

New 'bench top' machines open up DNA sequencing

April 27 2012

(Phys.org) -- Research carried out by scientists at the University of Birmingham have found that new 'bench-top' machines for sequencing DNA are capable of accurately identifying over 95% of a genome, signalling a major breakthrough for the diagnosis of infections caused by bacteria such as *E. coli*.

Traditionally this technology was the preserve of large-scale laboratories. However, these new lower-cost, bench-top machines open up the opportunity for far wider adoption. This is the first time an independent evaluation of these machines has taken place and the findings were published last week (April 23) in the journal *Nature Biotechnology*.

The Birmingham scientists, who worked in collaboration with scientists at the Health Protection Agency, compared the performance of three new bench-top instruments in genome-sequencing a strain of *E. coli* (*Escherichia coli* O104:H4). This strain was responsible for the food-poisoning epidemic in Germany in 2011, which resulted in over 4000 infections and 40 deaths. Whilst none of the bench-top sequencing instruments generated a completely accurate, joined-up, finished genome, all three recovered more than 95% of the strain's genome.

The instruments are around the same size as a laser printer and offer modest set-up and running costs. Each instrument can generate the data required for a draft bacterial genome sequence in days, making them attractive for identifying and characterizing microbes in the clinical setting. However, until now, none of the instruments had undergone

independent testing.

Research lead Professor Mark Pallen of the University of Birmingham School of Biosciences, said; “Over the last five years, there have been dramatic improvements in the speed, ease and cost of determining [DNA sequences](#), thanks to a range of new technologies that fall under the umbrella term "high-throughput sequencing" or "next-generation sequencing". However, until recently, the high set-up and running costs and the substantial space required in the lab, together with exacting and onerous technical requirements, have limited the adoption of these technologies in the average laboratory.

“Despite the tough tests we set, it is clear that all three platforms are capable of generating data quickly and easily and we can thus be confident that they are poised to make a decisive impact on diagnostic and public health microbiology in the near future.”

Study co-author, Dr John Wain, an expert on gastrointestinal infections at the Health Protection Agency, said: “Whole genome sequencing is the most powerful technology available for helping scientists to identify which form of bacteria, such as E. coli, is causing an outbreak. However, the translation of that potential into action on public health has so far been limited by unstable market place in sequencing technology, which has prevented public health scientists from taking advantage of these technological developments.

“We’re delighted that this study has shown that whole genome sequencing, using bench top technology, is now at a stage of development where it can be used in the front line. This will help us to identify the best equipment to use during an outbreak investigation, which, we hope, will in turn help to reduce the risk of infectious disease to the population.”

The three "bench-top" high-throughput sequencing instruments that were tested are: the 454 GS Junior (Roche), MiSeq (Illumina) and Ion Torrent PGM (Life Technologies).

Provided by University of Birmingham

Citation: New 'bench top' machines open up DNA sequencing (2012, April 27) retrieved 25 April 2024 from <https://phys.org/news/2012-04-bench-machines-dna-sequencing.html>

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