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Occurrence of Kanamycin-Resistant Bacteria Relative to Anthropogenic Pollution Along Richland Creek in Nashville, TN

Jolene Ho Mach

jolene.mach@bruins.belmont.edu

Annie Le

annie.le@bruins.belmont.edu

Brandon Torres Ramirez

brandon.ramirez@bruins.belmont.edu

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1Paulson, J. R., Mahmoud, I. Y., Al-Musharafi, S. K., & Al-Bahry, S. N. (2016). Antibiotic Resistant Bacteria in the Environment as Bio-Indicators of Pollution. *The Open Biotechnology Journal*, 10(1), 342–351. <https://doi.org/10.2174/1874070701610010342> 2Truong,T.;Hoang,T.L.; Tran, L.T.; Pham, T.P.T.; Le, T.-H. Prevalence of Antibiotic Resistance Genes in the Saigon River Impacted by Anthropogenic Activities. *Water* 2021,13,2234. <https://doi.org/10.3390/w13162234> 3Young, S., Juhl, A., & O'Mullan, G. D. (2013). Antibiotic-resistant bacteria in the Hudson River Estuary linked to wet weather sewage contamination. *Journal of Water and Health*, 11(2), 297–310. <https://doi.org/10.2166/wh.2013.131> [ps://doi.org/10.2166/wh.2013.131](https://doi.org/10.2166/wh.2013.131)

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The overuse of antibiotics has caused an increase in antibiotic-resistant (AR) bacteria, which is a serious public health concern. Previous studies showed a significant correlation between anthropogenic pollution and AR bacteria. This project aims to identify AR bacteria in Richland Creek relative to local anthropogenic pollution. Water samples were collected at four locations along Richland Creek in Nashville, Tennessee. Bacteria resistant to the antibiotic kanamycin were isolated from the water samples, identified to genera using DNA barcoding, and compared among the sites. We expect to see a greater abundance and diversity of kanamycin-resistant bacteria closer to the end than near the head of the creek. This research project can help describe the diversity of AR bacteria species present in the stream in different areas of Nashville and has public health consequences if the disparities in the distribution of AR bacteria correlate to human activity and/or socioeconomic differences along the stream.