

## 論文の内容の要旨

論文題目      Kinetics of virus inactivation by disinfection in drinking water treatment  
(浄水処理の消毒工程におけるウイルス不活化の速度論的解析)

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Virus is one of the major microbial contaminants to cause waterborne diseases. Due to its low infectious dose, the acceptable concentration in drinking water is extremely low. This requires the regulators to achieve a high reduction through water treatment. The conventional physical treatment has limited capacity to remove viruses: approximately 0 – 3-log for the activated sludge process (Hata et al., 2013; Katayama et al., 2008; Sano et al., 2016), 2-log for coagulation-sedimentation, and <1-log for rapid-sand filtration (Asami et al., 2016; Kato et al., 2018) in full-scale treatment plants. Thus, the current treatment system virtually relies on the disinfection process for reducing viruses. The allocable log reduction value (LRV) of the chemical disinfection is up to 6-log for chlorination, UV irradiation, and ozonation (Olivieri et al., 2016; Soller et al., 2018). Therefore, the efficacy and potential uncertainty of disinfection efficiency on virus reduction should be carefully examined.

In chapter 3, the inactivation kinetics of viruses were analyzed by a continuous quench flow reactor. Ozone has a strong oxidation power that allows effective inactivation of waterborne viruses. Few studies have accurately measured the kinetic relationship between virus inactivation and ozone exposure, because the high reactivity of ozone makes it difficult to measure them simultaneously. A continuous quench flow system (CQFS) is a possible solution for analyzing such a fast reaction; however, previous studies reported that CQFS provided different results of inactivation rate constants from the batch system. The objectives of this study were (1) to develop a CQFS to evaluate the kinetics of microbial inactivation accurately, (2) to evaluate the inactivation rate constants of the waterborne virus by ozone, and (3) to compare the results with previous studies. The results indicated that the simple plug flow

assumption in the reaction tube of CQFS led to an underestimation of the rate constants. The accurate measurement of rate constants was achieved by the pseudo-first-order reaction model that takes the residence time distribution (RTD; i.e., the laminar flow assumption) into account. The results of inactivation experiments suggested that the resistance of viruses were getting higher in the following order: Q $\beta$  < MS2, fr, GA < CVB5 Faulkner,  $\phi$ X-174, PV1 Sabin, CVB3 Nancy. Predicted CT values for 4-log inactivation ranged from 0.018 mg sec L<sup>-1</sup> (Q $\beta$ ) to 0.16 mg sec L<sup>-1</sup> (CVB3 Nancy strain). The required CT values for 4-log PV1 inactivation was 0.15 mg sec L<sup>-1</sup>, which was 166-fold smaller than those reported in the United States Environmental Protection Agency guidance manuals. The overestimation in previous studies was due to the sparse assumption of RTD in the reactor. Consequently, the required ozone CT values for virus inactivation should be reconsidered to minimize the health risks and environmental costs in water treatment.

In Chapter 4, the objectives of this study were (i) to examine a total of 35 environmental strains of F-RNA phage genotype GI collected in Tama and Sagami rivers for free chlorine resistance, and (ii) to develop the inactivation model to predict the overall inactivation efficiency of heterogeneous F-RNA phage GI strains by assuming a probability density function of free chlorine resistance. The results indicated that most environmental strains of F-RNA phage GI exhibited higher free chlorine resistance than MS2 and fr, laboratory strains of GI phage. The developed model suggested that the overall inactivation efficiency of GI phages was limited to 5.6 log and 5.3 log in Tama and Sagami river, respectively, in the case that 8 log MS2 inactivation was expected. Therefore, the heterogeneity in free chlorine resistance within specific reference pathogens should be incorporated into the model to accurately predict the inactivation efficiency in environmental water.

In chapter 5, the objectives were (1) to evaluate the variability in susceptibility to three major disinfectants (free chlorine (FC), UV254, and ozone) among environmental strains of coxsackievirus B5 (CVB5), (2) to characterize the genetic feature contributing to lower susceptibilities to the disinfectants, and (3) to develop a model to predict the overall inactivation efficiency of heterogeneous CVB5. A total of 12 strains of CVB5 and Faulkner strain were examined for disinfection susceptibility by bench-scale experiments. Inactivation kinetics were analyzed by the Chick-Watson model as a function of disinfectant exposure (i.e., CT value or UV dose). The whole genome was obtained by RNA sequencing. The disinfection susceptibilities were different by up to 3.4-fold in FC, 1.3-fold in UV254, and 1.8-fold in ozone among CVB5 strains. Interestingly, CVB5 in genogroup B exhibited significantly lower susceptibility

to FC and ozone than genogroup A, to which the Faulkner strain belongs. The capsid protein in genogroup B contained less number of sulfur-containing amino acids, which is readily reactive to oxidants. FC susceptibility showed a significantly positive correlation ( $r=0.66$ ,  $P<0.05$ ) with ozone susceptibility. To predict the overall inactivation efficiency of CVB5s, a probability density function (i.e. gamma distribution) of inactivation rate constants ( $k$ ) were incorporated into the conventional Chick-Watson model. The modified model indicated that 4.2-fold, 1.2-fold, and 1.5-fold larger CT or dose are required to achieve 6-log overall inactivation of heterogeneous CVB5 than the prediction based only on the lab strain (i.e. Faulkner stain) in FC, UV254, and ozone, respectively. The disinfection susceptibilities, especially in FC, were variable within the same genotype. Therefore, the homogeneous assumption of disinfection susceptibility should be avoided. A probability density function of disinfection susceptibility should be incorporated to predict the overall inactivation of reference pathogen.



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