

of internet sites with validated content and assessment tools, to bring medical microbiology and virology in line with other disciplines.

P2233 www.ccrbtyping.net – a web-based typing tool for staphylococci

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Objectives: ccrB typing, based on the DNA sequencing of an internal fragment of ccrB, was developed as a potential first-line SCCmec typing strategy for methicillin resistant *Staphylococcus aureus*, since the ccrB sequence is part of the ccrAB locus, whose allotypes are used for the definition of SCCmec types. Clustering of ccrB sequences has been shown to properly discriminate between different SCCmec types (I, II, III, IV and VI) (Oliveira et al, J. Antimicrob Chemother 58:23–30). To make this approach available to the general public, a web based typing tool interface was developed so that users can submit ccrB sequences and obtain an automatic assignment to a ccrB allele and presumptive SCCmec type classification.

Methods: The website serves as a front-end for a database and user management system, coupled with two sequence alignment programmes (MUSCLE and Clustal) and an alignment and tree viewer software (Jalview). For each SCCmec type, a set of known sequences are defined as a prototypes. The user submitted ccrB sequences are then, after an automatic trimming, compared by multiple sequence alignment with the defined prototypes, and the most similar prototype defines the ccrB allele, allowing the inference of ccrAB allotype and SCCmec type.

Results: The website (www.ccrbtyping.net) is being used since late October 2007. At the website launch date the database had 98 ccrB sequences, including 17 prototype sequences, with references and with other important isolate information. All the public information can be easily extracted to csv format and an online tutorial explains the users how to work with the web tool. The data can be saved privately or it can be submitted to the public database after being reviewed by a system curator.

Conclusion: Web-based applications have proved to be the best approach for the comparison of sequence based typing methodologies results. Anyone with internet connection can contribute with their data to the public database and help to validate and improve the typing methodology. The implemented website has demonstrated its usefulness for ccrB typing giving good results for several staphylococci species, allowing for an expanding database of curated ccrB sequences. Additionally the web based typing tool interface was implemented to be rapidly configurable, and can be used as a framework for other sequence based typing methods based either on direct sequence similarity or on the comparison of repeated patterns.

P2234 Development of a web-based learning tool to enhance healthcare workers' knowledge, attitude, and risk perception about safe work practices concerning methicillin-resistant *Staphylococcus aureus*

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Objectives: To develop a web-based learning tool based on the available national Methicillin Resistant *Staphylococcus aureus* (MRSA) policy, to enhance healthcare workers' (HCWs) knowledge, attitude, and risk perception concerning safe work practices.

Methods: A validated questionnaire and scenario-based tests were used to determine HCWs' key questions about safe work practices regarding MRSA. Next, the questions were categorised into groups by the Card Sort Method and analysed by WebSort software in order to provide a user-centred search structure for the web-based learning tool. The study was conducted among physicians, nurses, and domestic staff in four hospitals in Germany and the Netherlands.

Results: The results of 276 questionnaires showed inadequate levels of knowledge (97% of respondents) and risk perception (24%) about safe work practices, and negative attitudes (63%) toward complying with these practices. The 28 additional interviews demonstrated that lack of knowledge is mainly related to being uninformed about transmission routes of MRSA (14%), resulting in an inadequate perception of the personal risk to obtain and transmit MRSA (10%). A negative attitude is caused by HCWs questioning the usefulness of adhering to safe work practices (14%). These factors lead to non-compliance with safe work practices. HCWs seem to favour a more personal and social approach of safe work practice documents, stressing personal risks and the rationale behind applying the practices. In sum, 167 key questions were found about which the knowledge, the attitudes or the risk perceptions were unsatisfactory. The web-based learning tool should address these questions. The Card Sort Method (n=10) resulted in ten categories in which the key questions can be grouped. HCWs are best served with a web-based system in which they can actively search these questions in their own language both via a search engine and a table of contents representing HCWs' terminology and information needs.

Conclusions: Our study indicated that the mixed-methods design provides a powerful approach to analyse HCWs' key questions concerning safe work practices, and provides us with a search structure for a user-centred web-based learning tool. HCWs' involvement in the development of the tool might encourage compliance with safe work practices, which remains subject for further investigation.

P2235 National software system for microbiology laboratory management in Bulgaria: "Clinical Microbiology and Nosocomial Infections"

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Expedient software systems in clinical microbiology laboratories constitute very useful and effective component in laboratory and hospital management. Susceptibility test results of dozens of thousands of laboratories around the world are stored in paper or in computer files, which makes them inaccessible for analysis and comparison. The "Clinical Microbiology and Nosocomial Infections" (CMNI) programme provides a software through which data from each laboratory are entered into a common code and file format for the corresponding laboratory. These data could be shared with another laboratory working on CMNI programme for further collaboration, and utilised, through the main server, based in the National Center of Infectious and Parasitic Diseases, Sofia, Bulgaria, for a national data analysis and implementation of various control measures.

CMNI programme is web-based database software in Bulgarian language for the management of microbiology laboratory results and global surveillance of bacterial resistance to antimicrobial agents and control of nosocomial infections. Significant parts of HELICS protocols are implemented in the programme and CMNI software is also compatible to, and capable to interface with other Laboratory Information Systems – LIS (e.g. WHONET), the Antibiotic Consumption Calculator (ABC Calc), and other statistical packages and programmes.

The CMNI programme comprises the following three principal components:

- Laboratory configuration;
- Data entry;
- Data analysis

The analysis of the information facilitates:

1. The studying and understanding of trends of resistance;
2. The detection of epidemics and nosocomial infections;
3. The differentiation of epidemic from endemic infections;
4. The tracking and evaluation of financial expenditures in the laboratory;
5. The assessment of various risk factors;
6. The monitoring of antibiotic consumption;
7. The development of national antibiotic policy.

The ongoing equipment with LIS "CMNI" is a key component of the local and national surveillance of antimicrobial resistance,