18 October 2019

Mr Kelvan Smith
Independent chair *Mycoplasma bovis* Governance group

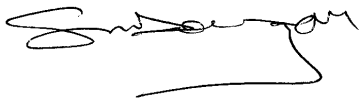
Dear Kelvan

Please find attached the report from the *Mycoplasma bovis* technical advisory group (TAG) in response to the terms of reference dated June 2019.

The first draft of this report was reviewed by MPI in the period 13th to 27th of September, 2019 and some revisions were undertaken in light of that feedback. Additionally, DairyNZ, Beef and Lamb and MPI have also commented on the second draft of this document.

The TAG would welcome the opportunity to provide any further commentary or feedback as required.

Yours



Scott McDougall

Chairman of the TAG, on behalf of the TAG

Report of the *Mycoplasma bovis* technical advisory group (TAG) in response to the terms of reference (June 2019)

18 October 2019

Glenn Browning, Jeff Caswell, Stephen Cobb, Larry Fox, Nigel French, Graeme Garner, Mark Humphris, Ben Madin, Scott McDougall, John Morton, Robin Nicholas

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Executive Summary

The New Zealand *M. bovis* programme is unique, as no other country has attempted to eradicate this organism. The TAG recognises that achieving biological freedom from *M. bovis* poses particular challenges and the programme will need to adapt and evolve over time to meet these challenges.

This report was undertaken following provision of terms of reference to the TAG by the *M. bovis* programme governance group in June 2019. To address these terms of reference, TAG received a number of documents, including copies of the Paskin and Roche reports, held a series of meetings with a range of programme personnel, requested further information, and was provided by the programme with additional material in late September. The TAG met with the board of DairyNZ in late July 2019, received oral and written feedback from MPI on the draft report, and has had written feedback on the draft report from Beef and Lamb and DairyNZ. Some revisions to the draft report were made after critical review of this feedback.

The TAG acknowledges that over the period June-September, during the preparation of this report, substantial changes were being made to the *M. bovis* programme largely as a result of the findings and recommendations of the Paskin and Roche reports. Changes have occurred in the directorate structure, resourcing (including employment of additional veterinary epidemiologists), improvements and streamlining of operating processes, implementation of new information management systems, and increased resourcing of communications. TAG supports these developments, but as many of these changes have only just occurred, or are still being implemented, objective assessment of the impact of such changes is not feasible at this time.

Key findings:

- After considering the available evidence, the TAG remains of the opinion that there has been a single introduction or a small number (3 or 4) of closely related introductions of *M. bovis* into New Zealand in 2015/16 and that *M. bovis* was not endemic prior to this time.
- The causes for the delay in casing and tracing in Summer 2018/19 have been well described in the Roche and the Paskin reviews. The TAG supports their findings.
- The TAG supports the substantial changes in information systems, resourcing, management and communications that have been made in response to the Roche and Paskin reports, but cautions that it is too early to fully quantify the impact of these changes on programme performance.
- There are some positive indications of improved operational performance, including a generally downward trend in the total number of infected places, the shorter duration of time that herds are in the casing queue, and that the conversion rate of high-risk traces to confirmed infected properties is lower than projections based on historical conversion rates.
- The historically long intervals between infection to placement of movement controls are of major concern due to the risk of movement of animals, and hence infection.
- However, evidence for reduced disease incidence or prevalence as a result of programme changes is not yet available.
- Development and reporting on key epidemiological measures such as the interval between the most likely date of infection to the application of movement control (NODs) is a key priority.
- Availability of these epidemiological measures will provide a clearer understanding of the impact of the surge and a better understanding of the rate of progress of the programme more generally.
- The programme is developing surveillance systems for cattle outside the dairy sector. The TAG sees this as a priority area given increasing evidence of infection in non-dairy herds. The TAG acknowledges the challenges in designing and implementing effective surveillance in these sectors but emphasises the importance of this work given the potential risks of transmission between the dairy and non-dairy sectors and vice versa.

- If transmission is occurring within the non-dairy sector, and if some of these infections are not detected due to incomplete recording of animal movements, there is a risk that there may be ongoing spillover from the non-dairy to dairy sectors, which may delay achievement of biological freedom.
- The TAG supports the changes made to bulk tank and individual animal level testing strategies, which will improve the sensitivity of testing protocols, as well as likely reducing the time required to resolve the status of a herd. The TAG also supports the use of latent class modelling to further assess, and potentially further improve, test performance.
- The surveillance and risk management strategies required to declare freedom from the presence of *M. bovis* in New Zealand are not yet defined. As it is not possible to "prove" freedom, stakeholders will need to be clearly informed about, and agree to, ongoing surveillance (and adoption of appropriate on-farm biosecurity measures) over an extended period. The TAG continues to believe that assessment of the options for long-term surveillance strategies required for declaration of biological freedom should be undertaken as a matter of high priority, given the impacts that such assessment will have in terms of prioritising for example non-dairy versus dairy surveillance efforts.
- The TAG understands that there are ongoing appointments of appropriately skilled and experienced individuals into key roles, with >85% roles now filled. Given acknowledged international shortages of technical staff it is important that the programme attracts and retains such skilled individuals.
- The TAG suggests that the programme be re-evaluated when the new information systems are fully functional and enough data have accrued to allow a more informed assessment. A more definitive assessment of the likely impact of the "surge" could then be undertaken, and this will inform the likelihood of the success of the eradication programme. The specific timing of this review will be dependent on how quickly the programme changes are implemented and how quickly data can be aggregated for review. The TAG suggests that early in the 2nd quarter of 2020 may be a suitable time for such a review.
- Whether achieving biological freedom remains feasible is dependent on a range of issues that are not just technical, but cultural, economic and logistical.
- Given currently available data, the TAG concludes that achieving biological freedom from *M. bovis* is feasible provided that the number of undetected infected herds is not large, infection has not established and spread within the non-dairy sector, and that the rate of transmission to new herds is reduced via continued shortening in the intervals from infection to application of movement controls. This requires adequate resourcing, appropriate metrics, effective programme management and ongoing support of stakeholders.

Recommendations

The recommendations are not in specific order nor does the order imply priority. The TAG believes recommendations 1, 3, 5 and 10 are the highest priority, but all are important and should be implemented within the next 6 to 12 months. The page number refers to the location of more detailed explanation/context for the recommendation.

Biological freedom

1. The surveillance options for defining and declaring biological freedom need to be assessed and the appropriate options selected (Page 14).
2. The economic benefits of achieving biological freedom should be re-evaluated, given the accrual of data on the incidence and prevalence of *M. bovis* infection and the on the clinical/production effects in New Zealand livestock systems (Page 22).

Information systems

3. The scoping, development and implementation of the next phase of the information systems (TIAKI phase 2) should be fast tracked. It should include measures of epidemiologically important outcomes, including indicators of the true incidence of infection, numbers of newly detected infected herds per week or month, estimates of the interval from infection to movement control and the estimated dissemination rate (Page 10/11).

New infection modelling

4. The casing, surveillance and tracing queue model developed by Drs Mackereth and van Andel to estimate the forward movement of infection is updated, externally validated and extended to develop a predictive tool to assess likely incidence of new infections and hence the efficacy of the programme over time (Page 12). Data on the likely estimated time of exposure derived from the modelling of Dr Firestone should be incorporated into this to further inform and improve precision of dissemination rate estimates.

Non-dairy surveillance

5. The proposed surveillance systems for non-dairy systems including cow calf operations, calf rearing enterprises, replacement dairy groups etc. be implemented as soon as possible, and this data should then be integrated into the surveillance decision tree model (Page 15).

Non-dairy transmission

6. The risks of transmission within non-dairy and from non-dairy to dairy need to be assessed (Page 15).

Diagnostic test validation

7. ELISA test validation should be repeated using additional data and with a revised definition of the gold standard uninfected herds. Latent class modelling should also be used to further assess the sensitivity and specificity of both the serum and bulk milk ELISA tests and determine optimal cut-off points (Page 16).

Safe stocking plan

8. A process should be established to allow herd managers to source stock with a low risk of being infected with *M. bovis* (Page 22).

Communication validation

9. Objective measures of effective communication (e.g. surveys of farmers to assess knowledge and implementation of programme recommendations and a user needs assessment) should be developed to optimise the effectiveness of communications (Page 21).

Ongoing review of the impact of the surge

10. The impact of the surge should be evaluated and feasibility of achieving biological freedom should be re-evaluated when the information systems are fully functional and enough data has accrued to allow a more informed assessment to occur (Page 9).

Terms of reference (TOR)

The TOR listed below are from the document provided to the TAG by the Governance group in June 2019.

The overarching mission for the *M. bovis* TAG is to provide an independent, science-based assessment and/or feasibility of the following:

A. In the first half of 2019, a backlog of farms requiring casing built up. The origins of this have been investigated in other reviews, which will be made available to the TAG.

i. Review the impact of this on the ability of the eradication programme to meet its objectives

ii. Review whether efforts to mitigate the impact of this backlog have been effective, and whether other measures could usefully be undertaken

B. The effectiveness of on-farm surveillance and bulk tank milk surveillance

i. Review the analyses which have been completed and the conclusions that have been drawn.

ii. Review the operational changes based on (i)

iii. Provide feedback on the proposed bulk tank milk surveillance (monthly BTM) for the coming season

C. Is the Programme operating according to best practice for disease management and elimination?

D. Provide feedback on updates on the following projects:

i. Pilot study for testing beef animals at an aggregation point – with a view to national surveillance

ii. Follow up of IHC false positive results from historical cases

The TAG was subsequently asked to provide an assessment of a written report requested by MPI from Dr Woodford (TOR E).

Report Structure

There is overlap between several of the terms of reference (TOR). To avoid unnecessary duplication, this report has been structured to provide an overarching review of the disease and the programme as currently understood by the TAG, with detailed discussion on the specific terms of reference under the following headings:

1. Assessment of the current situation
2. Impact of the 'surge' (TOR A)
3. Best practice for disease management and elimination (TOR C)
4. Changes in surveillance systems and testing (TOR B, D)
5. Dr. Woodford's report (TOR E)
6. Other matters

Assessment of the current situation

The situation report on the 9th of October 2019 indicated that there were 19 active confirmed herds, and 176 previously identified confirmed herds had been depopulated. There were 310 herds under a NOD and 327 herds under active surveillance.

The TAG considered a range of data including casing/tracing summaries, bacterial genomic analysis, surveillance reports and other information presented to the group during discussions. The TAG concludes, as it has previously done, that there has been a single introduction or a small number (3 or 4) of closely related introductions of *M. bovis* into New Zealand in 2015/16 and that *M. bovis* was not endemic prior to this time. In contrast to a number of other livestock diseases, there is no evidence for transmission of *M. bovis* via other pathways in New Zealand (e.g. aerosol spread of foot and mouth disease virus, wildlife spread of avian influenza virus, or 'area spread' of porcine reproductive and respiratory syndrome virus). The likely mechanism of spread remains movement of infected animals or contaminated milk between farms. On this basis, achieving biological freedom is feasible as long infected animals and herds are identified rapidly, and movement controls applied prior to onward movement of infected animals. Movements of infected animals from herds before those herds are identified as being infected pose a major risk to achieving biological freedom.

Modelling of estimated dissemination rates (EDR: an estimate of the rate of forward movement of the disease) raised the possibility that prior to the operational changes which occurred in response to the "surge" reports, that the disease had been moving faster than the response. The interval between the likely time of infection (i.e. animal or milk movements that introduce infection to a herd), and that herd being identified and placed under a notice of direction (NOD; i.e. effectively preventing further onward transmission of disease) was averaging 10 months, with some cases taking 2 or more years. It has been estimated that an average of 27, but in some instances up to 200, onward animal movements had occurred from infected properties over the period that the herd was infected. Taking into account the large number of movements that are a feature of the New Zealand cattle production systems, these delays provided the opportunity for infection to continue to spread. It remains unclear whether the changes in the programme have resulted in a reduction in the interval from infection to placement of a NOD, due to the lack of appropriate metrics available currently.

Impact of the 'surge' (TOR A)

The effect of the slowing of the casing, tracing and surveillance activities that occurred over summer 2018/19 may not be fully apparent for 6 to 12 months. However, it is highly likely that more farms became infected over this time than would have been the case if more rapid identification of risk movements and application of movement control had occurred.

In response to the Paskin and Roche reviews, the programme

- initiated a restructure of the directorate,
- increased responsibility for decision-making in the regional centres,
- reviewed and streamlined operational processes, resulting in potential shortening of the interval between identification of infected properties and the application of a notice of direction (NOD),
- employed more staff,
- increased focus on communication, and
- is developing of a new disease management database (TIAKI).

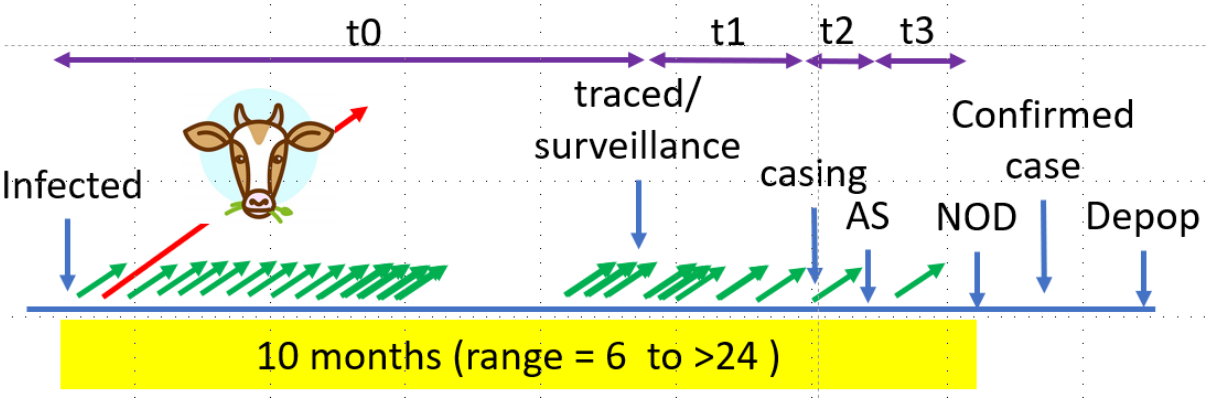
The TAG supports these changes but cautions that the full impacts of such changes may take 6 to 12 months to become apparent.

Development of key metrics to understand the rate of disease movement

A key measure of the effectiveness of the programme is that the interval between infection and institution of movement control is shortened sufficiently so that the rate of forward movement of infection (e.g. the true number of herds becoming infected herds per month) is lower than the rate at which infected herds are detected and placed under movement control. It is important that the intervals from identification of suspect herds (through tracing or surveillance) to NOD are reduced through operational efficiencies (i.e. time intervals t1, t2 and t3 in Figure 1). However, to minimise the possibility of forward movement of infected animals, the interval from infection to such identification (i.e. t0) must also be minimised. It is acknowledged that farming while under NOD or RP presents challenges to farm operators, but as long as movement control is effective, forward movement of infection should be halted. Hence, prioritisation of resources should be to find and contain infected farms.

In conjunction with effective and timely forward and backward tracing, the use of monthly bulk milk testing will likely reduce t0 in lactating dairy herds. However, with the currently limited programme surveillance in the non-dairy sectors, shortening t0 is dependent on improving the effectiveness and timeliness of forward and backward traces in these sectors. The primary aim of the surveillance systems being developed for non-dairy sectors must be to ensure shorter intervals from infection to application of movement controls. If t0 is not short, achieving biological freedom may be delayed or even preclude achievement of that goal.

Figure 1. Schematic of the disease management process. The critical interval from infection to application of movement control (i.e. NOD) is the sum of the interval from infection to initial indication that a farm has received animals from an infected farm or is identified by surveillance (t0), the interval from identification of the herd to casing (t1), the interval from casing to application of active surveillance (t2), and finally the interval to application of the NOD (t3). Arrows indicate cattle movements off the herd between infection and NOD; green arrows represent non-infected animal movements while the red arrow represents an infected animal movement.



The Paskin and Roche reports identified limitations of the animal disease response database (ADRB), including an inability to easily assess the current number of herds in each phase of the disease management process (i.e. casing, tracing, surveillance and depopulation), to define the date of infection (and hence the interval from infection to NOD) or of risk movements, or to enumerate forward traces. This lack of information was hampering resource allocation within the response and made it impossible for the programme to provide clarity about whether the response was getting ahead of disease movement.

Recent updates on programme activity provided to the TAG include information on some indirect indicators of control activities that appear promising, as is recent advice that the conversion rate of high risk traces to confirmed properties appears to be less than projections based on historical conversion rates. While metrics such as the number of NODs applied, the number of NODs revoked, and the duration of time that herds are in the casing queue are important operational metrics for the

programme, they do not provide direct measures of the interval from infection to application of a NOD (i.e. t0 + t1 + t2 + t3 in Figure 1), on the number of forward movements during this time, or on the likely proportion of currently infected, but undetected herds. More direct metrics, such as the interval from infection to detection (i.e. t0) and from infection to application of a NOD, are required to allow assessment of the efficacy of the programme. Account also needs to be taken of the fact that there will always be a lag between the time of infection and the time of detection and that current metrics reflect only those herds that have been detected, so those currently infected but undetected herds that are detected in the future will result in longer t0 intervals once they are included in the statistics. The total number of existing confirmed cases at any point in time (i.e. the prevalence of confirmed cases) is determined not just by the rate of detection of infected herds, but also by the rate of depopulation of infected herds. Reporting the number of newly detected herds per week would provide a more direct and meaningful metric. However, this metric on its own does not describe the current rate of spread of *M. bovis* to other herds, as there will always be a lag between infection and detection of infected herds. If intervals from infection to detection can be shown to be decreasing, then reducing numbers of newly detected herds per week may indicate reduced rate of spread some months previously, so the two measures assessed in combination would be useful.

An independent assessment of the effectiveness of tracing is provided by the programme surveillance. That is, if all herds detected by bulk tank milk screening and eventually confirmed as infected are within the known tracing networks, this would provide confidence that tracing is effective. Hence thorough assessment of the networks for those herds confirmed as infected following bulk tank milk surveillance is important. We understand that 3 of the 4 newly detected herds from the Spring 2018 bulk milk surveillance were from outside the network. This is of concern as it indicates incomplete tracing. The linkage (or lack thereof) between herds newly detected by the Autumn and Spring 2019 bulk milk surveillance will be very important information for the programme and the TAG in any future reviews.

Other key indicators apparently not being used and hence not available to TAG are the current numbers of herds in the casing, tracing, and surveillance queues, and the distribution of times from risk cattle movements into those herds by movement risk classification. The report by Drs Mackereth and van Andel in May 2019 (‘Mycoplasma bovis programme: How far through are we?’) contains comprehensive lists of indicators and performance measures covering the epidemiological situation, disease investigation measures and control effectiveness.

Information management

The development of a new information system (TIAKI) is a positive step. The improved ability to track interactions between the programme, farmers and laboratories will enable better tracking of operational performance. Additionally, it should improve communication. Phase 1 of TIAKI was not designed to provide the core epidemiological metrics outlined above. Hence the TAG recommends the development of the animal disease management component of the new database (i.e. TIAKI phase 2) be fast tracked and include input from the operational and strategic epidemiology teams, who will be amongst the end users of this system. Consideration should be given to ensuring interoperability of TIAKI with other database systems (e.g. NAIT) to ensure that data captured, for example about animal movements, in one system is available to other systems. Additionally, robust beta testing must be undertaken, and the database must deliver the appropriate key epidemiological metrics in real time and in a transparent manner. Assessment of disease response databases available internationally may help fast track development of the new systems in New Zealand. Communication of programme progress would be greatly enhanced with better representation of the number of farms by category over time. That is, clear graphical representation of number of new cases on a weekly or monthly basis (incident cases) and the number of cases resolved (depopulated) is required. It would also be prudent to ensure that the database can provide an overview of KPIs by regional centre so resources can be managed and reallocated as needed.

New infection modelling

The preliminary modelling of the estimated dissemination rate (EDR) should be extended and used for forecasting to provide more precise estimates of likely intervals from infection to application of movement control, and of animal movements within this period. This model should be used to provide indications of the likely number of herds still within the current casing, tracing and surveillance network that will be likely to test positive and the number of herds that are likely to be detected based on bulk milk ELISA surveillance. Delayed identification of and imposition of movement restrictions on infected herds will contribute to further spread of infection. In their analysis, Drs Mackereth and van Andel (22 May 2019) had estimated the impact of the backlog in terms of the number of undetected infected premises and the potential for further spread based on the estimated rate of spread. These estimates depend on a series of underlying assumptions and extrapolations from the response to date. The TAG now understands that an update of this modelling is underway and fully supports this.

Operational structure

The interval between risk movements and the application of NODs must be reduced, and robust and accurate assessment of this must be available in real time. To achieve this the implementation of the new programme structure should continue, the recent operational changes sustained, the regional management teams given clarity around their role, and, where feasible, decision-making decentralised and fast tracked with appropriate quality controls. Additionally, sufficient technical support must be available both in Wellington and regional centres to allow timely science-based decision-making to be made within a robust operating framework.

Best practice for disease management and elimination (TOR C)

The OIE and a number of reviews following disease eradication responses provide outlines of best practice standards for animal disease eradication or control. These include defining the objectives of the programme, maintaining social support, ensuring sufficient veterinary infrastructure, and organisational flexibility (see Text Boxes 1 and 2).

Text Box 1: The World Organisation for Animal Health (OIE) guidelines for animal disease control

(http://www.oie.int/fileadmin/Home/eng/Our_scientific_expertise/docs/pdf/A_Guidelines_for_Animal_Disease_Control_final.pdf)

- Identification of priorities, objectives, and the desired goal of the disease control programme, which take into account the importance of economic assessment of disease intervention options
- Clearly stating the rationale for establishing a disease control programme
- Defining the desired goal of the disease control programme from the outset
- Developing a disease control plan that identifies critical control points, identifies intervention options that take into account cost-benefit considerations, includes ongoing review of effectiveness, and considers non-financial factors (social, cultural, religious, etc)
- Implementation of the plan, based on the efficient and effective Veterinary Services, with any gaps in this identified and addressed through the OIE Performance of Veterinary Services (PVS) pathway (http://www.oie.int/solidarity/pvs-pathway/)
- Ongoing monitoring, evaluation, and review

It is acknowledged that each disease control/eradication process is unique, however, there is value in using guidelines and learnings from other disease eradication or control programmes to inform/improve the current programme.

It is recognised by the TAG that *M. bovis* poses particular challenges in terms of disease eradication including:

- Low clinical disease incidence on infected farms
- High frequency of animal movements in New Zealand
- Lack of highly sensitive and specific diagnostic tests at the animal or herd level
- Difficulty in gaining and maintaining wide stakeholder support for a disease that is endemic in nearly all other countries, which does not have any trade impacts, and which has a low incidence of clinical disease.

Text Box 2: Learnings from previous disease eradication programs (Goodman, 1998, Anderson, 2002, 2008).

- A need to deeply understand the disease before embarking on eradication
- Thorough consultation with all stakeholders prior to initiation of eradication
- Initiate and use surveillance data in real-time to assess the effectiveness of interventions
- Use a management structure that includes centralised direction, but decentralised execution
- Ensure high levels of supervision of training of all within the response including clear feedback loops, and the ability to update all personnel on changes in the programme
- Expect the unexpected: it is highly likely that will be regional variation in efficacy of eradication due to local epidemiological, economic and sociological factors
- Expect the need for variation in resources across regions
- Ensure that funders are fully engaged and take “ownership” of the programme
- Ensure ongoing political commitment at all levels is maintained
- Maintain positive and strong leadership during eradication but do not declare freedom of disease too early
- Set specific date targets for eradication

The Paskin and Roche reports identified issues with the programme, including insufficient staff to cope with the workload of the response, a critical shortage of appropriately skilled and experienced individuals in key roles, and poor systems and processes to support the response. The size of the tracing and casing backlog reported in the Roche review was clearly inconsistent with best practice. Such failures are commonly identified following the conclusion of disease eradication programmes and it is encouraging that these issues are being identified now, two years into a multiyear programme. Both reviews made a series of recommendations regarding improvements that could be made to the current response. Whilst the Roche review focused on operational improvements to avoid a future recurrence of the tracing backlog, the Paskin review adopted a more strategic approach and made recommendations to address shortcomings of the current response and ensure a more resilient system is in place to tackle any future animal disease incursions in New Zealand. This longer term vision is consistent with the third goal of the joint MPI, DairyNZ and Beef and Lamb NZ *Mycoplasma bovis* 2019 National Plan[1] - to leave New Zealand’s biosecurity system stronger. The recommendations of the Paskin review are broadly consistent with the guidelines of the OIE and the criteria published by Anderson and Goodman, summarised in the text boxes. The TAG supports the recommendations of the Paskin and Roche reviews and welcomes the program’s response to the recommendations of these reviews (https://www.mpi.govt.nz/dmsdocument/35544/direct).

The Paskin and Roach reports both recognise the need for the programme to develop and retain core skills to support the response, in common with previous disease eradication reviews (e.g. Anderson 2002, 2008). This highlights the critical importance of appropriate level of skills and resourcing of key

[1] https://www.mpi.govt.nz/dmsdocument/33708-m-bovis-2019-national-plan-summary

technical people, such as the operational and strategic epidemiologists and regional veterinarians. The TAG understands that there are ongoing appointments into these roles and welcomes this development and acknowledges the difficulty in finding appropriately qualified people for these roles. It also underscores the importance of ensuring that the programme encourages and supports those involved. It is acknowledged that is difficult to provide objective measures of organisational resilience, so undertaking and reporting on periodic staff engagement surveys and monitoring of indices such as staff turnover would provide the programme, Governance and the TAG with data to enable an objective assessment of this important part of the programme.

The OIE guidelines suggest that the desired goal and rationale for disease eradication be defined early in the program. The *Mycoplasma bovis* 2019 National Plan states that eradication, reduction of the impact of the disease and the programme on people and improving New Zealand's biosecurity system are the goals. What remains unclear is how it will be demonstrated that biological freedom has been achieved. Given the challenges of achieving biological freedom from *M. bovis* as outlined above, freedom from *M. bovis* (that is assurance that *M. bovis* is not present in New Zealand) will have to be defined on a probabilistic, rather than absolute, basis. There will need to be agreement amongst stakeholders that biological freedom is declared based on data demonstrating that *M. bovis* was not found following some number of tests in some number of herds over some time period. Understanding what is required to demonstrate biological freedom provides increased surety for stakeholders around the total time period required, the total number of tests required and hence the resources required. Undertaking this process would also likely identify current knowledge gaps, as well as potential areas of risk to the process.

Changes in surveillance systems and testing (TOR B, D)

The draft scenario tree surveillance model developed by Dr Mackereth ("Description of a decision support tool for designing surveillance to give confidence of freedom from Mycoplasma bovis" and associated spreadsheet model) is an important advance as it will help clarify thinking in design around surveillance required to define biological freedom. For it to be fully effective it should be validated, parameterised and used. The TAG has provided some feedback to Dr Mackereth, but this should not be seen as a full validation. As noted by Dr Mackereth, the current design parameters are based on international standards (for example, a design herd prevalence of 0.2% is based on OIE freedom of disease guidelines) or require further development or refinement based on, for example, data from response surveillance. Additional data will be required to enable this parameterisation to occur. For example, there appear to be no data on the animal-level prevalence of *M. bovis* in cow/calf operations, a critical parameter to determine sample size to define the prevalence of *M. bovis* in cow/calf operations. Using this scenario tree would then allow modelling of surveillance options, assessment of risks of transmission from beef to dairy, and definition of biological freedom. It would also enable the Governance group and the programme to undertake the detailed planning required for declaration of biological freedom. Detailed scenario modelling should occur using different assumptions and with various combinations of surveillance approaches (e.g. bulk milk ± cow-calf surveillance ± slaughter surveillance, etc.). This modelling will also be important for communication to farmers and other stakeholders. Decisions about biological freedom will not be simple or easy, and must incorporate technical, social and economic aspects. It is also highly likely that the model will need to be run on an iterative basis as additional data from the response become available.

One important role of undertaking scenario tree modelling is that it helps inform understanding of the risk of movement of infected animals between the dairy and non-dairy sectors. The current hypothesis of the programme team is that introduction of, and spread of *M. bovis* of, is predominantly in the dairy sector, that non-dairy herds are predominantly infected by movement of infected animals from the dairy industry, and that the rate of transmission within the non-dairy sector is low (i.e. there is a low estimated dissemination rate; EDR). Data presented to the TAG (for example in the Drs van Andel

and Mackereth report on the estimated dissemination rate of April 2019 and in discussions with the epidemiology team) suggest that while the proportion of infected properties that are defined as beef is currently greater than those defined as dairy (i.e. 106 of 195 confirmed properties are 'beef' as of October 2019), the majority of these beef properties have traces from the dairy industry, and the risk of forward movement from these properties is lower than from dairy farms. However, in the absence of surveillance of the beef industry more generally, a true understanding of the prevalence and incidence of *M. bovis* in the beef industry is lacking. If *M. bovis* is more widely spread in the non-dairy sector than is currently understood, transmission rates are higher than currently understood, or tracing is less than 100% effective in the non-dairy sector, there remains a risk of ongoing, undetected transmission, and spill over back into the dairy industry. Hence, the TAG believes that a greater understanding of prevalence and incidence within the non-dairy sector and an understanding of the transmission risks from this sector are vital to understanding the timeframe and resourcing required for delimitation of *M. bovis*, as well as planning for the post delimitation surveillance leading to a declaration of freedom. Optimising the surveillance systems by exploring the interrelationship between resource allocation, for example by exploring different intensities of surveillance (i.e. number of herds per unit time) and investigating different combinations of surveillance system components (e.g. slaughter versus bulk milk versus cow/calf surveillance), will allow decision-makers to make more informed and economically sound decisions.

Beef surveillance systems

The preliminary EDR estimates and analysis of trace forward data provide some support for the assumptions that the dairy industry is the primary focus of *M. bovis* and that forward transmission risk is lower in the non-dairy than dairy sectors. But this does not preclude the possibility that *M. bovis* has become established in non-dairy systems, which could then provide an ongoing source of infection back into the dairy industry. The explanation for the observed increase in number and proportion of infected non-dairy herds is either that there is ongoing movement of infected animals from dairy into non-dairy systems, that tracing/casing is still catching up with historical infectious movements from the dairy into the non-dairy sector, and/or or that there are non-dairy herds that remain infected, but have not yet been detected and hence are potentially still spreading infection. It is likely that all these scenarios are true, but the relative importance of each of them is unknown. With ongoing programme surveillance and tracing within the dairy industry, the probability of spill over from the dairy to non-dairy sectors should be reducing. However, if there remain undetected infected non-dairy herds that are acting as a source of ongoing new infection to other herds, the current systems will likely not identify these herds until infected animals are reintroduced into the dairy industry. Spill over to the dairy industry will ultimately be detected through bulk tank milk surveillance but the source of infection in the non-dairy sector may not be identified by back trace given the incomplete records of animal movements. There is also potentially a significant lag between infection and detection where dairy replacement stock or service bulls are infected as young animals. Detection may only occur when they start producing milk in the case of replacements or infect lactating cows in the case of service bulls. Co-grazing of potentially infected dairy replacement stock with other groups of replacement stock, introduction of service bulls, and possible interactions with beef animals are all potential routes for transmission of disease.

The report recently provided by Dr Crosbie on beef surveillance outlines a 4 pronged approach to beef surveillance, including surveillance of animals as they enter the Five-Star beef feedlot, blood sampling at the time of tuberculosis testing of cow/calf operations, sampling at slaughter, and enhanced syndromic surveillance. The proposed collaboration with Ospri is a positive step and should improve the likelihood that surveillance in the cow/calf operations may now occur and that this is done efficiently and with minimal impact on farming operations. Issues of perceived business risk by abattoirs cooperating with the programme for surveillance need to be resolved, presumably by implementing a national surveillance programme so that no single commercial abattoir is the sole

point of testing. The TAG supports all of these initiatives including early implementation of the proposed ELISA testing of cows within cow/calf operations in conjunction with TB testing and of the ongoing surveillance of animals entering feedlots. We recommend integration of the data generated by this testing into the decision support and surveillance modelling.

Risk assessment and risk mitigation of transfer of *M. bovis* from non-dairy to dairy herds (and vice versa) are linked to surveillance design. If the risk of transfer of *M. bovis* from non-dairy to dairy herds is extremely low, or if that risk can be mitigated so that it is extremely low, then less intense surveillance may be required in the non-dairy sectors. Assessment of the frequency and risk of animal movements between the dairy and beef industries requires further clarification and modelling.

Bulk tank milk (BTM) ELISA

The TAG supports changes in the bulk milk ELISA surveillance system (i.e. moving to monthly bulk milk testing to ensure that all herds, irrespective of calving pattern, are tested, and changes to the cut points used to declare herds positive), the recommended increases in sample sizes for serum ELISA testing, as well as the proposed changes in the serum ELISA cut points, which the TAG understands have already been implemented. All these changes are likely to increase the sensitivity of testing and/or enable confirmation of herd status more rapidly than is currently possible.

The results of the Spring 2018 bulk milk testing programme and the herd-level sensitivity and specificity of the current bulk tank ELISA protocol have been analysed, leading to the recommendations for future bulk tank milk (BTM) screening. Herds were tested once every four weeks for three months with the BTM ELISA. Of the herds from which three BTM ELISA results were available, the majority tested positive in only one of the three tests. Subsets of 24 'gold standard' infected herds, and 520 'gold standard' negative herds were identified. For the 11 infected herds with at least one BTM ELISA positive test result that had completed the three rounds of standard testing, 8 tested positive in either two consecutive tests or in all three tests. ELISA reactivity appeared to decrease over the three months for these Spring calving herds.

The BTM ELISA was estimated to be 54% sensitive and 94% specific based on the gold standard herds. The TAG suggests that further clarity is required about the definition and selection of those gold standard herds to fully assess the validity of the consequent sensitivity and specificity estimates. At an estimated herd-level prevalence of 2%, the BTM ELISA screening had a positive predictive value of 15% and a negative predictive value of 99%. There were only 31 herds, out of over 11,000 tested during the Spring 2018 BTM screening programme that yielded a false positive result, suggesting a specificity in excess of 99%, higher than the estimate of 94% based on the 520 gold standard uninfected herds. One possible reason for this difference in specificity estimates is the selection process for the 520 gold standard uninfected herds. Gold standard populations should be selected independently of the diagnostic test being assessed. An alternative explanation is that the on-farm surveillance had very poor sensitivity and so the 520 gold standard uninfected herds included undetected infected herds. Four negative herds that were tested at Milk Test NZ were positive on retesting at AHL, but these were regarded as negative in the analysis. A total of 3 previously unidentified infected herds were detected and confirmed positive by subsequent testing by the Spring 2018 bulk tank screening programme. BTM PCR testing did not identify any additional infected farms over those identified by ELISA.

The TAG recommends that the definition of gold standard used in this analysis be revisited, and that latent class modelling be undertaken. The TAG agrees with the recommendations in the paper that PCR testing should no longer be used for routine screening of BTM and that the ELISA be used as the primary BTM screening tool. The possibility that using PCR screening in parallel with ELISA may increase the joint sensitivity of testing is not supported by analysis of the actual Spring 2018 BTM screening data.

The screening of dairy herds supplying milk in Autumn 2019 has been completed, and the TAG supports the testing of all herds supplying milk at monthly intervals from 1 July 2019. There are no data available to compare fortnightly and monthly testing at this stage. The data provided following the review of bulk tank milk surveillance from Spring 2018 and Alysia Parker's work in long-term infected Australian herds (Parker et al., 2017) demonstrates that bulk tank ELISA titres are highest following calving or soon after onset of *M. bovis* clinical disease and decline rapidly after that. While sampling could be focused on early lactation by use of commencement of supply dates, the pragmatic decision to test all herds supplying milk is logical given the difficulty in defining the calving pattern in some herds. Some consideration could be given to introducing additional criteria to define a farm as positive based on BTM ELISA results, but it would be better if this is guided by the use of a more intensive modelling approach, such as Bayesian latent class analysis, as this might provide a better optimised approach than that proposed in the paper. We agree that a NOD should be placed on a farm after the first BTM ELISA positive result and that on-farm surveillance is undertaken immediately. Although there will be a number of false positives, which may lead to management pressure on farms, it should slow the rate of new infections and reduce the spread of infection to new herds. The high specificity of the BTM ELISA screening suggests that the number of false positive herds will be relatively low.

Serum ELISA vs PCR

The TAG was also provided with a report entitled "Evaluation of the IDVET serum ELISA on bovine serum in the New Zealand *Mycoplasma bovis* eradication programme" by Drs Mackereth and Marquetoux, dated 4th of April 2019. The objectives of this work were to describe the IDVET ELISA and PCR test results in likely *M. bovis* infected herds, to evaluate the accuracy of the IDVET serum ELISA in classifying herds as likely infected, using PCR as the gold standard, and to provide additional guidelines for herd-level test interpretation for *M. bovis* screening, with emphasis on the interpretation of ELISA results to classify herds as likely infected.

The main problem with this analysis is that the low sensitivity PCR was used as the animal-level gold standard, which could have biased the estimates of the sensitivity and specificity of the ELISA.

The on-farm surveillance programme that was being used to classify herds as infected has a low sensitivity (50%) and quite high specificity (90%). ELISA testing had been conducted in tandem with PCR testing. Given the current estimates of median animal-level prevalence in infected herds, this sampling scheme is unlikely to provide confidence about the absence of disease following a negative screen. An alternative herd screening process has been proposed.

The selection of animals for serum sampling in infected herds was not randomised, particularly when repeated sampling was conducted, so the analyses conducted in this study may have been affected by this biased sample collection. This should be considered in future analyses.

PCR and ELISA results appeared positively correlated, so ELISA results could be used to target or prioritise animals for PCR testing, with a focus on animals with the highest S/P ratios. The animal-level sensitivity of PCR was estimated at about 40%, while, at the current 'weak positive' cut point recommended by the manufacturer, the ELISA appears to have animal-level sensitivity of 89% and animal-level specificity of 95%. The authors advocate two thresholds/cut points for the ELISA depending on likely risk, which seems justified. The herd-level sensitivity of ELISA testing on a sample of animals was 50-75%, depending on the ELISA cut point used, the threshold proportion of animals that are required to test positive to declare a herd as positive, and on the estimated animal-level prevalence in infected herds. The ELISA results did not correlate with age or herd type, but no data were available to match ELISA results with clinical data.

The TAG understands that latent class modelling of the cow-level ELISA will be conducted to determine whether the suggested changes in terms of cut points (i.e. changes to the suggested S/P cutpoint of 90 and herd prevalence of 3%) are optimal. The TAG supports this approach.

The report also suggests performing analyses using the quantitative Ct values from the PCR analyses (in addition to the dichotomised positive/negative interpretation of the Ct values) could be useful, as it may indicate whether the animals that are still developing an immune response might have higher concentrations of the organism on the swabs; this may suggest an alternative approach to targeting the confirmatory testing.

Archived cases testing positive by immunohistochemistry (IHC)

IHC testing of tissue from a cow that died on 12 September 2004 yielded suspicious results that warranted further testing. MPI has been unable to conduct further tests on the formalin-fixed paraffin-embedded tissue from 2004, as the tissue block cannot be found. The source farm was sampled - all three cattle now present on the farm returned negative results on PCR testing of tonsillar swabs. Six forward-trace animals are still alive and tested negative by tonsillar swab PCR. In the opinion of the TAG, this negative testing indicates that this herd is not of importance in the current *M. bovis* incursion into New Zealand. It is not possible to conclude that this was a false positive test, because there was no further testing on the sample, but there is no evidence of current infection in the remaining animals. It should be noted that the sample size was very small, so the level of confidence that can be placed in any inference of freedom of disease is low. The small number of animals available precluded meaningful interpretation by serological testing and hence such testing was not performed. Therefore, while we would not completely rule out the possibility that *M. bovis* was introduced into NZ in 2004, it is apparent if this did occur, that it did not establish or spread.

IHC testing of a cow that died in March 2015 also yielded suspicious results that warranted further testing. The formalin-fixed paraffin-embedded tissue from 2015 was negative for *M. bovis* by PCR testing, and the positive and negative controls used in this analysis gave confidence that the negative result was valid. We note that further PCR testing could not detect any of 32 other Mycoplasma species in the sample, so it seems unlikely that the suspicious IHC result was due to cross-reactivity of the antibody with other Mycoplasma species. In addition, bulk milk testing (ELISA & PCR) of this herd was negative, 100 serum samples were tested by ELISA and found negative, and 30 nasal swabs were tested by PCR and were negative. Thus, the TAG considers that the investigation has been thorough and correct in concluding that the sample from this cow was negative for *M. bovis*.

Woodford report (TOR E)

Following a request from Dr Roche, Dr Woodford prepared a report for MPI and the TAG. In addition to this written report, a teleconference was held with Dr Woodford.

The 3 key points raised by Dr Woodford were that:

1. Given the data obtained from herd owners, Dr Woodford concluded that infections on some farms can potentially only be explained by animal movements prior to December 2015. Dr Woodford thus concluded that *M. bovis* must have been present prior to December 2015.
2. Dr Woodford suggests that the small number of isolates collected in 2017 for whole genome sequencing precludes precise estimation of the date of the common ancestor. He expressed concern about extrapolating back in time from the larger number of isolates collected in 2018/19. He expressed concern about the use of the movement data provided by the programme in modelling of the date of the common ancestor.
3. Dr Woodford expressed concern about test performance and infers that some herds have been incorrectly released from NODs (i.e. false negatives on testing).

Dr Woodford has indicated that he has more information than was provided in his written report and has offered to make himself available to discuss how this may help better inform decision making. The TAG encourages Dr Woodford to provide any additional relevant data he holds, or is aware of, to the *M. bovis* programme.

Dr Woodford asserts that communication to herd owners and other affected parties has not been entirely effective. The TAG acknowledges that some herd owners feel that they have not been listened to and their concerns apparently not acted upon. The TAG recommends that improved communication systems are developed such that there is an acknowledgement of information provided by stakeholders, and that feedback is provided to those providing information. The implementation of a new CRM package by the programme within TIAKI should enhance such communication.

The TAG shares Dr Woodford's concern about apparent delays in follow-up of forward and backward traces. These delays may have led to further spread of infection, as outlined elsewhere in this report.

Dr Woodford concludes that programme has taken too narrow a view of the likely time of introduction and infers that there has been selective data use by the programme. The TAG does not agree with this view, as the evidence still points to one or a small number of introductions of *M. bovis* into New Zealand in 2015 or 2016. The phylogenetic and molecular clock work continues to support this hypothesis. With more isolates being available for whole genome sequencing, and modelling being updated on a regular basis, there has been no substantive change in the estimate of the time of the common ancestor since the initial modelling was undertaken. The degree of relatedness of the now over 200 *M. bovis* isolates from 86 herds that have been sequenced continues to support the previous estimates of the time of introduction. If indeed *M. bovis* had been present and had established within New Zealand for an extended period of time, the diversity of the *M. bovis* isolates would now be considerably wider. The common ancestor modelling makes no use of the estimated date of introduction of *M. bovis* to a given herd. The only data used for the date of the common ancestor modelling are the date of isolation and the whole genome sequencing data itself. The rate of mutation of *M. bovis* is estimated from the isolates themselves, and no exogenous assumptions about the rate of mutation have been made. Tracing data is used in some (but not all) of the models assessing likely relatedness of isolates amongst farms. It should be noted that movement data is only used to support inferences made from the whole genome sequencing, not in place of the sequencing data.

Dr Woodford cites cases where farmers have reported clinical signs of mastitis or lameness prior to 2015 that bear resemblance to those associated with *M. bovis* as supporting evidence for the earlier presence of *M. bovis*. However, no supporting laboratory data were provided. There are multiple causes of lameness, recurrent and non-treatable mastitis and calf disease. Clinical signs are not sufficient to identify a specific cause of these disorders. Laboratory testing (e.g. culture, PCR) is required to make a specific diagnosis of *M. bovis* as the cause of these diseases. Given the multiple aetiologies potentially associated with such clinical signs and the lack of presentation of any laboratory results suggest limited weight can be placed on these reports. Thus, these reports do not indicate that *M. bovis* was present in New Zealand prior to 2015.

It is acknowledged by the programme that not all of the farms are linked by animal movements. As acknowledged by Dr Woodford, there are errors within the NAIT records both due to omissions and errors in movement records. The programme has clearly signalled that issues with the NAIT system have been a major impediment to their operations and there have been repeated calls from the Minister down to improve the NAIT system. The TAG agrees that the NAIT system needs to be improved to better enable the response to operate. The TAG is not aware of evidence for bias in terms of the NAIT records or in the use that the programme makes of these records. Dr Woodford has previously commented on inaccuracies of data within NAIT and he has been encouraged to provide

precise information either directly or to encourage affected herd owners to provide this to the programme. The programme is unable to act on information unless it is actually provided to it.

Dr Woodford expresses concern about the decision rules for declaring herds placed under NOD subsequently being declared free of disease. The programme is aware that the tests are not 100% sensitive or specific. Sensitivity and specificity should be understood not just in terms of an individual test at an individual time point, but in the context of the whole programme of testing using multiple time points and multiple tests. A number of herds have been released from a NOD but then had a NOD reapplied. The TAG understands that this is due to risk movements onto these farms across time, with NODs applied and/or infection being confirmed associated with movements which occurred after lifting of the initial NOD. Similarly, a small number of farms that have been destocked and restocked have subsequently tested positive. Again, the TAG understands that there were risk movements associated with the restocking which resulted in reinfection of these farms. The whole genome sequencing data supports the recorded movement data in these cases. Thus, such events appear related to subsequent animal movements, not to failures of earlier testing or to failure of the cleaning and disinfection processes.

Dr Woodford comments on the ELISA validation process. Test validation is complex, but as part of that validation process populations of animals that were likely uninfected, as well as populations of animals that were likely infected, were used to assess the test specificity and sensitivity, respectively. The TAG has noted that test validation could be improved and recommended further validation be undertaken. However, it should be noted that surveillance systems and testing strategies are developed accounting for the less than perfect tests, by selecting sufficient sample sizes and undertaking repeated tests across time to counter the limitation of the tests. Where NODs have been removed from dairy farms, these herds (along with all other dairy herds) remain in the national bulk tank milk surveillance programme.

Dr Woodford implies that the evolution of the testing strategy suggests a lack of transparency by the programme. As data from the response has become available and further analysis of these data has been undertaken, there has been optimisation of testing cut-points and strategies. Hence changes in decision rules have occurred over time, reflecting ongoing improvements in the testing systems. The TAG supports ongoing test evaluation and hence changes to test interpretation and programme testing strategies based on an improving understanding of test characteristics.

Dr Woodford mentions some animals that tested positive following export from New Zealand. The TAG is led to believe that there were a small number of test positive animals amongst a large shipment of animals. Given the known specificity of the tests, it is highly likely that these were false positives and, as the apparent prevalence was well below the threshold likely to be indicative of infection, these results are of little significance.

Dr Woodford suggests that there should be improved integration of information to understand disease movement. The core function of the casing, tracing and surveillance systems developed by the programme to deal with the epidemic is focused on achieving this. The Roche and Paskin reports identified limitations of the animal disease response database that have hampered integration of information. The programme has indicated that a new database is being developed that will improve the functionality in these areas.

The TAG does not have direct access to the response database and hence is not in a position to review individual cases. The TAG asked the programme to review the information provided by Dr Woodford and to assess whether this information was currently known to the response and/or whether it changed the inferences about specific chains of infection amongst farms. Dr Woodford makes a number of comments around the window of back tracing, inferring that the programme did not put sufficient weight on historical movements. However, the TAG understands from the

programme that all relevant back traces have now been investigated. The window over which back traces have occurred has expanded as knowledge of the disease has increased. The programme is using both NAIT records of animal movements, as well as NAIT tag purchases, even where those tags have not been entered into NAIT by the tag purchaser. The programme has provided verbal assurance to the TAG that they have investigated the information about specific animal movements provided by Dr Woodford that may have provided an alternative understanding of how disease may have transferred amongst farms. It is the TAG's understanding that the review of these cases has not resulted in any substantive changes in the programme's understanding of how and when disease transmission occurred. The programme also notes that some of the data provided by Dr Woodford has been proven to be inaccurate following further investigation by the programme team. The exotic disease incident reports (EDIR) are routinely shared in draft format with herd owners before finalisation. The programme has acknowledged that in a small number of cases early in the response this did not occur. It should be noted that the programme may hold additional data above and beyond the animal movements identified by the EDIR, where, for example, subsequent forward and back traces identify previously unknown animal movements. Similarly, the location of NAIT tags on farms not linked by NAIT movement records infer animal movements to those farms.

Dr Woodford infers that infection of certain animals must have occurred when they were calves to explain some infection links between farms. However, it appears that Dr Woodford has not considered that infection may occur in older animals. For example, commingling of rising 2-year-olds, or service bulls, may result in infection transferring between mobs. Hence, infection of calves say in 2013 or 2014 is not required to explain how movement of animals from one farm to another results in infection in 2015 or 2016. Additionally, pass through events (i.e. animals transferred from Herd A to Herd B to Herd C with animals resident in Herd B not becoming infected and hence testing negative) may explain some linkages where the intermediate farm is not confirmed positive. The programme also has evidence of animal movements within farming organisations with multiple physical locations that may not be ascribed to the appropriate farms within the organisation. Thus, linkages between farming organisations can occur, but incorrect NAIT records may result in an inference that these movements did not occur.

The TAG agrees with Dr Woodford's suggestion that there is a need for high level overview and integration of data. There is an ongoing requirement for robust strategic oversight of the programme. In the new directorate structure, the strategic epidemiologist is reporting in at a senior level. Additionally, the intelligence function is being separated from the operations function, so an alternative view of the response is being provided to senior leadership. Decisions about application and revocation of NODs, as well as other operational decisions, are made by the operational epidemiology team, with input from a number of sources, not by one individual.

Other matters

The TAG acknowledges the efforts undertaken by the programme to improve communication, including efforts by key staff to attend face-to-face meetings, the establishment of regional groups including mayors, presentation by programme staff at technical meetings such as the Annual Conference of the Dairy Cattle Veterinarians of New Zealand and via teleconferences, and the expansion of the regional veterinarians role to include communications with local veterinary practitioners. The role of the industry partners (Beef and Lamb, DairyNZ) in supporting farmers, in facilitating the compensation process, and in communication amongst other activities, is a positive sign of industry engagement in the program. Reports of improved NAIT compliance are positive evidence that messaging from the programme is making an impact. Additionally, implementation of a CRM system within TIAKI phase 1 should allow collation of all relevant data for a herd and hence should enhance communication. However, feedback from Dr Woodford and others indicates a perception amongst some that the programme historically was not sufficiently responsive to concerns

or inputs by stakeholders. Hence the TAG recommends that systems to record, act upon, and report back on information provided by farmers, clinical veterinarians and other stakeholders be implemented and monitored. Key performance indicators around the communication strategy should be developed, monitored and acted upon if not being met. It is critical for the continued stakeholder support for the programme that this occurs as soon as possible. Further dialogue between the response teams and local clinical veterinarians should occur. In many cases, affected herd owners will turn to their local veterinarians as an independent and trusted source of information. A number of clinical veterinarian's report frustration with their inability to be able to provide technically sound information to herd owners and to understand the context for decision-making about individual herds. While it is recognised that, because of confidentiality and resourcing issues, high levels of detail about every decision cannot necessarily be provided to herd owners or their veterinarians, a system enabling herd owners to provide permission for their veterinarians to be privy to, and involved in, discussions with response staff would be highly desirable.

Development and implementation of a herd accreditation programme that would allow farmers to purchase cattle that are unlikely to be infected is recommended. Given current limitations of testing at the individual animal level, such a programme would have to be based on a risk assessment of the herd (number of animal movements, operational structure, etc.) as well as on the basis of the accumulated herd-level testing data. Such programmes have been used to provide risk assessments of likely herd level status for diseases such as Johne's disease (Geraghty et al., 2014). Such a system could be an extension of current industry efforts to improve NAIT compliance but would need to involve integration of a risk assessment and test results and require development of a scoring system that would allow herd owners to assess risk of disease introduction with cattle purchases.

The TAG recommends that the economic modelling used to inform the decision to proceed to biological freedom be updated in the light of the additional data now available. Studies assessing the impact of *M. bovis* on dairy herds, cow-calf operations, beef finishing units and other herd types should be fast tracked to provide robust estimates of the impacts of *M. bovis* in New Zealand management systems. The models should also include uncertainty (i.e. be converted to stochastic models), and external validation of these models is required.

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