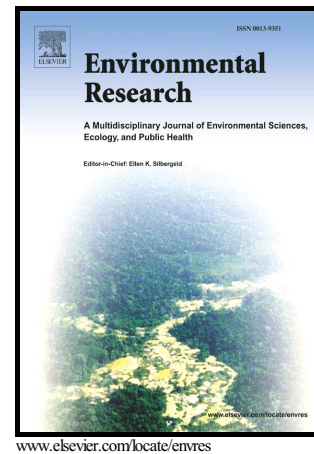


# Author's Accepted Manuscript

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PII: S0013-9351(18)30509-7  
DOI: <https://doi.org/10.1016/j.envres.2018.09.022>  
Reference: YENRS8078

To appear in: *Environmental Research*

Received date: 7 June 2018  
Revised date: 21 August 2018  
Accepted date: 17 September 2018

Cite this article as: Blaise P. Bougnom, Cheikna Zongo, Alan McNally, Vito Ricci, François X. Etoa, Sören Thiele-Bruhn and Laura J.V. Piddock, Wastewater used for urban agriculture in West Africa as a reservoir for antibacterial resistance dissemination, *Environmental Research*, <https://doi.org/10.1016/j.envres.2018.09.022>

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## Wastewater used for urban agriculture in West Africa as a reservoir for antibacterial resistance dissemination

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### Summary

State of art metagenomics were used to investigate the microbial population, antibiotic resistance genes and plasmids of medical interest in wastewater used for urban agriculture in Ouagadougou (Burkina Faso). Wastewater samples were collected from three canals near agricultural fields in three neighbourhoods. Assessment of microbial population diversity revealed different microbial patterns among the different samples. Sequencing reads from the wastewaters revealed different functional specializations of microbial communities, with the predominance of carbohydrates and proteins metabolism functions. Eleven pathogen-specific and 56 orthologous virulence factor genes were detected in the wastewater samples. These virulence factors are usually found in human pathogens that cause gastroenteritis and/or diarrhoea. A wide range of antibiotic resistance genes was identified; 81 are transmissible by mobile genetic elements. These included seven different extended spectrum  $\beta$ -lactamase genes encoding synthesis of four enzyme families, including two metallo- $\beta$ -lactamases (*bla*<sub>AIM-1</sub> and *bla*<sub>GES-21</sub>). Ten different incompatibility groups of *Enterobacteriaceae* plasmid replicons (ColE, FIB, FIC, FII, P, Q, R, U, Y, and A/C), and 30 plasmid replicon types from Gram-positive bacteria. All are implicated in the wide distribution of antibiotic resistance genes. We conclude that wastewater used for urban agriculture in the city represents a high risk for spreading bacteria and antimicrobial resistance among humans and animals.

**Keywords:** Antimicrobial resistance, metagenomics, urban agriculture, low and middle-income countries

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