Update of EARS-Net Microbiological Protocol

Session 2: EARS-Net

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Content

Breakpoints

- Interpretation of results
- Standardisation of methods

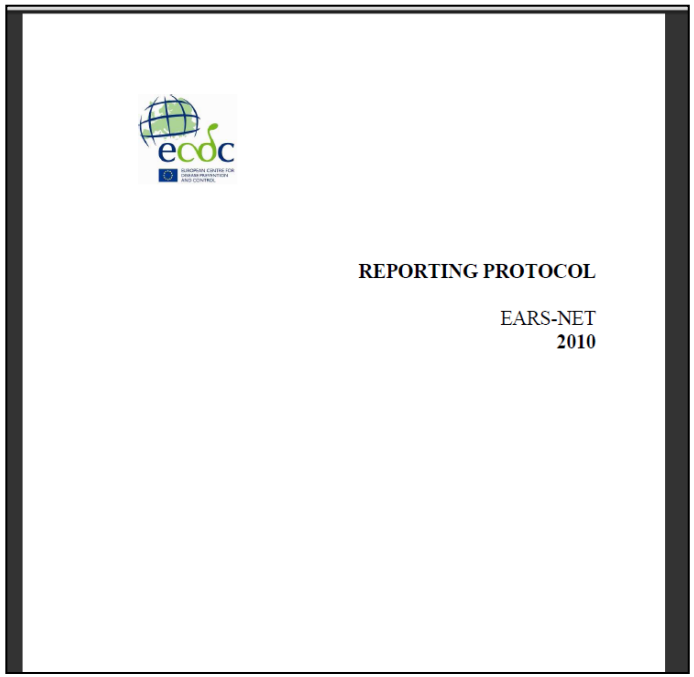
ESBL & carbapenemases

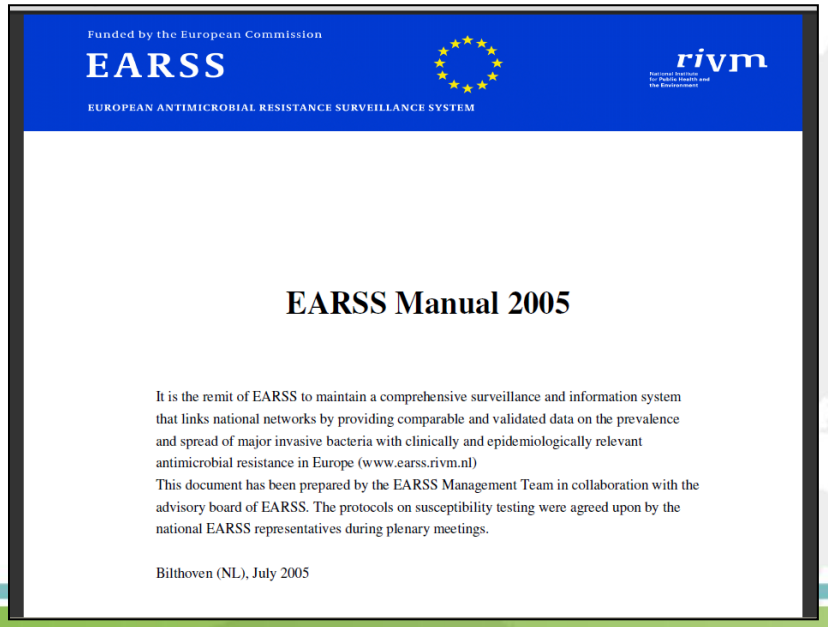
- The need for data of resistance mechanisms?

Note: Issues discussed in this presentation will also be addressed with the EARS-Net coordination group

Background

- EARS-Net Reporting protocol 2010 and EARSS Manual 2005 (to be updated)
- Adherence to EUCAST guidelines and breakpoints





Interpretation of results (breakpoints)

- At the moment, reporting of *S. pneumoniae* penicillin non-susceptibility is based on EARSS 2005 protocol
- WHONET and EARSS (at RIVM) used **meningitis breakpoints** for interpretations because they were closer to epidemiological breakpoints and (at that time) were consistent between CLSI and the various European groups
- EARS-Net will continue to recommend use of the meningitis breakpoint

Penicillin and *S. pneumoniae*

- EUCAST breakpoints (clinical breakpoints v. 1.3) are:
  - Penicillin S≤0.06 and R>2
    - For Meningitis, only isolates with MIC ≤0.064 mg/L should be categorized susceptible to penicillin, otherwise report resistant
- CLSI 2011 breakpoints for penicillin are:

1.	Meningitis:	S≤0.06		R≥0.12
2.	Nonmeningitis:	S≤2		R≥8
3.	Oral:	S≤0.06	I=0.12-1	R≥2

  - For "Meningitis" there is no longer any intermediate category, whereas for "Oral" there is

- Intermediate category is not shown in the EARS-Net Report!

Breakpoints

- The EARS-Net Coordination group suggested (March 2010) that an annex with additional data from the laboratories, incl. **breakpoint** information, should be included in the Annual report

- A questionnaire* for laboratories to collect the additional denominator data could be structured in two sections:

1) Questions about the breakpoint guidelines and their versions and the testing systems or methods used

☐ EUCAST breakpoints ☐ CLSI breakpoints

☐ VITEK II
☐ Phoenix
☐ Micro
☐ Other

2) Details on the breakpoints used for each specific drug/bug combination

E. coli:	S	I	R
AMP	≤		>(or≥)
CTX	≤		>(or≥)

*Based on Gunnar Kahlmeter's suggestions

Breakpoints –Summary / Questions

- Should we collect the data concerning breakpoints and guidelines?
  - Is it valuable information?
- Is it too much work for participating laboratories?
- Comments for interpretation-issue?

ESBL & carbapenemases

Variables in the present metadata set are:

VariableName	**23 – ESBL**
Description	Detection of ESBL
Required	No
Data type	Coded value
Code	POS = positive NEG = negative UNK = unknown

Phenotypic or genotypic?

Only phenotypic? Genetic confirmation test?

VariableName	**24 – ResultCarbapenemases**
Description	Detection of Carbapenemases. This refers to phenotypic test for carbapenemase activity ( )
Required	No
Data type	Coded value
Code	POS = positive NEG = negative UNK = unknown

The Modified Hodge test is not reliable and should not be used!

ESBL & carbapenemases

- Do we need genetic characterization?
  - "Performance of *phenotypic* and *molecular testing* for screening and confirmation of the presence of carbapenemases would add a significant and important layer of information to the existing data"
    (Chapter 2, AMR Annual report, 2010)
  - "For carbapenemases it might be useful to add genotype, as they are still relatively rare in most parts of Europe, and the battle against them is not lost (yet)"
    (Correspondence with Christian Giske and Gunnar Kahlmeter)
  - "Can we manage?"

ESBL

- For ESBLs collection of genotype data may not be feasible
  - –Only few laboratories will have a high-quality data on the presence of CTX-M, TEM and SHV

- Suggestion for ESBL reporting:

VariableName	**24 - ResultESBL**
Description	Detection of ESBL. This refers to phenotypic test for ESBL production (e.g. the double disk test with **clavulanic acid**).
Required	No
Data type	Coded Value
Code	POS=positive NEG=negative UNK=unknown

More detailed determination

- Comments? More ideas?

Carbapenemases

- For carbapenemases we could use similar reporting as for MRSA:

Specific rule to define Carbapenem-resistant *Enterobacteriaceae* (CRE)

The antibiotic considered for this resistance are: Imipenem (IPM) and Meropenem (MEM). Other tests (equivalents) are also considered as confirmation tests: PCR detection of KPC, IMP, VIM, NDM-1 or OXA-48 gene.

Hierarchical levels to assess the CRE	Priority sequence of the results
1. E-test (SIR result of IPM, MEM)	R→I→S
2. Other MIC tests (SIR result of IPM, MEM)	R→I→S
3. Other test (SIR result of IPM, MEM)	R→I→S
4. **Confirmation test (PCR carbapenemase genes)**	**POS→NEG**

- What do you think? Is this too complicated or demanding?
- Is it possible to report carbapenemase gene data?

Thank you for your attention!