Title:

Exploration of AMR Enrichment Techniques for Monitoring Environmental Waters and Wastewater

Authors:

M.F. Blair, K. Beck, and H. Bürgmann

Institution(s):

Eawag, Swiss Federal Institute of Aquatic Science and Technology, Department of Surface Waters - Research and Management, Kastanienbaum, Luzern

Abstract (300 words maximum): :

Antimicrobial resistance (AMR) is a complex global issue both within Switzerland and abroad. AMR is genetically encoded by thousands of ever-evolving antibiotic resistance genes (ARGs) with varying antibiotic targets, hosts, mechanisms of action, mobilities, and potencies. These factors make studying AMR a particularly challenging task that is further complicated by the numerous environments in which is it found, and the unique dynamics present within those environments. Metagenomics is one of a few tools that have been successfully utilized to broadly explore these complex dynamics through deep sequencing of environmental DNA and identification of thousands of ARGs simultaneously. While a promising tool, metagenomics remains limited in its application for widespread environmental monitoring, in part due to the cost of deep sequencing that is required to capture low abundant targets. However, recent advancements in enrichment-focused library preparations show promise in improving the feasibility of AMR monitoring by more effectively utilizing sequencing depth on targets of interest, in the process eliminating the need for more costly, deeper sequencing.

This study looks to explore enrichment-based library preparations and their suitability for applications in environmental waters. Specifically, four enrichment kits are being compared across a range of environmental samples with varying degrees of suspected AMR contamination and potential inhibition. The selected sample matrix is representative of environmental waters that are of interest to AMR researchers including wastewater influent, wastewater effluent, wastewater impacted lake water, and non-wastewater impacted lake water. Overall, the study design will allow for a direct comparison of enrichment mechanism (i.e. hybridization capture vs amplification), gene selection (ranging from approximately 400 to over 2000 shared and unique ARGs), kit performance, associated costs, ease of implementation, and suitability for their application in environmental waters while also assisting in characterizing the impact of wastewater discharge on water sources through a more targeted assessment of AMR.