to a smartphone (-) No perceived value (-) Strong technological fear and trust issues (-)
Implications for new agricultural apps	Will be open to trialling new apps if they are user friendly	May trial new apps if shown how and supported in their use	Unlikely to use
Recommendations	Embed user experience (UX) studies during app development	Provision of wider training and support networks	Consider unintended impacts (e.g., increased digital divide and isolation)

FIGURE 1: Thematic map reflecting the landscape of smartphone app use among Irish farmers, key barriers/motivators associated with their (lack of)/use, and recommendations for future development of apps aimed at the farming community.

highlighted across all groups, such as: age; knowledge and skill; fear and a lack of technological self-efficacy; (a lack of) trust; cost; internet connectivity; (a lack of) perceived value and interest; prior negative experiences with technology; and, a preference for more traditional farming methods. The key facilitators of smartphone engagement included: an enhanced sense of empowerment; a more flexible lifestyle; a reduction in stress; an improvement in time efficiency; an enhanced level of communication between farmers and their respective governing bodies; and, an ability to make data-driven decisions on the farm.

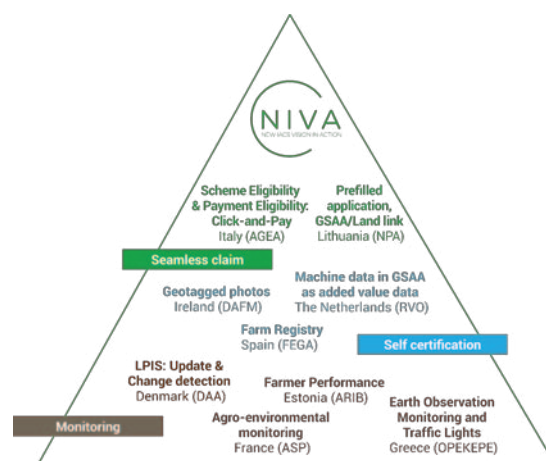
A thematic map was also developed to further illuminate the landscape of smartphone app use (motivations for/barriers against use) (Figure 1).

Conclusion

The practical findings of this research outline the importance of understanding the barriers and enablers of farmers’ engagement with smartphones and agricultural apps in Ireland. The findings may be of interest to researchers in the field of smart farming technology, as well as developers and providers of agricultural-related smartphone apps, since this research is one of the first studies to provide information about the underlying factors driving or preventing smartphone use among farmers.

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