

PCR SCREENING REVEALS THE EXISTENCE OF QUINOLONE RESISTANCE GENES IN ANTHROPOGENICALLY AFFECTED WATERWAYS OF BADULLA AND KANDY DISTRICTS

M.H.M.I.M. Gunawardane¹, C.D. Gamage^{2*}, S. Rajapakse¹, G.M.T.M. Herath², A.K.U.I. Karuadasa², E.W.M.A. Ekanayake², T. Furukawa³, M. Amarasiri³ and K. Sei³

¹Department of Molecular Biology and Biotechnology, Faculty of Science, University of Peradeniya, Peradeniya, Sri Lanka

²Department of Microbiology, Faculty of Medicine, University of Peradeniya, Peradeniya, Sri Lanka

³Department of Allied Health Sciences, Graduate School of Medical Sciences, Kitasato University, Japan

*chandika.gamage@med.pdn.ac.lk

Aquatic ecosystems serve as reservoirs for the emergence and dissemination of antibiotic resistance genes. Though fluoroquinolone resistance is of global concern, data from Sri Lanka is scattered and sparse. Therefore, we aimed to investigate the presence of quinolone resistance genes in two districts: Badulla and Kandy, to understand the magnitude of the distribution of fluoroquinolone resistance in the environment. We used molecular tools such as PCR amplification, DNA sequencing, and phylogenetic trees to evaluate the evolutionary relationship of the detected operational taxonomic units. We detected *quinolone resistance (qnr)* genes; *qnrA*, *qnrB*, and *qnrS* using PCR screening of environmental DNA samples collected from human-interacted waterways in those districts, using a convenient sampling method. Six out of 30 (20.0%) sites in the Kandy district and five out of 30 (16.7%) sites in the Badulla district harboured *qnr* genes. In both districts, the detection frequency of *qnrB* genes was relatively high compared to *qnrA* and *qnrS* genes. Two-sample-proportion tests conducted at a significance level of 0.05 showed no statistical difference between the *qnr* gene detection proportions observed between the two districts. The *qnr*-positive sites in the Kandy district were confined only to the samples from waterways adjacent to hospitals. However, in the Badulla district, we detected *qnr* genes from the waterways adjacent to dairy farms, agricultural fields, and hospitals. The presence of environmental bacteria comprised of antibacterial resistance genes is a significant health risk toward humans' wellbeing. Therefore, in-depth studies based on the One-Health approach are required to understand whether there is an interaction between intensive agriculture practice and the emergence of fluoroquinolone resistance in the environmental microbiome. The PCR protocols used during the study can be used as a rapid screening tool to detect *qnr* genes in countrywide environmental DNA samples.

Keywords: Aquatic ecosystem, Environmental DNA, Fluoroquinolones, Plasmid-mediated quinolone resistance (*qnr*), Rapid screening tool