Whole genome sequencing of bacterial isolates

Resistance surveillance and outbreak analysis in Region Östergötland

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Clinical applications of WGS

- **MRSA**
  - Subtyping (Spa typing, MLST)
  - Identification of PVL gene

- **ESBL-A, -M and -CARBA**
  - Identification of resistance genes
  - Subtyping (MLST)
  In extended spectrum beta lactamase- and carbapenemase-producing bacteria
  *(Enterobacteriales, Pseudomonas and Acinetobacter)*

- **Outbreak analysis**
  - Epidemiological typing by SNP analysis, on any species
  - Can also be performed on previously produced data

*Whole genome sequencing (WGS) is performed on DNA from bacterial isolates*
Clinical applications of WGS

- Several molecular methods have been replaced by a single laboratory workflow
- Accredited by SWEDAC
Clinical use

- Routine analysis once a week since December 2017
- 450 clinical samples/year (2018)
- Capacity: 22 samples + 2 controls/week

- Research projects
  - Epidemiological typing
  - Identification of virulence genes, plasmids, new resistance genes, and more

WGS workflow

DNA extraction

Libary preparation

Sequencing

Bioinformatics

2 days

2 days

(EZ1, Qiagen)

(QIAseq, Qiagen)

(2x300 bp, MiSeq, Illumina)

(Pipeline created in CLC, Qiagen + Spa typing in BioNumerics, Applied Maths)
Clinical reports

- Relevant genes and subtypes (MLST/spa) are reported
- Additional information on request
Outbreak analysis

- Usually requested by the Department of Infection Control and Hygiene
- Reported with phylogenetic tree and genetic distances
- Interpreted in view of epidemiological information
Outbreak analysis

Suspected infection spreading of *Corynebacterium striatum* at the Intensive Care Unit for burn injuries

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> 18 000 SNPs

6188 SNPs

Patient 1, ward A (sepsis)
2 SNPs

Patient 2, ward A (wound)
3 SNPs

Patient 3, ward A (wound)
7 SNPs

Patient 4, ward A (wound)

Patient 5, ward B

Patient 6, ward C
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Outbreak analysis

Suspected infection spreading of *Enterococcus faecalis* at the Hospital Eye Clinic
Outbreak analysis

- *Stenotrophomonas maltophilia* at the Intensive Care Unit
  - Identified in respiratory tract samples in three patients within a few days
  - *S. maltophilia* was found in samples from sinks and medical equipment...
  - ... and later in a fourth patient

Phylogenetic tree
Conclusions and future

- Several medical questions answered by one laboratory analysis
- New species and genes can be validated continuously
- High resolution comparison of isolates, where previously only subtyping was available
- Close contact with Department of Infection Control and Hygiene in suspected outbreak situations
- Future national collaboration and data sharing
Thank you

Clinical Microbiology, Diagnostic Center

Department of Infection Control and Hygiene

QIAGEN

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