QMRA DATA EXPERTS

Streamlined ENVIRONMENTAL

# Responses to S92 Questions: Quantitative Health Risk Assessment for wet weather wastewater discharges

25th January 2021

Gisborne District Council
PO Box 747
Gisborne 4010
New Zealand

**Attention**: Wolfgang Kanz

Dear Wolfgang,

**Re: S92 Questions - Gisborne QMRA Report**

Thank you for the opportunity to respond to the S92 questions raised with respect to the Gisborne QMRA. This report was attached to the application as Appendix M, and is referenced below (Dada 2020).

We have been advised that our responses to the technical questions can be provided in memo form and that a report, or update to the existing report, is not required.

Kindly find below, in a tabulated form, responses to each of the S92 questions.

We trust that this addresses the relevant S92 issues raised.

Kind regards,

**Dr Christopher Dada**

**Tabulated responses to S92 comments.**

| *S/no* | *S92 Comments* | *Response* |
|---|---|---|
| *(xi)* | Several aspects of the Quantitative Microbial Risk Assessment (QMRA) report (Streamlined Ltd) require clarification to understand all of the assumptions which apply.<br><br>For example, it is unclear what "a limited microbiological analysis of the WWTP influent samples" (p18) means in practice, in terms of the number of samples and conditions under which sampling was undertaken. | To the best of our knowledge, and consistent with several previous NZ QMRAs (e.g. several NIWA QMRA reports), the assumptions of the Streamlined Environmental Ltd QMRA have been duly acknowledged in the report. We considered it appropriate to use this approach to allow for consistency and ease of comparison across multiple QMRA reports in New Zealand. However, we have now provided additional clarification as requested by the S92.<br><br>As stated on page 18 of the QMRA report, Dnature Diagnostics & Research Ltd NZ was commissioned by GDC in 2019 to conduct a microbiological analysis of the WWTP influent samples, based on a three-day grab sampling program. Because of the sporadic nature of wastewater pathogen concentrations and the short duration of the sampling, it is possible that the data generated was not representative of the full range of wastewater pathogen concentrations. Ideally, sampling is conducted over a period of at least two years to capture temporal variabilities in pathogen concentrations that may be associated with the various seasons. However, this approach is very time and cost intensive.<br><br>It is noted that the three-day samples showed low adenovirus and norovirus concentrations (see attached Dnature Diagnostics Report). Also, Giardia was detected at very low concentrations. Enterovirus and Salmonella were not detected at all. This may be due to the sensitivity of the methods used to enumerate the samples or alternatively, that higher concentrations of these pathogens may have been detected, had the sampling been repeated across different seasons.<br><br>Due to the limited sampling information, the Gisborne QRMA applied pathogen concentrations typical of the ranges found in New Zealand. This is the approach that has been applied in a number of recent QMRAs (e.g., Hudson 2019 -NIWA Queenstown Stormwater QMRA, McBride 2017- Bell Island WWTP QMRA). This approach was acknowledged on page 18 (re-pasted below):<br><br>Given the limitations with the limited monitoring data, *"a precautionary approach [consistent with previous NZ QMRAs] that relied on previously published ranges of pathogen concentrations was applied in this QMRA*".<br><br>This approach may be considered conservative (i.e., over-protective) as:<br><br>• The overflow pathogen concentrations applied in the Gisborne QMRA are several orders higher than |

| S/no | S92 Comments | Response |
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| | | concentrations reported in the limited Dnature sampling.<br>• Pathogen concentrations in raw WWTP influent documented in several previous NZ QMRAs were applied as wastewater overflow pathogen concentrations based on a conservative assumption that the wastewater overflow is not diluted by stormwater. Realistically, as stormwater ingress into the wastewater network is the cause of wet-weather overflows, dilution and reduction of the pathogen concentrations will occur in the resulting mixture of wastewater and stormwater. Although GDC has advised that Gisborne's wastewater overflows are expected to be at 75-88.3% stormwater, as a conservative approach, we have assumed in this QMRA that the content discharged is 100% raw wastewater. This is also already stated in the report on page 19. |
| *(xi)*<br>*Cont'd* | It is also unclear what methods the raw pathogen concentrations listed in Table 3 were based on (e.g. infectious units vs PCR analysis for adenovirus) and whether or not some 'harmonisation' of data was needed for the influent concentrations to be applied to the dose-response model. | For adenovirus, enterovirus and norovirus, the concentrations are expressed in qPCR-based genome copies per litre consistent with previous NZ QMRAs (e.g. McBride 2007, 2011; 2012; 2016a,b- Snells Beach and Warkworth WWTP QMRA, McBride 2017-Bell Island WWTP QMRA, Dada 2018a; 2018b). For Cryptosporidium and Giardia, the detection was based on recoverable oocysts per litre. For Salmonella, the detection was based on culturable cells expressed per litre.<br>Harmonisation of data is usually applied to norovirus because of the disparity between norovirus concentrations detected by currently available PCR methods and those used for enumeration of virus concentrations in the Teunis et al. (2008) clinical trial[1].<br>Hence, some NZ QMRAs (e.g. McBride 2007, 2011; 2012; 2016a,b- Snells Beach and Warkworth WWTP QMRA, McBride 2017-Bell Island WWTP QMRA) divided norovirus concentrations by a "harmonization factor" i.e. 18.5 before using the "harmonized" (i.e. reduced) concentrations in the QMRA. It is important to note that this "harmonization factor" may be variable and dependent on the recovery efficiency of the laboratory where the PCR was performed. In this Gisborne QMRA, we did not reduce the norovirus concentration by 18.5, thus making it even more conservative (it may overestimate |

[1] Dose response model was developed based on data generated in the Teunis et al (2008) clinical trial.

| S/no | S92 Comments | Response |
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| | | health risks associated with norovirus, which is a preferred outcome from a public health protection perspective). |
| *a.* | Provide a copy of the GDC-DNAture 2019 pathogen results. | The DNAture pathogen results are attached. As above, however, please note that a more conservative range of concentrations were used in the Gisborne QRMA. |
| b. | Clarify if the enterovirus and adenovirus dose response curves were developed using cultured virus counts based on qPCR-based measures of enterovirus and adenovirus. If so, this may yield either over or underestimates of risk because molecular methods of PCR may over or underestimate the number of infectious viruses (e.g. adenovirus has been detected more frequently by qPCR in urban rivers than by infectivity assay).<br><br>This needs to be acknowledged in the report to provide a more complete understanding of the QMRA's assumptions. | The dose response curves applied were based on qPCR-based measures of viruses. This is conservative and consistent with the approach that has been used in several previous NZ QMRAs (e.g. McBride 2007, 2011; 2012; 2016a,b- Snells Beach and Warkworth WWTP QMRA, McBride 2017-Bell Island WWTP QMRA, Hudson, 2019-Queenstown QMRA, Dada 2018a; 2018b).<br><br>It is important to note that the more frequent detection of adenovirus by qPCR than is observed in infectivity assays, as the reviewer suggests, is simply because the detection of viral genetic material does not necessarily equate to infectivity (even degraded DNA is detected by the PCR-based methods). From a public health perspective, as we have done in the Gisborne QMRA report, consistent with several previous QMRAs (e.g. McBride 2007, 2011; 2012; 2016a,b- Snells Beach and Warkworth WWTP QMRA, McBride 2017-Bell Island WWTP QMRA, Dada 2018a; 2018b, Dada and Gyawali, 2020), it is safer to assume a conservative stance during modelling, that all the detected viral genetic materials are infectious. |
| c. | Clarify if the concentrations of norovirus in Table 3 are based on both GI and GII. Currently there is only one dose response model available for norovirus (for GI). Consequently, the quoted norovirus risks may represent an under or over-estimation of the actual risks depending on the | The concentrations of norovirus in Table 3 are applicable to both GI and GII.<br><br>Although the clinical trial which birthed the dose response model for Norovirus (as reported by Teunis et al. 2008) was for the genotype group GI.1, several similar viruses have been identified in genogroups I, II, III, IV and V. It is best practice, consistent with previous NZ QMRAs (e.g., McBride 2017, Bell Island WWTP QMRA), to assume that the infectivity of norovirus GI.1 is similar to all noroviruses which affect humans (especially GI and GII). Consistent with previous NZ QMRAs, no differentiation is usually made with respect to genotype I or II in reported QMRA input tables (as was also the case in a more recent Queenstown Stormwater QMRA- Hudson, 2019). |

| S/no | S92 Comments | Response |
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| | infectivity of the GII norovirus. | |
| d. | Advise what assumptions have been made regarding the proportion of the adenovirus concentration shown in the Table 3 that relate to Adenovirus 4 – the report says adenovirus is used as a model virus for respiratory disease using the dose response model for Adenovirus 4 but Adenovirus 4 will only make up a small proportion of adenovirus species. If no assumption has been made and the concentration range shown in Table 3 (2,000 – 30,000,000) is used to randomly sample potential concentrations of AdV 4 in the QMRA model, then this will markedly over-estimate the risk of respiratory illness from contract recreation | We assumed that 10% of the overflow adenovirus concentrations listed in Table 3 (i.e., 10% of 2,000 – 30,000,000) were Adenovirus type 4. This is consistent with literature published on the populations of adenovirus prototypes in raw wastewater (Fong et al. 2010). Hence the adapted concentrations do not over-estimate health risks. |
| *(xii)* | River sediments and beach sands have been recognised as reservoirs for pathogens and epidemiological studies have shown that exposure to these can increase the risk of gastroenteritis. Please comment on the potential risk of exposure to pathogens during dry weather when tidal and wind conditions can | During dry weather, tidal and wind conditions may resuspend pathogens (from catchment flows and the WWTP overflow) that have been deposited in bottom sand/sediment back into the water column (Walters et al 2014). Reliable estimates for pathogen sedimentation and resuspension rates are rarely available in literature (for instance, see Sterk et al 2016) and complex processes associated with the fate of pathogens in sediments generally tend to be location- and pathogen-specific and are associated with many uncertainties (Hassard et al 2016). Therefore, we can't provide an accurate risk of exposure of pathogens from resuspension of sediment. Notwithstanding, we note that solar-based inactivation will play a crucial role in reducing residual pathogen concentrations in the river sediments. Furthermore, risk will also substantially decrease |

| S/no | S92 Comments | Response |
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| | resuspend bottom sand/sediment and into the water column. | following the reduction in overflow frequency and volume, as proposed in the upgrades. |
| *(xiii)* | Please comment on the types of shellfish found and typically harvested at each of the locations modelled by MetOcean and discussed in the QMRA report. In particular, the health risk from consumption of raw shellfish is predicted to reduce from "high" (current risk) to "moderate" at sites 6, 7 and 8 under the future 10-year ARI scenario. Are shellfish present at and harvested from these sites?<br><br>(**note**: This may require response from Council if the sites were provided to Streamlined. However, any rationale for the selection of these sites should be provided). | Sites were provided to Streamlined Environmental Ltd by GDC. I understand that GDC will respond to the question of what shellfish are present at the modelled sites. |

# Cited references


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McBride, G. , Stott, R., Miller, W., Bambic, D., & Wuertz, S. (2013). Discharge-based QMRA for estimation of public health risks from exposure to stormwater-borne pathogens in recreational waters in the United States. Water research, 47(14), 5282-5297.

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Sterk, A., de Man, H., Schijven, J. F., de Nijs, T., & de Roda Husman, A. M. (2016). Climate change impact on infection risks during bathing downstream of sewage emissions from CSOs or WWTPs. Water research, 105, 11-21.

Teunis, P. F. M., Moe, C. L., Liu, P., Miller, S. E., Lindesmith, L., Baric, R. S., Le Pendu, J. & Calderon, R. L. (2008) Norwalk virus: how infectious is it? J. Med. Virol. 80(8), 1468–147

Walters, E., Schwarzwälder, K., Rutschmann, P., Müller, E., & Horn, H. (2014). Influence of resuspension on the fate of fecal indicator bacteria in large-scale flumes mimicking an oligotrophic river. Water research, 48, 466-477.

# Water Testing Report

Client: Gisborne District Council c/- Wolfgang Kanz
Address: Gisborne
Report Date: 3rd December 2019
Purchase Order: N/A

**Testing**
Samples 12479 and 12480 are duplicate water samples to re-assess sampling and processing performance.

Water samples collected: 14/08/2019 and 16/08/2019

Processed: 16/08/019 – 20/08/2019 (external)

Extracted and tested: 22/08/2019 – 24/08/2019

Results (copies per 100ml - DNA equivalents)

| Sample ID | BTF site 1 14/8/2019 | BTF site 1 16/8/2019 | BTF site 1 dup 16/8/2019 |
|---|---|---|---|
| **dnature #** | **12478** | **12479** | **12480** |
| **Bacteria** | | | |
| Bacteroides | 32,392,746 | 33,295,693 | 36,658,873 |
| Campylobacter (*C. coli* & *C. jeuni*) | 1,155 | 921 | 1,124 |
| Cryptococci | Trace | N | N |
| *E. coli* | 23,288,206 | 19,530,540 | 19,746,687 |
| Enterococci | 2,765,611 | 2,564,220 | 2,494,680 |
| Giardia | 60 | 36 | 34 |
| Salmonella | N | N | N |
| | | | |
| **Viruses** | | | |
| Adenovirus | 19,611 | 23,288 | 26,355 |
| Enterovirus | N | N | N |
| Norovirus Group I | N | N | N |
| Norovirus Group I | Trace | Trace | Trace |
| Polyomavirus | 813,616 | 605,426 | 626,594 |
| Rotavirus | 1,2205 | 6,223 | 6,529 |

| | | | |
|---|---|---|---|
| **Helminths** | | | |
| *N. americanus* | TBC | TBC | TBC |

N Not detected
Trace Very low levels detected

Comments: NIL

Author: John Mackay
molecular biologist
dnature diagnostics & research Ltd