

EGU22-2616

<https://doi.org/10.5194/egusphere-egu22-2616>

EGU General Assembly 2022

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Distribution of pathogens and antibiotic resistance genes in the vadose zone of soil-aquifer treatment (SAT) system.

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The main objective of this study was to quantify the distribution of pathogens and antibiotic resistance genes in the vadose zone of the soil aquifer treatment (SAT) system. Soil samples were collected from a treated wastewater infiltration basin to a depth of 25 m in two sampling events: (i) at the end of flooding and infiltration and (ii) following three days of drying before the subsequent flooding event. Viable count parallely of bacteria compared with microscopic live/dead count and enzymatic activity FDA hydrolysis. The abundance of the total bacteria, coliform, antibiotic resistance bacteria (ARB), were examined. In addition, total genomic DNA was extracted from soil samples (n-28 for both flooding and drying cycle), and quantitative PCR (qPCR) was used to determine the relative abundance of antimicrobial resistance genes (ARGs), including 1 integron-integrase *intI1*, *blaTEM*, *blaCTX-M-32*, *sul1*, *qnrS*.

In both sampling events, the results demonstrate that the distribution of antibiotic resistance genes in the vadose zone exhibits a similar pattern to the one obtained for the examined pathogen. We observed a high concentration of pathogens in topsoil layers and a gradual decline with depth. In this presentation, the profile obtained will be described and discussed with pathogens and ARGs transport and retention in the SAT system.