

Hidden communities revealed by new DNA sequencing

October 20 2010

(PhysOrg.com) -- Half a bucket full of sand from an unassuming beach in Scotland has revealed a far richer and more complex web of microscopic animals living within the tiny 'ecosystem' than have previously been identified.

A paper published in the new online journal [Nature Communications](#) shows how this was achieved using a new method that allows DNA sequencing of large communities of very small multi-celled creatures and animals. The new technique, being dubbed environmental metagenetics, has the potential to transform current methods of species identification and environmental analysis, providing new insights into the structure and composition of those communities as well as new potential applications.

The work was conducted by an international team, led by Dr. Simon Creer at Bangor University's School of Biological Sciences, and funded by the Natural Environment Research Council. The project was part of the PhD thesis work of Vera Fonseca, at Bangor University's School of Biological Sciences, funded by the Portuguese Foundation for Science and Technology.

The team were able to identify the genetic diversity of almost all the animal species ranging between 45 microns- 1mm in size throughout the Scottish beach site. They were able to quantify numbers of different groups of animals for the first time. Developed to be used to assess communities within seabed sediments, the technique could be adopted

for any ecosystem inhabited by microscopic organisms.

“The sequencing techniques are orders of magnitude faster and cheaper than traditional approaches. To complete the same work using traditional methods would take unquantifiable centuries of working hours to manually identify each individual species from a sample,” said Vera Fonseca, lead author and PhD student at Bangor University.

The new method paves the way for future research into topics as diverse as climate change, the effect of pollution on ecosystem health and the distribution of microbial life from the deep sea to the polar environments.

“Adding the DNA sequence of the samples to a database will ultimately enable scientists to track where individual species occur- and over time- to gauge their reaction to climate change or to pollution or other human induced events,” explains Dr. Creer of Bangor University.

Professor Kelley Thomas, a collaborator from the University of New Hampshire is already using identical approaches to assess the impact of the recent oil spill on the microbial metazoan communities of the Gulf of Mexico.

“By being able to look objectively at all animal groups simultaneously, for the very first time, we have been able to identify substantial genetic diversity and quantify the relative abundance of different forms of animal life,” says Dr. Creer of Bangor University’s School of Biological Sciences.

“For example, the data revealed that a group of predatory flatworms has been overlooked in traditional assessments. This is akin to a savannah grassland ecologist realising that the whole cat family had previously been missed in ecological studies of the savannah grassland.”

One of the paper's authors, Prof. P John D Lamshead of the University of Southampton's School of Ocean & Earth Science commented:

"In the early eighties, I spent three years studying ten thousand microscopic worms from the Firth of Clyde by eye, one at a time, using high power light microscopes, and identified 113 species. Our new DNA study identified 182 types of nematode worms from the same region in just one month."

Provided by Bangor University

Citation: Hidden communities revealed by new DNA sequencing (2010, October 20) retrieved 6 May 2024 from <https://phys.org/news/2010-10-hidden-revealed-dna-sequencing.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.