Fate of Antibiotic Resistant Bacteria from Wastewater to Water Environment

Ryo HONDA¹, Norihisa MATSUURA¹, THAN Van Huy ², SORN Sovannlaksmy ², Yuta MORINAGA², Hiroe HARA-YAMAMURA ¹, Ryoko IKEMOTO-YAMAMOTO ¹, Toru WATANABE³

¹ Faculty of Geosciences and Civil Engineering, Kanazawa University, Kanazawa, Japan ² School of Environmental Design, Kanazawa University, Kanazawa, Japan ³ Faculty of Agriculture, Yamagata University, Tsuruoka, Japan

rhonda@se.kanazawa-u.ac.jp

Abstract – Municipal wastewater is a major source of the antibiotic resistant bacteria (ARB) in the environment. Wastewater treatment plants (WWTPs) are considered as "the final gate" to prevent ARB's spread into the environment. An important question on role of a WWTP in spread ARB is whether WWTP serves as a barrier to avoid the spread of ARB from wastewater, or as the reservoirs of ARB which are potentially discharged to the environment. We have investigated fate of antibiotic resistant bacteria in wastewater treatment process by using metagenomic analysis and culture assays. According to our recent studies and literature review, sludge bacteria are likely to have low abundance of antibiotic resistance when compared to cultivable fecal bacteria. Wastewater and activate sludge showed distinctly different antibiotic resistance gene (ARG) profile as well as 16S-based microbial community. Meanwhile, treated effluents were characterized to have both features of wastewater and sludge. These result implies that some of ARB in wastewater from fecal origins pass through the treatment and remain in treatment effluent with sludge bacteria. ARB in wastewater plays important roles in possible discharge of ARB through WWTP. It is important to focus on fate of ARB in wastewater to make WWTPs effective barrier to prevent ARB spread from wastewater into the environment.

Keywords: Antimicrobial resistance (AMR); Antibiotic resistance gene (ARG); Metagenome; E. coli; Wastewater treatment; Activated sludge