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25 March 2022

Central Hawke's Bay District Council
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Attention: Fiona Clark, Senior Project Manager

Dear Fiona

Pōrangahau Wastewater Discharge to Land - QMRA s92 Response (P:D.68)

Further to the letter from Hawke's Bay Regional Council (HBRC) 'Request for Further Information' dated 7 March 2022 in relation to resource consent application APP-126770, the following sets out our response to the first question raised in respect to the Quantitative Microbial Risk Assessment (QMRA) under Section 92 of the Resource Management Act.

Further Information Request

The s92 letter (HBRC states):

"The QMRA conducted to assess the risks of human illness due to the Pōrangahau WWTP discharge uses currently accepted methodology for assessments of this sort. However, there are several aspects of the QMRA that require further elaboration to justify the decisions made in the formulation of the model. These are:

a) *The derivation of log removal values for the application of UV treatment*
b) *The derivation of dilution estimates for sites 2-4*
c) *The use of marine microbiological guidelines, rather than the freshwater NPS for assessment of the risks"*

This letter responds to (a) above and draws reference to the ESR review (Review of QMRA for the Porangahau WWTP Discharge, February 2022).

Response

Table 1 provides the estimates of pathogen inactivation that were provided to QMRA Data Experts to undertake the QMRA.

Table 1: Estimates of Pathogen Inactivation

1 **Pond only**

Pond	Min	ML	Max	Dist.n
Adenovirus	0	1	2	Pert
Enterovirus	0	1	2	Pert
Norovirus GI	0	1	2	Pert
E.coli	1	2.5	3.5	Pert

Pond e.coli projection based on actuals from Te Kauwhata Aquamat plant
Pond viral inactivations are conservative based on an absense of data

	Min	ML	Max	Distribution

2 **Pond + UV**

Pond	Min	ML	Max	
Adenovirus	0	1	2	Pert
Enterovirus	0	1	2	Pert
Norovirus GI	0	1	2	Pert
E.coli	1	2.5	3.5	Pert

UV	Min	ML	Max	Distribution
	0.2	0.5	0.9	Gamma or Loglogistic
	1	2	4	Gamma or Loglogistic
	1.3	3	5.5	Gamma or Loglogistic
	1.5	4	7	Gamma or Loglogistic

Based on IUVA dosimetric data

Modelling Notes
No Flow Split: The inactivation rates above assume that 100% of the flow passes through the unit process
If Bypass: Where there is a bypass envisaged, the Log inactivations will need to be calculated on a mass balance basis
Correlation: For each unit process, a STRONG Correlation is to be applied between individual species because the state of the process at the time / instant will have a similar i
Sequential unit Processes: The log reductions presented here are NOT to be added numerically. They need to be sampled sequentially in the QMRA Monte Carlo model.

The following comments were provided by ESR in their review. Our responses are listed below.

HBRC/ESR query

Influent concentrations of norovirus, enterovirus and adenovirus were taken verbatim from studies by McBride (McBride, 2016; McBride and Hudson, 2016) and represented by custom distributions (hockey stick) to include less common, very high viral concentrations observed in one study (the Mangere scoping study (DRG, 2002)). The very high concentrations of adenovirus and enterovirus seen in the Mangere scoping study have not been subsequently reported in any New Zealand or international studies and these results should be viewed as being questionable. The use of these data for the Pōrangahau WWTP QMRA is potentially overly conservative.

Beca response

We agree – Mangere influent concentrations (well the extreme right hand end of the distribution) are probably very conservative. But bear in mind that this is represented by a 'Hockey Stick' distribution that makes extreme values an outside possibility but highly improbable. These were selected by the modeller as appropriate.

HBRC/ESR query

The impact of the wastewater treatment plant on viral concentrations was modelled in terms of three scenarios covering combination of the current treatment (oxidation pond) and the potential addition of UV treatment. The viral removals by the processes were reported to be based on a literature review carried out by Beca. The literature review was not provided or summarised.

Beca response

A heavy reliance was not placed up literature reviews but rather judgement based on many years of practical experience with the use of UV disinfection in the New Zealand wastewater context. Some of the literature used in support is listed below.

HBRC/ESR query

The mean log reductions used in the QMRA model were 1 log_{10} removal for all virus types due to the oxidation pond.

Beca Response

Pond:

- The majority of disinfection occurring in waste stabilization ponds is due to solar UV irradiation. Shilton and Harrison: 2003 demonstrate the effect of maximising hydraulic retention time in the pond system.
- IUVA 2009 report 17 studies where *E.coli* inactivation is at the rate of 1 x $\log_{10}$ for 2 to 7 mWs/cm2. In the same data, caliciviruses (norovirus belongs to this family) at the rate of 1 x $\log_{10}$ for 4 to 8 mWs/cm2. Human adenovirus 20 to 55 mWs/cm^2
- Therefore the caliciviruses are inactivated at a similar but slightly lower rate than *E.coli* in the pond system. It is reasonable to assert that a similar inactivation rate is seen at similar UV doses in the IUVA report and therefore it is reasonable to expect a similar inactivation in the pond system which is largely UV driven per first bullet point above.
- McBride et al , 2011 Health risk assessment for Westland Milk Products Wastewater Disposal – Hokitika
    - WW Pond HuNov min 40%, Max 99% (0.2 to 2.0 $\log_{10}$ reduction)
    - WW Pond HuAdv min 5%, max 99% (0.02 to 2.0 $\log_{10}$ reduction)
- Hickey et al 1989, regarding waste stabilization ponds in the New Zealand context reported:
    - 50%ile effluent FC of 104/100ml. This compares to a normal raw sewage influent concentration, in New Zealand, of 1E7/100ml. This implies a median of 3 $\log_{10}$ removal of FIBs
- Sinton et al 2002, from a series of 10 experiments in New Zealand reported similar inactivation rate constants for *E.coli*, Somatic coliphages and F-RNA phage (but much higher summer inactivation rates for enterococci).
- Verbyla et al, 2015, took a fresh look at " A review of virus removal in wastewater treatment pond systems" and concluded, from literature pertaining to 71 WW pond systems with a range of HRTs and over a range of virus types, that "1 $\log_{10}$ reduction of viruses was achieved for every 14.5 to 20.9 days of retention". Typical HRTs seen in New Zealand Waste Stabilization ponds range upwards from 20 days.
- Shotover Ponds exhibited summer and winter influent *E.coli* 95th%iles of 2.40E7 and summer and winter final effluent *E.coli* 95th%iles of 2.6E3 and 7.1E4 respectively implying 3 to 4 $\log_{10}$ removals.
- A three year study on the Te Kauwhata ponds showed an effluent E.coli median of 2E3 cfu/100ml , 95th percentile of 7E3/100 ml. The median represents approximately a 3 $\log_{10}$ reduction from influent.
- During a 2 year study at Waipawa (single pond) median influent *E.coli* was 2.75E6 and median effluent *E.coli*, pre-UV was 1.6E3. This is a 2.25 $\log_{10}$ reduction

On the basis of the above and due to the paucity of virus specific performance data from pond discharges, a conservative 1 $\log_{10}$ inactivation was adopted across the board as the most likely viral inactivation in the pond system.

UV System:

HBRC/ESR query

"and additional mean reductions of 3.4 and 2.5 log_{10} for norovirus and enterovirus, respectively, due to UV treatment (Appendix 1). Additional log removal of adenovirus is not reported in Appendix 1, but according to Figure 4 appears to be minimal."

Beca response

This is not correct, P_{50} inactivation (not reduction as no viral particles can possibly be removed by UV irradiation) for norovirus, enterovirus and adenovirus used were 3, 2 and 0.5 log_{10} respectively.

HBRC/ESR query

These viral log removals appear very high, based on our own review of the literature. Studies on norovirus inactivation by UV treatment typical show removals of less than 1 log_{10} (Barrett et al., 2016; Campos et al., 2016; Qiu et al., 2015; Qiu et al., 2018; Simhon et al., 2020).

Beca response

We do not agree with the reviewer's assertion of low norovirus inactivation by UV disinfection.

- HuNov is one of the family of calicviruses similar in type and structure to murine, feline and canine caliciviruses. The difficulty with HuNov is that it, historically (some researchers are saying that this may now be possible but this seems to be far from agreed), has not been able to be cultured in the laboratory. So influent and effluent sampling have rendered essentially the same physical enumeration. The active and inactive genetic material is there in the same quantities upstream and downstream of the UV system. Theoretically, enumeration (e.g RT-qPCR) pre and post UV should give near identical results as no viral particles can have been physically removed.

Considering the papers cited by the reviewer:

- Barrett et al 2016 does not appear applicable: In their 'Results and Discussion', they acknowledge ("Therefore in this incidence, RT-qPCR was not appropriate method of assessing the inactivation of NoV and FRNA bacteriophage (GA) via PUV post UV treatment") that the use of RT-qPCR was not appropriate for enumeration of viable versus no viable viral particles. So it doesn't really matter how high the dose went (6,900mJ/cm^2 is off the scale in terms of normally applied UV disinfection doses), the enumeration across the UV reactor would probably change little and any difference only represents debris created by the ultra-long (60 – 120s) exposures to the UV light that were used in that experiment.
- Campos et al 2016 does not appear applicable: It discusses the presence and absence or reduction in replicates found in different processes. It does not discuss inactivation. Primary treatment, trickling filter and activated sludge would all be expected to remove viral particles and therefore significantly reduce the number of virion replicates found downstream as opposed to upstream of the process. UV is not a physical barrier it would not be expected to result in any reduction in HuNov (or any other virus particles) between upstream and downstream measurements. UV disinfection results in viral inactivation, not reduction.
- Qiu et al 2018 does not appear applicable: They considered a number of human infectious viruses at two WWTPs in Canada. Again they used qPCR enumeration technology and again determined little difference between pre and post UV replicate numbers (In most cases, qPCR concentration estimates of pre- and post-UV were similar for all viruses, suggesting that qPCR itself is not a good measure of UV-inactivation across all the genetic variants of selected virus species that may be present in full-scale wastewater treatment plants) and, as with Barrett et al concluded that this method was not suitable for addressing viral inactivation by UV disinfection. They estimate that the

applied UV doses ranged between 8 and 24 mJ/cm^2, which is low – normally a minimum of 40 mJ/cm2 is targeted. It is surprising that they even measured the 1.2 Log_{10} reduction that they quote.

- Qiu et al 2015: The first part of the report deals with virus removal through various wastewater treatment processes. Table 1 presents essentially completely predictable results of almost nil removal of viruses across the UV process. Again the quantification method is qPCR so it is just counting an aggregate of the viable and non-viable carcasses upstream and downstream of the process. For UV, the only difference between upstream and downstream will be because of non-homogeneity of viral concentration in the water. The second part of the report considers viral inactivation across the processes and discusses that HuNov cannot be assessed in the laboratory. The results (Table 2) of this part of the study therefore do not cover HuNov and for the other viruses considered in the study, only report the presence or absence of viable replicates and not an enumeration. Interestingly the report mentions, briefly in passing, that "*The dose of UV is important for disinfection with dose response curves shown for various viruses shown in ……..".* this is an understatement. The UV dose is critical to the performance of UV systems. UV dose is not considered at all in the report and it is questionable as to how any assessment of the effectiveness of UV alone or against other processes, can be made without knowledge of the dose applied during the research.

The upshot of all this is that prediction of the performance of a particular UV system in inactivating HuNov can really only be done by association with the dose response pattern of a similar organism.

- IUVA publish (used in this study) biodosimetric data upon which WW UV disinfection systems around the world are designed. Individual columns reflect dose rates for 1 to 6 log_{10} inactivation respectively.

Calicivirus canine	MDCK cell line	LP	7	15	22	30	36		Husman et al. 2004
Calicivirus feline	CRFK cell line	LP	7	16	25				Husman et al. 2004
Calicivirus feline	CRFK cell line	N/A	4	9	14				Tree et al. 2005
Calicivirus feline	CRFK cell line	LP	5	15	23	30	39		Thurston-Enriquez et al. 2003

Other:

- Park et al (2011) considered 3 mammalian NoVs as surrogates for HuNov, alongside echovirus 12 and MS2 phage. The report concluded that "A UV dose of c. 30 mJcm−2 was able to achieve a 4-log_{10} reduction of three mammalian NoV surrogates. Thus, it is likely that human NoV could be effectively controlled by 40mJ cm−2, which is the UV disinfection practice for drinking water (ANSI/NSF, 2002)". The same study showed that the resistance of MS2 phage to UV irradiation was approximately three times that of the NoVs, which is consistent with the biodosimetric data published by IUVA. IUVA has not published echovirus 12 data (just 1 and 2).

HBRC/ESR query

While less information is available for enteroviruses and adenoviruses, inactivation by UV treatment appears to be similarly low (<1 log10) (Qiu et al., 2015; Qiu et al., 2018). Unless information is provided to substantiate the log removal figures used in the QMRA then the results of scenarios based on UV treatment should be viewed with caution.

Beca response

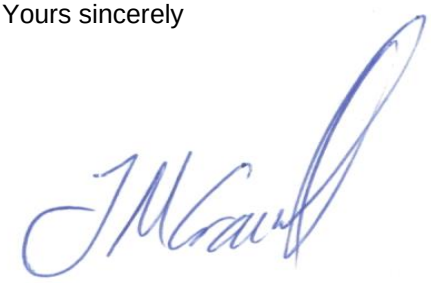
Further to the discussion above:

- IUVA publish (used in this study) biodosimetric data upon which WW UV disinfection systems around the world are designed. Individual columns reflect dose rates for 1 to 6 log_{10} inactivation respectively.

- Therefore for a target UV dose of 40mJ/cm2, the expected (P50) inactivation is 1x $\log_{10}$. We have suggested a Most Likely of 0.5 due to the practical difficulty in rendering pond effluent in an ideal state for delivering the design dose.

Adenovirus type 2	A549 cell line	LP	20	45	80	110			Shin et al. 2005
Adenovirus type 2	Human lung cell line	LP	35	55	75	100			Ballester and Malley 2004
Adenovirus type 2	PLC / PRF / 5 cell line	LP	40	78	119	160	195	235	Gerba et al. 2002
Adenovirus type 15	A549 cell line (ATCC CCL-185)	LP	40	80	122	165	210		Thompson et al. 2003
Adenovirus type 40	PLC / PRF / 5 cell line	LP	55	105	155				Thurston-Enriquez et al. 2003
Adenovirus type 40	PLC / PRF / 5 cell line	LP	30	ND	ND	124			Meng and Gerba 1996
Adenovirus type 41	PLC / PRF / 5 cell line	LP	23.6	ND	ND	111.8			Meng and Gerba 1996

Yours sincerely



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