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Venter takes a shot at the sea

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New horizons in oceanography and genomics were opened up this week with the [publication](#) by Craig Venter and colleagues of a pilot study to shotgun clone and sequence microbial genomes filtered from seawater in the Sargasso Sea, off the coast of Bermuda (*Science*2004, DOI:10.1126/science.1093857).

More than 1.2 million new genes were identified, revealing a level of microbial diversity in seawater that was only previously guessed at. More than 700 of those were new rhodopsin-like photoreceptors.

"At the time of writing the paper, there were roughly 180,000 genes and proteins in [Swiss-Prot](#) [the curated protein database]," Venter told us. "In one paper, we're adding 1.2 or 1.3 million [genes]"

Venter said his group had extended the shotgun method to take it from single genomes to entire environments. "The level of discovery is truly extraordinary," he said.

The results, published in *Science*, suggest there must be between 10 and 20 billion different genes in the planet Earth's repertoire, said Venter, who heads the Institute for Biological Energy Alternatives.

"This leap gives us a new method and new tools to actually get access to that and start to understand it. I think it's more important as a method and a philosophy, an approach," he said.

[Sallie Chisholm](#), from the Department of Civil and Environmental Engineering at the Massachusetts Institute of Technology (MIT), said it was not surprising to find all these new genes, considering less than 1% of the microbes that live in the ocean are in culture.

"We basically know very little about the genomic composition of the microbial community in the ocean, and the genes that we know about are only from the tiny fraction of cultured organisms," she told us.

Chisholm, who was not involved in the study, said she didn't think people in the field would be surprised that Venter had found such extraordinary diversity. "That's what we've been working on, but it's tremendously exciting to see the differences, to see it in these sequences."

[Martin Polz](#), from the same department at MIT, told us that traditionally, the marker for estimating diversity in the environment had been ribosomal RNA genes.

His group had also been using a large-scale approach to estimate how many of those genes are present in a typical ocean sample. "I would say there's about a few hundred [of] what we might call species out there per milliliter of sea water," he said.

At least 1800 different species are represented by the 1.045 billion base pairs of non-redundant sequences generated from the survey, Venter estimates. This includes 148 novel bacterial phylotypes.

[Paul Falkowski](#), at Rutgers University, who wrote an accompanying article in *Science*, said he was impressed with the technical prowess of Venter's feat but felt that there wasn't yet a lot of scientific 'meat'.

"There is a long way before we can use this as a scientific tool in an oceanographic context," he told us. "I think if Craig collaborates - or if people with his capabilities collaborate - with microbial ecologists with a lot of experience in the ocean, he can make a lot of headway pretty quickly."

What oceanographers are trying to do is to look for patterns of nature on large temporal and spatial scales, he said. Sampling the oceans using this approach was not going to be done easily or cheaply by sequencing the genomes on a shotgun basis.

"There has to be some kind of approach that is a kind of compromise between this incredible quasi-industrial technique and a lower resolution technique, such as the ribosomal RNA analyses," he said.

Venter also told a news conference that he has begun an expedition around the world partly inspired by Charles Darwin's voyages in the 1830s. His aim is to sample ocean water every 200 miles, as well as some places on land. His yacht, the *Sorcerer II*, which is in the Galapagos Islands, has been converted into a research vessel.

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