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Spanish researchers sequence the genome of global deep ocean

by Staff Writers
Madrid, Spain (SPX) Jun 17, 2013

A team of Spanish researchers, coordinated by the Spanish National Research Council (CSIC), has started to sequence the genome of the global deep ocean. They are using more than 2,000 samples of microorganisms collected in the Atlantic, Indian and Pacific Oceans during the Malaspina Expedition. This collection of marine microbial genomic, the first in the world on a global scale, will provide new clues about a reservoir of biodiversity yet to explore, considering that it could imply the discovery of tens of millions of new genes in the coming years.



Malaspinomics preliminary results reveal a wealth of unknown species of microorganisms in the deep ocean, characterized by an intense biological activity. Credit: CSIC Communications Department.

The works of sequencing (framed in the Malaspinomics project) focus on the viruses, bacteria and protists that inhabit the ocean to 4,000 meters deep. Most of the biomass of marine organisms is composed of microorganism. Of these, a 72% inhabit the dark ocean, from 200 meters deep. However, so far, the DNA or RNA sequencing had been almost exclusively limited to the ocean surface waters.

Malaspinomics preliminary results reveal a wealth of unknown species of microorganisms in the deep ocean, characterized by an intense biological activity. Specifically, 60% of the bacterial species of the deep ocean detected by massive sequencing techniques are unknown.

Carlos Duarte, CSIC researcher and coordinator of Malaspina Expedition, asserts: "Malaspinomics means a leap forward because, for the first time, we are analyzing samples from the deep ocean, covering the great oceans. The new protocols of sequencing and analysis allow us to extract quite more information than in previous studies, which were limited to specific regions or surface waters, to an unprecedented level of resolution".

Researchers have already detected some bacteria which are capable of degrading highly toxic compounds that have gradually gathered in the seabed. Silvia Acinas, CSIC researcher at the Institute of Marine Sciences (ICM-CSIC), states: "We have found bacteria with metabolic pathways that are capable of degrading methylmercury derived from human activity. Other bacteria, the methanotrophs, use the degradation products of these toxic compounds as a carbon and energy source.

The detection of these recycling plants in the deep ocean allows us to identify those regions with the greatest accumulation of toxic substances and to use these bacteria as biosensors of the ecological status of such an unknown environment so far".

Analysis are being conducted by a team that includes researchers from the Institute of Marine Sciences (CSIC), the Mediterranean Institute for Advanced Studies -joint centre of CSIC and the University of the Balearic Islands (UIB)- and the National Genome Analysis Centre of Barcelona (CNAG). They also count on the collaboration of MareNostrum -National Supercomputing Centre (BSC) in Barcelona-, the Joint Genome Institute (USA) and the European Molecular Biology Laboratory (Germany).

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WATER WORLD

Ocean acidification killing oysters by inhibiting shell formation

Washington DC (SPX) Jun 17, 2013

For the past several years, the Pacific Northwest oyster industry has struggled with significant losses due to ocean acidification as oyster larvae encountered mortality rates sufficient to render production no longer economically feasible. Now, a new study has documented why oysters appear so sensitive to increasing acidity. It isn't necessarily a case of acidic water dissolving their she ... read more



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Millions of new genes

According to Josep Maria Gasol, CSIC researcher at the Institute of Marine Sciences and leader of the Malaspina block of microorganisms, samples "are especially valuable because they come from areas that have been poorly studied in a scientific sense up to now, such as the Indian and South Pacific Oceans. Recent evidences suggest that the deep ocean contains active and highly diverse bacteria, as well as archaea, protists, viruses and zooplankton".

Jesus Maria Arrieta, CSIC researcher at the Mediterranean Institute for Advanced Studies, explains: "The number of marine species used as a source of genes with commercial interests grows at a rate of 12% per annum. The biotechnological potential of marine organisms is immense, especially in the deep ocean. We hope that the genes collected in Malaspina Expedition open the door to multiple biotechnological applications in fields such as bioenergy, food or cosmetics".

Duarte emphasizes: "This collection has an incalculable strategic value because no country has this kind of samples on a global scale. We are going to provide international databases with hundreds of millions of new genes with unknown metabolic capabilities so far and with potential applications. When we started to manage Malaspina, we didn't expect that it was possible to sequence in Spain. However, we have the necessary technology now to carry it out".

[Next Gen Sequencing,Spain](http://WWW.lifesequencing.com)

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