Successful, multiresistant bacterial clones

Neil Woodford*

Antibiotic Resistance Monitoring and Reference Laboratory, Centre for Infections, Health Protection Agency, 61 Colindale Avenue, London NW9 5EQ, UK

Multilocus sequence typing gives us unparalleled insights into the population biology of bacterial species, including those that cause healthcare-associated and/or community-acquired infections. For many of these species, we now recognize the existence of internationally prevalent clones, which are often resistant to multiple antibiotics.

Keywords: E. coli, Enterococcus, Staphylococcus, MLST

Bacteria are ‘typed’ most frequently to monitor the spread of strains during suspected outbreaks of infection. Numerous techniques have been developed, with molecular methods now standard, and with PFGE the most widely used. However, interpretation of PFGE results for disparate groups of isolates is often complicated by the lack of obvious epidemiological connections. PFGE is comparative, rather than definitive, with patterns prone to change through mutation, DNA transfer and rearrangement events; such events may hide fundamental relatedness. Multilocus sequence typing (MLST; http://www.mlst.net) frequently offers a more fundamental perspective of the population biology of a species, defining ‘sequence types’ (ST) based on polymorphisms within strongly conserved ‘housekeeping’ genes. MLST has been used, in concert with more traditional typing methods, to document the international occurrence of healthcare-associated and community clones of methicillin-resistant Staphylococcus aureus, a hospital-adapted multiresistant clone of Enterococcus faecium and multiple clones of penicillin-resistant pneumococci.

In this issue, Nicolas-Chanoine et al. use MLST to extend our knowledge of successful clones to include extended-spectrum β-lactamase (ESBL)-producing Escherichia coli. They describe an internationally disseminated clone (O25:H4-ST131) with CTX-M-15 ESBL and found representatives of it in Canada, France, Lebanon, Portugal, South Korea, Spain and Switzerland. The clone also occurs in the UK, where it includes five major PFGE-defined strains with CTX-M-15 enzyme. Their study shows, once again, the power of MLST, which has the potential to reveal relationships even among isolates that appear distinct by other molecular methods, such as PFGE. Recognition of a successful clone, regardless of species, is an essential first step that may lead eventually to the design of intervention strategies aimed at preventing its spread.

Critical questions relating to the biology of this ST131 E. coli clone remain unanswered, yet have huge bearing on public health. How common is this lineage among non-ESBL-producing E. coli, and how widely is it carried in the gut in the general population? In other words, was ST131 an established, successful clone before it acquired plasmids encoding CTX-M-15 ESBL, or did acquisition of these plasmids help to make a minor E. coli lineage successful? The distinct PFGE patterns and virulence factor profiles observed among ST131 isolates indicate considerable diversification of this clone, but did this occur after plasmid acquisition? Or, have the prevalence and/or biological characteristics (e.g. ability to receive plasmid DNA) of multiple variants of the clone predisposed them to acquire related CTX-M-15 plasmids on multiple occasions?

Similarly successful, disseminated clones have been found in many bacterial species. Representatives of these lineages should be prioritized for genome sequencing. When armed with this information, we may be better able to define which biological attributes give these successful, multiresistant clones their competitive ‘edge’.

Transparency declarations

N. W. has received research grants and accepted speaking engagements/conference invitations from various companies, but is not aware of any conflicts of interest with the content of the current paper.

References


