

Harnessing Deep-Level Metagenomics to Explore the Three Dynamic One Health Areas: Healthcare, Domiciliary and Veterinary

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Abstract : Deep-level metagenomics offers a useful technical approach to explore the three dynamic One Health axes: healthcare, domiciliary and veterinary. There is currently limited understanding of the composition of complex biofilms, natural abundance of AMR genes and gene transfer occurrence in these ecological niches. By using a newly established small-scale complex biofilm model, COMBAT has the potential to provide new information on microbial diversity, antimicrobial resistance (AMR)-encoding gene abundance, and their transfer in complex biofilms of importance to these three One Health axes. Shotgun metagenomics has been used to sample the genomes of all microbes comprising the complex communities found in each biofilm source. A comparative analysis between untreated and biocide-treated biofilms is described. The basic steps include the purification of genomic DNA, followed by library preparation, sequencing, and finally, data analysis. The use of long-read sequencing facilitates the completion of metagenome-assembled genomes (MAG). Samples were sequenced using a PromethION platform, and following quality checks, binning methods, and bespoke bioinformatics pipelines, we describe the recovery of individual MAGs to identify mobile gene elements (MGE) and the corresponding AMR genotypes that map to these structures. High-throughput sequencing strategies have been deployed to characterize these communities. Accurately defining the profiles of these niches is an essential step towards elucidating the impact of the microbiota on each niche biofilm environment and their evolution.

Keywords : COMBAT, biofilm, metagenomics, high-throughput sequencing

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