**Background**
Antimicrobial resistance poses a growing threat to public health as bacterial infections are becoming increasingly challenging to treat successfully. Primarily arises in one of three ways:
- **Acquisition of antimicrobial resistance genes**
- Accumulation of DNA in gene-encoding proteins targeted by antibiotics
- Insertion of a transposon mediating or altering the expression of genes related to resistance

The spread of resistant bacteria and transmission of resistance mechanisms is alarming. Detection and surveillance is key to preventing and controlling infection.

Whole genome sequencing (WGS) has gained acceptance as a tool for the prediction of antimicrobial resistance patterns, because it offers a sensitive and reproducible alternative to antimicrobial susceptibility testing. The advantage over alternative approaches is the potential to reveal the full complement of resistance determinants, including resistance towards compounds that are not routinely tested. In addition, WGS data offer insight to the mechanisms by which antimicrobial resistance is transmitted.

**Aim**
Our aim is to demonstrate the application of WGS for the detection of resistance genes and resistance-carrying regions using tools from the QIAGEN Microbial Genomics Pro Suite.

This poster shows the application of resistance detection in three different settings: *Klebsiella pneumoniae*, *Actinobacillus pleuropneumoniae* and *Mycobacterium tuberculosis*.

**Resistance Detection in *Klebsiella pneumoniae***

**Background**
Carbapenem-resistant Enterobacteriaceae, such as *K. pneumoniae*, are a major public health threat with an associated economic burden due to the lack of efficient antibiotics, extensive transmission and high mortality rate. Carbapenem resistance arises from several mechanisms. One is the production of carbapenemases, which hydrolyze almost all β-lactams. These are encoded by genes that reside on plasmids or transposons and are thus easily transferable.

Detection and tracking of plasmid-encoded resistance is difficult using short read technologies due to mobile elements and the repetitive nature of plasmids. Long read technologies have the potential to resolve and fully assemble genomes and accompanying plasmids.

**Methods**
Carlon et al. (2014) described carbapenem resistance in isolates of *Enterobacteriaceae* in a hospital setting. Using their data we demonstrate the assembly of single-molecule real-time sequencing (SMRT) reads to discriminate and resolve plasmids from chromosomally encoded resistance genes in *K. pneumoniae*.

**Resistance Detection in *Actinobacillus pleuropneumoniae***

**Background**
Antimicrobial resistance in animals destined for food production is of increasing concern. Because farm animals may serve as a reservoir from which antibiotic-resistant bacteria can spread to humans, there is increasing concern about antimicrobial resistance in this setting. A. pleuropneumoniae is a major contributor to swine respiratory disease, and antimicrobials are routinely used to limit disease severity and transmission. Resistance profiling is important for treatment decisions and surveillance purposes.

**Methods**
We combined the tools Trim Sequences, De Novo Assembly and Find Resistance in a custom workflow to assemble the data processing of the 94 isolates.

**Resistance Detection in *Mycobacterium tuberculosis***

**Background**
Antimicrobial resistance in *M. tuberculosis* is predominantly caused by mutations that interrupt drug-target interactions rather than by uptake of mobile elements that carry resistance genes.

**Methods**
Carbon resistant database

The resulting custom database contained nearly 1500 variants in 51 target genes conferring resistance towards 15 different drug classes.

**Conclusions**
The tools of QIAGEN Microbial Genomics Pro Suite allow accurate detection of antimicrobial resistance markers. Workflows and bullpen access to public databases streamline data analysis and help users get started easily.

**References**

For up-to-date licensing information and product specific details, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

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**Sample to Insight**