Genomic epidemiology: Tracking superbugs to their source

As concern grows over an increasing risk of deadly antibiotic-resistant bacteria, a budding field of microbial research, ‘genomic epidemiology’, may also be delivering a solution.

The advantage of [whole genome sequencing], in comparison to pre-existing standard operating procedures used in clinical service laboratories, is that genome analysis can be used to compare microorganisms down to the last nucleotide. In our own work in New South Wales, Australia, with the human pathogen*Streptococcus pyogenes*, closely related isolates may vary by only 50 or 60 nucleotides across a 2 million nucleotide bacterial genome. Thus, genomic technology can determine whether a patient has been infected with a different bug that is nonetheless closely related (i.e. 50-60 nucleotide differences) versus the identical bug (0 nucleotide differences). These small differences have large consequences. If multiple patients are infected with the identical bug, it suggests a breakdown in clinical practice. This can be addressed to prevent further transmission by sterilisation of surfaces, treatment of patients, treatment of patient contacts, and treatment of potential carriers of the infection. It has not previously been possible to figure out whether patients had been infected with the same bug due to a breakdown in patient management practices, or alternatively closely related bugs, that happen to cause otherwise unrelated infections.

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