Epidemiology and economic impact
of Johne's disease in Irish dairy herds

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1. SUMMARY

This project addressed two aspects of an emerging infectious disease of Irish cattle; the epidemiology and the economic impacts of Johne's disease (paratuberculosis). Though this disease has been present in Irish cattle herds for decades, only since the introduction of the Single European Market in 1992 has it become more widespread. In addition to this change in the epidemiology of the disease in Irish cattle, there is increasing evidence that the causative organism, *Mycobacterium avium* subsp. *paratuberculosis* (MAP) may be implicated in a human illness, Crohn's disease, though proof of a zoonotic link is currently disputed (Tremblay, 2004). Against this background a collaborative research project was set up by Teagasc and funded by Irish dairy farmers.

The first three studies dealt with epidemiology of Johne's disease in Irish dairy herds.

Heretofore there has been no data available on the national sero-prevalence of this disease in Irish cattle herds. In order to address this knowledge gap, the Department of Agriculture, Fisheries and Food (DAFF) carried out a national bovine paratuberculosis sero-survey in 2005. The first study reported here was conducted to validate the sampling methodologies used during the collection of the 1,000 serum samples for that survey. The aim of the study was to assess the external validity and precision of two field data sets (605 samples selected randomly, 295 selected opportunistically). Limited prior knowledge was available about the population, with respect to Johne's disease. Therefore, a range of methods were used to conduct a *post hoc* assessment of external validity (spatial distribution, nearest neighbour method, kernel density plots) and precision. Based on this post-hoc assessment, results from the randomly selected samples would provide an externally valid, albeit relatively imprecise, estimate of national disease prevalence and of the disease prevalence in three of the four provinces (Munster, Leinster and Connacht) and in beef and dairy herds.

While the national sero-prevalence was being established, a linked study was set up to investigate the herd and management risk factors associated with the introduction and transmission of paratuberculosis into dairy herds in Ireland. A case-control design was used and data were gathered by structured tele-questionnaire interview. Case herds were selected on the basis of having one or more positive faecal cultures for *Mycobacterium avium* subsp *paratuberculosis* (MAP). Control herds were selected on the basis of being seronegative for MAP in a national serosurvey. Control herds were matched to case herds on the basis of the year of diagnosis of MAP in the case herds. Factors relating to disease history, herd size, neonatal feeding and management and grassland management were found to be significant in the univariate analysis. The multivariate analysis found the feeding of waste milk

prior to diagnosis, the absence of individual calving pens, the herd size, and herd depopulation for a notifiable disease to be significant risk factors for the occurrence of paratuberculosis.

The demography of bovine infections caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is poorly defined and documented in Ireland. The objective of the third study on the epidemiology of Johne's disease was to describe the demographics of cattle positive to MAP on faecal culture, based on submissions to the Cork Regional Veterinary Laboratory between 1989 and 2006. The study focused on all available faecal samples from adult cattle with non-responsive chronic diarrhoea that were submitted by private veterinary practitioners to Cork RVL for MAP culture. No positive bovine submissions were recorded between 1989 and 1993. The first bovine faecal culture positive submission was a pedigree Limousin cow in 1994 (MAP had been isolated from farmed deer faeces in 1993 and 1994). The percentage of MAP culture positive bovine samples in each year varied between approximately 10 and 40% (mean yearly proportion = 18.3%, SD 6.7). These data show an increase in the number of submissions with requests for MAP culture over time, particularly from 2002, when the Department of Agriculture, Fisheries and Food took a proactive approach to Johne's disease. While the number of positive submissions also increased over time, the proportion of positive submissions has not increased in recent years. This study indicates that increased awareness of Johne's disease has resulted in increased submissions for MAP culture in the CVRL catchment area but the proportion of positive samples has remained constant in recent years.

The next four studies dealt with the economic impacts of Johne's infection, either subclinical or clinical, in Irish dairy herds.

The fourth study utilised the data from the national Johne's disease serosurvey in conjunction with the national milk records database to investigate the impact of Johne's disease sero-status on milk yield, fat, protein, somatic cell count and calving interval in Irish dairy herds. The ICBF database was interrogated to find milk–recording herds that were sampled in the national Johne's disease serosurvey. Serum from all animals over twelve months of age (n=2,602) in 34 dairy herds was tested for antibodies to *Mycobacterium avium* subsp. *paratuberculosis* using an ELISA. Herds were categorised by sero-status into positive, non-negative and negative, where a positive herd contained two or more positive cows, a non–negative herd contained only one positive cow and a negative herd contained no positive cows. Data at animal, parity and herd-level were analyzed by multiple regression using general linear models. The true animal-level prevalence of paratuberculosis was 2.9%. At the herd-level, 25% of herds had two or more positive cows and 50% of herds had at least one positive cow. Positive herds (mean herd size=129 cows) and non-negative herds (81 cows) were larger than negative herds (72 cows) (P<0.01). Negative herds had the highest

economic breeding index (EBI) while positive herds had the highest estimated breeding value (EBV) for milk yield. There was no significant effect of paratuberculosis sero-status at animal, parity or herd-level on milk yield, milk fat or protein production, somatic cell count score (SCCS) or calving interval. Negative herds tended to have a lower SCCS than positive and non-negative herds (P=0.087). This study could only examine the effects of paratuberculosis sero-status (subclinical Johne's disease), but not the clinical effects of Johne's disease at the farm or dairy industry levels.

The fifth study arose from an investigation of a large dairy herd which presented with a clinical Johne's disease outbreak. This study examined the herd Johne's disease epidemiology, investigation and control recommendations. The study followed the DAFF Johne's disease control model of the local veterinary practitioner leading the investigation with support from other agencies as required. The objectives of the study were to carry out an historic analysis of the herd to determine the likelihood of the presence of Johne's disease and the projected level of Johne's disease if present and to develop an on-farm Johne's control programme. The investigation confirmed the presence of Johne's disease in the herd, the likelihood that it had been brought in by imported cattle and the occurrence of a large recent outbreak of the infection. In one year 19 cows died on the farm and Johne's disease was a major contributory factor. Control recommendations were formulated with the local veterinary practitioners and documented in reports to the farm manager. Follow up farm biosecurity measures were also outlined. This study highlighted the potential extent and impact of some of the more serious outbreaks of Johne's disease in Irish dairy herds and the on-farm operation of the disease control model.

The sixth study, a retrospective case study, was undertaken on a commercial dairy herd with a documented history of Johne's disease. Individual animal production records were interrogated to assess the effect of JD on milk yield and somatic cell count and reasons for culling, cull price and changes in herd structure over time. Lactations from all cows in milk from 1994 to 2004 were compared between JD and non-JD cows using clinical signs and test results to define JD status. Six separate multivariate regression models were conducted. There was a significant negative association between clinical JD infection status and milk yield, SCC and culling price in the study herd. In contrast, little effect was noted for sub-clinical infections. These direct effects, in combination with increased culling for infertility and increasing replacement rates, had a negative impact on the economic performance of the farm. Results from this study provide preliminary information regarding the effects of JD status on both herd and animal-level performance in Ireland. The findings confirm those of the previous studies indicating that while clinical Johne's disease can have a serious economic impact subclinical infection may not.

Given that there are very few published data on the economic impacts of Johne's disease under Irish farming circumstances, in the final study, the economic impact of Johne's disease was simulated. A whole farm bioeconomic model has been developed in Moorepark; the MDSM. While this model includes production derived economic data, it did not contain an animal disease component. The objective of this seventh study was to upgrade the existing MDSM with a disease component using Johne's disease as an example. The predicted effect of disease on a 100-cow dairy herd using international effects of disease on production was to lower farm net profit by €7,693 per year for an infected herd. This is an estimated loss of net profit of 15.2% per year. This estimate could be improved by using Irish-based input data, adding a stochastic element to the model and calculation of economic performance accounting for changes in herd health status over time and with and without disease control.

With the increased global demand for dairy products and the abolition of the EU milk quota in 2015, many Irish dairy herds will be undergoing expansion in the future. Such herdowners need to be aware of Johne's disease and take precautions to avoid its introduction and spread.

2. INTRODUCTION

Paratuberculosis (Johne's disease; JD) is a chronic, granulomatous enteritis of ruminants caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). The disease is characterised by persistent diarrhea, weight loss and protein-losing enteropathy. Paratuberculosis can cause significant economic loss in affected herds, as a result of reduced milk yield, increased incidence of mastitis, altered milk constituents, increased somatic cell counts, poor feed conversion, increased susceptibility to disease in general, reduced reproductive efficiency, premature culling and reduced cull cow values (Hasonova and Pavilk, 2006). There are also potential concerns relating to the safety of dairy products derived from the milk of animals infected with paratuberculosis (Ghadiali *et al.*, 2004). Should the putative causal link between MAP and Crohn's disease be substantiated, Johne's disease could become the most important infectious disease affecting the Irish and international dairy industries.

Paratuberculosis has been a scheduled and notifiable disease (though non-compensatable) in the Republic of Ireland since 1955. Prior to the mid 1990's, disease was rarely reported (92 cases between 1932 and 1992), primarily in imported animals (DAFF, unpublished). The introduction of the Single European market in 1992 facilitated the free movement of goods and services within the EU. Cattle could be imported into Ireland from continental Europe without any of the previous requirements for testing and certification prior to import and 6-month quarantine and additional testing following importation. The indications are that the prevalence of paratuberculosis in Ireland has increased since the introduction of the Single European market.

Given these unique and changing national circumstances, the Department of Agriculture, Fisheries and Food took a proactive role in Johne's disease control in 2002/03 organising a series of national farmer and veterinary meetings addressed by invited international experts. This greatly raised awareness of the disease and stimulated farmer interest and concern about out national Johne's disease status. Whilst Teagasc had an active research programme on the pasteurisation aspects of MAP (Murphy and Lynch, 2005), its last involvement in research on the veterinary aspects of the disease was over ten years ago (O'Doherty et al., 1998). Hence, it was decided to initiate a joint Teagasc/DAFF/CVERA/ICBF project on the current epidemiology and economic impacts of Johne's disease in Irish dairy herds.

2. STUDIES

The seven studies reported here cover both the epidemiology (Studies 1-3) and the economic impact (Studies 4-7) of paratuberculosis in Irish dairy herds. In parallel with these studies, the Department of Agriculture, Fisheries and Food has conducted other collaborative studies with Teagasc on paratuberculosis in Irish beef herds (Mullowney et al., 2007).

Epidemiology of paratuberculosis in Irish dairy herds.

Study 1.
External validity and precision of samples used to carry out a national sero-survey of the Irish cattle population for Johne's disease

Introduction
External validity refers to the accuracy with which a sample represents the population of interest. Precision is directly related to sample size, where generally, increasing sample size gives increased precision. A sampling error occurred during collection of samples to investigate the sero-prevalence of Johne's disease (JD) in Irish cattle, which resulted in approximately a third of the data being collected opportunistically, rather than randomly. This created concern over the potential for sampling bias in the data set. As data collection is expensive, a post-hoc analysis of both external validity and precision was considered necessary to ascertain if the samples could be usefully used for the purpose intended. The purpose of the study was to assess the external validity and precision of the two field data sets (selected randomly and opportunistically), and to assess the level of sampling bias if the opportunistic and random field data sets were combined.

Materials and methods
In this study, the reference population included the 97,455 (breeding) herds where at least one home-born calf had been registered in 2003. A simple random sample of 1,000 herd numbers ('the proposed dataset') was selected from the reference population, using computer-generated random numbers. This sample size is sufficient to estimate a national herd level prevalence of 10%, with a 95% CI and a precision of 2%. Arrangements were then made, through the national brucellosis testing laboratory, to collect all sera from each selected herd. A computer programme was used to notify staff when relevant samples were available. Between June and November 2005, the sera from 644 herds (so-called 'random field dataset') were collected in this way. However, a computer error occurred in mid-November, and no further samples were collected using this approach. Once the error was detected, sera from a further 367 herds were collected opportunistically during early winter 2005 to make up for the earlier missed samples. Samples in this 'opportunistic field dataset' were selected by laboratory staff as brucellosis samples came in, without any formal methodology or stratification of the sampling. A further

three datasets were generated ('generated datasets' A, B and C), using the random number selection in the Animal Movement extension of Arc View (version 2.4), to provide a comparison group (with an equivalent number of herds) to the random, opportunistic and combined field datasets, respectively.

In Ireland, herd numbers are geo-referenced to digitised parcels of land, constructed for calculating EU land based farming aid. Mapping was conducted using ArcVIEW 9.1 (ERSI, Redlands, CA, USA). We visually compared the spatial distribution of the random and opportunistic field datasets. Then, we used the nearest neighbour method (ArcVIEW 9.1) on the field data (random, opportunistic and combined) and three generated datasets to determine the degree of clustering in each (high: neither dispersed or clustered; medium: dispersed but possibly random; low: <5% likelihood that clustering is randomly distributed; very low: <1% likelihood that clustering is randomly distributed). Nearest neighbour ratios and qualitative outputs from ArcVIEW were reported. The nearest neighbour analysis was restricted to a rectangular area or 'window' that incorporated as much of Ireland (but as little sea or Northern Ireland) as possible. We also developed a kernel density plot (ArcVIEW 9.1) for each data set, except the combined field and generated datasets, to further examine sample distribution within the window. The kernel density plot was conducted using a 10km search radius, with a 100m grid. Results are presented as points per square kilometre.

We calculated the precision of the original proposed sample (n=1000) and of each field sample (n=644, n=367), at different prevalence levels and given a 95% confidence level. Precision was displayed as margin of error and was calculated using:

(1)
$$L = \sqrt{\frac{1.96^2 * pq}{n}}$$

where L=precision, p=prevalence, q= 1-p and n=sample size.

We determined the percentage of herds within each of the 26 counties, based on data from all breeding herds (n=94,261), the random data set (n=644), the opportunistic data set (n=367) and the combined field data sets (n=1011). The original herd datasets were stratified by province (4 categories: Connacht, Leinster, Munster, Ulster), county (26) and enterprise type (3: dairy, beef, mixed). Enterprise type was determined based on the proportion of beef and dairy breeds among mature cows in each herd (beef: >66% beef breeds; dairy: >66% dairy breeds; mixed: all other herds). The strata-level distribution of herds was compared between datasets using the chi-square test.

Results

During 2003, there were 97,455 (breeding) herds in Ireland where at least one home-born calf had been registered. Of these, 90,807 (93.2%) were geo-referenced, including 58,285 (59.8% of all breeding herds) located within the target window. The distribution of all geo-referenced cattle herds across the country was visually homogeneous, except for areas obviously not suitable

for grazing, such as lakes, bogs, forest and upland areas. Herds in the opportunistic field dataset (n=295) were distributed in clusters across the country, whereas those in the random field dataset (n= 605) were evenly dispersed (Figure 1). Based on results of the nearest neighbour analysis, herds in the field datasets were more clustered than those in the generated datasets. Areas of higher sampling density were present in the kernel density plots of the opportunistic field dataset and to a lesser degree the random field dataset, but not of the equivalent generated datasets. There was a significant difference between the county distribution of herds in the national data set and the random data set compared with the opportunistic field dataset (p<0.001), but not between the national data set and the random field datasets (p = 0.576). There were significant differences in the ratio of percentages between the field dataset with the national database, both by province and by enterprise type (each P<0.001).
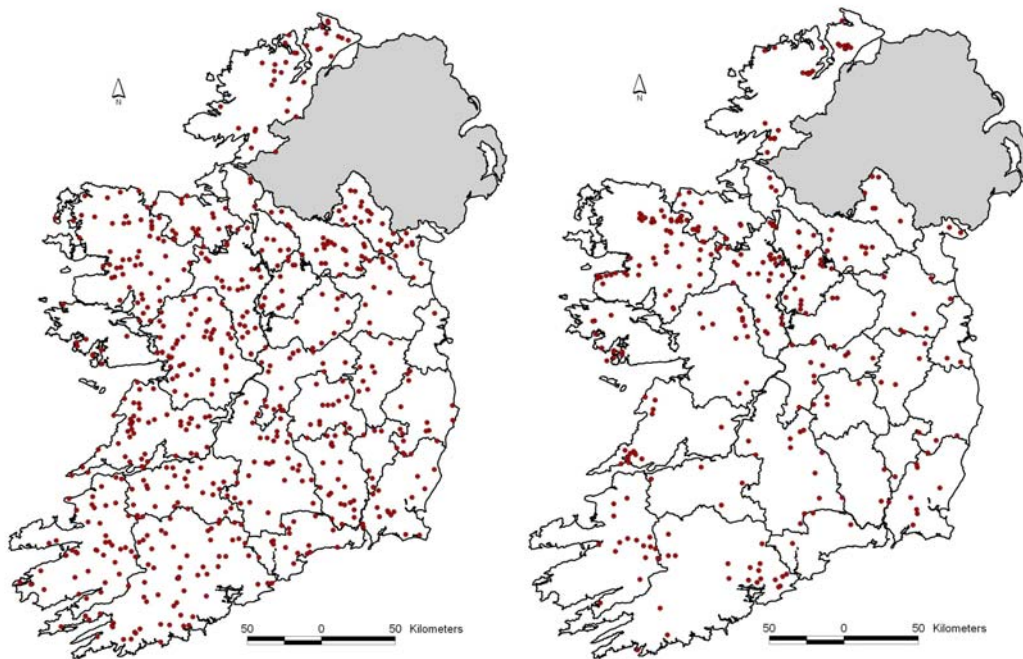

Figure 1. Distribution of geo-referenced herds in the random (left; n=605) and opportunistic (right; n=295) field datasets of the national paratuberculosis sero-survey.

Discussion
There were substantial differences between the opportunistic field dataset and the national database, highlighting problems of sampling bias with the opportunistic field dataset. This was most clearly seen in the artificially even distribution of the proportion of herds selected from each county in the opportunistic sample. Similarly the proportion of cattle types were skewed towards higher numbers of beef cattle in the opportunistic sample, which

essentially would not accurately represent the level of disease prevalence in dairy cattle across the country. These findings were consistent with the widely accepted practice that when data is collected in an opportunistic manner it does not follow the conventional random sampling frame considered necessary to produce reliable inferences about a population (Norman and Streiner, 2003). Based on each of the methods used, the random and target populations were similar. Therefore, disease prevalence in the random field database is likely to provide a reliable estimate of disease prevalence in the target population.

Due to sample size constraints, imprecise prevalence estimates would be obtained following separate analysis of each of the two field datasets. Clearly, these estimates would be more precise if the two datasets were combined. Combining the two field data sets in this study resulted in a roughly averaged value of the two; showing that one field data set would bias the other were the two combined. However, based on the post hoc assessment conducted here, it is clear that the random and opportunistic field datasets should not be combined as they do not share the same demographic profile. Results from the opportunistic selected herds will be biased due to being clustered in certain areas and occurring in a different proportion by county and enterprise to the rest of the herds in the country. The difference in the proportion of beef to dairy herds between the random and opportunistic data sets may be a result of the bias in the opportunistic data set towards sampling a comparatively lower number of herds from Munster, which characteristically has a high proportion of Ireland's dairy herds. Overall, the results from the opportunistic sampled herds will need to be interpreted with caution as they do not appear to represent the target population of Irish breeding herds. Based on this post-hoc assessment, results from the randomly selected samples would provide an externally valid, albeit relatively imprecise, estimate of national disease prevalence, and of the disease prevalence in three of the four provinces (Munster, Leinster and Connacht) and in beef and dairy herds.

Study 2.
Management risk factors associated with paratuberculosis (Johne's disease) in Irish dairy herds

Introduction

Prior to the introduction of the single European market in 1992, Johne's disease was only reported sporadically in Irish dairy herds (92 cases, primarily in imported animals; 1932-1992). However, following the removal of pre-importation test certification and post-importation quarantine in 1992, the number of cattle imported from countries within the EU where paratuberculosis is present, increased dramatically (85,000 cattle between 1992 and 2004). However, there have been no studies published on the management factors associated with paratuberculosis in Irish dairy herds.

Materials and Methods

A case-control study of herd and management factors associated with the occurrence of paratuberculosis (PTB) in Irish pastoral dairy herds was conducted by telephone questionnaire interview. Case herds (n=67 respondents) were defined as those with one or more positive individual animal faecal cultures for *Mycobacterium avium* subsp *paratuberculosis* (MAP). Control herds (n = 85 respondents) had no animals (>12 months of age) seropositive (ELISA) for MAP in a national whole herd serosurvey. Control herds were matched to case herds on the basis of the year of diagnosis of PTB in the case herds. Statistical analyses were performed using uni- and multivariate conditional logistic regression with the herd as the experimental unit.

Results

Factors relating to disease history, herd size, neonatal feeding and management and grassland management were found to be significantly associated with herd PTB status (P<0.05) in the univariate analysis. In the multivariate analysis the feeding of waste milk prior to diagnosis, the absence of individual calving pens, large herd size, and herd depopulation for a notifiable disease were all significant risk factors for the occurrence of PTB (P<0.05). Potential faecal contamination of feed and a longer residency time of the newborn calf with its dam prior to the reference year were protective against the occurrence of PTB (P<0.05), both possibly indicating less intensive herd management.

Discussion

With the increased global demand for dairy products and the abolition of the EU milk quota in 2015, many European dairy herds will be undergoing expansion. Hence, European farmers need to be aware of paratuberculosis and take precautions to avoid its introduction and spread. Farmers who are unaware of their herd's infection status need to establish it. Where PTB is present, management practices must be put in place to control and eradicate it. This study has identified significant modifiable risk factors which Irish

dairy farmers and their veterinary practitioners can address in order to control this disease (Barrett et al., 2008).

Conclusions

This study identified feeding of waste milk prior to PTB diagnosis, the absence of individual calving pens, large herd size, and herd depopulation for a notifiable disease as significant risk factors for Johne's disease in Irish dairy herds.

Study 3.
Descriptive regional epidemiology of paratuberculosis from bovine submissions to the Cork Regional Veterinary Laboratory (1989-2006).

Introduction
The demographics of bovine infection caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is poorly delineated in Ireland. Recent studies have shown the economic impact of clinical (Barrett et al., 2006) and subclinical (Hoogendam et al., in press) Johne's disease in Irish dairy herds. Internationally, the prevalence of paratuberculosis is increasing, however, there have been no studies published on the temporal trends in paratuberculosis in Irish herds The objective of this study was to describe the longitudinal temporal characteristics of submissions from cattle which tested positive for MAP on faecal culture within the catchment area of an Irish regional veterinary laboratory.

Materials and Methods
This is a retrospective study of laboratory results obtained from bovine faeces samples submitted to Cork Regional Veterinary Laboratory (CRVL) from 1989 to 2006. This laboratory provides a diagnosis service to private veterinary practitioners in County Cork, and some parts of the bordering counties of Kerry, Waterford and South Tipperary. Faeces samples were cultured using the conventional Herrold's egg yolk agar (HEY) at the Central Veterinary Research Laboratory. This report deals with all culture positive bovine submissions. SPSS, Excel and Ucinet were used to sort and analyse parameters of interest.

Results
There were 110 faecal culture positive bovine samples in the CRVL database between 1994 and 2006. The total number of bovine samples submitted for MAP culture from 1997-2006 was 547. Records for total submissions are not reliable between 1994-1996 due to changes in staff and recording procedures.
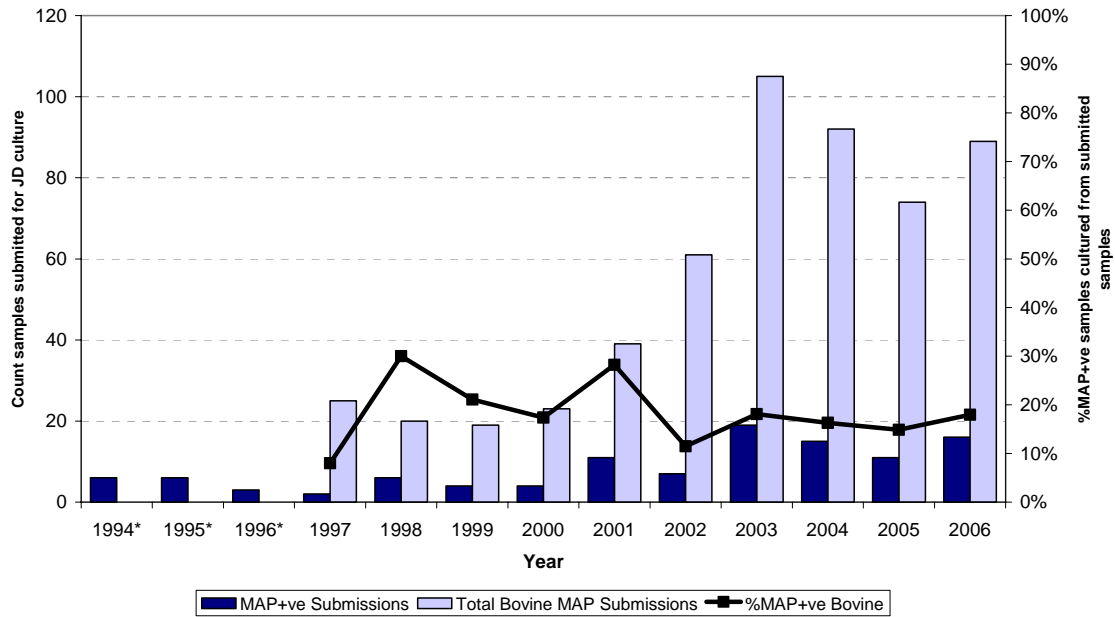
*15 MAP culture positive bovine submissions were processed by the lab between 1994-1996 (n=6,6,3, respectively).

Figure 2: All MAP faecal culture positive bovine animals in the CRVL database (n=110)

No positive bovine submissions were recorded between 1989 and 1993. The first bovine faecal culture positive submission was a pedigree Limousin cow in 1994 (MAP had been isolated from farmed deer faeces in 1993 and 1994). Figure 2 shows the percentage of MAP culture positive bovine samples in each year (mean yearly proportion = 18.3%, SD 6.7) from total submitted samples.

Discussion
These data show an increase in the number of submissions with requests for MAP culture over time, particularly from 2002, when the Department of Agriculture took a proactive approach to Johne's disease. While the number of positive submissions also increased over time, the proportion of positive submissions has not increased in recent years.

Conclusions
Increased awareness of Johne's disease has resulted in increased submissions for MAP culture in the CVRL catchment area but the proportion of positive samples has remained constant in recent years. This work may contribute to the development of a surveillance strategy for MAP by regional veterinary laboratories. The pattern of JD in Ireland is in agreement with international reports. Further work is required to determine the spread and rate of spread and prevalence of JD in Irish cattle herds nationally

Study 4.
Effect of Johne's disease sero-status on milk production, SCC and calving interval in Irish dairy herds.

Introduction
The consequences of paratuberculosis for farm economics in Ireland may differ from estimates found in other countries due to the seasonal, pasture-based systems of milk production practiced here. The effect of paratuberculosis on farm production in the USA was estimated as a loss of $200 million (Losinger et al., 2005). The effects of paratuberculosis infection on milk yield are very inconsistent, varying between increased yield in infected cows (Johnson et al., 2001), no significant effect (McNab et al., 1991) and up to a 24% reduction in yield (Barrett et al., 2006). While the majority of studies show no significant effect of paratuberculosis on SCC (Gonda et al., 2007, Lombard et al., 2005), some studies showed an increase in either mastitis (Buergelt and Duncan, 1978) or in SCC (McNab et al., 1991, Van Leewen et al., 2007). The impact of paratuberculosis infection on herd fertility is similarly variable with Gonda et al., (2007) and Lombard et al., (2005) finding better fertility in infected cows, McNab et al., (1991) finding no significant effect and Johnson-Ifearulundu et al., (2000) finding significantly reduced fertility in infected cows. In general, impacts on production and reproduction are much lower in subclinically infected animals (test-positive only) than in clinically affected animals.

The aim of this study was to investigate the impact of paratuberculosis sero-status on the economically important variables milk yield, milk fat and milk protein, somatic cell counts (SCC) and calving interval in dairy herds in the Republic of Ireland. The hypothesis tested was that paratuberculosis infection has a significant negative effect on milk yield, milk solids, SCC and calving interval in both infected animals and in infected herds. To address this hypothesis, the study examined the effect of paratuberculosis at the animal-level between paratuberculosis test-negative and test-positive cows, and at the herd-level between test-negative, non-negative and positive herds.

Materials and methods
The Department of Agriculture, Fisheries and Food (DAFF) conducted a national bovine paratuberculosis sero-survey in 2004 and 2005 using blood samples collected for the brucellosis eradication scheme. Samples were collected from all lactating and non lactating animals (male and female) older then 12 months. Within this dataset, serology results from animals (n=2,602) in dairy herds (n=34) which were milk-recording in 2004 and 2005 were extracted. Milk and reproduction records for each paratuberculosis-tested cow (estimated breeding value [EBV] for milk yield, milk fat, milk protein, SCC, calving interval and economic breeding index [EBI] and predicted 305-day milk yield, milk fat, milk protein, SCC and calving interval) were

retrieved from the Irish Cattle Breeding Federation (ICBF) database and matched to the test results from DAFF by animal tag number. After checking for errors and outliers, data were available for 993 lactating cows in 32 herds. The dataset was comprised of 95.6% Holstein-Friesian cows. Therefore to remove the effect of breed on production and reproduction variables, all other breeds were deleted leaving 949 cows in 32 herds. The EBV of the cow (not the sire) was recorded for 259 of the 949 cows. Paratuberculosis status was established using an ELISA (Elisa Bovine Paratuberculosis Serum Verification, Institut Pourquier, France) with a specificity of 99.8% (CI 95% 99.6-99.8) and a sensitivity of 40.8% (CI 95% 35.3-46.7), in a DAFF laboratory. A sample to positive (S/P) ratio of $\geq$70% was considered positive. The true prevalence of paratuberculosis in this population was estimated by calculating the apparent prevalence and adjusting this with the specificity (Sp) of 99.8% and sensitivity (Se) of 40.8% of the ELISA. A case-control study design was used to match each paratuberculosis test-positive cow (case) with five negative cows (1:M) (controls) all of which had data available for their current lactation. The cows were paired on parity and calving date, where the calvings of the controls were within one month of the cases. The herds were categorised into three groups: test-negative, non-negative and positive. A herd had to contain two or more positive animals before it is classified as a positive herd. A herd was classified as a negative herd if all the animals in the herd had negative test results. A herd with only one animal that tested positive for paratuberculosis was categorised as non-negative.

Univariate general linear models were used for each dependent variable, with herd paratuberculosis status, herd size and parity as fixed factors and lactation length (in logarithmic form) and the EBVs of the dependent variables as covariates. Milk yield was included as a covariate to analyse effects on protein and fat production, because they are linked to milk yield. An adjustment was made in the models for a significant interaction between herd paratuberculosis status and herd size. Results were considered significant at a P-value of $\leq$0.05. The statistical analyses were conducted using SPSS version 14.0.1 (2006).

Results

Of the 949 cows in the final dataset, there were thirteen cows that were paratuberculosis sero-positive with OD values ranging from 84 to 241; an animal-level apparent prevalence of 1.37%. Adjusting for the specificity (Sp 99.8%) and sensitivity (Se 40.8%) of the ELISA (equation 2) resulted in a calculated true animal-level prevalence of 2.88%. Of the 32 herds (949 cows) tested, there were eight positive, eight non-negative and sixteen negative herds. This means that 25% of these herds had two or more positive cows and 50% of these herds had one or more positive cows. The positive herds (mean herd size=129 cows) and the non-negative herds (81 cows) were larger than the negative herds (72 cows) (P<0.01).

The mean (range) age, milk yield, SCC and lactation length of the sero-positive cows was 50 months (28-73), 6,292 kg (3,810-8,795), 169,083 cells/ml (44,000-1,090,000) and 250 days (175-304), respectively. Two of the eleven positive cows were in first parity; therefore for calving interval [mean (range) 371 days (335-424)] only nine positive cows could be matched with 45 negative cows. At the animal-level, paratuberculosis sero-status had no effect on any of these dependent variables (P> 0.05). Table 1 shows the outputs from the multiple regression models comparing positive, negative and non-negative herds using the restricted dataset with EBV records. Overall, herd paratuberculosis sero-status had no significant effect on milk yield, milk fat or milk protein production or on calving interval. Negative herds tended to have a lower SCCS than the positive and the non-negative herds (P=0.087). The positive herds had a significantly higher EBV for milk yield, SCC and calving interval than the negative herds. However, the negative herds had a significantly higher EBV for EBI than the positive herds. EBVs for milk fat and protein did not differ between negative and positive herds. Non-negative herds had significantly lower EBVs for milk yield, protein, calving interval and EBI than negative or positive herds but did not differ for SCC and fat. When the data were examined at parity-level, there were no significant differences between positive, non-negative and negative herds in the four parity groups for milk yield, milk fat, milk protein, SCC or calving interval.

Table 1: The effect of herd paratuberculosis sero-status (positive, negative or non-negative) on milk, fat and protein yield, somatic cell count score (SCCS) and calving interval [mean (95% CI)].

Variables	Positive	Non-negative	Negative	F-value	Adjusted R^2	P-value
Milk (kg)	6981.44 (6594-7369)	6928.00 (6594-7369)	6601.85 (6408-6795)	1.995	0.447	0.138
Fat (kg)	242.20 (231-253)	238.50 (226-251)	238.03 (232-244)	0.213	0.7	0.809
Protein (kg)	222.09 (216-228)	220.79 (214-228)	215.75 (213-219)	2.031	0.871	0.133
SCCS (score)	3.26 (2.7-3.8)	3.38 (2.7-4.0)	2.76 (2.5-3.0)	2.469	0.021	0.087
Calving interval (day)	386.42 (368-405)	391.63 (364-419)	381.67 (372-391)	0.696	0.063	0.5

Discussion

The true animal-level prevalence of paratuberculosis in this study (2.88%), is similar to that found internationally, for example, in Spain (3%) (Dieguez et al., (2007), the Netherlands (3.3%) (Muskens et al., 2003) and the United States (3.8%) (Lombard et al., 2005). Though the animal-level prevalence of paratuberculosis in the present study was low, the herd-level prevalence was

high with 25% of herds having two or more positive cows and 50% of herds with at least one positive cow, albeit in a limited number of herds. These figures are higher than those found in the only previous Irish paratuberculosis random sero-survey, where 30% of the 143 herds had one or more positive animals, albeit only in three counties (Barrett et al., 2006). Internationally, the herd-level prevalence of paratuberculosis in dairy herds varies widely in MAP-positive countries between 11% in Spain (Dieguez et al. 2007) and 85% in Denmark (Nielsen, 2007).

The hypothesis that there would be a reduction in production and reproductive performance between paratuberculosis-positive and negative herds was rejected. This study showed no significant effect of herd paratuberculosis sero-status on milk yield, fat, protein, SCCS and calving interval. The fit of the General Linear Models was good for milk yield (R^2=0.45), and fat and protein yield ($R^2 \geq 0.70$), but poorer for SCCS and calving interval (R^2<0.10). Though the SCCS was numerically higher for positive and non-negative herds than for negative herds, all of the herd SCCS scores indicated mean herd SCC of between the 36 and 283,000 cells per ml. While clinical paratuberculosis has been shown to have significant negative economic impacts in both pasture-based (Barrett et al., 2006) and confinement systems (Benedictus, et al., 1987), the impact of subclinical paratuberculosis (test-positive only) is less clear. For example, in the UK, with management systems not greatly dissimilar from those in Ireland, Stott et al., (2005) found that the financial effect of paratuberculosis is considerably lower than for other major endemic diseases of dairy cows.

In the present study, the large positive herds had a significantly higher EBV for milk, while the smaller negative herds had a higher overall EBV, and when adjusting for EBV, the difference in milk yield was no longer significant. It might be the case that the selection for high milk yield in the positive herds made the cows more vulnerable to infection with paratuberculosis. There is a general consensus that when selecting for a higher milk yield, the genetic merit for health decreases (Jakobsen et al., 2003). Koets et al., (2000) provided evidence for the presence of genetic variation in the susceptibility of cattle to paratuberculosis. The average milk production in the non-negative and positive herds was higher than the average milk production (6,677 kg/cow) of Irish milk-recorded herds. The fat and protein production was similar to that of Irish milk-recorded herds (244 kg fat and 221 kg protein). There is another possible reason for the relationship found between larger herds, the number of positive cows and high EBV milk yield. It is posited that farmers with large herds may have imported cows with high genetic merit for milk yield from abroad and inadvertently imported MAP carriers, as genetics at the time were mainly sourced from countries where paratuberculosis is now recognized. The non-negative and negative herd had higher EBV_EBI values than the positive herds but lower EBI_milk. This also suggests that these herds may not have selected as strongly for EBV_milk, as

they had higher EBV_SCC and EBV_CI cows which would have contributed to a higher EBV_EBI found in these herds.

However, it should not be concluded that paratuberculosis is an economically unimportant disease in the Irish dairy industry. On a very small number of Irish farms there have been major outbreaks of Johne's disease (e.g. Barrett et al., 2006) which caused huge financial loss. At the Irish dairy industry level, paratuberculosis presents a continual threat to our export of dairy products given the uncertainty regarding the link with Crohn's disease and the progress on national control programmes internationally. In addition while this study examined the effects of paratuberculosis sero-status it could not address the impacts of clinical Johne's disease on veterinary costs, culling rates and animal welfare.

Study 5
Investigation and clinical impact of paratuberculosis in a dairy herd

Introduction
While most dairy herds in Ireland are free of infection with MAP, a minority have been infected to some extent and a very small number experience clinical signs either at the individual animal or the herd level. Outbreaks of Johne's disease, though uncommon, can cause serious economic losses in individual affected herds. In this study a large dairy herd presented with a Johne's disease outbreak. The study reports the herd Johne's disease epidemiology, investigation and control recommendations. The study followed the DAFF Johne's disease control model of the local veterinary practitioner leading the investigation with support from other agencies as required. The objectives of the study were to carry out an historic analysis of the herd to determine the likelihood of the presence of Johne's disease and the projected level of Johne's disease if present and to develop an on-farm Johne's disease control programme.

Case investigation and control recommendations.
An on-farm analysis of management procedures was carried out to develop a flow diagram of farm activities and using this, examine the risk areas for transmission of Johne's disease via Johne's infected faecal material to calves and young animals (F), Johne's infected milk fed calves and young animals (M) and vertical transmission from infected dam to calf (V). Having identified the Johne's spread critical control points (F, M or V), preventative strategies were developed to limit the spread of Johne's disease. The above procedure in essence is an on farm HACCP (Hazard Analysis and Critical Control Point Program).
Prior to 1993 herd was closed but from 1993 onwards Dutch and French in-calf heifers and calves were purchased in addition to cattle from Irish herds. Since 2002, the herd had suboptimal milk yield and fertility with occasional cases of diarrhoea in cows. Prior to 2005 some 2-3 clinical cases of Johne's per year were detected. In 2006 some 19 cows died and there was a noticeable deterioration in animal health (retained foetal membranes/ "bottle jaw"/ diarrhoea/ fertility problems / reduced BCS / increased SCC). Two animals were submitted for laboratory post-mortem in 2006 and Johne's disease was confirmed in both. Based on the above, the local veterinary practitioners carried out a Johne's Disease pre-assessment and assigned a MAP (Johne's disease) score (Table 2).

Table 2. Johne's disease risk assessment scores

	Max Score	Actual Score
Closed/Open Herd	20	19
Clinical cases/ Pos tests	70	60
Previous/current management	<u>10</u>	<u>9</u>
	100	88

This assessment indicated that this was a Johne's disease high risk herd, adult stock (>2 y.o. females) needed a serological survey and a management program was necessary for Johne's Disease. Each area of farm management (e.g. pregnant cow management) was assessed following farm visits, the hazard profile for Johne's Disease was documented and suggested control measures were detailed.

Pregnant Cows/Heifers

Hazards   F-yes   M-yes   V-yes

Hazard Detail

- Calves born in dry cow cubicles or in communal dry cow paddock or dry cow pad may be in a faeces contaminated environment.
- Cross-suckling possible in these areas
- Udders/teats may carry faecal contamination to calving areas.

Johne's control program cannot co-exist with concept of communal calving

Suggestions:

1. Clean out and disinfect the cubicle and slatted housing before the winter housing period with, for example, Osmodex.
2. Consider udder singing at springing if needed based on observation of cows' udders precalving.

Pre calving segregation and calving and suckling

Hazards   F-yes   M-yes   V-yes

Hazard Detail

- Calving areas (pad and strip grazing) are communal leading to environmental faecal contamination and risk of cross suckling
- Faeces on teats/udder/boots/wheelbarrow/other fomites.
- MAP from positive or doubtful cows

Suggestions:

1. Employ extra labour unit for the spring to manage calving and newborn calf care
2. Run two separate calving mobs based on blood ELISA test results
3. Increase frequency of calving pad visits to move cows on the point of calving into the calving pens, assist newborn calves to suckle and remove calves.
4. Install individual calving pens on the calving pad using sheep wire to prevent calves from getting out
5. Maintain beds frequently and consider disinfecting beds between calvings with, for example, Osmodex.
6. Cease calving in calving paddocks and move all calvings to the pad.
7. In order to free up space on the pad, accommodate far-off dry cows and pregnant heifers elsewhere, not on the pad.
8. Assist calves to suck, as necessary, in the calving pens before calf removal

9. Pick up calves thrice daily at calving check and bring them to a nearby lorry.
10. Consider night time or early morning (pre 5.30am) calving supervision
11. Consider installation of CCTV cameras and lights on pad to facilitate calving supervision at night
12. Manage calves from test positive dams for beef, not replacements.

Calf Rearing
Hazards F-yes   M-yes   V-yes
Hazard Detail
  - Faecal contamination from grazing and paddocks
  - Faecal contamination from drinking soiled water

Milking cow management
Hazards F-no   M-no   V-no
Hazard Detail
  - No contact and therefore no risk

Yearling/6 month old replacement heifers
Hazards F-yes   M-no   V-no
Hazard Detail
  - Faeces from adult heifers or cows via leader/follower systems or from slurry spread on grass from adults
Suggestions:
1. Graze heifer calves in a separate area of the farm which does not receive slurry in the same year as the calf grazing.
2. In order to keep the heifer calves separate from the adult stock, consider grazing them on aftergrass (not previously grazed by adult stock) and use sheep to clean up the paddocks after them in a separate rotation from the adult cattle.
3. Provide separate water troughs for the heifer calves from the cows.
4. If heifers are to be accommodated on cubicles as dry cows, house them on cubicles in their first winter. If not, then slats are adequate.

Breeding management
Hazards F-yes   M-no   V-yes
Hazard Detail
  - Bull shedding MAP in faeces

Suggestions:
1. Consider sexing of feti (60-90d) and separation and priority management at calving of pregnant stock carrying heifer calves.

Farm biosecurity

Suggestions:
1. Install foot baths at most contaminated areas if environmental sampling reveals such areas
2. Need to inform relief workers of the need for biosecurity precautions
3. Sell surplus heifers only for slaughter, not into other herds.
4. Consider installing a wheel bath at the farm entrance(s)
5. Consider pre-movement testing for added animals

These findings and the associated recommendations were documented in reports to the farm manager through the local veterinary practitioners.

Conclusions

It was concluded that monitoring of above programme should be carried out regularly (2-3 months) especially during calving season, the programme should be reviewed each year and an annual serological review was necessary. This case study highlighted the complexity of Johne's disease investigation and the central role played by the committed farmer and his staff along with their local veterinary practitioner in dealing with this disease.

Study 6

Direct and indirect effects of subclinical and clinical Johne's disease on farm and animal productivity in an Irish dairy herd

Introduction

Johne's disease (JD) is considered to adversely affect farm performance and so economic profit. As yet, little data are available about the impact of JD on farm production in Ireland. Based on international studies, JD infection is associated with reduced milk production (Lombard *et al.*, 2005) and increased involuntary culling rates (Ott *et al.*, 1999), increased calving interval and infertility (Johnson-Ifearulundu *et al.*, 2000). This paper aims to describe the impact of JD on an Irish commercial dairy herd, and the effect of animal JD status on several measures of production.

Materials and methods

The study was conducted over 11 years (the 'study period') from 1994 (the year prior to detection of the first JD clinical case) to 2004. A detailed JD herd investigation, including documentation of clinical signs and the widespread use of faecal culture and ELISA testing on individual animals in the case herd, commenced in 2002. A JD control programme commenced in 2002, concurrent with the detailed herd investigation, as described previously (Good *et al.*, 2006). For each study animal, we collected both general data (animal identification number, dates of entry to and exit from the herd, reason for culling and culling price [the monetary value received by the farmer]) and data about each lactation (parity number, calving date, year of lactation, days in milk, milk yield [total kg per lactation] and geometric average somatic cell count). Data were also collected about JD-related events, including clinical observations and test results (ELISA and faecal testing dates, test type and test result). Data analyses were conducted using SPSS (SPSS Inc., Chicago, IL, USA), Excel and SAS v9.1.3 (SAS Institute Inc., Cary, NX, USA).

Reasons for culling and changes in herd structure over time were examined using data from all study animals. The JD status of each study animal was determined on the basis of available clinical observations and test results. Two groups of case animals were defined:

- *Clinical cases* - all animals that presented with clinical signs consistent with JD, including scouring, bottle-jaw development and/or significant body weight loss.

- *Test-positive cases* - all animals that were test positive (faecal culture and/or ELISA) but without clinical signs consistent with JD.

Testing did not commence until the latter part of the study period. These two groups of case animals were mutually-exclusive as only non-clinical test positive cases were included in the second group.

The effect of JD status on cull price was examined between 1994 and 2002, prior to the start of the herd investigation and subsequent control

programme. Cull price of clinical cases was compared to that of all other animals, using an independent t-test. Where applicable, the cull price in punts was converted to euro at the rate of 1 punt = 1.27 euro.

The effect of JD status on production was examined after first identifying three series of case lactations, and three control series of lactations for comparison. The following methodology was used to select the case lactations:

- *Clinical lactation,* being a single lactation from each clinical case, either the lactation in which clinical signs were first detected, or the prior lactation if the former had not been completed;

- *Pre-clinical lactation.* For each clinical case, the lactation immediately preceding the above-mentioned clinical lactation; and

- *Test-positive lactation,* being a single lactation from each test-positive case, either the lactation during which the animal first tested JD positive, or the prior lactation if the former had not been completed.

A series of three control lactations were selected:

- *Control 1 lactation* (for comparison with clinical lactations) being a randomly selected lactation from all study animals except clinical cases.

- *Control 2 lactation* (for comparison with pre-clinical lactations) being a randomly selected lactation from all study animals except clinical cases.

- *Control 3 lactation* (for comparison with test-positive lactations) being a randomly selected lactation from all study animals except clinical and test-positive cases.

Therefore, three case-control comparisons were used: clinical comparison (clinical lactation, control 1 lactation), pre-clinical comparison (pre-clinical lactation, control 2 lactation) and test-positive comparison (test-positive lactation, control 3 lactation).

Multivariate modelling was conducted to separately determine the effect of JD on two outcome variables: milk yield (total kg per lactation) and somatic cell count (SCC, lactation geometric mean). Four independent variables were considered, including year, parity, days in milk (DIM) and JD status. Three separate linear regression models (one for each case-control comparison) were conducted for each outcome variable (six models in total) using backwards stepwise procedures based on Akaike inclusion criteria values and *P*-value <0.2 for inclusion in the model. Regression models were run using PROC MIXED in SAS 9.1.3 (SAS Institute Inc., 2003). Year, parity and JD status were each entered as class variables.

Results

On the study farm, there were an average of 71 cows in milk during the study period, with an annual average milk production of 5550.3 kg/year (SD=431.2). Over 64% of the herd had Holstein or Friesian genetics, with the balance being a mix of other dairy and beef bloodlines. During the study period, production data were available for 283 study animals and 717 lactations. On-farm JD investigations commenced in 2002. During 2002 to 2004, 765 JD tests (ELISA and faecal culture) were conducted on 211 animals, leading to the identification of 22 and 98 animals that were positive on faecal culture and ELISA, respectively. ELISA positive animals were detected during 2002 to 2004. In total, 58 clinical cases were identified in the study herd, the first in 1995. Testing was conducted on 25 of these animals. Widespread culling commenced in 2002 as part of the JD control programme, and clinical signs consistent with JD were not observed after 2003.

During the study period, infertility and 'other reasons' (which includes animals culled with clinical signs consistent with JD) were the main reasons for culling, accounting for 31.3% and 32.8% of culls, respectively. However, infertility was a more frequent reason for culling at the start, compared to the end, of the study period. During 2002-2004, 73% of cows culled for reasons other than infertility had been removed as part of the JD control programme. Other recorded culling reasons included abortion, accident, bad legs, damaged udder, late calving, low production, mastitis, old age, pining, slow milker, surplus and TB.

There was a significant difference in cull price for 18 clinical cases compared to 59 non-JD culls (mean difference of €516, *P* <0.001). The adjusted effect of JD status on milk yield for each case-control comparison, after controlling for DIM, year and parity, is presented in Table 3. The adjusted effect of JD status on average lactation SCC yield for each case-control comparison, after controlling for year, parity, DIM and yield is presented in Table 4. JD status was associated with a significant difference in both milk yield and SCC in the clinical and pre-clinical lactations (but not the test positive lactation), compared to control lactations.

Table 3. The adjusted effect of JD status on milk yield for each case-control comparison, after controlling for DIM, year, parity

Case-control comparison	Overall model fit (R^2 value)	Milk yield difference (kg)[d]	*P*-value
Clinical comparison[a]	0.673	-638.55	<0.0001
Pre-clinical comparison[b]	0.716	-285.09	0.047
Test positive comparison[c]	0.582	5.1	0.971

a. Model statement used: yield = JD status, DIM, year, parity
b. Model statement used: yield = JD status, DIM, year, parity
c. Model statement used: yield = JD status, DIM, parity
d. Negative value indicates that average yield was lower in case compared to control lactations.

Table 4. The adjusted effect of JD status on average lactation SCC for each case-control comparison, after controlling for year, parity, yield, DIM

Case-control comparison	Overall model fit (R² value)	SCC difference (000's) [d]	P-value
Clinical comparison[a]	0.129	1.45	0.018
Pre-clinical comparison[b]	0.227	1.46	0.022
Test positive comparison[c]	0.116	1.29	0.221

a. Model statement used: log(SCC) = JD status, year, parity
b. Model statement used: log(SCC) = JD status, year, parity, yield
c. Model statement used: log(SCC) = JD status, year, DIM
d. Positive value indicates that the average SCC was higher in case compared to control lactations.

Discussion

This study highlights the adverse impact of JD on herd fertility, parity structure, milk production and SCC in a single Irish dairy herd. Direct impacts of JD on production included a decrease in milk yield and cull price, along with an increase in average SCC in animals with clinical signs. Indirect impacts of JD noted in the herd were high levels of culling for infertility and changes to parity structure. There was a change in parity structure during the study period as a consequence of increasing replacement rates. At the beginning of the study period, the milking herd was predominantly mature milking cows. However, this changed during the study period towards younger cows with lower productivity. High replacement rates are inefficient, noting that a parity one cow milks at approximately 75% of her mature equivalent.

These impacts combined to have negative economic consequences for the herd (Barrett *et al.*, 2006). Significant losses in milk production in the last full lactation (-638.6 kg) and second to last lactation (-285.1 kg) compared to non-clinical cows support concerns that JD is associated with reduced milk production in the herd. Similar results have been noted elsewhere (Lombard *et al.*, 2005). Bulk milk tank SCC is considered a measure of milk quality, and counts greater than 200,000 cells/mL have been found to constitute economic loss (Ott *et al.*, 1999; Losinger, 2005). Culling price was significantly lower (€516 on average) for clinical animals compared to animals culled without clinical signs. High rates of culling due to infertility and increasing replacement rates result in indirect (long-term) costs to production.

In the current study, definitions of JD status were used that can be applied in a practical context. The study investigated three different stages of JD infection on production: animals showing clinical signs, the year prior to the animal showing clinical signs, and test positive animals not showing clinical signs. As the farmer (and possibly his/her assisting veterinarian) can only cull on the information available to them, the approach used here may help to inform culling decisions. For example, our results suggest that test positive animals did not show any milk loss. In contrast, clinical signs were associated

with considerable milk loss and an increase in SCC. This information, combined with knowledge that clinical animals often shed high bacterial counts, can inform culling decisions. Further work is needed to extrapolate these findings and apply them practically.

No effect of JD on production was noted for animals positive by test only. This finding is consistent with results from three out of four herds investigated in a New Zealand study (Norton, 2008) which used repeated ELISA testing to identify JD in cattle. However, in the current study all clinical test positive animals were removed from the test positive group before the analysis which may have affected the results for the test positive group.

Because this study was conducted on a single herd, these findings are difficult to extrapolate. Nonetheless, the impacts of this disease are unlikely to be dissimilar in other Irish herds where JD has established, or is establishing.

The effect of JD on measures of fertility was not quantified in this study. Tight culling practises on infertility was considered to have affected the calving interval data for cows as Good *et al.* (2006) noted there was a marked increase in involuntary culling due to infertility between 1994 and 2000 in the case herd. As a consequence, it seems certain that calving interval data was confounded by culling practises.

Conclusions

Clinical JD infection negatively impacted milk yield and culling price in the study herd. In contrast, little effect was noted for sub-clinical infections. These effects, in combination with infertility and high replacement rates, contributed to economic losses for the farm over this period (Barrett *et al.*, 2006). This case study has provided preliminary information regarding the effects of JD status on both herd and animal-level performance in Ireland.

Study 7

Estimation of the economic impact of Johne's disease using a whole farm simulation model [Moorepark Dairy Systems Model (MDSM)]

Introduction

A whole farm bioeconomic model has been developed in Moorepark (Shalloo et al., 2004). While this model includes all production derived economic data flows, it did not contain an animal disease component. The objective of this study was to upgrade the existing MDSM with a disease component using Johne's disease as an example. The Johne's disease (JD) model could potentially be used to investigate two important questions: What is the cost of JD at farm, regional and national level to Irish agriculture? What is the economic benefit to Irish farmers and the Irish dairy industry of changing current management practices on farms to those proven to lower the incidence of JD in Irish herds?

Materials and Methods

The MDSM is a series of inter linked worksheets in MS Excel 2003 (Figure 3).
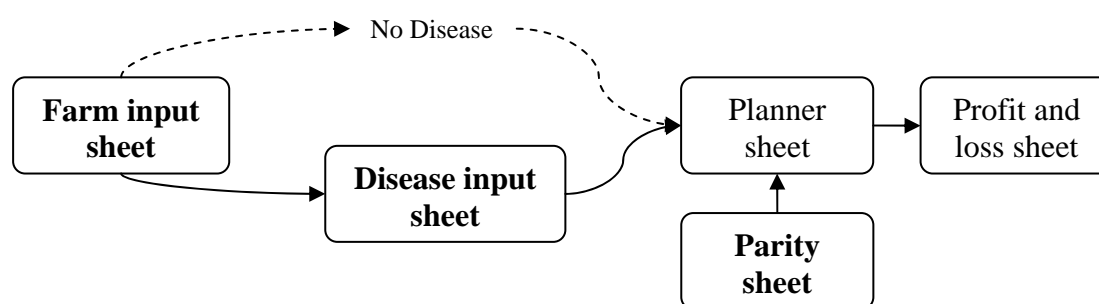
Figure 3. The newly added input sheets feed into the pre-existing Planner sheet and subsequently the Profit and loss sheet from the original model.

The original MDSM ran its calculations from a single main 'Planner' sheet. The values in this sheet were either calculated cells or cells containing a 'single' number (that is they are an inputted value that is not calculated from another part of the sheet). Originally changes in the model inputs were typed directly into the relevant cells in the Planner sheet. The first step in altering the MDSM to calculate disease effects was to add a new 'Farm input' sheet. The aim of the Farm input sheet was to have all the main input cells affecting the economic calculations in the MSDM grouped in one location making them more accessible and updateable. Values were then changed in the model by entering new values into the cells of the Farm input sheet that then linked back to the original cells in the Planner sheet (Figure 4).
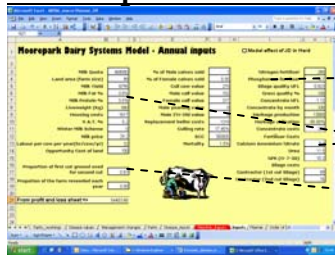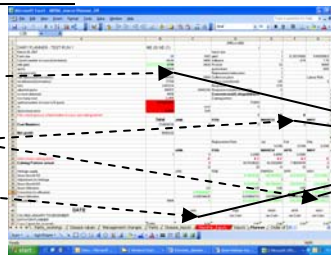
Original MDSM
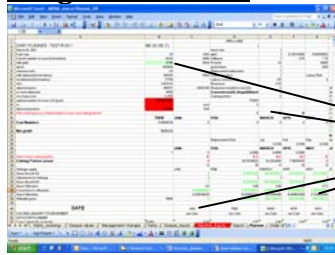
Planner sheet

Farm input sheet added to MDSM

Farm input sheet   **Planner sheet**

Figure 4. A readily accessible Farm input sheet was added to the pre-existing model to collate the primary input cells into one location.

The variables in the MDSM, such as milk yield and culling rate, which were considered likely to be affected by Johne's disease were assembled in a further 'Disease input sheet'. Having a separate sheet for disease impacts allows the model to run with or without accounting for disease effects, as shown in Figure 5. The sheet was edited so that affected production parameters were not weighted for disease more than once throughout the planner calculations (e.g. slaughter value and market price).
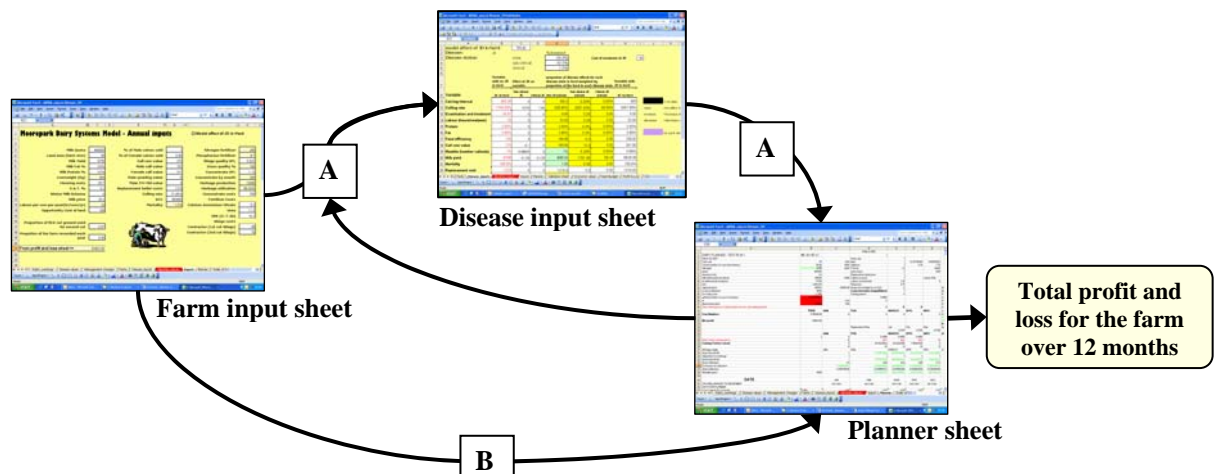

Figure 5. The Disease input sheet added to the MDSM allowed the model to calculate either option A (calculate the economic effect of disease on the farm) or option B (calculate farm economics without allowing for disease costs).

The Disease input sheet recalculated the original values from the Farm input and the Planner sheets to model the effect of disease on production and subsequent economics on the farm over 12 months. The Disease input sheet was set up to calculate the overall effect of clinical and sub-clinical disease in proportion to the number of animals in the herd affected (Table 5). These recalculated values then fed into the Planner sheet.

Table 5. Equations used to calculate the overall effect of disease on the herd with values from culling rate used as an example.

	JD -ve herd	Sub-clinical JD	Clinical JD	Non JD animals	Sub-clinical JD animals	Clinical JD animals	JD +ve Herd
Equations	A	B	C	$X=D*A$	$Y=((A*B)+A)*E$	$Z=((A*C)+A)*F$	$P=X+Y+Z$
Example	17.4	0.90	0.85	14.6	5.0	0.3	19.9

Where: D= 84%; E= 15%; F= 1%

Due to the increased culling rates that may result from disease causing a change in the parity structure of the dairy herd, a separate 'Parity sheet' was added to calculate the effect on average milk yield per cow due to changes in herd parity structure. Culling rate was used as the replacement rate to model a static herd size. Culling rate was then used to estimate the subsequent changes in production per parity group which gave the average change in milk yield per cow to be incorporated directly into the planner.

National and international literature was researched and all studies related to the effect of JD on farm production and economics were collated into a database. Values from the database were further summarised into a magnitude for entry in the Disease input sheet. Using inputs from international literature, the model was run to show the effect of disease in a 100 cow dairy herd with 1% of animals showing clinical signs of disease, 15% of cows sub-clinically infected, and 84% of cows not infected.

Results
The expected effect of disease on a 100 cow dairy herd using international effects of disease on production is to lower farm net profit by €7,693 per year for an infected herd. This is an estimated loss of net profit of 15.2% per year. This estimate would be improved by using Irish-based input data and adding a stochastic element to the model. Few studies on JD and economics have been carried out in Ireland. So these data need to be collected from people who have had extensive experience in dealing with the disease to gain a better understanding of the effect of the disease on production at farm level in Ireland.

Discussion

The next step in the development of this upgraded model would be to look at disease economics over time, where the disease status of the herd is either worsening or improving. This could be carried out in co-operation with an institution (e.g. Cornell University) with an in-house Johne's simulation model. Preliminary collaborative work with Cornell indicated that the outputs of their model would be the number of animals in a typical 100 cow herd that are sub-clinically or clinically affected at differing rates over a 20 year period. The number of disease affected animals in each group would then be added into the Disease input sheet and used to drive further calculations of economic performance to account for changes in herd status over time and with and without disease control. Future developments in disease modelling could help farmers to make sound economic decisions in regard to disease impact and disease control.

Conclusions

The MDSM has been modified to include a disease component which can be used to assess farm level and national costs of JD. Further work would involve using the model to look at farm economics over time during periods of disease spread and control and using the MDSM to investigate the economic impact that other infectious diseases have on the dairy industry.

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