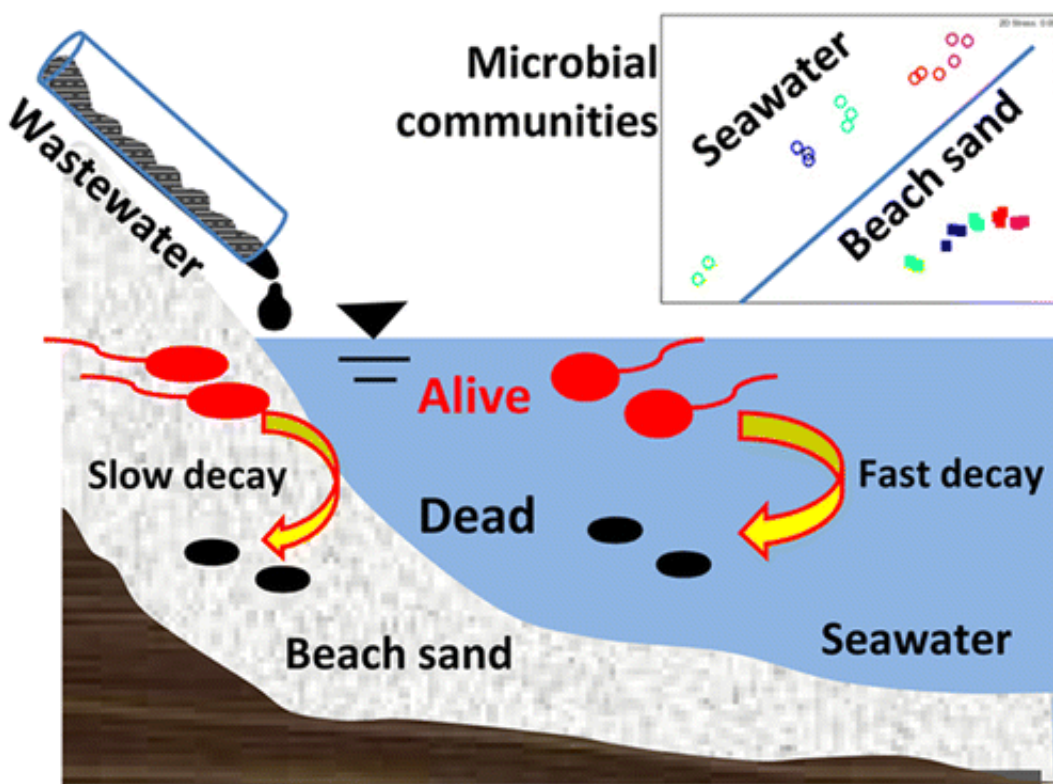


Attention beachgoers: Fecal contamination affects sand more than water

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"No swimming" signs have already popped up this summer along coastlines where fecal bacteria have invaded otherwise inviting waters. Some vacationers ignore the signs while others resign themselves to tanning and playing on the beach. But should those avoiding the water be wary of the sand, too? New research in the ACS journal *Environmental*

Science & Technology investigates reasons why the answer could be "yes."

Sewage-contaminated coastal waters can lead to stomach aches, diarrhea and rashes for those who accidentally swallow harmful microbes or come into contact with them. But over the past decade, scientists have been finding fecal bacteria in beach sand at levels 10 to 100 times higher than in nearby seawater. Tao Yan and colleagues wanted to find out why.

In the lab, the researchers created microcosms of beach sand and seawater contaminated with sewage to see how the overall bacterial populations, including fecal dwellers responsible for causing illness, would change over time. They found that microbial communities tended to decay much slower in the simulated beach [sand](#) environment than in the water, which could help explain why more [fecal bacteria](#) are found on sandy beaches affected by wastewater pollution than in the waves.

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More information: Differential Decay of Wastewater Bacteria and Change of Microbial Communities in Beach Sand and Seawater Microcosms, *Environ. Sci. Technol.*, Article ASAP. [DOI: 10.1021/acs.est.5b01879](https://doi.org/10.1021/acs.est.5b01879)

Abstract

Laboratory microcosm experiments were conducted to determine the decay kinetics of wastewater bacteria and the change of microbial communities in beach sand and seawater. Cultivation-based methods showed that common fecal indicator bacteria (FIBs; *Escherichia coli*, enterococci, and *Clostridium perfringens*) exhibited biphasic decay patterns in all microcosms. Enterococci and *C. perfringens*, but not *E. coli*, showed significantly smaller decay rates in beach sand than in

seawater. Cultivation-independent qPCR quantification of 16S rRNA gene also showed significantly slower decrease of total bacterial densities in beach sand than in seawater. Microbial community analysis by next-generation sequencing (NGS) further illustrated that the decreasing relative abundance of wastewater bacteria was contrasted by the increase in indigenous beach sand and seawater microbiota, and the overall microbial community dynamics corresponded well with the decay of individual FIB populations. In summary, the differential decay of wastewater bacteria in beach sand and in seawater provides a kinetic explanation to the often-observed higher abundance of FIBs in beach sand, and the NGS-based microbial community analysis can provide valuable insights to understanding the fate of wastewater bacteria in the context of indigenous microbial communities in natural environments.

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