132 MRSA epidemiology: a different diffusion in Italian cystic fibrosis centres

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Background: Persistent MRSA infection in CF patients can affect clinical status. The geographical diffusion of MRSA clones remains poorly investigated. The aim of this study is to highlight MRSA epidemiology in a national survey.
Strains and Methods: 443 MRSA strains belonging to 235 patients attending 11 CF Italian centres were collected over a 4-year period. SCCmec typing was performed according to published protocols, as well as Multi Locus Sequence Typing (MLST) analysis.
Results: SCC*mec* typing was performed on 371 MRSA strains: 156 (42%) strains were characterised by SCC*mec* IV (mainly associated with CA-MRSA), while 175 (47%) had SCC*mec* I, II or III (associated with HA-MRSA). The prevalence of SCC*mec* IV was 42% in Nothern Italy while in the Centre and in Southern Italy it was 28% and 31% respectively. MLST analysis was performed on 111 out of 443 strains, showing that the majority of clones were ST228-MRSA-I (26%) and ST8-MRSA-IV (9.9%).
Conclusions: This preliminary data shows that SCC*mec* IV, mainly associated with CA-MRSA, have a higher diffusion in Northern Italy. Different hospitalisation rates and/or segregation practices, can be hypothesised to explain these findings. More data is needed to clarify these differences in MRSA epidemiology.
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133 Genetic diversity among isolates of *Stenotrophomonas maltophilia* in patients with cystic fibrosis

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Objective: The purpose of this study was to investigate the genotype distribution of *S. maltophilia* isolates from patients with cystic fibrosis (CF) by repetitive sequence-based PCR using the DiversiLab® System.
Methods: Sputum samples (n = 787) from 169 CF patients were inoculated onto a selective medium for improved isolation of *S. maltophilia*. Suspected isolates were identified by established phenotypic methods, as well as by DNA sequencing. A total of 63 *S. maltophilia* isolates from 14 CF patients were detected. For genotyping, DNA extraction was performed with the UltraCleanTM microbial DNA isolation kit (Mo Bio Laboratories, Carlsbad, CA, USA), according to the manufacturer's instructions. DiversiLab® bacterial DNA fingerprinting kit (bioMérieux, Marcy L'Etoile, France) was used for typing. The relatedness degree of the isolates was determined by cluster analysis using Pearson's Correlation coefficient. Isolates with a similarity of ⩾95% were considered as "clinically related" (clone), and isolates with a similarity >98% were considered as "indistinguishable" genotypes.
Results: DiversiLab profiles from all patients' isolates exhibited one dominant colonising/infecting clone. It was also observed that two patients (15%) had more than one genotype. Only a small proportion of isolates from different patients (n = 5) were indistinguishable genotypes (9.52%), suggesting either cross-transmission or a common source of exposure of unclear origin.
Conclusions: CF patients possess a dominant *S. maltophilia* clone and genotypic variants may coexist. Further epidemiological studies are required to elucidate the route of colonisation/infection in CF patients.

134 Validity of a symptom questionnaire for the diagnosis of viral respiratory infection in adults with CF

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Introduction: Viral respiratory infections are common in CF and are frequently associated with pulmonary exacerbations. PCR-based assays are highly sensitive for respiratory viruses but are limited by high processing costs and variable availability.
Objectives: We investigated whether symptoms of an upper respiratory tract infection (URTI) predict laboratory-confirmed viral respiratory infection in adults with CF.
Methods: 100 adults with CF were recruited to a prospective study examining the incidence & impact of viral infections. Sputum, nose- and throat-swabs were collected and tested with PCR-based assays for adenovirus, influenza, metapneumovirus, parainfluenza virus, respiratory syncytial virus & rhinovirus. A 27-point URTI symptom score (Johnston *et al* BMJ 1993) was recorded. A score of ⩾4 has previously been used to diagnose URTI. Receiver operating characteristic (ROC) analysis was performed.
Results: 19/100 recruitment visits were positive for ⩾1 virus (9 rhinovirus, 7 influenza & 3 metapneumovirus). Mean (SD) URTI score was 9.6 (7.4) in the virus-positive group & 5.0 (4.7) in the virus negative group (p = 0.01). ROC analysis revealed an area under the curve of 0.69 for the URTI score. An URTI score cut-off of ⩾4 gave a sensitivity & specificity of 74% & 51% respectively. Optimal performance of the URTI score was achieved with a cut-off of ⩾12 which gave a sensitivity & specificity of 42% & 88% respectively. Positive & negative predictive values for a score of ⩾12 were 44% & 87%.
Conclusions: Symptoms of an URTI as measured by this symptom score are poorly predictive of laboratory-confirmed viral respiratory infection in adults with CF.

135 Is the lung of cystic fibrosis patients a reservoir of extended-spectrum beta-lactamase-producing Enterobacteriaceae?

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Aims: To:
- define the prevalence of CF patients colonized by extended-spectrum beta-lactamase-producing Enterobacteriaceae
- establish length of colonization
- emphasise the role of such pathogens in spreading resistance determinants

Material and Methods: Sputa of pts with CF and Schwachmann Syndrome found positive for Enterobacteriaceae producing extended-spectrum beta-lactamases were evaluated. Cultures were processed according to the National and International Guidelines for the research of bacteria and fungi.
ESBL production was confirmed in accordance with CLSI recommendations. Pulsed field gel electrophoresis was used to define the clonal relationship.
Results: Between 1 September 2010 and 30 August 2011, we evaluated the cultures of the respiratory secretions of 350 pts; 15 pts (13 CF and 2 with Schwachmann Syndrome, 9 males, average age 3.5 years, range 1–32 years) resulted colonized by Enterobacteria producing extended-spectrum beta-lactamases (13 *Escherichia coli*; 1 *Klebsiella oxytoca*; 1 *K. pneumoniae*).
Prevalence rate was 4.2%; in 5 pts colonization was higher than 6 months and in 2 higher than 1 year. Three pts showed only 1 isolate; for the others the observation period was too short.
Conclusions: In the last year, we observed an increase of number of pts colonized by Enterobacteria producing ESBL that have a key epidemiological role for spreading the resistance genetic determinants. As a long time persistence of such pathogens in CF lung makes it a reservoir of resistance determinants, strict infection control measures must be taken in order to avoid dissemination.