Untangling the complexity of diseases such as calf diarrhoea is crucial to future productivity.

As the world hurtles to 2050 carrying with it the prospect of a human population estimated to be 9.6 billions, the challenge of feeding this number of people is becoming ever more apparent (Mellody et al., 2014). There has been much discussion around strategies to increase agricultural production; however, limitations on arable land and impending key resource scarceness, in particular water, suggest that at some point a ceiling will be reached that caps production. Faced with this impending agricultural austerity, it will be necessary to increase food production while minimising associated increases of the footprint of agriculture. A crucial part of this equation will be minimisation of food loss, which has been estimated at account for 25% of world food production (Kummu et al., 2012).

A complementary strategy which has received less of a coordinated response is to increase the efficiency of agricultural production prior to products enter food supply chains. In the cattle industry, there are opportunities to maximising production and the use of current inputs of finite resources by reducing farm losses. These gains in productivity will likely include enhancing conception rates, improving feed usage and the incorporation of superior genetics. It will also be necessary to more effectively address highly complex diseases that currently reduce cattle productivity. Historically these diseases have been described by generic, somewhat simplistic names, such as bovine respiratory disease (BRD).
undifferentiated fever, neonatal calf loss, and calf diarrhoea or calf scours to name a few.

These generic terms are used to describe diseases with complex aetiologies where a range of pathogens in association with other factors, such as animal management, contribute to disease expression. To reduce production losses associated with these complex issues, the first step will be to more accurately define the underlying aetiology of these diseases.

Calf diarrhoea is one such disease which requires this approach to reduce its impact on production. Calf diarrhoea is the most common cause of calf mortality which can exceed 20% in some instances (Uetake, 2013). Currently, the list of infectious agents associated with calf diarrhoea includes viral pathogens (such as bovine rotavirus and coronavirus), bacterial pathogens (such as *Escherichia coli* K99, *Clostridium perfringens* Type C and *Salmonella* spp.) and some parasitic pathogens. In this issue of *The Veterinary Journal*, Di Felice et al. (2015) have proposed the extension of the list of viral pathogens associated with calf diarrhoea to include bovine norovirus (BoNoV). The authors have reviewed the associated literature in regard to BoNoV and bovine/calf diarrhoea. The authors also drawn parallels with the more extensively studied area of human norovirus biology to draw links that support the inclusion of BoNoV on the list of pathogens considered during diagnostic investigation of calf diarrhoea. The strategy used by Di Felice et al. (2015) to draw on the extensive literature for parallel human diseases to identify putative pathogens for less well characterised bovine diseases is an excellent one.

Technology developments will undoubtable also play a critical role in untangling the complex web of pathogens associated in with diseases such as calf diarrhoea. Metagenomics using next generation sequencing (NGS) technology being applied to veterinary disease
investigations will be central to elucidating complex aetiologies. Ng et al. (2015) have recently applied metagenomics to BRD and the resulting data, albeit novel, were hardly surprising. The authors report a list of pathogens commonly linked to BRD, for which vaccines and diagnostics are readily available. However, a range of other viral agents were also identified and linked to BRD, thereby demonstrating the value of this approach. The principle advantage of metagenomics is that there is no need to isolate or propagate the pathogen from diseased tissues. Therefore, it has the capacity to remove experimental bias that can be inherent in disease investigations focused on pathogen isolation for disease causation. Investigations based on pathogen isolation are obviously more likely to find those pathogens that are readily amenable to growth in laboratory conditions. As BoNoV cannot be grown in vitro, it is not surprising that it has been previously left of the list during calf diarrhoea investigations (Di Felice et al., 2015).

There is no doubt that the availability of efficacious vaccines will be crucial to the future control of calf diarrhoea and other complex diseases. Improved diagnostics will also be required to accurately monitor and track disease incidence and aid long-term control. For BoNoV, there is potential for considerable genetic diversity that needs to be considered for effective vaccines and diagnostics (Di Felice et al., 2015). Again metagenomics has the capacity to provide the information required to support improved control.

The presence of a potential pathogen is obviously not sufficient to attribute causation for complex diseases. In this respect, epidemiological studies can play an important role to identify risk factors that may either increase or decrease likelihood of disease. For epidemiology to support gains in productivity, the use of complex analyses will be required
to not only identify, but also quantify risk factors. The challenge for farmers in controlling complex diseases with multiple contributing risk factors is making the right decision at the right time. To do this, the outputs of complex epidemiological studies need to be distilled down into a farmer-friendly decision support tools. These will undoubtedly be in the form of tools available on smart devices, whereby the farmer can enter known information regarding the risks for a particular group of cattle. This input data could include results from crush-side diagnostics, farm disease history, vaccination status, animal movement data and weather data, which could then be used to generate specific advice on the optimal management of particular cattle groups. The overall result of this process will be informed proactive management as opposed to the current reactive management.

For too long there has been an acceptance of loss as part of the animal production business model. This may have been partly driven by ineffective measures used to combat the disease in question, as the underlying aetiology was poorly understood. For example, this could result in vaccinating for bovine coronavirus based on clinical signs of calf diarrhoea when BoNoV or another pathogen might have been the primary cause. With so many challenging aspects in the future on our planet, the time to act is now to increase product efficiencies. This is particularly important for diseases such as calf diarrhoea and BRD that have widespread negative impacts on cattle production. Fully defining these complex aetiologies is only the first step in the process, since the development of intervention strategies, such as vaccines and other management strategies, is going to take time to develop and implement.

Timothy J Mahony
Queensland Alliance for Agricultural and Food Innovation
References


