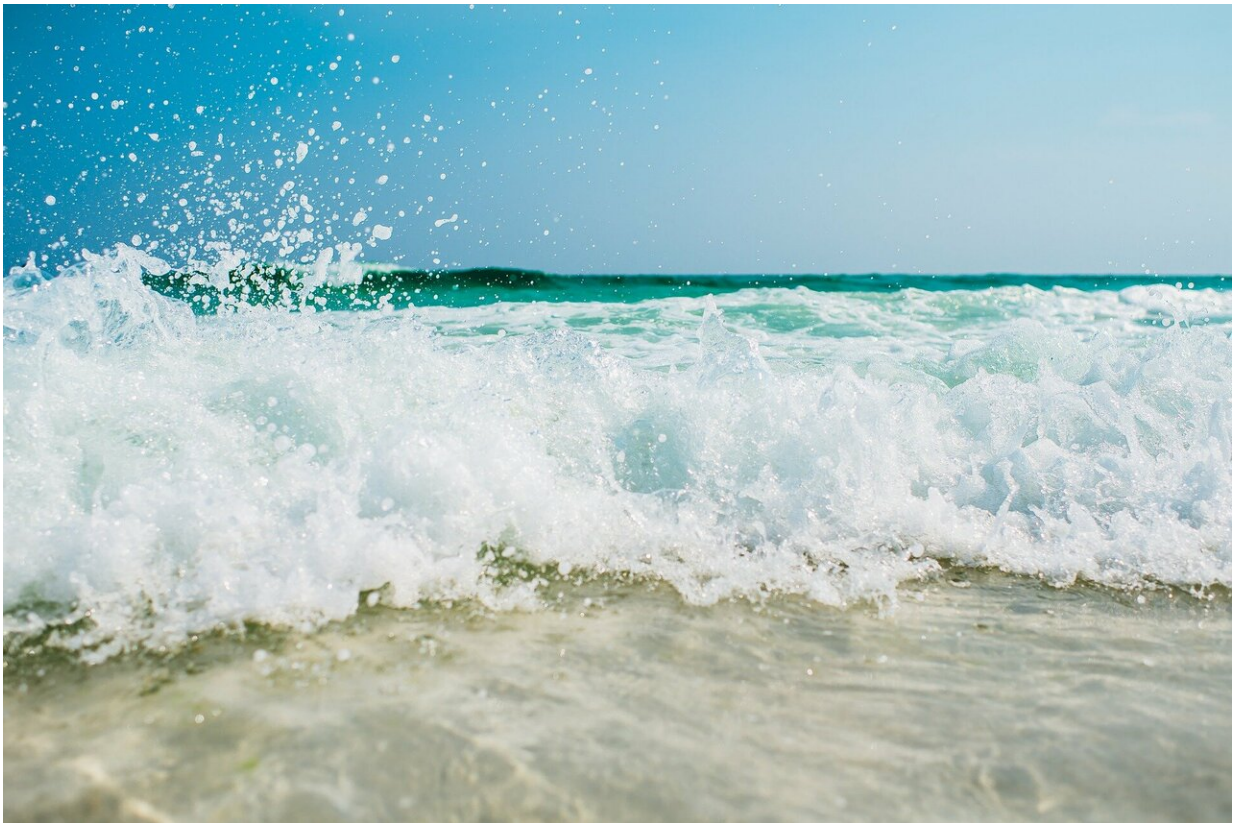


Study: Presence of *E. coli* is a poor indicator of fecal pollution

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Escherichia coli is best known as a gastrointestinal pathogen in warm-blooded animals. For the last hundred years, its presence on beaches has been assumed to indicate fecal pollution, leading to beach closures. New

research examines the genetic basis for recent findings that many strains of *E. coli* thrive harmlessly in soil, water and beach sand. The research is published in *Applied and Environmental Microbiology*.

In the study, the researchers isolated *E. coli* from human sewage, gull droppings and beach sand. They then buried bacteria from each of the three sources together in sand, inside small polyvinyl containers with tiny holes that could let moisture and oxygen pass in and out, but that kept the bacteria inside. These were buried for 45 days, half a meter deep, in sand on a freshwater beach on Lake Michigan.

There are core genes that are mostly identical in different strains of *E. coli*. "Accessory genes" often differ from one strain to another. That's partly because they can be acquired by "horizontal transfer," mostly from other strains of *E. coli*, though possibly from other closely related bacteria. Horizontal transfer of accessory genes is a quick way to attain new capabilities, such as the ability to thrive in extra-intestinal habitats such as beach sand.

At the end of the 45 days, the investigators unearthed the containers. They compared the accessory genes of the *E. coli* that survived the 45-day burial in beach sand with those in *E. coli* that had not undergone the ordeal, finding several accessory genes related to survival in beach sand.

The impetus for the research was the lack of ways to differentiate *E. coli* indicating the presence of [fecal pollution](#) from harmless conspecifics that occur naturally in [beach sand](#), the latter leading to "unnecessary beach closings, with lost recreational and economic opportunities," said co-author Elizabeth Alm, Ph.D., Professor, Department of Biology and Institute of Great Lakes Research, Central Michigan University.

"This work has real world implications for the field of applied and

public health microbiology," said first author Sandra McLellan, Ph.D., Professor, School of Freshwater Sciences, University of Wisconsin-Milwaukee. Previous work examining the evolution of *E. coli* has focused on pathogens, with much less attention paid to commensal strains, and virtually no research on strains that thrive outside of the host in a secondary environment.

"Perhaps the study's most striking finding was that many of the genomic traits enriched in the surviving isolate collections are broadly distributed across strains of *E. coli*," said McLellan. "The one exception to that broad distribution is the B2 phylogroup of *E. coli*, which contains mostly human pathogens."

Previous research demonstrated that B2 has been selected for in human hosts. In the current study, the investigators show that traits linked to survival in the environment appear to be ancestral in *E. coli*, but largely lost in B2 lineages.

The research, McLellan says, "may finally lead to development of indicators that are more directly related to human health."

More information: Natalie A. Rumball et al, Genetic Determinants of *Escherichia coli* Survival in Beach Sand, *Applied and Environmental Microbiology* (2022). [DOI: 10.1128/aem.01423-22](https://doi.org/10.1128/aem.01423-22)

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