

New genomic technique uncovers transcriptome of a reef-building coral

May 12 2009



This is a picture of coral. Credit: Meyer et al.

Using a new technique for cDNA preparation combined with the latest sequencing methods, researchers have uncovered the larval transcriptome of a reef-building coral (*Acropora millepora*). Their study, described in the open access journal *BMC Genomics*, features the most extensive database of genes and genetic markers currently available for any coral.

A collaborative team of researchers from the University of Texas at Austin and Indiana University, led by Mikhail Matz and John Colbourne, developed a new method for transcriptome analysis based on next-

generation 454 sequencing technology. De novo transcriptome analysis is a cost-efficient alternative to genome sequencing when the goal is discovery of protein-coding genes and genetic markers. According to Eli Meyer, the primary author on the paper, "Our method specifically addresses problems that had hindered the sequencing of transcriptomes with 454, such as homopolymer (A/T) tracks, adaptor artifacts, and uneven transcript coverage".

The new method requires as little as 1 microgram of total RNA, eliminates the need for a strand-selection step prior to emulsion PCR, and results in 2-5 fold greater 454 sequence output than in any previously reported attempts. Meyer said, "These tools allow for the rapid development of sequence resources for any organism at a low cost - a few weeks and a few thousand dollars".

The protocol outlined in the paper was developed for 454-FLX. The current version of the protocol (available from the authors' website) is already modified and tested to work with the latest 'Titanium' version of 454.

As well as demonstrating the technical power of the method, the study has identified approximately 11,000 genes on the basis of sequence similarity with known proteins, over 30,000 markers of [genetic variation](#), and a number of novel candidate genes for stress-related processes. The characterization of the larval transcriptome for this widely studied coral will enable research into the biological processes underlying stress responses in corals and their evolutionary adaptation to global climate change.

Find the coral genes online at www.bio.utexas.edu/research/matz_lab/matzlab/454.html.

Source: BioMed Central ([news](#) : [web](#))

Citation: New genomic technique uncovers transcriptome of a reef-building coral (2009, May 12) retrieved 24 April 2024 from <https://phys.org/news/2009-05-genomic-technique-uncovers-transcriptome-reef-building.html>

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