Public Health
England

Media backgrounder

Whole Genome Sequencing (WGS) and antibiotic-resistant bacteria

Background

Antibiotic resistance is one of the biggest threats to public health.

To tackle this issue there is a five-year cross-government strategy and Public Health England (PHE) has been assigned four key elements on surveillance, infection control, optimising prescribing and improving the education in those that prescribe.

The cycle of antibiotic resistance is complex and includes use of antibiotics for any purpose; people and circulation of resistant bacteria between people; pets, livestock and the circulation of resistant bacteria between animals; sewage and its treatment or lack of treatment; manure from animals; wildlife; food crops and the environment (water and soil).

How do bacteria develop resistance?

Bacteria become resistant to antibiotics through natural evolution and this cannot be stopped, only managed. Resistant strains of bacteria are unaffected by antibiotics that would kill susceptible strains and so are harder to treat if they cause infections. The spread of resistance is encouraged by antibiotic use, so if we expose bacteria to fewer antibiotics we may slow the emergence and spread of resistance. Some types of resistance emerge by random mutation, whereas other types are spread via loops of genetic material called plasmids which can jump from one species of bacteria to another thereby magnifying the problem.

How does PHE test for antibiotic resistance at the moment?

PHE mainly uses methods that measure levels of resistance directly; these include paper discs or plastic strips impregnated with antibiotics. The mechanisms responsible for resistance may be detected using genetic tests, including PCR.

For the future, PHE will increasingly use whole genome sequencing (WGS) to detect resistance genes. One day WGS might even replace the need for measuring levels in some laboratories, but this isn’t likely to happen for several years. For resistance analysis, PHE has, for example, started to use WGS on *Staphylococcus aureus* and carbapenemase-producing bacteria (these are bacteria which have an enzyme which confers resistance to carbapenem antibiotics – those of ‘last resort’). The aim is to perform WGS regularly on isolates received to provide an archive for future comparison purposes.

How can WGS help the fight against resistance?

- **Strain Evolution** – Sequencing the whole genomes of bacteria will enable scientists at both a national and a global level to see which strains of bacteria are circulating, to track the emergence and spread of new strains and to understand how resistance flows through bacterial populations.
- **Outbreak investigation** – At a hospital level, microbiologists will be able to investigate transmission of bacteria within wards to see whether harmful infections have passed from patient-to-patient or are new infections brought into the hospital.
- **Novel resistances** – Wide use of WGS will assist the discovery of new resistance mechanisms, and will allow scientists around the world to respond faster when assessing the importance of a new resistance found in any country.
- **Faster Diagnosis** – WGS will lead to new generations of tests, which will enable doctors to assess quickly whether an infection is caused by bacteria and whether those bacteria are resistant to a particular antibiotic.
- **Better treatment** – Faster and more accurate diagnosis will reduce unnecessary antibiotic use (they are not needed if an infection is caused by a virus). Doctors can make sure that patients get the right treatment as soon after admission as possible. This would reduce use of so called ‘broad spectrum’ antibiotics. These are powerful antibiotics and those of last resort. Avoiding using them will reduce the pressure for spread of resistance and will maintain their efficacy for the future.