Epidemiology and dynamics of virulent and resistant S. aureus clones

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The SRL working group
Task

“Identify specific clones or mobile genetic elements that should be incorporated into surveillance systems to understand the epidemiology and dynamics and how this can be done.”
Approach

- Inventory of high risk clones of bacteria and their high risk mobile genetic elements.

- Conceptual approach on how to identify high risk clones and high risk mobile genetic elements.
Approach

- Inventory of high risk clones of bacteria and their high-risk mobile genetic elements.

- Conceptual approach on how to identify high risk clones and high risk mobile genetic elements.
Conventional distribution of activities in AMR surveillance

- **Patient**
  - optimising empirical antibiotic therapy
  - local, timely, syndrome-based, inclusive

- **Population**
  - estimating burden for public health
  - sentinel laboratory-based using routinely available data

- **Pathogen**
  - identifying emergence and spread
  - sentinel laboratory-based WGS data
Pathogen oriented AMR surveillance improves

- Risk identification
- Risk assessment
- Risk management
What are Pathogen-related Risks? (host perspective)

- Risk of developing disease (infection)
- Risk of transmitting this disease (infection)
- Risk of not being able to receive effective therapy
What are Pathogen-related Risks? (pathogen perspective)

- Virulence/pathogenicity
- Transmissibility/tenacity
- Antibiotic resistance

=> Any of the above define a High Risk Clone
Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe

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Risk identification: High Risk Clones

- Genetic relatedness
- Abundance
- Geographic structure
Microreact: tool for geo-visualisation and analysis of WGS data

http://www.microreact.org/project/EkUvg9uY?tt=rc
CC22

A

EMRSA-15
SCCmec IVh
UK
Germany
Portugal

MRSA
MSSA

B
Possible transmission of EMRSA-15 from the UK to Germany via Berlin
(colour gradient indicates the direction inferred from phylogenetic signal)
Mobile Genetic Elements in *S. aureus*
Sharing of accessory genes: pairwise comparison
Accessory genome (MGEs) statistically associated with abundance

- integral to success
- or the result of hitchhiking?
MRSA are more likely to pick up MGEs than MSSA!
## Prediction of antibiotic resistance: WGS vs. Phenotypic testing in NRLs

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Reference: In-silico prediction vs. EUCAST Development Laboratory (EDL) and Staphylococcal Reference Laboratory (SRL)
Crucial components for future pathogen surveillance

- Unbiased strain collections from large scale structured surveys
- WGS analysis
- Community-oriented databases and analysis tools
Pathogen surveillance based on WGS

- provides biological meaningful data

- offers the means for a robust ascertainment of the presence or absence of genomic resistance and virulence markers

- resolves pathogen dynamics (emergence, spread, transmission across ecological interfaces) at all geographical levels
Thank you!