Hunting for new genes by sequencing seas samples

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(Phys.org) —Mass DNA sequencing has led to a better knowledge of marine micro-organisms in their environment and helps to discover new genes of interests. However, it is only part of the answer for biotech applications.

One litre of sea water contains about one billion bacteria. This represents at least one thousand species, in addition to the single-cell organisms

different from bacteria—referred to as protists—which make up plankton, according to Daniel Vaulot, a researcher at the Station biologique de Roscoff, located in the Brittany region of France. Studying each of these organisms by mass-sequencing their genome could lead up to discover new species. It could also help study species potentially interesting for fundamental research on the origins of life and climate change, or for applications in the industry. Raising the awareness of the possibilities of marine genomics among the wider research and industry communities is precisely what the EU-funded Marine Genomics for Users (MG4U) project is designed to do. Its coordinator, Bernard Kloareg who is the director the Roscoff station, is himself an advocate of marine genomics.

The types of technologies that the project is attempting to showcase include metagenomics, which has been used extensively since the 2000s. Few of the organisms found in sea water samples can be cultivated in the laboratory to extract enough DNA for genome sequencing. Instead of deciphering each genome one by one, geneticists had the idea to mass-sequence the whole sea water sample in a single run. This involves cutting DNA extracted from the sample into thousands of small fragments. These are then processed by high-throughput sequencing machines. As the DNA originating from each individual of a given species is randomly cut, the fragments overlap and longer sequences can therefore be reconstructed.

This technique does not allow deciphering complete genomes. But it could help to detect unknown genes possibly belonging to new species. It can also be used to assess the presence of well-documented genes in the samples. "To do so, researchers need to compare their results with huge databases of genetic sequences", Vaulot tells youris.com.

Originally, metagenomics helped marine biologists to study the relationship between genomes and their environment and to discover

metabolic processes relevant to applications. For example, extensive sampling campaigns have been carried out, by expeditions such as Tara Oceans, during its round-the-globe sail from 2009 to 2011. Subsequent programme Oceanomics is planning to sequence the Tara samples at the Genoscope facility in Evry, France. These samples may contain bacteria or algae, which host enzymes able to degrade or synthesise molecules of interest in the field of pharmaceuticals, biofuels, etc. By transferring the genes coding for enzymes of interest, identified as a result of metagenomics, into standard bioprocessing bacteria contained in bioreactors, these molecules could be produced on an industrial scale. But this is not so simple.

Although the potential applications brought by marine metagenomics are real, they have not yet delivered significant innovations. "Marine metagenomics is not as developed as 'terrestrial' metagenomics used, for example, in the field of human health, because investments in marine research have been lower. So far, it has not yielded a molecule that became a blockbuster," comments Patrick Durand, head of the Biotechnology and Marine Resources Unit at Ifremer, the French research institute for exploitation of the sea, based in Nantes, France. He tells youris.com: "It may take a while before it happens."

Indeed, even though industries such as the biotech sector are avid of novel applications, metagenomics may be the kind of tools required to bring them one step closer to finding the solutions they seek. "The biotech industry is looking for enzymes that will be combined to synthesise artificial compounds on an industrial scale," says Jürgen Eck, CEO of a bioactive compound discovery biotech company called Brain, which is based in Zwingenberg, near Frankfurt, Germany. For this purpose, metagenomics is a useful tool to screen biodiversity in search for these enzymes, as the latter are coded by a small number of genes.

However, finding actual therapeutic solutions may be much more

complex. "Bioactive compounds, like potential anti-cancer agents, are often the product of complex metabolic ways involving several genes," Eck tells youris.com, explaining that it would make it difficult to clone them into bioprocessing bacteria susceptible to produce desired compounds. He adds: "Improving the traditional approach of cultivating organisms is preferable in this case."

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