

# New tool cracks genomic code quicker than ever

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US and Australian scientists have pioneered a new hybrid method for genomic sequencing that is faster and cheaper than state of the art technologies.

The breakthrough will be welcomed in medical and biotechnology circles where there is rising demand for genome-sequencing technologies. The new hybrid method combines the best of new and old code cracking methods for "fingerprinting" the genetic basis of life.

Scientists from the US-based J. Craig Venter Institute and the University of New South Wales in Sydney, Australia published the findings in the *Proceedings of the National Academy*.

"Cracking the entire, genetic code of an organism is expensive and until recently has relied in its fundamentals on a 30 year old technology that involves a physical separation of gene fragments," says Dr Torsten Thomas, a study co-author and senior research fellow at the University of New South Wales.

"A newer method which has emerged in the past year uses real-time, light-based observations of gene synthesis to reveal genomic information. It produces genomic information up 100 times faster than the old technology."

Using the genomes of six ocean bacteria, the scientists evaluated the utility and cost effectiveness of the old and new methods to show that a

hybrid method was better than either method on its own. They found that combining the advantages of the two sequencing methods in a hybrid approach produced better quality genomic information.

The team found that the traditional method known as 'Sanger' sequencing worked best at sequencing large segments of the genomes, while the newer method known as '454 pyrosequencing' was more adept at sequencing smaller, more difficult sections, such as unclonable regions and gaps induced by secondary structures. The hybrid sequencing approach enabled the scientists to more easily close sequencing gaps between genome fragments compared with previous techniques.

The researchers suggest that the hybrid technique will become the preferred method for sequencing small microbial genomes, as the Sanger method is more capable of sequencing larger segments of DNA. "The new hybrid approach has generated exceptional results for several, marine microbes and we hope that our findings will kick-start other genome projects that were previously constraint by economic considerations", Dr Thomas says.

Source: University of New South Wales

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