

Study finds evidence of bacteria spread throughout the global ocean

March 5 2013, by Bob Yirka



(Phys.org) —A joint team of American and British researchers has found evidence that suggests that all bacteria in the ocean migrate to all parts of the ocean. In their paper published in the *Proceedings of the National Academy of Sciences*, the group says that their findings indicate that different ocean locations account for different proportions of the number of bacteria to be found, rather than different bacteria altogether.

To gain a better understanding of bacteria in the ocean, the research team used monthly samples of seawater pulled from the English Channel over the course of five years (2003-2008). To distinguish one [species of bacteria](#) from another and to compare what was found with other species throughout the worlds' oceans, the researchers sequenced their DNA.

[Bacterial DNA](#) sequencing doesn't find every instance of every bacteria in a sample in one go, instead, it takes several passes—the higher the number of passes, the more accurate the results become. To uncover all the species in a sample requires millions of passes, a process known as deep sequencing. The researchers were able to perform such sequencing on just one of the samples from the English Channel, but remarkably found that 44 percent of all known oceanic bacteria were represented. This led them to theorize that if they were to deep sequence even deeper, they'd eventually prove that 100 percent of the world's bacteria would be represented, which they say means that all of the bacteria in the world's oceans is in all of the world's oceans, just in different amounts.

This means that "unique" bacteria found near hot vents, for example, would also be found in the [Chesapeake Bay](#), if scientists looked hard enough. Likewise bacteria found in mangrove colonies in the tropics would be found in seawater beneath [arctic ice](#). The researchers acknowledge that their conclusions represent a bit of a jump, but add that they plan to back them up by continuing to analyze samples and perform deep sequencing analysis until they gather conclusive proof. They note that prior research has shown that any small bit of water in the ocean can be dispersed to the rest of the ocean in as few as 10,000 years. Bacteria in the ocean have had millions of years to do the same.

More information: Evidence for a persistent microbial seed bank throughout the global ocean, *PNAS*, Published online before print March 4, 2013, [doi: 10.1073/pnas.1217767110](https://doi.org/10.1073/pnas.1217767110)

Abstract

Do bacterial taxa demonstrate clear endemism, like macroorganisms, or can one site's bacterial community recapture the total phylogenetic diversity of the world's oceans? Here we compare a deep bacterial community characterization from one site in the English Channel (L4-DeepSeq) with 356 datasets from the International Census of

Marine Microbes (ICoMM) taken from around the globe (ranging from marine pelagic and sediment samples to sponge-associated environments). At the L4-DeepSeq site, increasing sequencing depth uncovers greater phylogenetic overlap with the global ICoMM data. This site contained 31.7–66.2% of operational taxonomic units identified in a given ICoMM biome. Extrapolation of this overlap suggests that 1.93×10^{11} sequences from the L4 site would capture all ICoMM bacterial phylogenetic diversity. Current technology trends suggest this limit may be attainable within 3 y. These results strongly suggest the marine biosphere maintains a previously undetected, persistent microbial seed bank.

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