

Detection of the *sul1*, *sul2*, and *sul3* genes in sulfonamide-resistant bacteria from wastewater and shrimp ponds of north Vietnam

Phuong Hoa P.T., Nonaka L., Hung Viet P., Suzuki S.

Center for Marine Environmental Studies (CMES), Ehime University, Matsuyama, 790-8577, Japan; United Graduate School of Agricultural Science, Ehime University, Japan; Research Center for Environmental Technology and Sustainable Development (CETASD), Hanoi University of Science, Hanoi, Viet Nam

Abstract: To assess the presence and distribution of the *sul* genes (*sul1*, *sul2*, and *sul3*) and plasmids in human-mediated environments of north Vietnam, we examined a total of 127 sulfonamide-resistant (SR) bacterial isolates from four shrimp ponds (HNAQs), a city canal (HNCs) and three fish ponds that received wastewater directly from swine farms (HNPs). Results from the SR isolates revealed that *sul* genes were most frequently detected in the HNPs (92.0%), followed by HNCs (72.0%), and the HNAQs (43.0%). Among the *sul* genes detected, *sul1* was the most prevalent gene in all three environments (57.0, 33.0 and 60.0% in HNPs, HNAQs, and HNCs, respectively) followed by *sul2* (51.0, 19.0, and 20.0%, respectively) and *sul3* (14.0, 6.0, and 8.0%, respectively). All combinations of paired different *sul* genes were detected, with the combination between *sul1* and *sul2* being the most frequent in all three environments (20.0, 8.0, and 8.0% in HNPs, HNAQs, and HNCs, respectively). The combination of three *sul* genes was detected at low frequencies (2-3%) in the HNPs and HNAQs, and was absent in the HNCs. The *sul* genes were more frequently located on the chromosome than on plasmids. The identification of SR isolates positive for the *sul* genes and plasmids showed that *Acinetobacter* was the most dominant. Our study revealed that the *sul* genes were common in SR bacteria from the aquatic environments we examined from northern Vietnam. Wastewater from swine farms might be "hot spots" of the *sul* genes and plasmids and may be reservoirs for the exchange of the *sul* genes among bacteria. © 2008 Elsevier B.V. All rights reserved.

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Correspondence Address: Suzuki, S.; Center for Marine Environmental Studies (CMES), Ehime University, Matsuyama, 790-8577, Japan; email: ssuzuki@agr.ehime-u.ac.jp

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Authors with affiliations:

- Phuong Hoa, P.T., Center for Marine Environmental Studies (CMES), Ehime University, Matsuyama, 790-8577, Japan, United Graduate School of Agricultural Science, Ehime University, Japan
- Nonaka, L., Center for Marine Environmental Studies (CMES), Ehime University, Matsuyama, 790-8577, Japan
- Hung Viet, P., Research Center for Environmental Technology and Sustainable Development (CETASD), Hanoi University of Science, Hanoi, Viet Nam
- Suzuki, S., Center for Marine Environmental Studies (CMES), Ehime University, Matsuyama, 790-8577, Japan

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