



enilabAMR project (expansion of network and improvement of lab capacity for better AMR surveillance)

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Background, aims

Increasing prevalence of resistant Gram-negative bacteria

- Emerging spread of carbapenemases (KPC, NDM, OXA-48, OXA-23, VIM etc)
- Incomplete data about ESBL- CARBA epidemiology in Baltic Sea region and neighbouring countries
 - Prevalence/incidence
 - Molecular classes
 - MLST (Multilocus sequence typing) types
 - etc
- Need for standardized methodology, algorithms
- Application of new techniques

Some project details

- 9 participant countries: Estonia, Latvia, Lithuania, Russia, Belarus, Ukraine, Georgia, Poland and Moldova
 - 5 new participants to BEEp team
- Focus of interest carbapenem screening positive/R/I Enterobacteriaceae, *Pseudomonas aeruginosa*, *Acinetobacter* sp.
- Collection period of 3 months April till June 2015
- Clinically relevant strains (infection site, no colonisation/enviromental strains)
- Sensitive strains from each participation country (sequencing)

Management team

Sweden – Petra Edquist and Karin Sjöström

- Financial support and management
- Estonia Paul Naaber, Marina Ivanova, Anastasia Pavelkovich, Tiiu Rööp
 - General management
 - Data collection
 - Consumables planning and delivery
 - Workshop arrangements
 - Strains collection, storage and maintenance

Achievements and first results



Final participants' number

- Georgia workshop March 2015
 - 9 countries
 - 38 participant labs
- Estonia workshop October 2015
 - 9 countries (Moldova, + Finland)
 - 38 participant labs (Moldova, 1 Estonian lab,
 - + 1 Finnish lab, + 1 Ukrainian lab):
 - 10 labs provide service only for hospitals
 - 3 labs provide service only for outpatients
 - > 23 labs: "mixed" service, reference service, public health

Collected screening positive strains



Screening positive Enterobacteriaceae



Collected sensitive strains



Updated 29.11.15

Screening positive strains from all screened strains



First stage – Enterobacteriaceae



Enterobacteriaceae investigations

- Maldi identification
- DNA extraction
- CTX-M genes detection by Luminex in-house multiplex panels
- Carbapenemases genes (IMP, VIM, KPC, GIM, OXA48, NDM) detection by Luminex
- Whole Genome

Sequencing by Illumina



Results – CTX-M genes

- 156 Klebsiella pneumoniae confirmed isolates
 - 140 have CTX-M1 group gene
 - I strain has both CTX-M1 and CTX-M9 group genes
 - > 2 strains have CTX-M2 group gene
 - in 13 strains no CTX-M genes were found



Results – carbapenemase genes

Carbapenemase genes were found in 75 K. pneumoniae strains

- ▶ The most dominant was NDM gene 48 strains
- OXA-48 23 strains
- VIM (Latvia) 1 strain
- KPC (Russia) 1 strain
- GIM (Poland) 1 strain



Distribution by country



OXA-48 positive

NDM positive



Future plans

- Molecular tests
- WGS to all Enterobacteriaceae strains
- MALDI subtyping
- Data analysis
- Publications

Investigations in PA and AC strains

Visual evaluation of spectra. Peak list creation



Totally list of 37 peaks were created

Application of Principal Component Analysis (PCA) in 2D/3D



PCA analysis indicates 2 clusters of *Klebsiella pneumoniae* isolates corresponding to NDM producers and non-producers

Application of Main Spectrum (MSP) dendrogram



What is right distance level score to securely distinguish cluster difference?