ESR
Science for Communities

Refinement of the Framework for Assessment of Recreational Water Quality

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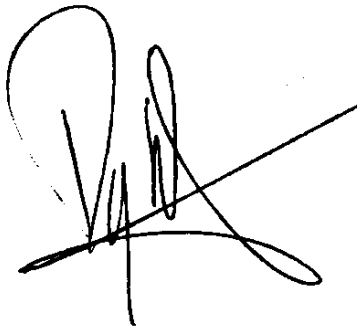

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EXECUTIVE SUMMARY

Protecting the health of New Zealand's freshwater resources, in recognition of Te Mana o te Wai, is the fundamental focus of the National Policy statement for Freshwater Management (NPS-FM) 2020. Under the NPS, councils are required to assess the quality of their freshwater sources, and where unacceptable levels of contamination are found take practicable steps to improve water quality.

A key component of this quality assessment relies on measurement of concentrations of the faecal indicator bacterium *Escherichia coli* as a proxy for the presence of pathogenic microbes. When *E. coli* levels exceed acceptable limits, councils are expected to take actions to identify the source of contamination and implement interventions to ameliorate the situation. Little guidance, however, is provided in the NPS as to what steps councils should take when contamination is identified.

In 2020, the Ministry for the Environment commissioned a Quantitative Microbial Risk Assessment (QMRA) pilot study (Leonard et al. 2020) with the aim to integrate new pathogen detection technologies and faecal source tracking approaches into the toolbox for assessing water quality. As part of that report a three-step framework for evaluating water quality based on a range of evidence assessments was presented.

The aim of this report is to further develop the water quality framework and provide step-by-step guidance to councils on what to do when *E. coli* concentrations exceed acceptable levels (Fig. 1). Development of this modified framework was informed by partnership with iwi/hapū/rūnanga and consultation with local authorities and communities, and is supported by evidence from case studies undertaken at contaminated freshwater sites. The revised framework can be summarised as follows:

- ***Step 1: Initial monitoring of water quality***
  This is monitoring of *E. coli* concentrations as mandated in the NPS. It may also include evaluation of environmental parameters indicative of water quality.

- ***Step 2: Characterisation of faecal sources and mitigation***
  Where *E. coli* concentrations exceed acceptable levels, the next step is to identify the source of contamination. This involves catchment surveys to identify features of the catchment likely to affect water quality. It is also involves identification of sources using a toolbox for faecal source tracking (FST). In FST, tools are used to identify the source of contamination by targeting specific microbes/chemicals in the faeces of animals, such as humans, ruminants, avian species, and dogs. Decision trees for assessing contamination from human, livestock and non-human/non-livestock sources are presented.

    - ***Human sources***

      Human sources present the highest health risk and as such are the highest priority for mitigation. Special consideration must be given where sources are aged or from treated wastewater as this may result in low *E. coli* concentrations despite considerable risk posed by persistent pathogens such as viruses and protozoa.

- ***Livestock sources***

  Faecal contamination from livestock sources can occur as point sources, for example, where animals have direct access to waterways, or diffuse inputs such as agricultural run-off from land-based activities. Where there are multiple tributaries into a contaminated waterway, flow-weighted measures for determining *E. coli* loads can be used to identify and prioritise for mitigation those contributing the most faecal pollution. Localised land mapping or tracers can be used to identify/confirm sources of contamination. Seasonal variations in climate and farming practices, such as calving, must be taken into consideration when evaluating contamination sources.

- ***Non-human/non-livestock sources***

  For sources not attributable to human or livestock contamination, there are other possibilities, such as avian or feral sources, which must be considered. Avian sources can result in sporadic exceedances in *E. coli* concentration and are often hard to control/mitigate. FST markers are available for some feral animals to evaluate their potential contribution. However, the FST toolbox for feral species and indigenous avian species is currently limited. Where no source can be identified using current methods, the contribution of naturalised *E. coli* or *Escherichia* species may be considered.

  Where a source is identified, potential mitigations are considered and implemented. Re-assessment of water quality is then performed to evaluate the success of each of the interventions. Development of potential mitigations must occur in partnership with iwi/hapū, and in consultation with farmers/landowners and the community. Evaluation of mitigation measures requires an assessment of Māori mātauranga and tikanga and the values that communities place on taonga, and local practices. For example, seeking consensus/compromise from interested parties where the proposed control measures impact on local feral and/or avian populations.

- ***Step 3: Site or source specific assessment and QMRA***

  Where a contamination source cannot be identified, or a source is identified but mitigations are unsuccessful or impractical, risk assessments may be conducted to determine the potential health risks posed by the contaminated site.

  - ***Step 3a – site-specific assessment and QMRA***

    Where a contamination source has not been identified, the site is assessed using a range of techniques to provide information on potential health risks. These assessments may include site-specific pathogen detection, and FST using additional markers for cryptic sources of contamination. This may involve development and validation of FST markers for new host species. The microbial community present at the contaminated site can also be assessed using novel research approaches such as metagenomic analyses. The contribution of naturalised *E. coli*/*Escherichia* species. may also be considered. As part of this site-specific assessment a QMRA may be undertaken, informed by the additional data gathered during this site evaluation.

- ***Step 3b***

  Where a source is identified but interventions are unsuccessful or impractical, a source-specific QMRA is performed. As the source is known, this is mostly a desk-top exercise where current knowledge about the contamination source is used to identify the potential pathogens present and determine suitability for recreational contact. The QMRA will include hazard identification, exposure assessment, dose-response assessment, and risk characterisation.

This framework provides valuable guidance and support to council scientists tasked with driving improvements in microbial water quality. This framework is equally applicable to an assessment approach for drinking water sources. It is recognised that this framework addresses only the microbial aspect of water quality and should be viewed in conjunction with all NPS-FM (2020) requirements for progressing environmental outcomes that improve the health and wellbeing of freshwater ecosystems and water bodies throughout Aotearoa New Zealand.

Protection of Recreational Water & Source Water

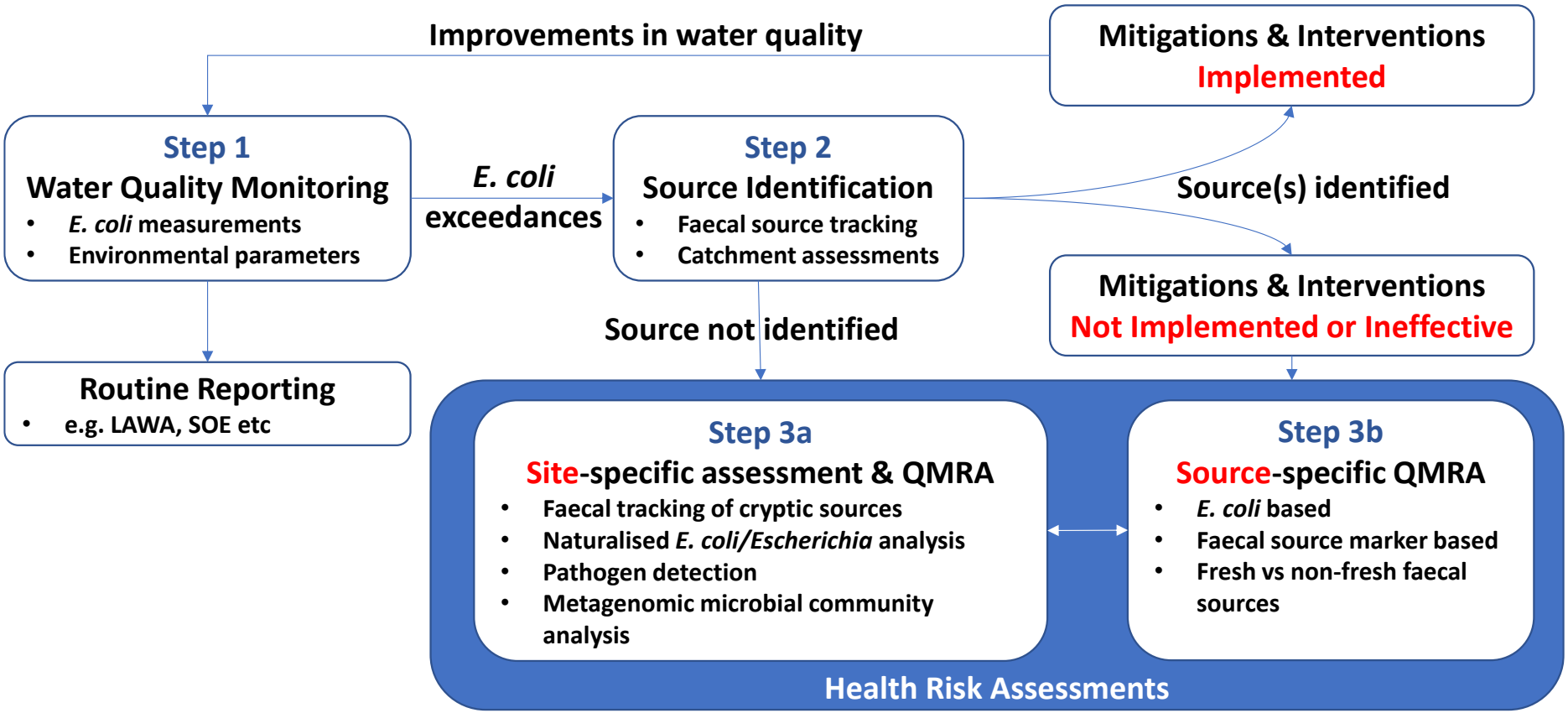

Figure 1 Refinement of the framework for assessment of water quality where elevated *E. coli* levels are detected in freshwater sites. Maximum benefits will be gained from partnering with iwi/hapū and consulting with communities throughout the assessment process.

1. INTRODUCTION

1.1 BACKGROUND

In the National Policy statement for Freshwater Management (NPS-FM, 2020), there is a requirement to increase the number of rivers in Aotearoa New Zealand that are suitable for recreational contact, and to improve the overall health and wellbeing of freshwater ecosystems and water bodies (NPS-FM, 2020). This is driven by the fundamental concept of Te Mana o te Wai, which recognises the importance of water health and its flow-on effects for individual and community well-being. Under the National Objectives Framework within the NPS-FM, each regional council must monitor 16 attribute states indicative of overall freshwater quality and establish acceptable targets and action plans for improvement of these attributes. The attributes relate to the compulsory values of ecosystem health, human contact, threatened species and mahinga kai. Two attributes¸ *Escherichia coli* and cyanobacteria concentrations, relate to human contact. The focus of this report is on *E. coli,* but this must be viewed in the wider context that it is only one of the attributes used to assess overall water quality.

The criteria for assessing microbial water quality in freshwater sites are based on monitoring concentrations of the faecal indicator bacterium (FIB) *E. coli* (NPS-FM, 2020). *E. coli* concentration is used as a proxy for the presence of pathogens to minimise public health risks during recreational contact with the freshwater body (e.g., swimming). The *E. coli* concentration limits for primary contact are based on the risk of acquiring an infection from *Campylobacter* based on the results of the 2002 Freshwater Microbiology Research Programme (McBride et al, 2002) (refer Appendix A). For example, if a single water sample contains between 130-260 *E. coli*/100 mL, 95% of the time there is a ≤1.0 % risk of acquiring a *Campylobacter* infection during a swimming event. This risk increases to ≤5 % if the concentration of *E. coli* is between 260-540 *E. coli*/100 mL. Aside from these guidelines, the NPS-FM (2020) provides little further advice for council water managers on what to do next when *E. coli* concentrations exceed acceptable standards. Advanced tools for identifying faecal sources were not available to the freshwater study of McBride et al. (2002), and subsequently, the incorporation of FST in multiple studies has proven their efficacy for faecal source tracking (Ahmed et al. 2019, Korajkic et al. 2019, Unno et al. 2018, Weidhaas et al. 2018). The aim of this report, therefore, is to provide stepwise guidance for regional and city councils to inform their responses to elevated *E. coli* concentrations, including identification of potential sources of faecal contamination.

In 2020, the Ministry for the Environment commissioned a Quantitative Microbial Risk Assessment (QMRA) pilot study (Leonard et al. 2020) to investigate the practicality of integrating advanced molecular techniques for pathogen detection and faecal source tracking (FST) tools into recreational water quality monitoring. These tools can be incorporated into risk assessment analyses to advise water managers about the relative public health risks associated with a contaminated waterway. Water samples were collected from 16 rivers across NZ characterised as having either urban, dairy farming, or sheep and beef farming in the surrounding catchment. Results of this study identified the frequent occurrence of more than one source of faecal contamination in each river and confirmed *E. coli* as a valuable indicator of faecal contamination (Leonard et al. 2020). Potentially pathogenic micro-organisms were detected in 94% of the samples, but generally at very low concentrations. It

was also observed that land use categories (urban, dairy or sheep and beef) did not always match the identified sources of contamination. The pilot report, therefore, concluded that future studies should include both visual confirmation of land use and FST.

The QMRA (2020) study also highlighted that to understand the health risk associated with a water body, water managers need to go beyond relying on *E. coli* measurements. *E. coli* is a suitable indicator of faecal contamination in a water body, and as such is an indicator of the potential presence of faecal pathogens. Multiple studies, however, have noted varying correlations between *E. coli* and pathogens. The die-off rates of *E. coli* and faecal pathogens differ depending on how recently the faecal material entered the water environment and the type of treatment it has undergone. Aged or treated sewage, for example, will have lower correlations between *E. coli* and more persistent pathogens such as viruses and protozoa, due to faster die-off rates for *E. coli*. When *E. coli* is identified in exceedance, therefore, further investigation is required to determine the source(s) of that contamination. Information on the type of faecal source will advance knowledge about which pathogens are likely to be present (Devane and Gilpin 2015, Soller et al. 2010, Soller et al. 2014). This information can be incorporated into a QMRA study to inform the decisions made by councils and local communities as to the health risk associated with *E. coli* exceedances in a water body.

Importantly, the QMRA (2020) report also presented a conceptual framework for assessing water quality using a three-step approach designed to help councils better understand and identify the causes/sources contributing to poor water quality in their locale (Fig. 2). This framework was adapted from a source water protection framework for drinking water developed by Andreas Farnleitner and colleagues at the Karl Landsteiner University of Health Sciences in Austria (Farnleitner et al. 2018, Savio et al. 2018).

The purpose of this report is to refine the conceptual framework, in consultation with councils, scientists, iwi/hapū and community groups, to provide step-by-step advice for councils on what to do when *E. coli* concentrations exceeding acceptable standards are identified. This refined framework will also be informed by results from case studies at contaminated freshwater sites. It is anticipated that the refined framework will simplify assessment of potential health risks posed by contaminated water sources and expedite potential mitigations. Similar to the original conceptual framework, it will focus on the three main steps involved in assessing water quality:

1. Is there a problem with faecal pollution?
2. If yes, what is the reason for it?
3. What are the health risks associated with the identified faecal contamination source?

1.2 AIM

The main aims of this report are to:

- Refine the water quality framework presented in the 2020 QMRA pilot study to provide clearer guidance to councils and communities tasked with remediation of freshwater bodies affected by faecal pollution. This will include advice on assessment of faecal indicators to identify contamination sources, and source-informed quantitative microbial risk assessments.

- Provide additional guidance for cases where mitigations are impractical or do not lower *E. coli* concentrations below those required by the recreational water quality standards.
- Identify knowledge gaps and limitations of the refined framework for improving water quality outcomes based on feedback from councils and community groups.

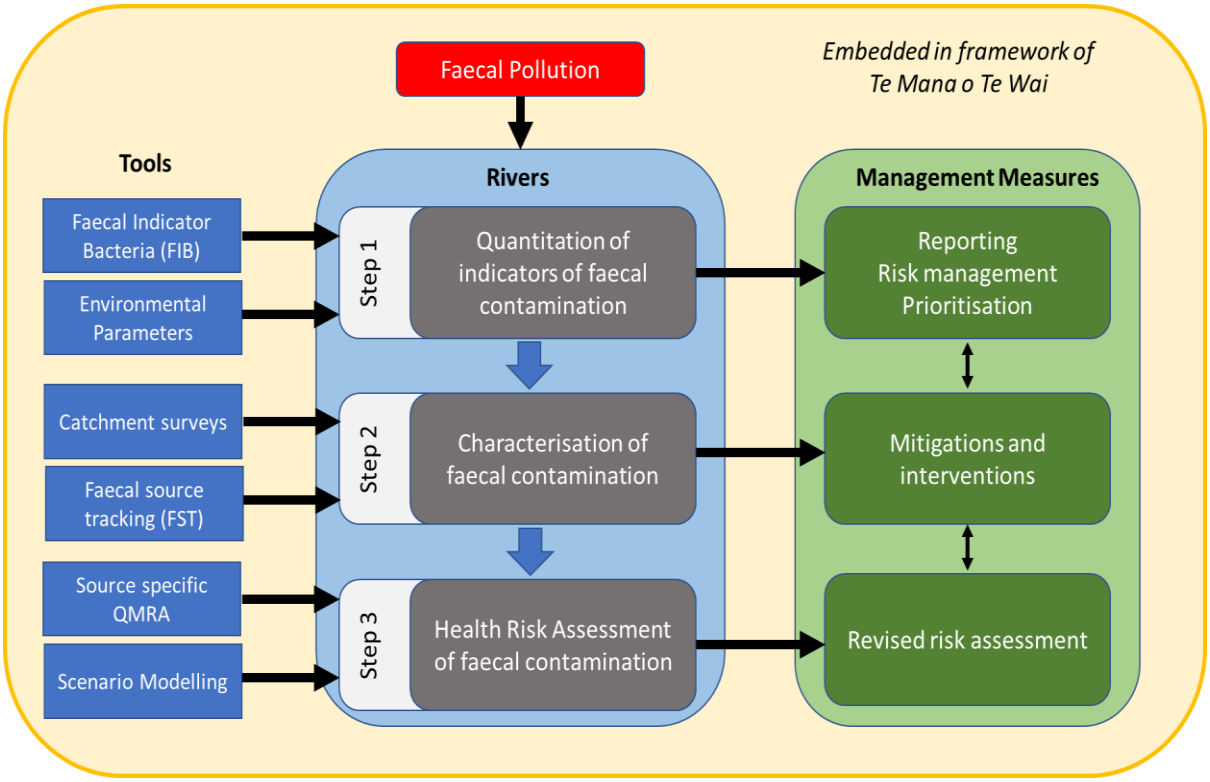

Figure 2 Conceptual framework for water quality assessment

Reproduced from Leonard et al. (2020).

2. COMMUNITY AND COUNCIL CONSULTATION AND FEEDBACK

This section outlines the various platforms that were employed to consult stakeholders on the proposed refinement of the water quality assessment framework and to obtain feedback. Presentations were given to stakeholders at four conferences/meetings across Aotearoa NZ and included reference to results from the 2020 Ministry for the Environment Freshwater QMRA pilot study (Leonard et al. 2020). Full presentation details are provided in Appendix B. Meetings were also held with councils. A short document summarising the main findings of the Leonard et al. (2020) QMRA pilot study was distributed following the conclusion of that study (Appendix C), and the Executive Summary of the main report with the proposed framework was distributed before meetings. A summary of the feedback received is provided in this section. Note that comments summarised in this section do not represent the views of all councils and reflect our interpretation of feedback gathered during discussions.

2.1 FEEDBACK FROM DISCUSSIONS WITH COUNCILS

Councils currently employ a range of measures for identifying and managing faecal contamination of freshwater sources. Eight councils were asked about how they manage poor water quality, what the biggest challenges were, whether a framework might assist in their investigations of faecal sources where contamination is indicated by elevated *E. coli* concentrations and what knowledge gaps existed. To obtain a broad range of responses, discussions were held with both small and large councils as they face different challenges. Anonymised responses have been collated and combined into common themes detailed below. The questions posed by ESR during these meetings and key feedback from councils are presented in Appendix D and E, respectively.

2.1.1 DRIVERS

Councils identified a variety of driving forces for improvement of water quality including The Three Waters Reform Programme for drinking water, stormwater and wastewater[1],[2] Te Mana o te Wai[3] and the routine requirements for monitoring and mitigation of sources required under the NPS for Freshwater Management. Expectations of council, community groups and District Health Boards (DHB) also drove the response to management of poor water quality. During discussions, it was noted that water quality improvements may require significant changes in infrastructure for sewage and stormwater systems including the management of septic tanks. As such, the importance of mitigation targeted at sources was emphasised.

2.1.2 CURRENT PROCESSES AND CHALLENGES

The degree of response to elevated *E. coli* levels was influenced by resource availability, the level of DHB involvement and council and community expectations. Interactions between councils and the local DHB vary. This is perhaps due, in part, to inconsistencies between the description of their roles in the 2020 National Policy Statement for Freshwater Management and the 2003 Ministry for the Environment (MfE) and Ministry of Health (MoH) Microbiological

[1] The Three Waters Reform Programme is a three-year programme designed to improve how councils deliver drinking water, wastewater and stormwater services, with particular focus on stormwater regulation and dealing with sewage overflows

[2] https://www.dia.govt.nz/Three-Waters-Reform-Programme

[3] Te Mana o te Wai recognises the importance of water health as paramount and giving effect to Te Mana o te Wai is a central component of the National Policy Statement Freshwater Management.

Water Quality Guidelines for Marine and Freshwater Recreational Areas (MfE, 2003). Additionally, both the 2020 National Policy Statement and 2003 Microbiological Water Quality Guidelines require daily sampling when *E.* coli levels exceed 260 *E. coli*/100mL, which was not always viewed as practicable by councils. Some councils are sufficiently resourced to investigate individual exceedances. Others use data trends to enable resources to be targeted at the most problematic sites, or specific sampling programmes e.g., during spring when there are elevated flows.

When councils do retest a site if there is an exceedance, it can take five days before notification of a public health issue by which time the contamination may have passed. It was noted that compliance with the 95th percentile over 12 months of the year for five years can be difficult as it only requires three samples (out of a total of 60 samples) to exceed the criteria for that five-year period. Sudden convergence of wildfowl in an area may easily elevate *E. coli* concentrations and result in non-compliance. Low flows could be problematic as they may lead to high concentrations of *E. coli* but either may not represent a significant *E. coli* contribution due to the low volume or may be indicative of stagnant areas with the potential for growth of naturalised *Escherichia*.

The Sanitary Survey was seen as a coarse tool in need of some additional guidance and perceived as having limited use for the investigation of faecal sources. Faecal Source Tracking (FST) was seen as a useful tool, but several councils noted budget constraints may limit its application.

2.1.3 HEALTH RISK ASSESSMENTS

Several important issues were identified in relation to health risk assessment. The ability to distinguish between different faecal contamination sources, their contribution and their accompanying potential health risks were recognised as important issues. In particular the health risk from avian sources was raised. Councils had also encountered feedback from stakeholders that *E. coli* was either 'not a problem', or the presence of 'naturalised *E. coli*' was the issue. Better communication is therefore required around the health risk associated with what is meant by 'naturalised *E. coli*', and the linkages between *E. coli* and pathogens. Communication with farmers about mitigation is often also hampered where undeveloped sites such as bush or forest have the same concentrations of *E. coli* as farmed sites.

2.1.4 KNOWLEDGE GAPS AND FUTURE INITIATIVES

Several scientific knowledge gaps and potential future initiatives were identified through the consultation process. It is anticipated that addressing these will maximise the effectiveness of the refined framework. These include:

- Being able to detect FST markers at lower *E. coli* concentrations was identified as important in certain situations.
- Requests for additional FST markers to be added to the toolbox of tests depended on a council's location. These included horses, goats, pigs, possums, wallabies, deer, shags, pigeons, pūkeko, stoats, cats, dogs, and rats. Pig was the most requested additional source marker.
- Reduced costs for FST analyses so it can become a useful part of a monitoring programme.
- Data on attenuation rates of faecal microorganisms once discharged into waterways.
- Information on the persistence of pathogens in sediment and their role in disease transmission would provide valuable information for health risk assessments.
- The ability to track concentrations of micro-organisms over a hydrograph would be informative.
- Another approach was raised to use shellfish as sentinel indicators because they accumulate contaminants during biofiltering.

2.1.5 COUNCIL AND COMMUNITY FEEDBACK ON THE FRAMEWORK

The concept of the refined framework was generally well received. However, it was suggested that it may not be helpful to be a requirement for councils because, as noted above, there are often insufficient resources, and it would need to be adaptive. Additionally, there was consensus that the benefits of the refined framework would need to be clearly communicated to councils and staff across the different groups especially monitoring groups and the groups that oversee the impacts of implemented mitigations. In these circumstances, it will be necessary to ensure that these groups are co-ordinated to maximise communication and improve outcomes. Furthermore, councils were hesitant about adding more guidelines into the requirements. Several councils noted that they already implement Steps 1 and 2 using FST to identify faecal sources. Additional guidance on the third step would be helpful with site-specific risk assessments for different contamination sources to understand the health risks. However, in contrast, some councils questioned whether health risk assessments were the best next step after identifying the source of contamination.

It was suggested that a framework could help inform water managers to ensure effective mitigation occurs, and to identify where implementation of mitigations is impractical, e.g., where contamination is derived from wildfowl, or mitigation is too expensive. A common community response was wanting to know what their personal contribution was to faecal contamination. Guidance on communication of the risk to different sectors of the community to support proposed mitigation would be useful. In rural settings lifestyle block owners may overstock or there may be issues with septic tanks, in addition to issues with livestock. It would be useful to provide examples of how mitigation manages health risk e.g., the benefits of fencing to keep cattle from accessing streams. It was also thought that the refined framework and associated health assessments may be beneficial for understanding the potential impacts on the gathering and consuming of freshwater mahinga kai.

3. CASE STUDIES OF CATCHMENTS WITH CHRONICALLY ELEVATED *E. COLI* CONCENTRATIONS

This section contains a summary of three case studies undertaken by ESR at chronically contaminated freshwater sites. These case studies were undertaken to inform refinement of the water quality assessment framework presented in Section 4. The summaries provided in this section are drawn from interactions with relevant local stakeholders, with whom the ESR Water and Waste team interact on a regular basis for water quality monitoring advice. These stakeholders include council scientists, members of hapū and rūnanga and both commercial and non-productive landowners. All views and responses have been amalgamated and anonymised, unless otherwise advised. These studies provided useful background to the consideration of framework modifications by ESR for councils who are seeking assistance with the next steps for addressing chronically elevated *E. coli* concentrations that exceed recreational water quality standards.

Information about the three case studies, which illustrate the usage of the proposed new framework, the data required, steps to be taken, and possible impacts is provided. Case study sites were chosen from known contaminated sites that included key pollution source categories (human, livestock, wildfowl/feral animal and non-faecal impacted), and where interventions were being implemented or identified. These studies were supplemented with microbial investigation, where necessary.

3.1 CASE STUDY 1 – MULTIPLE LAND USE CATCHMENT

The following case study in a catchment containing multiple land uses on steep hill country was undertaken in collaboration with council scientists who have been partnering with tangata whenua throughout the restoration process.

The stream under investigation (Stream A) was a tributary of a stream that discharges into a harbour estuary. Summer monitoring has identified persistently elevated *E. coli* concentrations in Stream A prompting an in-depth investigation of the catchment by council scientists. These results indicate that water quality does not meet contact recreational water quality standards, and a permanent health warning has been put in place for Stream A, which includes a major swimming attraction. There is also concern that contamination of the estuary may occur from Stream A outputs.

Council scientists initiated a robust investigation into the sources of elevated *E. coli* levels in the catchment of Stream A. The results of multiple years of monitoring and estimations of *E. coli* loadings (concentration plus flow data) have been collated in a council report. Faecal source testing by ESR has identified that the main source of elevated *E. coli* is ruminant with the bovine signature specifically identified in some samples. Secondary faecal signatures from avian species have also been identified at consistently lower levels. This catchment has steep hill country, and therefore, the greater potential for land runoff of contaminants directly into streams highlights the role of first order streams as significant contributors to pollution as discussed in McDowell et al. (2017). There is no irrigation of land in this catchment, therefore, irrigation is not providing a pathway for contamination to enter waterways. It is important to note that most of this water quality monitoring has been undertaken during base flow scenarios, underlining the chronic problem of pollution, and that it is not always related to heavy rainfall initiating land runoff and resuspension of *E. coli* stored in sediments.

Flow-weighted measurements of *E. coli* highlighted that although some waterways reported high *E. coli* concentrations, their actual contribution to the catchment was small due to their lower flows in comparison with two tributaries in the upper catchment of Stream A. This investigation has narrowed down the major sources of diffuse pollution to these two tributaries where there is also significant native bush. This study established the importance of flow gauging for understanding the actual discharge of *E. coli*/second to appreciate the contribution from different tributaries into a waterway and allow targeting of the dominant critical sources.

In discussion with council scientists, ESR is investigating water samples from these upper reaches for selected pathogens and faecal source markers including non-human/non-livestock faecal sources, which will include feral animals such as deer and possum and application of metagenomic assays for microbial community analysis (Figs. 3 and 4).

3.1.1 ACTIONS TAKEN BY COUNCIL INCLUDING MITIGATIONS

- Removal of beef cattle from bush areas.
- Fencing of streams to reduce cattle egress and subsequent direct defecation. Ephemeral streams were targeted for fencing to reduce contamination pathways to main streams.
- Riparian planting has been undertaken along streams in portions of the catchment.
- Swampy sites were identified where there is potential for development of wetlands.
- At the request of the landowner, the council analysed samples from various sites including a groundwater seep (<10 *E. coli*/100 mL), and a waterway within the native bush area but near its edge (range of 200-1100 *E. coli*/100 mL) and deeper within the bush in the upper catchment (approx. 100 *E. coli*/100 mL)) to check for other sources of *E. coli*. These results were included in catchment assessments and council scientists concluded that these sites were not consistently contributing the highest *E. coli* loads to the downstream catchment. Mitigations, therefore, focussed on other tributaries with higher *E. coli* loads.

3.1.2 SUMMARY OF THE MAIN POINTS OF DISCUSSION BETWEEN COUNCIL SCIENTISTS AND ESR

- Investigate potential contamination pathways into streams where land runoff etc. can carry faecal pollution including faecal microbes into the waterways.
- An extensive watering system has been put in place to provide water sources for livestock. ESR is aware that stock water troughs can be a source of faecal contamination runoff to streams. Where stock congregate around a water trough, the splashing of water is likely to cause cattle stock to defecate within that trough area. Therefore, it is important to site troughs away from potential contamination pathways that flow (in)directly into water bodies.
- Check installation of tile drains (recent and historical) in paddocks by asking local farmers and using old drainage maps to look for tile drains in that catchment.
- In consultation with ESR, the council initiated sampling at a headwater site high in the native bush where faecal sources should be non-human/non-livestock. The council also collected water from two sites further downstream of the native bush and above recreational areas. These samples have been analysed by ESR for faecal source markers and selected pathogens. In addition, novel faecal source tracking using bacterial community analysis may be informative of faecal sources from deer and possums which frequent the native bush areas. Local iwi have noted increases in the deer population in the upper catchment.
- ESR and council scientists discussed naturalised *E. coli*, which has been raised by local farmers as a confounding factor. However, the bovine faecal signature is strong in this

waterway, and therefore, naturalised *E. coli* or *Escherichia* species are unlikely to be the issue because in this area naturalised *E. coli* will most likely be derived from bovine faecal pollution. The only time it is suggested to investigate if naturalised *E. coli* or *Escherichia* species are contributors to *E. coli* exceedances is when elevated *E. coli* are identified at a “pristine”, non-anthropogenic impacted site and no additional feral animal/avian faecal sources can be identified.

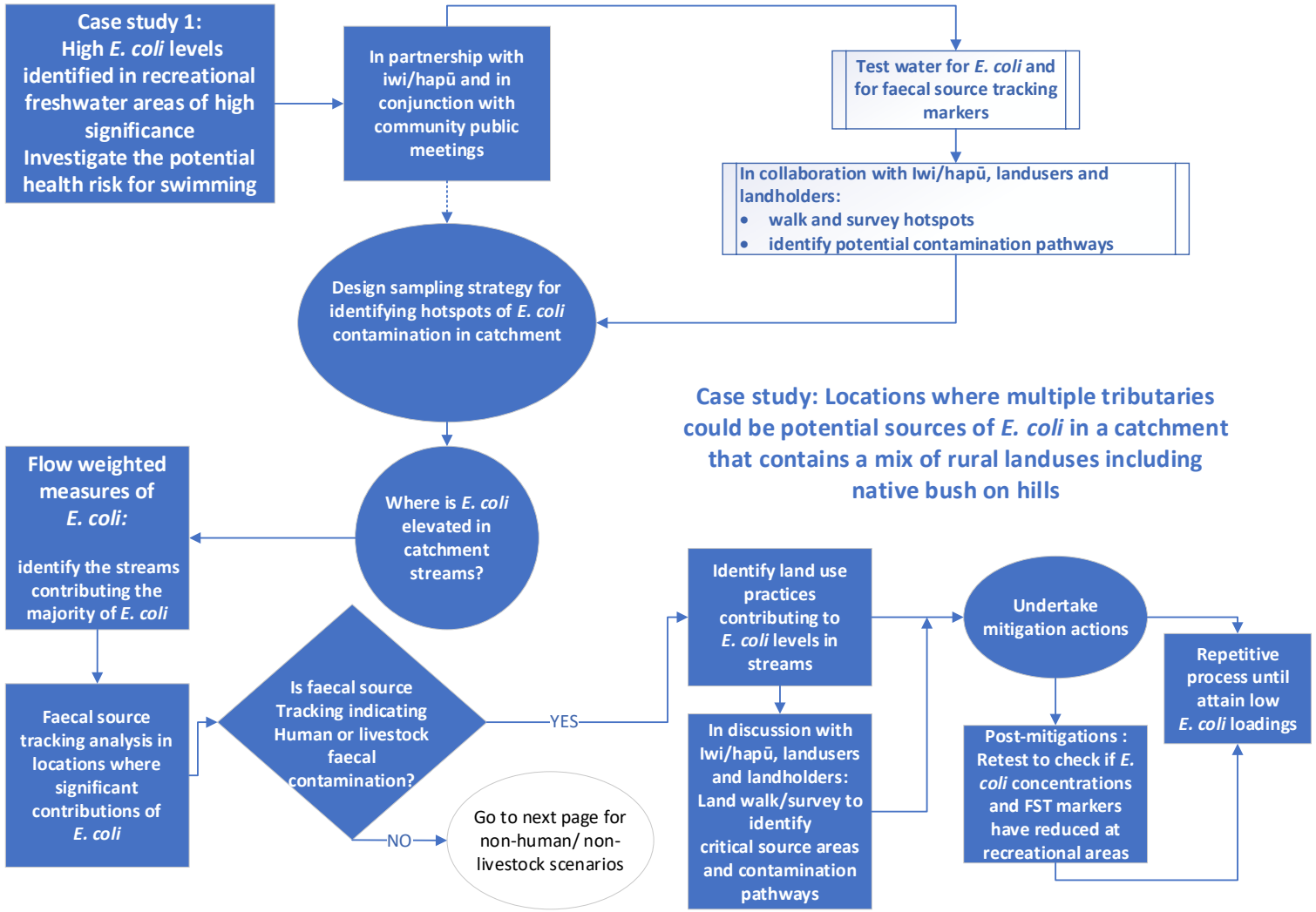

Figure 3 Decision tree for Case Study 1

Decision tree highlighting next steps when chronic levels of *E. coli* are identified in a multiple land use catchment, that includes agriculture, residential septic tanks and areas of native bush.

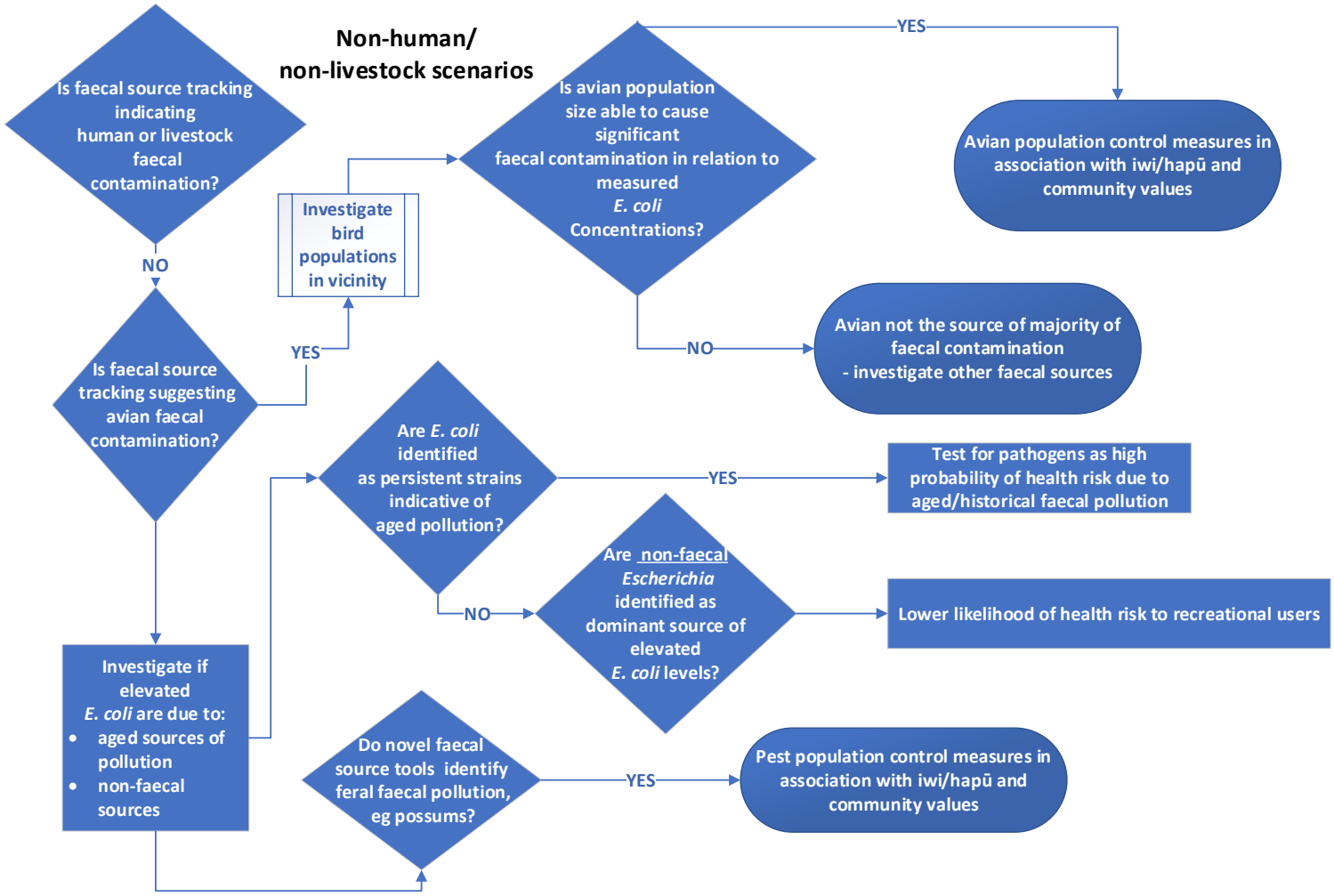

Figure 4 Decision tree for Case Study 1 assessing non-human/non-livestock scenarios

Decision tree highlighting suggestions for additional investigation in cases where neither human nor livestock faecal pollution are identified by faecal source tracking.

3.2 CASE STUDY 2 – ON-FARM STUDIES

This case study of farms represented in Figure 5 is a composite of information drawn from several on-farm studies where the identity of the location and stakeholders is anonymised to protect pro-active, champion farmers and landowners who have opened their land and farming practices up to scrutiny for identification of pathways of faecal contamination. Essential to the process outlined in Figure 5 is the time taken to establish robust relationships between council representatives and their constituent landholders. In particular, the farmers in the area need to have formed a trusted relationship with their council land management advisor.

Community meetings led by local District Council and/or regional councils were held to address the issues of elevated *E. coli* concentrations and its impacts on swimmability at local recreational areas. The councils invited local stakeholders, such as farmers, Dairy/Agricultural Industry interests (for example, Fonterra and Dairy NZ, Federated Farmer representatives), Fish and Game, and Living Waters (a partnership between the Department of Conservation and Fonterra) and all interested residential parties. The community meetings discussed the problem supported by relevant recent scientific data made available in non-scientific language for consideration by all parties. These community meetings discussed the next steps and decided that co-ordinated monitoring sampling plans in the catchments were required. Rūnanga meetings were held between ESR scientists and Māori representing whānau interests in Māori land leased for farming.

The collation of local information from all stakeholders was important to understand the current mitigations in place such as the extent of fencing of streams/drains in the area, riparian planting (including the average width of planting from stream edge), the presence of sediment traps and wetlands. All land uses were categorised and investigated including lifestyle blocks, ponds frequented by wildfowl and non-productive land use where fencing is not required. Targeting both non-agricultural areas and farms within a catchment was essential to maintaining an unbiased view of potential faecal sources. However, Figure 5 concentrates on the on-farm sources for identifying the *E. coli* hotspots but still includes areas in the sampling plan where lifestyle blocks and duck ponds may be sources of contamination. If avian sources or non-livestock sources are identified then this figure directs the reader to Section 4, Figure 9 where specific guidance is provided to investigate potential sources of avian and feral faecal contamination and contributions from naturalised sources of *E. coli*/*Escherichia* species.

A frequent question raised at these community meetings is the contribution of wildfowl populations compared with ruminant (cows and sheep) to the *E. coli* concentrations in streams (Muirhead et al. 2011). In one scenario, high numbers of pūkeko frequent farmland and landholders have voiced concern that they may contribute to *E. coli* concentrations in waterways. Although, pūkeko are targeted by the general wildfowl DNA faecal source markers, it is unknown what types of microbes they carry and whether the *E. coli* concentration in their faeces impacts on water quality issues. This information is known for general wildfowl such as ducks (Moriarty et al. 2011).

The role of wildfowl is a difficult question to answer as the DNA faecal source markers target different bacteria in the faeces of wildfowl compared to the bacteria in livestock faeces. This factor means that the markers for wildfowl and livestock are not directly comparable in terms of estimating quantitative contributions to *E. coli* concentrations. This issue can be addressed, in part, by an intensive temporal sampling programme to establish levels of the two marker types and frequency of detection. On farms with fenced streams, most livestock pollution will be detected as non-fresh/aged sources of land runoff/subsurface transport from land applied effluent and decomposing cowpats. While this type of aged livestock faecal contamination still exports high levels of *E. coli*, the ruminant faecal markers are present in lower concentrations (Devane et al. 2020). These lower levels of aged ruminant faecal markers add another layer of complexity when endeavouring to compare with contributions from avian sources, which

under baseflow conditions, will most likely be derived from fresh faeces deposited directly into a water body.

From community meeting inputs and collective farmer/landholder meetings, potential hotspots of faecal contamination were identified and included duck ponds, dairy farm streams where cow paths to dairy sheds run alongside streams, and unfenced streams where lifestyle blocks or farms carry livestock including beef/cattle and sheep. An intensive sampling programme of daily monitoring over several weeks was developed in some catchments to identify potential hotspots of *E. coli* contamination. The aim of the intensive sampling plan was to monitor for *E. coli* initially and then target selected areas with *E. coli* and quantitative faecal source tracking markers, and potentially a suite of pathogens at identified hotspots. Part of this process required asking farmers to provide a record of all daily farming practices in the areas of interest to allow identification of on-farm practices potentially associated with *E. coli* elevations.

In the long-term, the plans include extending these sampling programmes to different seasons and farming stages e.g., a comparison of over-winter sources and calving/lambing seasons. In the latter stages of the sampling programmes where hotspots are targeted then flow-weighted measures of *E. coli* may be important to ascertain the pathways associated with the dominant sources of *E. coli* so that mitigations can be directed to the biggest contributors. Flow-weighted *E. coli* data may be difficult to acquire where farm drains have low/intermittent flow during the summer season, therefore, evaluations may negate the collection of data on *E. coli* loadings for all seasons.

Important to this process of identifying contamination pathways was the local knowledge of landholders. Environment walk surveys proved to be important for ground truthing as farmers/landholders know about the topography of individual paddocks including variations in slope and hidden/old stream channels and the presence of hidden tile drains. This local knowledge was essential for identifying likely contamination pathways to farm drains/streams and again emphasizes the requirement for well-established relationships based on trust between landholders and council staff/scientists. It also alerts farmers to take topographical features into consideration prior to applying fertilizer or animal effluent and reinforces the concept of runoff potential from hill slopes and soils with high moisture content.

Scientific evidence collected from these types of in-depth surveys will help inform the community stakeholders as to the next steps for targeted mitigation interventions.

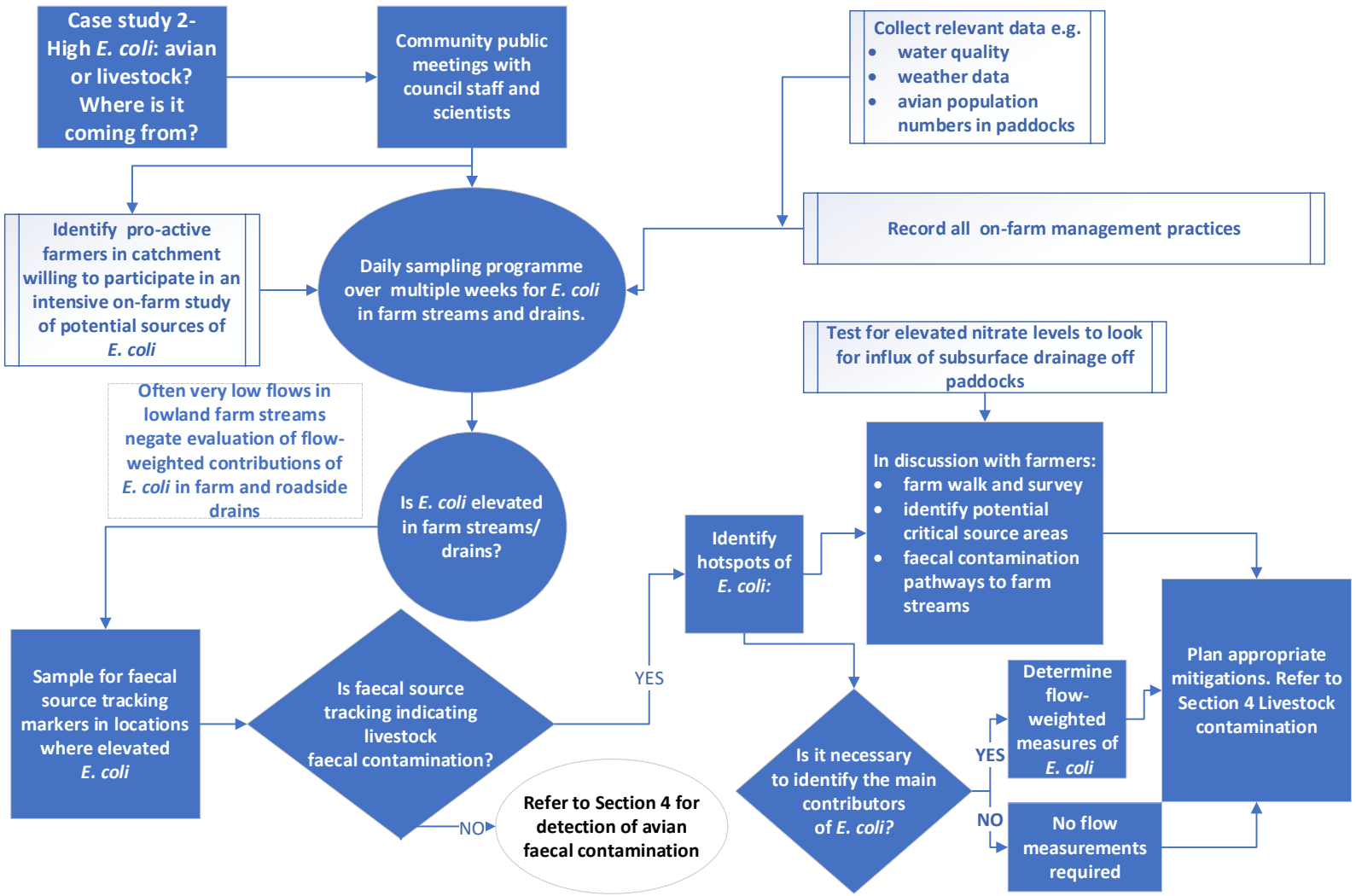

Figure 5 Case Study 2

Decision tree summarising discussions with farmers to identify hotspots of *E. coli* contamination and potential mitigations.

3.3 CASE STUDY 3 – DISTRICT COUNCIL INVESTIGATION

Case Study three is sited within Tasman District Council and represents years of extensive monitoring (1996-present) and investigations by Senior Resource Scientist, Trevor James, to track down intermittent exceedances of enterococci (10% of 234 samples between 2003-2015) at a popular public beach site.

During one of these investigations, a sanitary survey in the summer of 2006-2007, a significant faecal discharge from a residence was identified and repairs undertaken of the household's sewerage system. This remediation resulted in a reduction of the FIB exceedances for the following three years. Subsequently, FIB exceedances have increased to 13% including sporadic transgressions over 1000 enterococci/100 mL. The sampling frequency at this beach was increased to 20/year in every year (as recommended in the guidelines for a popular site with higher risk) and additional sanitary surveys undertaken. On a couple of occasions (the last time being in January 2015, when two consecutive samples were above 140 enterococci/100ml), warning signs were placed at five sites along the beach to discourage recreational activity in the area due to enterococci exceedances in samples collected during that month. After sampling at a total of four sites along the beach over the period, it was hypothesised that the beach water contamination may have originated from a plume associated with a creek. Low flows from this creek, however, may negate a significant contribution to the beach water. Subsequent samples identified an area about 200 metres either side of the creek mouth. There had been no previous warnings of contamination issues identified during water quality monitoring in the preceding months before this event. Furthermore, there was no pattern of exceedances associated with the peak holiday period in the years prior to this January event. The only pattern is that almost all the high results during fine weather are due to samples taken closer to high tide.

In consultation with ESR and council scientists, sampling was undertaken in March 2020 at this beach site and surrounding waterways. Seven locations were sampled on each of three consecutive days at high tide including 15 coastal water and 6 freshwater samples and, included the creek and beach sites discussed above. Marine water samples were analysed for enterococci and *E. coli*, and freshwater samples were analysed for *E. coli*. All samples with elevated FIB were analysed for faecal source markers, with additional testing of selected samples undertaken for analysis of pathogens, and metagenomic bacterial community analysis by next generation sequencing to further inform faecal source tracking. Follow-up assays testing for pathogens detected *Campylobacter jejuni* and *C. coli* in river samples containing ruminant and avian pollution sources. No faecal sources have been identified to explain the source of elevated FIB in the creek and *Campylobacter* was not detected in these creek samples. Exploratory research using bacterial community analysis for faecal source tracking has potentially identified non-recent ruminant faecal sources at the creek, but this finding awaits further validation. Additional investigations may target whether these elevated FIB are due to naturalised sources of FIB persisting in the creek and related to historical faecal inputs to this waterway or whether the river outflow is the main contributor. The pathway of this investigation is now including the decision tree in Section 4 that is targeting non-human, non-livestock sources of contamination to investigate these potential historical sources of naturalised FIB. Additionally, the follow-up investigation may include flow-weighted FIB measurements in relation to the creek, and also the river where faecal sources were identified.

4. REFINEMENT OF THE WATER QUALITY FRAMEWORK

The water quality framework presented in the Leonard et al. (2020) QMRA pilot commissioned by the Ministry for the Environment is at the concept stage and requires refinement to provide specific guidance to councils and communities tasked with remediation of freshwater bodies affected by faecal pollution. In this section, information gained from community/council consultation and from the case studies presented in Sections 2 and 3 is used to refine the water quality framework to provide realistic and quality solutions for water contamination scenarios. The refined framework is designed to simplify the assessment of health risk and expedite action. Adoption of such a framework can be expected to have an immediate impact on recreational water quality management by providing specific advice on what should be done and how to do it, when *E. coli* transgressions are encountered. Additionally, this framework has the advantage of being similar to the requirements for source water protection for drinking water and, is therefore, timely for councils and Taumata Arowai, the new water services regulator for Aotearoa NZ.

This section will be divided based on the three steps of the framework:

1. Water quality monitoring
2. Characterisation of faecal sources
3. Site or source-specific health risk assessments including QMRA

Decision trees will be presented for each section illustrating the specific actions to be taken at each step.

4.1 STEP 1 – WATER QUALITY MONITORING

This step is based on the requirements for monitoring freshwater sites for *E. coli* as outlined in the NPS-FM (2020) (refer Table 1 and 2 in the Appendix). Primary contact sites (those used for swimming or other recreational activities) must be monitored weekly during the bathing season. If a single sample taken during this time has between 260-540 *E. coli*/100 mL the council must increase to daily sampling and try to identify and mitigate the source of contamination. If a single sample has over 540 *E. coli*/100 mL the site is no longer suitable for recreational use and must be sign-posted accordingly. It will remain unsuitable until further testing indicates concentrations have dropped below 540 *E. coli*/100 mL.

In conjunction with monitoring *E. coli* concentrations, it is also important to examine other environmental parameters indicative of water quality. Careful consideration should be given to which additional environmental parameters are important for monitoring in concert with *E. coli*. The types of environmental parameters used for water quality assessment will depend on the catchment under investigation. Important parameters could include dissolved oxygen, rainfall, water temperature, flow rate (if gauging stations present), sediment coverage, macrophyte presence (plants/weeds in the water) or the macroinvertebrate community index (MCI, where polluted rivers have a low MCI).

When *E. coli* concentrations exceeding 260 *E. coli*/100 mL are detected there are a few factors that need to be considered prior to advancing to Step 2 of the framework. These factors relate

to whether additional sampling is required to assess the dynamics of the contamination and include:

- Is the investigation triggered by a single exceedance of *E. coli* levels or does it rely on 95th percentile data?
- Were the samples significantly influenced by wet weather conditions?
    - Is there sufficient data to understand the influence of seasonal variations and wet versus base/dry flow scenarios? What is the influence of these variations on average *E. coli* concentrations versus peak concentrations?
- Are there potential seasonal influences related to farming practices such as: de-stocking during winter, pugging (trampling of pasture by livestock during winter), calving/lambing in spring (known to produce higher *E. coli* concentrations)
- Has resuspension of sediments occurred prior to or during sampling, which would increase *E. coli* concentrations?

The recommendations of this step are summarised in Fig. 6. When sufficient samples have been collected to make informed decisions on chronically elevated levels of *E. coli*, proceed to Step 2 of the framework.

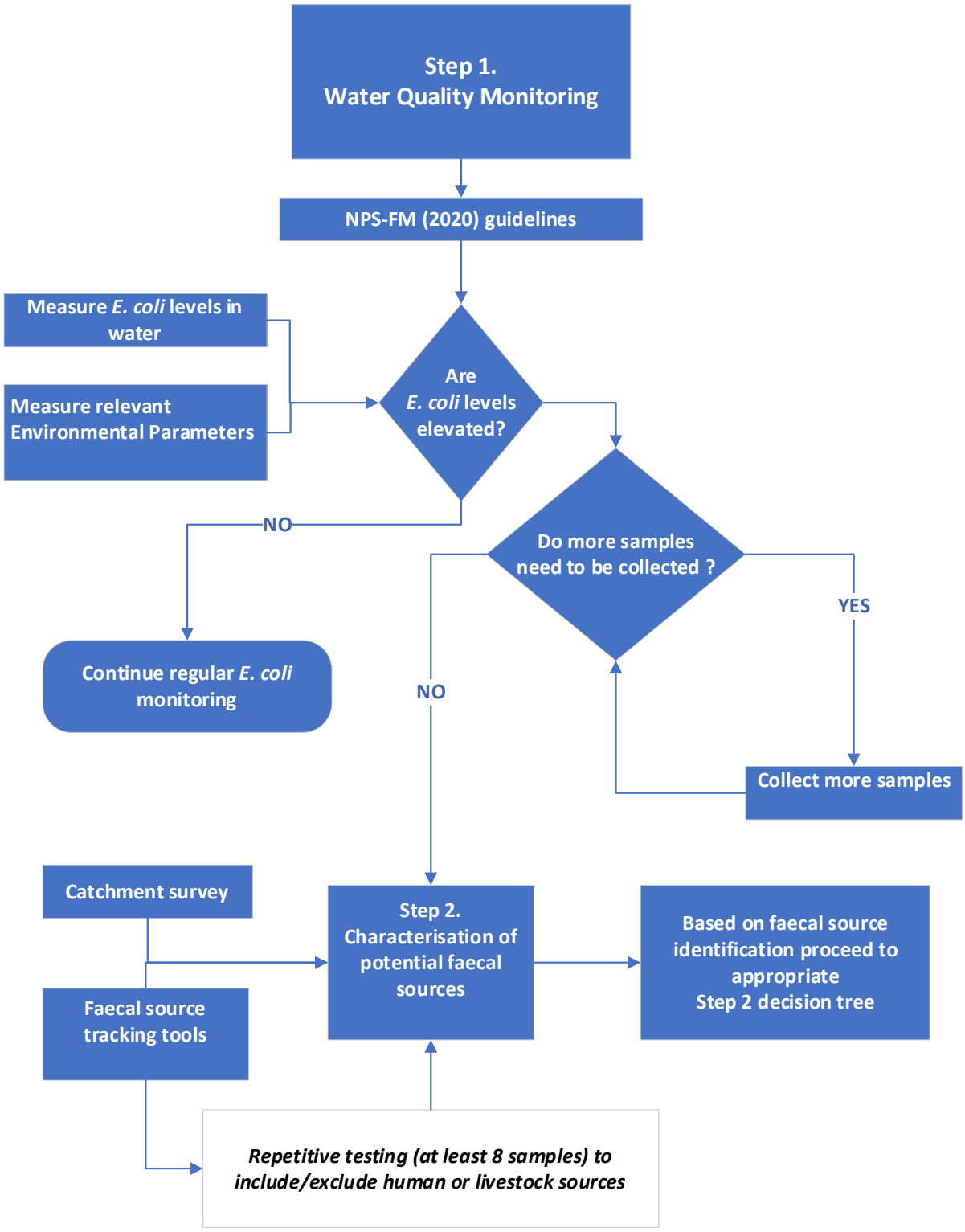

Figure 6 Decision tree outlining initial steps in the refined water quality framework

4.2 STEP 2 – CHARACTERISATION OF FAECAL SOURCES

This step involves the characterisation of the source of the faecal contamination event(s) contributing to the elevated *E. coli* levels and consists of two major actions: catchment surveys and faecal source tracking (FST), summarised in Figs. 6-9.

4.2.1 Catchment surveys

Catchment surveys assess the likelihood of features associated with a given water catchment affecting water quality. Important considerations include topography (e.g., the effect of slope on surface runoff); stream order (how many tributaries feed into the contaminated waterway); land uses within the catchment; local resource consents; sanitary surveys, which are visual inspections (e.g., environment/farm walks) of the local environment to assess potential sources of faecal contamination (Kinzelman et al. 2012); and assessment of the cultural health index by local hapū. Surveys may include information gained from assessments using the River Environment Classification (refer NPS-FM (2020) Table 26).

4.2.2 Faecal source tracking overview

Faecal source tracking (FST) involves using molecular tools to identify the likely sources of faecal contamination by screening contaminated water for markers specific for certain faecal sources e.g., human, ruminant, avian. FST may utilise one or more of the following tools (reviewed in Devane et al 2018):

- **Quantitative Polymerase Chain Reaction (qPCR) markers**

These are faecal source markers that target the DNA of microbes that inhabit the gut of a particular animal species/group and are associated with (but not specific to) that type of animal host. Multiple qPCR markers can be tested on DNA extracted from water and sediment and testing can be retrospective on stored DNA if new potential sources are identified at a later stage. The main qPCR markers available for faecal source tracking include:

    - Human markers: two or more markers that target different microbes specifically present in human faecal pollution.
    - A ruminant marker that targets cows, sheep, deer and goats.
    - Cow and sheep specific markers, used where levels of ruminant marker are identified at >>1000 copies/100 mL (Devane et al. 2020).
    - Avian markers including a general wildfowl marker known to target ducks, Canada geese, seagulls, black swans and pūkeko. There is also a duck-specific marker.
    - Dog marker.

- **Faecal sterols**

Faecal sterols, such as cholesterol, are particularly useful for tracking non-fresh or historical faecal sources in water. In addition, they are very stable in (benthic) sediments and soils. In FST, ten different sterols including their breakdown products (stanols) are analysed. The ratios between these ten sterol/stanols is then used to build a sterol fingerprint specific to either humans, herbivores (e.g., cows and sheep) or avian species.

- **Fluorescent whitening agents (FWA)**

FWA are commonly used in washing powders. As the grey water from washing machines is generally mixed in with wastewater from toilets, FWA can be used as an indicator of human faecal contamination. Assessment of FWA is particularly good for low volume waterways such as stormwater drains.

- **Next generation sequencing metagenomic tools**

These FST tools are used to identify the microbial community present in a water sample, which is then compared to the microbial communities present in the faeces of different animal species. These metagenomic tools are still under development but hold great potential for the future and can be used in conjunction with qPCR markers as both utilise the DNA extract obtained from the contaminated water source. DNA extracts can be stably stored for restrospective analyses as required. This metagenomic approach is being investigated for its ability to distinguish additional host species such as horses and feral animals. If successful, this may allow the development of host-specific faecal signatures in a more timely and cost-effective manner than the qPCR markers, which each require identification of specific microbes unique to the gut of an animal host followed by validation against multiple non-host faecal samples.

When characterising the faecal source(s) present in a waterbody it is important to base decisions on multiple water samples and to collect samples under the same conditions where *E. coli* concentrations have been elevated in past sampling trips. Repetitive sampling at different sites within a location where chronic *E. coli* levels are detected and at different times/flow rates/weather conditions is important to confirm the inclusion/exclusion of livestock or human contamination as faecal sources. It is recommended that a minimum of eight samples per location are tested before undertaking remediation (Meijer, 2012). This multiple sampling regime avoids missing critical sources (human and livestock) and maximises the cost-effectiveness of mitigations.

4.2.3 Faecal source tracking where human sources are identified

When human faecal contamination alone or in conjunction with other sources is detected by FST analysis, it represents the highest public health risk, and therefore, the highest priority for mitigation as outlined in Fig. 7. This will require implementation of catchment surveys, including a sanitary survey to identify potential contamination sources/pathways. Tracer techniques such as dyes, synthetic tracer DNA markers and in-situ cameras for drains and pipes can be utilised to identify potential faecal sources and sewer pipe breakages (Devane et al. 2018, Pang et al. 2017, Water New Zealand, 2019). In rural areas where human faecal contamination is detected sanitary surveys will include identifying local resource consents for on-site wastewater management systems (OWMS) with follow-up inspections of potential contamination tanks and their disposal fields.

An ESR review of tikanga Māori frameworks for wastewater management systems acknowledged that Māori had well-established procedures and protocols for the management of all types of waste, including sewage sludge (Feltham, 2021). Furthermore, contemporary Māori views have been shaped by colonisation and have a heightened focus on protection of water and the reversal of damage compared with traditional views. The review recommended that professionals working in the waste management sector should prioritise early, effective engagement with local iwi and/or hapū. This interaction should be led from a tikanga Māori

perspective and non-Māori stakeholders should familiarise themselves with the correct protocols.

Where faecal contamination is derived from treated wastewater or non-fresh human faecal inputs such as OWMS it is important to recognise that *E. coli* concentrations may not be as high as in recent/fresh source inputs to a surface water. These lower *E. coli* concentrations, however, can still pose significant health risks due to pathogens such as viruses and protozoa (e.g., *Giardia*) that can persist in aquatic environments, including in sediments (Devane et al. 2014, Garcia-Aljaro et al. 2017, Mackowiak et al. 2018). Resuspension of sediments, therefore, should be considered when evaluating the health risk associated with recreational activity in a waterway.

The impact of non-fresh faecal sources on the concentration of faecal source markers in receiving environments is under investigation (Boehm et al. 2018, Boehm and Soller 2020, Boehm et al. 2015, Brown et al. 2017, Schoen et al. 2020). In the future, faecal source markers may be incorporated into the risk characterisation step of the QMRA discussed in Section 4.3 Step 3. Current research is investigating the different concentrations of human faecal source markers in water bodies associated with inputs of raw sewage versus treated human effluent and scenarios where there are mixed sources such as from human and birds at beaches (Boehm and Soller 2020). This may be particularly important in situations where mixed sources are encountered as noted in the Leonard et al. (2020) QMRA Pilot study, where all river sites contained avian pollution often in association with human and/or livestock contamination.

Contrasting rates of decay between pathogens, indicator bacteria and faecal source markers are particularly evident with viral and protozoan pathogens having longer degradation times in treated effluent and aquatic environments. For example, Boehm et al. (2018) performed a meta-analysis of decay rate constants measured for pathogenic bacteria, protozoa and enteric viruses to account for persistence of these microorganisms in surface waters containing aged sewage. The U.S. Environmental Protection Agency has set a threshold of 3 illnesses/100 swimmers as their level of risk for swimmers. Boehm et al. (2018) observed that the health risk increases with a fixed concentration of the human qPCR faecal source marker HF183 as the faecal source ages. The reason for the difference in risk evaluation is due to the faster decay rate of the human source marker compared with the pathogens, norovirus and protozoa. The age of a sewage contamination event is often unknown, and in some circumstances, inputs are continuous due to a broken sewerage system and will represent contamination of mixed age as occurred during the Christchurch/Ōtautahi earthquakes (Devane et al. 2019, Devane et al. 2014). Therefore, Boehm et al. (2018) present thresholds that take into account the uncertainly of contamination age and concluded based on updated decay rates, the human source marker HF183 would need to be identified in the surface water at a concentration of 4100 copies/100 mL to exceed the risk threshold for swimmers.

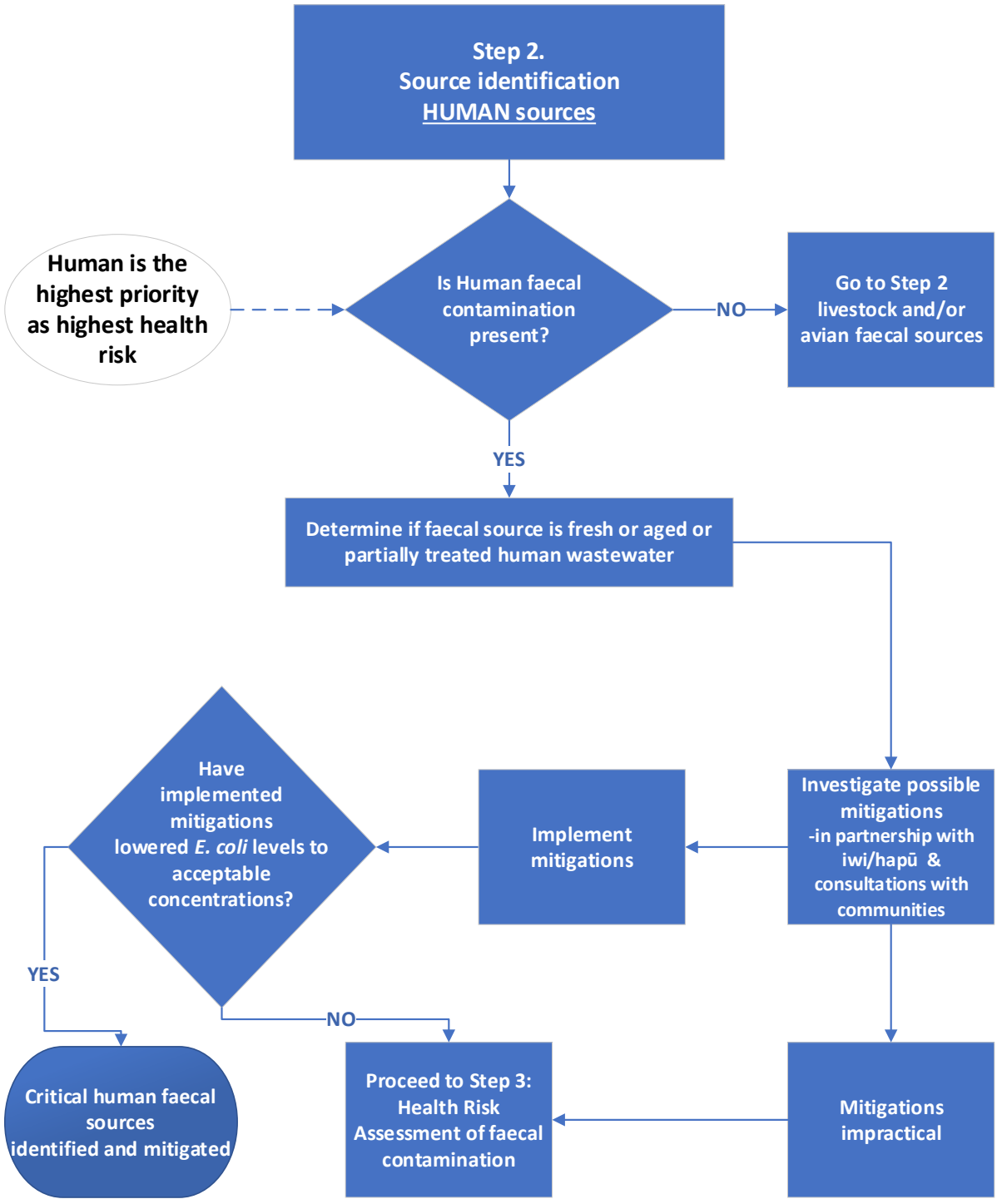

Figure 7 Decision tree for cases where human faecal contamination is identified.

4.2.4 Faecal source tracking where livestock sources are identified

Faecal contamination derived from agricultural sources such as livestock can be either from direct inputs to a waterbody or from diffuse sources. Direct inputs include faecal deposition directly into a stream where livestock have access to the waterway. Cattle are likely to defecate during river crossings, whereas sheep tend to avoid streams (McColl and Gibson 1979, McDowell et al. 2017). On dairy farms, however, this problem of direct livestock access to waterbodies has been widely mitigated by fencing streams and building culverts across

streams for the daily treks of cows to the milking shed. Diffuse pollution from surface run-off and tile/mole-pipe drains are well-recognised contamination pathways for *E. coli* from faecal deposition on paddocks/tracks and land-applied animal effluent (Devane et al. 2020a, Monaghan and Smith 2004, Monaghan et al. 2016). Fig. 8 outlines specific actions for council scientists to undertake where faecal source analysis of a waterbody has identified livestock as a major source of contamination, either as a single source or in conjunction with mixed sources. Prior to investigating potential mitigations on-farm, it is important to identify critical sources or contamination pathways that are contributing to *E. coli* measurements.

Specific guidance for identifying critical sources or contamination pathways is provided below:

- **Flow-weighted *E. coli* measurements**

Where there is convergence of multiple waterways, it may be important to compare flow-weighted *E. coli* measurements to determine which streams contribute the highest *E. coli* loads. Prioritisation of highest load contributors for targeted mitigation can maximise the resulting impact and reduce cost. A NIWA report for a regional council illustrates the value of including flow-weighted *E. coli* measurements to assess which tributaries are contributing the highest *E. coli* loads (NIWA, 2019). However, roadside drains and small streams/drains within a farm may contain very low flows, particularly during summer conditions (e.g., <0.2 metres/second), making it impractical for flow gauging and requiring time-consuming manual collection of data when assessing individual contributors within a farm.

- **Localised land mapping for agricultural point sources**

This involves detailed mapping of the agricultural land surrounding contaminated waterways to try and identify potential point sources of contamination. Considerations include:

  – Fencing of waterways, including information on the distance between the fence and waterway
  – Presence of riparian planting, including the width of planting from waterway
  – Local resource consents for effluent ponds, OWMS (septic tanks) etc.
  – Geology of soils, land cover, topography

Common sources or pathways for diffuse pollution include:

  – Leaking effluent ponds/unintended pond discharges
  – Effluent land application
  – Water troughs where cattle congregate and defecate
  – Local topography e.g., hill slopes increase run-off
  – Topography within a paddock where uneven slopes facilitate runoff and/or ponding
  – Subsurface flow e.g., tile drains
  – Shallow groundwater flow
  – Stock holding areas
  – Soil pugging (trampling) by livestock and dairy shed tracks alongside waterways

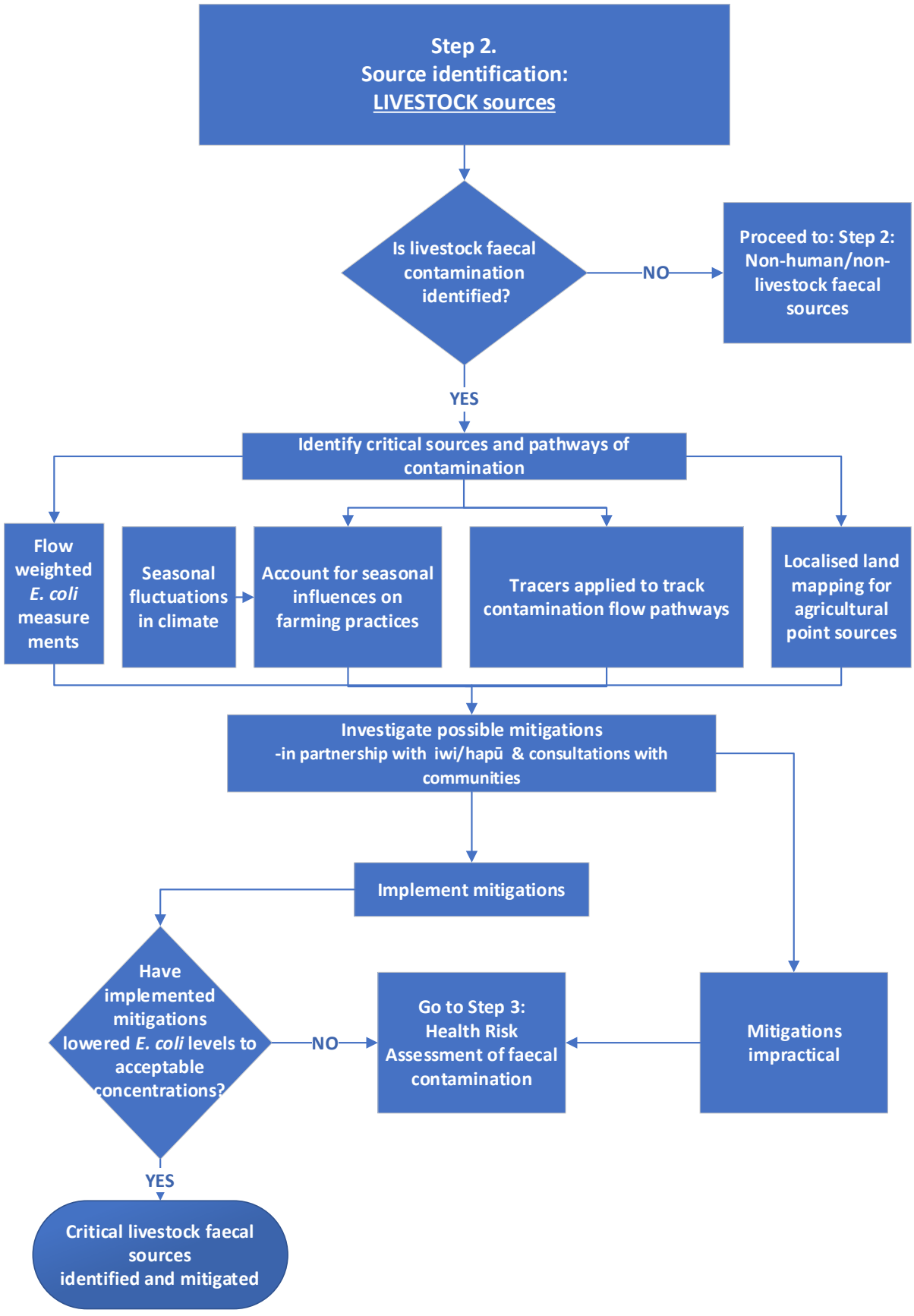

Figure 8 Decision tree for cases where livestock faecal contamination is identified.

- **Seasonal variations**

An important aspect of measuring diffuse pollution from agricultural settings is the sporadic nature of the pollution inputs (Muirhead et al. 2011). Seasonal patterns in both weather and farming practices, such as lambing/calving or de-stocking during winter, can have substantial impacts on *E. coli* loads in waterways and should be taken into account during scoping of contamination pathways. To obtain a representative evaluation of pollution, multiple samples need to be collected in a spatial and temporal manner within an area taking into account seasonal climate patterns and farm management practices.

- **Tracers to track contamination flow pathways**

Where potential contamination pathways have been identified, a range of tracers can be used on-farm to assess the potential contribution of these pathways to the waterway. These include:

  – Temporal measurement of nitrate fluxes at identified critical inputs to the waterway (e.g., tile drain outlets)

  – Dyes and synthetic DNA tracers (Pang et al. 2017). These require resource consent from the local council.

  – qPCR markers. Note that ruminant, sheep- and cow-specific faecal source markers degrade in the environment more quickly than *E. coli*. As such, lower levels of ruminant marker compared with *E. coli* or avian markers must be viewed in context with farm management practices. For example, diffuse pollution sources that result in low levels of ruminant faecal source markers due to non-recent faecal inputs include tile drainage, surface runoff from cowpats and land applied effluent. When sheep and cow specific qPCR markers are identified in a waterway it suggests recent faecal inputs and will be in association with higher levels of the ruminant marker (>>1,000 copies/100 mL) (Devane et al. 2020a). When only the ruminant qPCR marker is identified then diffuse/non-recent sources should be considered as the source.

  – If sources are diffuse or historical inputs, analysis of sediments by faecal sterols and/or FST qPCR markers may reveal higher levels of faecal contamination compared with water samples.

- **Scoping/identification of potential mitigations**

When identifying potential mitigations, it is important to differentiate between point and diffuse contamination sources. Targeting of point sources should be considered first as these are more readily identified and remediation may have a bigger impact on reducing contamination. For example, the prevention of direct access of livestock to water bodies may be achieved by fencing of water bodies and building bridges across streams to connect dairy tracks. The direct discharges of dairy shed runoff and effluent into waterways requires mitigations that may address issues of dairy effluent storage, such as increasing effluent pond capability.

Targeting diffuse pollution sources, such as surface and sub-surface runoff, requires elimination of critical contamination pathways identified using tracking techniques outlined above. It also necessitates an understanding of the sediment sources in farm streams/drains, as sediments tend to harbour faecal microbes including *E. coli* and pathogens. Erosion control measures along stream banks, including re-battering of banks and riparian planting to minimise stock damage to bank edges, could be implemented. However, in-stream sediment traps that slow the stream flow and increase the deposition of sediment carrying phosphate and attached faecal microbes may be an efficient, lower cost mitigation. Trials of wood chip filters fitted to the end of tile drains is also underway to identify benefits for nitrate reduction and potential impacts on *E. coli* concentrations. However, subsurface flows remain problematic for mitigation measures. A significant diffuse source of faecal contamination is application of animal effluent to land. Communication of best practices to farmers is required

to increase understanding of critical flow paths, particularly on occasions where application exceeds the moisture capacity of the soil (Muirhead et al. 2011) and paddock slopes allow for surface runoff into waterways.

It is important to consider whether there are any possible negative side-effects for a given mitigation. Examples of unintended side-effects include growth of persistent *E. coli* in sediment traps if the traps are not regularly cleaned out. It is also important to dispose of the sediment from the trap on to land where there is reduced opportunity for *E. coli* or other pollutants to flow back into the waterway. This means siting disposal on non-sloping paddocks and applying in a thin layer that maximises opportunity for sunlight inactivation of faecal microbes and evaporation to reduce water availability, which supports microbial growth.

Mitigations may require input from communities and affected iwi/hapū with recognition of Māori mātauranga in relation to local waterways and mahinga kai and places of significance. In addition, iwi/hapū may be leaseholders of farmed land, and farmer interactions with Māori values and tikanga is important as Māori re-gain their rightful place in Aotearoa NZ society. The uptake of indicators for identifying faecal contamination is on the increase by iwi/hapū, who see this accumulated data as a valuable resource for communicating the issues of water quality within their community and to the wider nation.

During this consultation process it was recognised that champion farmers and landholders who identify and implement mitigations are important contributors to the community evaluation of remediation steps. They can lead the way to improved pollution outcomes by modelling appropriate behaviour to fellow landholders. However, as outlined in Case Study 2, the critical step in developing champion farmers within a community is the establishment of a trusted relationship between the farmer and council representatives, all working in liaison with farm industry representatives and the local iwi/hapū.

When repeated trialling of mitigations to reduce faecal contamination as measured by *E. coli* concentration and faecal source markers is not effective, or only partially effective then the requirement is to proceed to Step 3 of the framework to assess the health risk posed by the non-compliant location. Furthermore, Muirhead et al. (2011) noted that when all practicable best farming practices have been implemented but *E. coli* concentrations in-stream are still above the NPS-FM guidelines, then an evaluation of the contribution from avian faecal sources may be a valid next step as outlined below.

4.2.5 Faecal source tracking for non-human and non-livestock sources

In cases where both human and livestock sources of faecal contamination have been ruled out, thorough visual assessments of the catchment including environment walks are essential for identification of potential contamination sources (refer Fig. 9).

- **Avian sources of contamination identified by FST**

Where faecal source tracking tools identify avian sources as a major contributor to faecal pollution at the contaminated site, this can represent a health risk but generally implies a lower likelihood of illness compared to human or cattle (dairy and beef cattle) derived faecal contamination (Devane and Gilpin 2015, Soller et al. 2010, Soller et al. 2014).

Quantitative faecal source tracking measures such as qPCR using avian faecal source marker(s) will be valuable for understanding the level of impact of avian sources on *E. coli* concentrations. Assessment of the avian contribution based on the quantitative markers will require multiple samples over time as avian faecal inputs will be direct inputs to the waterways when measured under baseflow conditions and could represent high or low levels depending on how recent the faecal deposition. These sporadic but direct inputs from avian sources are in contrast to the often-diffuse pollution sources from livestock, where fencing and bridges limit direct access to streams. Lower levels of the ruminant qPCR marker (and non-detection of sheep and cow specific qPCR markers) compared with *E. coli* levels or avian markers may

indicate ruminant inputs are diffuse/non-fresh (Devane et al. 2020a) rather than lower than avian contributions.

It is important to identify the likely candidates contributing to the identified avian pollution to differentiate between inputs from non-indigenous wildfowl and indigenous bird species. Careful evaluation of candidate bird numbers by collation of local observations will help determine if the bird populations are likely to be the source of the elevated *E. coli* concentrations. These factors may impact on management decisions taken by iwi/hapū and community groups who consider some birds as taonga, while other groups may place recreational value on game birds or be sensitive to any bird population control measures.

- **No avian source of contamination identified by FST**

Where FST has not identified an avian faecal contamination source, faecal sterols and qPCR source markers can be used to determine if there is any contribution from non-livestock animal sources including feral deer, goats, and possums. Where the ruminant qPCR marker is identified in native bush/forest areas then surveys and environment walks must be undertaken to exclude wild cattle/sheep inhabiting these areas. If surveys do not suggest such agricultural faecal sources then the ruminant qPCR marker may indicate feral ruminants such as wild deer and goats, although there is currently no specific marker for confirmation of these two animal species. qPCR and faecal sterol markers are available to test for possum faecal pollution (Devane et al. 2013, Gilpin et al. 2012). In addition, aquatic animals including fish have been identified as sources of *E. coli* in aquatic environments (Coxon et al. 2019, Frick et al. 2018).

- **No faecal sources identified by the current FST toolbox**

Non-detection of faecal sources may signal that the current toolbox does not contain a suitable marker to identify the source of faecal *E. coli*. Additional tools are required for host-specific markers relevant to the Aotearoa NZ environment including indigenous avian species and feral animals. Discussions with council scientists in Section 2 provided a list of species of interest that were considered important additions to the faecal source tracking toolbox. The use of next-generation sequencing metagenomic tools that target host-specific microbial communities may be promising for determining the contributions from non-livestock animals.

There is growing evidence for contributions from naturalised sources of *E. coli* and/or other *Escherichia* spp. to measured *E. coli* concentrations. When the current suite of faecal source tracking tools does not identify a potential source for the elevated *E. coli* then naturalised sources should be considered. Some naturalised *E. coli* may indicate a non-recent/non-fresh source of faecal contamination and should be given a high priority from a public health risk perspective. Analysis of these sources is beyond the scope of this document and readers are referred to the review of Devane et al. (2020b) for an explanation of the different *Escherichia* spp. that may confound water quality monitoring tests such as Colilert.

In brief, there are two types of naturalised *Escherichia* that can be identified by *E. coli*-based water monitoring tests:

1. True *E. coli*

This category represents *E. coli* that are detected in waters with non-fresh/aged sources of faecal material. When the contamination has been released into a waterbody several days (>3) prior to detection, some *E. coli* subtypes, especially those belonging to phylogroups B1 and B2, are able to persist in the aquatic environment. Although they may be identified at lower levels and in the absence of faecal markers, these persistent faecal *E. coli* may still be associated with persistent pathogens, and as such represent a health risk.

2. Non-*E. coli* / *Escherichia* spp.

Microbes in this category do not belong to the species *E. coli* but are phenotypically the same as *E. coli* and are identified by current water quality methods used to measure *E. coli* (e.g., Colilert). Investigations are underway to explore the relevance of these *Escherichia* species. However, they are currently thought to infrequently inhabit the intestines of mammals and humans, and therefore, their identification in water may represent a non-faecal input of *Escherichia*.

If naturalised *Escherichia* clades are identified as the dominant/sole source of elevated *E. coli* levels, then this exceedance may represent a lower likelihood of health risk to recreational users of the target water body. A threshold for *E. coli* monitoring data may need to be established for a location where high percentages of cryptic *Escherichia* have been identified as contributing to the *E. coli* exceedance (Table 7, Envirolink Report Devane 2019). Establishment of this threshold for contributions from naturalised cryptic *Escherichia* would require multiple sampling events, which account for seasonal effects. Routine monitoring of this water body would be required to detect spikes in faecal *E. coli* above the threshold, with appropriate tools such as faecal source tracking used to evaluate sources and monitor health risks.

It is important to recognise that these naturalised sources of *E. coli*/*Escherichia* species should only be investigated in circumstances **where faecal sources have not been identified** as the source of elevated *E. coli* levels.

- **Scoping/identification of potential mitigations**

Consideration of potential mitigations first requires wide consultation with all affected community groups including iwi/hapū to gain an understanding of all relevant factors that may impact a proposed remediation plan.

Where avian or feral animals are identified as major contributors to elevated *E. coli* concentrations that are of concern for recreational water quality then consultations with iwi/hapū and community groups are of paramount importance to ascertain the Māori and community values placed on such animals. Any proposed mitigations will require thorough investigation of all value systems within the community and may require social systems expertise to gain consensus for appropriate actions.

It is important to consider whether there will be any negative side-effects for a particular mitigation. An example of an unintended side-effect, is where dogs are used to disrupt wildfowl populations from river beaches but also disturb the nests of rare indigenous avian species. Effective mitigations for faecal inputs from avian and/or feral animals will follow an iterative process as outlined for livestock sources, with implementation of the mitigation(s), retesting for reductions in *E. coli* concentrations and faecal source markers, then repeating the process until all major source contributors are remediated.

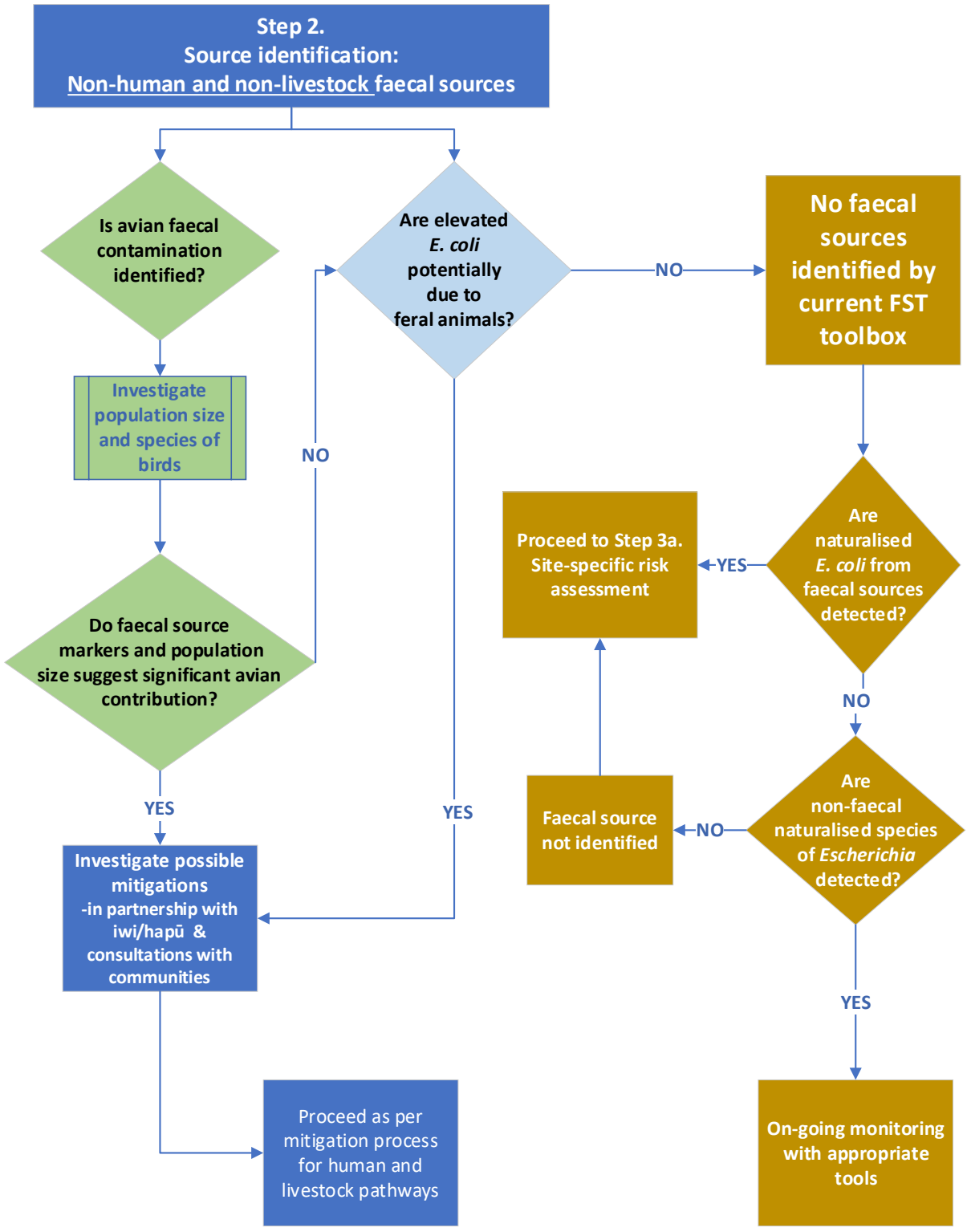

Figure 9 Decision tree for cases where contamination is non-attributable to human or livestock sources

4.3 STEP 3 – HEALTH RISK ASSESSMENT FOR UNMITIGATED FAECAL CONTAMINATION SCENARIOS

This step of the framework is initiated when mitigations are either impractical to implement or are ineffective or the faecal source has not been identified. There are a range of possible reasons for mitigations not being implemented, including financial constraints, timing delays due to infrastructure issues, or community decisions based on Mātauranga Māori and/or community values. In some circumstances, despite repeated trialling of different mitigations the observed reduction in *E. coli* levels and faecal source markers may still be insufficient and require council scientists to conduct health risk assessments.

Two types of risk assessment can be employed at Step 3, dependent on whether the faecal source(s) of contamination have been identified at Step 2. These are summarised below:

4.3.1 Step 3a – Site-specific assessment and QMRA

This step outlines site-specific risk assessments to be undertaken when the source of pollution at a location with chronically elevated *E. coli* levels is unknown. Lack of source identification can be due to a range of factors, such as lack of a marker or method in the FST toolbox for identification of that particular animal/bird source. Elevated *E. coli* concentrations could also be due to naturalised sources of *E. coli*/*Escherichia*. It is important to determine if the *E. coli* detected is derived from faecal material or from *E. coli*-like bacteria that naturally inhabit a particular aquatic environment. In the case of non-recent/non-fresh pollution, the faecal source markers may no longer be associated with the persistent *E. coli* in the water due to degradation of those markers, but the *E. coli* present still indicates past faecal contamination.

Under this step, additional investigations are required to identify the cause of the elevated *E. coli* concentrations and establish if these elevated levels are indicative of a potential health risk from pathogens associated with faecal material. These investigations may include re-sampling of the target environment, supplemented by re-analysis of stored DNA extractions from previously sampled water. Additional analyses using the extended faecal source toolbox may include:

- **Site-specific pathogen detection**

  An essential step used to identify the types of pathogens associated with the contaminated water body when the source of contamination cannot be identified. It may be of value to sample from both water and sediment in this aquatic environment as sediments are known to harbour persistent pathogens such as the protozoan, *Giardia* (Devane et al. 2014).

- **Additional faecal markers for cryptic sources**

  This may be required at locations where the FST toolbox does not identify a source for the elevated *E. coli*. The current suite of faecal source tools employed for tracking contamination detect pollution from human, livestock, ruminants (cows, sheep, deer and goats) and common wildfowl species (ducks, Canada geese, seagulls and black swans). Additional faecal markers may need to be employed where available, e.g., possum, or research directed to identifying and validating new host markers. One potential method being investigated to identify uncharacterised faecal sources is microbial community analysis where the microbes present in a water sample are compared with and attributed to the microbial communities present in faecal sources from different animal species.

- **Microbial community analysis by metagenomic assays**

  This can be employed retrospectively on stored DNA extracts from contaminated water samples to investigate microbial communities associated with different faecal sources including feral animals and indigenous avian species.

- **Naturalised sources of *E. coli*/*Escherichia***

  This may be investigated in circumstances where both the catchment surveys and faecal source analysis do not suggest contamination from human, livestock or avian species. If the elevated *E. coli* levels detected by water quality methods such as Colilert are found to be due to naturalised *E. coli* derived from non-recent/non-fresh faecal sources then this contamination must be given high priority from a public health risk perspective (refer to Step 4.2.5).

Information gathered from site-specific assessments, including identification of cryptic sources, could then be incorporated into a QMRA investigation for that location, as will be outlined for Step 3b below.

4.3.2 Step 3b – Source-specific QMRA

Where a faecal contamination source(s) is identified but unable to be mitigated, a source-specific Quantitative Microbial Risk Assessment (QMRA) can be undertaken as outlined in previous ESR reports (Horn et al. 2018, Nokes et al. 2017). The QMRA will provide information on the public health risk attributed to pathogens from the water body under consideration. The QMRA is one part of the local water quality knowledge that needs to be considered alongside the other attributes and guidance in the NPS-FM (2020). Collation of all information will enable councils and communities to make informed decisions about what is an acceptable risk. The actions required to ameliorate that risk will be region/location dependent and decisions should be made in partnership with iwi/hapū. Public consultations will enable communities to take ownership of the values important to the local community and iwi/hapū. Outcomes from these investigations may lead to communities deciding that a water body is unsuitable for all recreational activities and mahinga kai and this outcome would require appropriate signage to inform the public of the health risks. Other possibilities may be a restriction on primary contact activities, mahinga kai and fishing, while boating/rowing may be acceptable.

A public health QMRA considers the four steps outlined below:

- **Hazard Identification**

  This step identifies which pathogens are important to consider in the given scenario, where information about the identified faecal source allows incorporation/exclusion of appropriate pathogen(s). For example, viruses in animals are generally not considered to be zoonotic because it is believed that there are strong barriers to prevent viruses crossing between animal species. A QMRA, therefore, may exclude viruses hosted by non-human animal species.

- **Exposure Assessment**

  This step identifies how people are exposed to pathogens using information on the volume of water and the concentration of the target pathogen ingested (dose) by people during exposure to recreational water.

- **Dose-Response Assessment**

  This step assesses people's response (infection, illness) to the given dose and how likely it is to occur. The QMRA may also consider more vulnerable groups such as the immunocompromised and children who have a lower dose-response than healthy adults.

- **Risk Characterisation**

  This step integrates the above three components to indicate the public health risk for the given scenario. Risk characterisation is generated by running mathematical models based on modelling the exposure and effect assessments for each pathogen.

The QMRA will utilise published scientific information on the types and concentrations of pathogens found in each faecal source, average volume of water ingested during recreational activity and dose-response curves for each pathogen. The use of known information allows the QMRA to be a desk-top exercise, minimising additional sampling requirements and expediting risk assessments.

4.4 REFINEMENT OF THE WATER QUALITY ASSESSMENT FRAMEWORK

The previous sections of this report have drawn together insights and recommendations on water quality issues from a wide range of sources including feedback from consultations with councils, communities, iwi/hapū and scientists, and evidence from case studies of chronically contaminated waterways. The starting point for consultation was the conceptual water quality framework presented in the Leonard et al. (2020) QMRA pilot study (Fig. 2). Based on the findings detailed in this report, this framework has been further refined to provide clearer guidance to councils on what steps to take when *E. coli* exceedances are encountered (Fig. 10). The refined framework maintains the three-step approach of the initial version. Features of note include:

- Step 2, which is tasked with source identification, has been supported by decision trees (Figures 6-9), which outline specific steps for human, livestock or non-human/non-livestock sources of contamination.
- Step 3, the health risk assessment, has been divided into two separate paths based on the outcome of source identification in Step 2.
- Where a source is not identified, Step 3a is initiated. This involves site-specific assessments, which can include a QMRA and pathogen testing in the aquatic environment of concern. It is recognised that non-detection of a faecal source may be due to limitations of the markers in the faecal source toolbox, which mainly target human, livestock and wildfowl sources. These limitations potentially negate the detection of many indigenous avian species and feral animals, and recommendations have been made with regards to expansion of the faecal source toolbox.
- Where a faecal source is identified an iterative process is followed to ensure improvements in water quality by trialling various mitigations. Prior to instigating pollution interventions, consultations with iwi/hapū and communities are strongly advised to ensure Māori tikanga and community values are upheld. Success of mitigations will be confirmed by reduced *E. coli* concentrations in compliance with water quality standards in Step 1.
- Where mitigations are either impractical, ineffective or only partially effective in reducing *E. coli* levels, councils are required to move to Step 3b and initiate a source-specific QMRA. This will be based on published scientific information rather than the additional site investigations outlined for Step 3a.

This revised framework will provide councils with specific guidance on what should be done when *E. coli* guidelines are exceeded and how to advance the process of remediation. Many of the components for this framework are in existence and contained within current guidelines such as the NPS-FM 2020 and State of the Environment (SOE)[4] monitoring and reporting. However, consolidation of these components within this framework has the advantage of streamlining council decisions on the next steps to take when *E. coli* exceedances are encountered as the framework and decision trees deliver clear guidance on actions rather than representing new regulations.

[4] Environment Aotearoa 2019 provides an overview of the state of our environment. Using five broad themes the report presents nine priority environmental issues including rural and urban impacts on pollution in our waterways. https://environment.govt.nz/publications/environment-aotearoa-2019

Protection of Recreational Water & Source Water

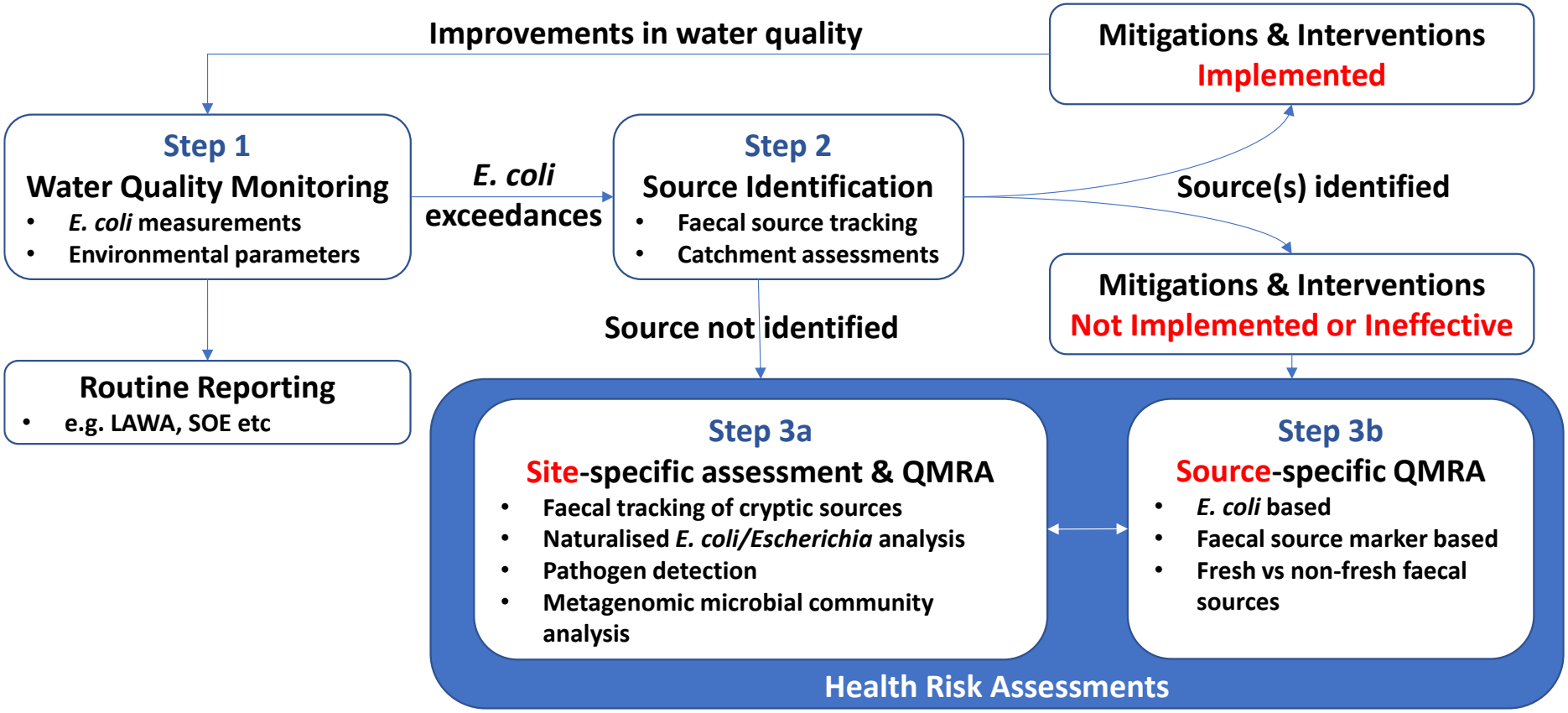

Figure 10 Refinement of the framework for assessment of water quality where elevated *E. coli* levels are detected in freshwater sites. Maximum benefits will be gained from partnering with iwi/hapū and consulting with communities throughout the assessment process.

5. CONCLUSIONS

Protecting the health of New Zealand's freshwater resources, in recognition of Te Mana o te Wai, is the fundamental focus of the National Policy statement for Freshwater Management (NPS-FM) 2020. Under this policy, councils are required to assess the quality of their freshwater sources, and where unacceptable levels of contamination are found take practicable steps to improve water quality. A key component of this quality assessment relies on measurement of concentrations of the faecal indicator bacterium, *Escherichia coli*, as a proxy for the presence of pathogenic microbes. When *E. coli* levels exceed acceptable limits, councils are expected to take actions to identify the source of contamination and implement interventions to remediate the situation.

An ongoing concern with the current Recreational Water Quality Guidelines is the lack of clear guidance when water quality criteria are exceeded. The NPS-FM 2020 requires councils to prepare action plans where attribute numeric values such as *E. coli* levels are exceeded in a catchment (Tables 1 and 2, Appendix A). The aim of this report was to further develop the recreational water quality framework proposed in the Quantitative Microbial Risk Assessment (QMRA) pilot study (Leonard et al. 2020) commissioned by the Ministry for the Environment (Figure 2). This framework outlined a three-step approach to water quality evaluations with the first step aligning to the routine monitoring of *E. coli* mandated under the NPS (Leonard et al. 2020). Elevated concentrations of *E. coli* alert authorities to potential faecal contamination events and require appropriate responses from council scientists to mitigate risk. Advances in technology have enabled incorporation of faecal source tracking tools into water quality assessments when *E. coli* exceedances trigger further investigations.

The focus of this report was to provide guidance for council scientists on how to respond to *E. coli* exceedances. The refined water quality framework is presented in Figure 10 and is supported by decision trees which outline specific guidance for faecal source identification (Step 2; Figures 6-9). This report drew on feedback from consultations with community and council scientists to revise the framework including case studies of various faecal contamination scenarios. Feedback from the consultation process was incorporated into the decision trees to outline steps for identification of human, livestock and avian faecal contamination as well as mixed sources. Further advice is provided, and additional tools are suggested, for cases where the sources of chronic *E. coli* contamination are not identified. The health risk assessments outlined in Step 3, including QMRA, are to be initiated in three circumstances: where the contamination source is not identified, mitigations are unable to be implemented, or mitigations prove ineffective. Valuable feedback collected during meetings has highlighted that council staff have had multiple renditions of the NPS-FM over the last decade and are hesitant to accept new recommendations on water quality monitoring, particularly in light of budgetary constraints. It is hoped that this revised framework for water quality assessments will be viewed as providing clearer guidance and reduced workloads when councils confront faecal contamination events.

The consultation process and case studies further highlighted that mitigations require input from communities and partnership with iwi/hapū who bring into view the value of local knowledge and the historical background relevant to the remediation process. Recognition of Māori mātauranga was perceived as critical in relation to local waterways, mahinga kai and

places of significance. In addition, iwi/hapū may be leaseholders of farmed land, and farmer interactions with Māori values and tikanga is important to re-establish the rightful place of Māori in Aotearoa NZ society. The uptake of indicators for identifying faecal contamination is on the increase by iwi/hapū, who see this accumulated data as a valuable resource for communicating the issues of water quality within their community and to the wider nation. The case studies also highlighted the role of champion farmers who recognise and implement mitigations. They can lead the way for improved pollution outcomes by modelling appropriate behaviour to fellow farmers. However, as outlined in Case Study 2, the critical step in developing champion farmers within a community is the establishment of a trusted relationship between the farmer and council representatives, all working in liaison with farm industry representatives and the local iwi/hapū.

Overall highlights from this project are listed below and include the consultation process and case studies that informed the outcome of refining the water quality assessment framework:

- Consultation meetings with eight councils were undertaken and feedback collated
- Dissemination to councils of a two-page summary of the main findings of the Leonard et al. (2020) QMRA pilot study
- Four oral presentations (including one paper presentation) to national conferences in 2020, which involved discussions of water quality issues and referenced results from the Leonard et al. (2020) QMRA pilot study.
- Three case study analyses were undertaken by ESR, which presented contamination scenarios for varied faecal sources with input from council scientists, communities and hapū/rūnanga.
- Specific step-by-step guidance has been provided to council scientists when exceedances of *E. coli* concentrations are encountered during routine water quality monitoring.

  Guidance includes advice on:

  - The stepwise implementation of the faecal source tracking toolbox to identify the source(s) of elevated *E. coli.*
  - When it is necessary to investigate whether naturalised *E. coli* or *Escherichia* species are contributing to elevated *E. coli* concentrations
  - When flow-weighted measures of *E. coli* lead to a better understanding of what the major pollution contributors are in a catchment. This evaluation allows prioritisation of the most effective mitigations.
  - The circumstances when a health risk assessment should be initiated:
    - The faecal source is not identified
    - Mitigations are unable to be implemented
    - Mitigations prove ineffective
  - Future directions for expansion of the faecal source tracking toolbox to cover non-livestock animals and indigenous avian species.

5.1 KNOWLEDGE GAPS AND FUTURE DIRECTIONS

Several scientific knowledge gaps and potential future initiatives were identified through the consultation process and refinement of the framework. It is anticipated that addressing these will maximise the effectiveness of the refined framework. These include:

- There is a lack of information on the faecal indicator bacteria (*E. coli* and enterococci) and pathogen concentrations in feral animals and in native and indigenous birds of New Zealand such as the ubiquitous pūkeko.

- Are naturalised faecally-derived *E. coli* associated with pathogens in sediment and water?
- More information is required on the effectiveness of various mitigations for reducing FIB levels to below Recreational Water Quality standards.
- Health risks associated with sheep faecal pollution have not been well characterised by international QMRA studies as large-scale sheep farming is more likely in Australasia than other countries where these types of analyses have been conducted (Soller et al. 2010, Soller et al. 2014).
- The incorporation of faecal source marker concentrations and the effects of non-recent/treated faecal sources into QMRA investigations.

Suggestions and requests from Regional Council scientists:

- Faecal source tracking methods that can detect sources at lower levels of *E. coli* i.e., <<260 *E. coli*/100 mL. This would be significant for drinking water sources such as groundwater bores.
- Additional faecal source markers for non-livestock/non-human sources with the most requested marker being for pigs.
- Sufficient resourcing of testing for faecal sources in Step 2 of this assessment framework.
- Real-time methods are necessary for measuring *E. coli* exceedances and to avoid situations where notification of a public health issue takes days to confirm by which time the contamination may have passed.
- Information on attenuation rates of faecal microbes once discharged into waterways.
- Investigation of the persistence of pathogens in sediment and their role in disease transmission.

The refined recreational water quality assessment framework presented herein, is equally applicable to an assessment approach for sourcing drinking water. This framework will therefore, be supportive of the new Water Services Regulatory environment of Taumata Arowai.

To make an impact on recreational water quality management, we propose progressing the adoption of the water quality assessment framework (Figure 10) and the accompanying decision trees (Figures 6-9). Many of the components for this framework are in existence and contained within current guidelines such as the NPS-FM 2020 and State of the Environment monitoring and reporting. This framework provides councils with specific guidance on what should be done when *E. coli* guidelines are exceeded and how to advance the process of remediation of polluted water bodies.

APPENDIX A: WATER QUALITY GUIDELINES

Table 1 *E. coli* water quality guidelines as presented in Table 9 of the NPS-FM (2020)

Value			Human contact	
Freshwater body type			Lakes and rivers	
Attribute unit			*E. coli*/100 mL (number of *E. coli* per hundred millilitres)	
Attribute band and description			**Numeric attribute state**	
Description of risk of *Campylobacter* infection (based on *E. coli* indicator)	% exceedances over 540/100 mL	% exceedances over 260/100 mL	Median concentration /100 mL)	95th percentile of *E. coli*/100 mL
A (Blue) For at least half the time, the estimated risk is <1 in 1,000 (0.1% risk). The predicted average infection risk is 1%.	<5%	<20%	≤130	≤540
B (Green) For at least half the time, the estimated risk is <1 in 1,000 (0.1% risk). The predicted average infection risk is 2%.	5-10%	20-30%	≤130	≤1000
C (Yellow) For at least half the time, the estimated risk is <1 in 1,000 (0.1% risk). The predicted average infection risk is 3%.	10-20%	20-34%	≤130	≤1200
D (Orange) 20-30% of the time the estimated risk is ≥50 in 1,000 (>5% risk). The predicted average infection risk is >3%.	20-30%	>34%	>130	>1200
E (Red) For more than 30% of the time the estimated risk is ≥50 in 1,000 (>5% risk). The predicted average infection risk is >7%.	>30%	>50%	>260	>1200

Attribute state should be determined by using a minimum of 60 samples over a maximum of 5 years, collected on a regular basis regardless of weather and flow conditions. However, where a sample has been missed due to adverse weather or error, attribute state may be determined using samples over a longer timeframe.
Attribute state must be determined by satisfying all numeric attribute states.
The predicted average infection risk is the overall average infection to swimmers based on a random exposure on a random day, ignoring any possibility of not swimming during high flows or when a surveillance advisory is in place (assuming that the *E. coli* concentration follows a lognormal distribution). Actual risk will generally be less if a person does not swim during high flows.

Table 2 *E. coli* concentrations relevant for swimmability (primary contact sites) as presented in Table 22 of the NPS-FM (2020)

Value	Human contact
Freshwater body Type	Primary contact sites in lakes and rivers (during the bathing season)
Attribute unit	95th percentile of *E. coli*/100 mL (number of *E. coli* per hundred millilitres)
Attribute band and description	**Numeric attribute state**
Excellent Estimated risk of *Campylobacter* infection has a < 0.1% occurrence, 95% of the time.	≤ 130
Good Estimated risk of *Campylobacter* infection has a 0.1 – 1.0% occurrence, 95% of the time.	> 130 and ≤ 260
Fair Estimated risk of *Campylobacter* infection has a 1 – 5% occurrence, 95% of the time.	> 260 and ≤ 540
National bottom line	**540**
Poor Estimated risk of *Campylobacter* infection has a > 5% occurrence, at least 5% of the time.	> 540
The narrative attribute state description assumes "% of time" equals "% of samples".	

APPENDIX B: PRESENTATIONS TO INTEREST GROUPS

Date: 17 October 2020

Conference: Water New Zealand

Title: Prevalence of pathogens in New Zealand

Author and presenter: Margaret Leonard

Location: Hamilton

Key audience: Water industry practitioners and scientists

Impact: Well received

Date: 27 November 2020

Conference: Special Interest group for Regional Councils: SWIM (Surface Water Integrated Management)

Title: Prevalence of pathogens in New Zealand

Presenter: Margaret Leonard

Location: online webinair

Key audience: Regional council scientists

Impact: Special Interest group for Regional Councils: 48 people attended

Date: 3 December 2020

Conference: Joint conference of New Zealand Freshwater Sciences Society, Hydrological Society and River NZ

Title: Indicators and pathogens in New Zealand Rivers – A pilot study.

Presenter: Brent Gilpin

Location: Invercargill

Key audience: Regional council scientists

Impact: 60 people attended from regional and city councils

Date: 9 December 2020

Conference: One Health Aotearoa

Title: Pathogens and indicators in freshwater.

Presenter: Margaret Leonard

Location: five regional hubs around the country which were connected online via Zoom

Key audience: Scientists and academics

Impact: included international speakers

APPENDIX C: 2020 QMRA PILOT STUDY SUMMARY DOCUMENT

ESR
Science for Communities

www.esr.cri.nz

FIGURE 1
Location of rivers

River recreation is an activity that is highly valued by New Zealanders. The guidelines which assess the risk of getting an infection are based on a large study undertaken in 1998–2000. Much has changed in the last 20 years and it is important to determine if the data used for the guidelines reflects the current concentrations and prevalence of pathogens in rivers.

The Ministry for the Environment funded a pilot project to:

- determine the current prevalence of pathogens in rivers.
- confirm methodologies.
- determine the logistics and costs for a larger study.
- engage with iwi and hapū.

Project outline

Sixteen rivers across New Zealand were selected. They had a history of high concentrations of the bacteria *Escherichia coli* (*E. coli*) and reflected different land uses – urban, sheep & beef and dairy.

What was measured?

Traditional methods and PCR[1] were used to detect:

- bacterial pathogens: *Campylobacter*, *Salmonella*, Shiga toxin-producing *E. coli*
- protozoa: *Giardia*, *Cryptosporidium*
- human viruses: adenovirus, enterovirus, norovirus GI and GII.
- Faecal Source Tracker[2] (FST) markers to identify the faecal pollution from humans, ruminants and birds.

What we found

As expected all of the samples had *E. coli* present, with 45% above 540 MPN/100 mL which is the guideline value for safe recreation (the blue line in Figure 2). The major source of faecal contamination in each sample was determined from the FST concentration and mostly reflected the observed land use (Figure 2). However, at two sites bird FST was dominant so they were classified as wildfowl impacted sites.

What pathogens were present and how much?

All target pathogens, except for adenovirus, were present in at least some samples from each river, mostly at low concentrations. The results presented in the Figure 3 (next page) are based on traditional culture methods. Even sites classified as "wildfowl" sometimes had pathogens present.

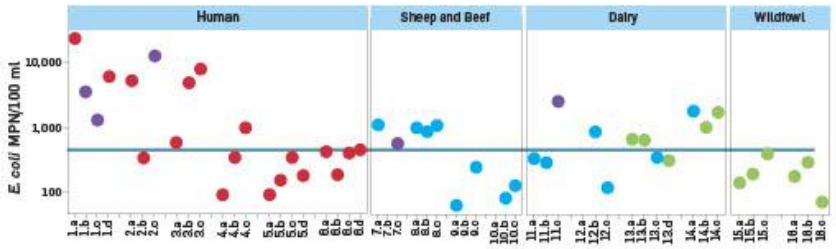

FIGURE 2 (right): Concentration of *E. coli* by river (1-16) with dominant faecal source for each sampling event (a-d) within the different categories.

NOTE the data is anonymised and in the same order as the table.

[1] PCR is a method which detects the genetic material. It does not determine if the micro-organism is infectious.
[2] FST markers are micro-organisms specific to the gut of an animal and can be used to determine the origin of faecal contamination, such as human, ruminant or birds

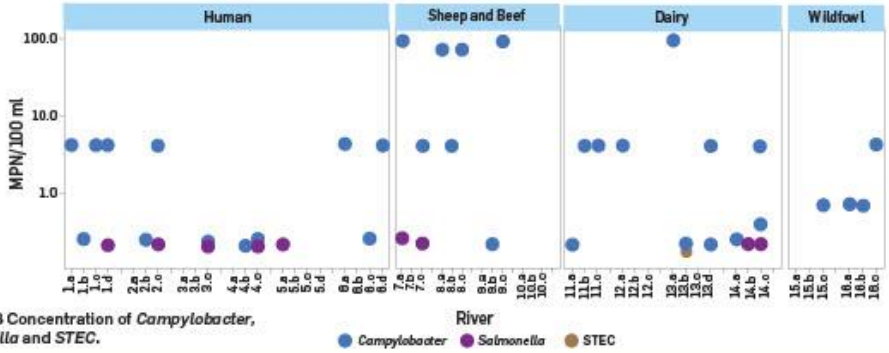

FIGURE 3 Concentration of *Campylobacter*, *Salmonella* and *STEC*.

Bacteria

- *Campylobacter* was present in 68% of samples in 14/16 rivers, but only 36% of all samples had concentrations greater than 1 MPN/100 mL, with five samples ranging from 72 to 92 MPN/100 mL.
- *Salmonella* was found in 18% of all samples and in 7/16 rivers with a maximum concentration of 0.25/100 mL.
- STEC was only found once (2%) at 0.14 MPN/100 mL.

Protozoa

- Both protozoa were present at low concentrations.
- *Giardia* was the most frequently present pathogen in 81% of all samples and in 15 rivers.
- *Cryptosporidium* was present in 42% of samples in 13 rivers.

Viruses

- No adenovirus was detected.
- The other viruses were present in 11 samples (12%) and at such low concentrations they couldn't be quantified.

PCR Methods

- In some samples pathogens were detected by PCR, but not traditional methods e.g. STEC was detected at low concentrations by PCR in 22% of all samples in 10 rivers
- A good correlation was found for *E. coli* using both methods.

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What next?

Engagement with Māori

The pilot study provided an opportunity to engage with iwi and hapū for the selected awa. Because sites with problems were specifically selected to test methods and maximise the likelihood of pathogens being present, cultural significance for iwi was not a criterion in the pilot study. The next phase of the project will include cultural significance and a Cultural Health Index, or similar. Pathogen data may also help to understand potential impacts on mahinga kai. Incorporation of Māori values and approaches responds to Te Mana o Te Wai, in the National Policy Statement Freshwater 2020.

- Expand collection and analysis of samples. There was low rainfall in many places during this pilot study which may have resulted in lower concentrations of micro-organisms. Higher concentrations may occur in a year with normal rainfall.
- Collect more samples New Zealand-wide, over different seasons. Some pathogens are more prevalent in spring when lambing and calving occur. This pilot study was done in summer.
- Analyse bacteria and protozoa using traditional and PCR methods.
- Use FST to determine sources of faecal contamination.
- Collect enough samples to enable statistical analysis e.g. association between pathogens and *E. coli*, the impact of land use and rainfall
- Engage with iwi on site selection and Cultural Health Index, or similar
- Revise the Quantitative Microbial Risk Assessment using the new data.

Determining the sources of pathogen contamination and prevalence of pathogens allows mitigation measures to be targeted. This supports the National Environmental Standards for Freshwater and the National Policy Statement for Freshwater Management to increase recreational water quality for recreational use.

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Full report available at https://www.mfe.govt.nz/publications/fresh-water/quantitative-microbial-risk-assessment-pilot-study

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APPENDIX D: QUESTIONS ASKED AT MEETINGS WITH COUNCILS

Examples of questions that may be asked to prompt responses

1) Do you think there is a need /demand for a consistent framework for water quality assessments?
2) What are the barriers? Does this framework address those issues?
3) Step 1: What is the process you follow when there are elevated *E. coli* concentrations detected?
4) Step 2: Which types of faecal pollution would you like more direction for identifying faecal sources so Council can implement mitigations?
5) Which faecal sources are of greatest importance to your council? Prioritisation of sources.
6) When a faecal source is identified: What are the drivers/barriers to implementing a mitigation(s)?
7) What are the knowledge gaps in terms of the types of faecal sources we currently target?
8) Step 3: What information would help Council with the health risk assessment (HRA) process?
9) Would a range of scenarios for HRA for different faecal contamination events be useful?
10) How do you view the efficacy and value of Step 3?
11) How important are correlations between indicators and pathogens and understanding the different contamination scenarios that will impact on these relationships?

APPENDIX E: SUMMARY OF COUNCIL RESPONSES

Figure 11 Word cloud representing key responses from councils

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