The end of a long-term outbreak with highly transmissible *Burkholderia cenocepacia* ST32

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Persons with CF can acquire *Burkholderia cepacia* complex (Bcc) infection through patient-to-patient contacts or from the environment. The former way of acquisition was well documented in the Prague CF centre where infection rate with a single *B. cenocepacia* strain ST32 reached over 30% in 1997–2003.

The aim of this study was to compare epidemiological situation in the Centre in 2003 vs. 2010, and to evaluate efficacy of infection control in tackling the spread of ST32. System of surveillance exploiting typing techniques (RAPD and MLST) was set up in 2008.

A total of 76 out of 211 patients examined by the end of 2003 (36.0%) were infected with Bcc; majority of them (78.9%) harboured epidemic strain ST32. Seven years later, Bcc positivity was detected in 72 out of 374 patients who attended the Prague CF clinic (19.3%). While 39 patients still suffered from infection with ST32 (54.2% of infected), a substantial portion of patients carried strains other than ST32 (see Table; note that ST number is specified only if more than two patients harboured the strain). Notably, only 2 patients within the ST32 group became positive after 2003, with the last case dated in May 2007.

Epidemiological situation characterized by increasing heterogeneity of the Bcc population and no occurrence of new ST32 cases is a likely consequence of both healthcare workers’ and patients’ good compliance with strict infection control rules.

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<th>Strain distribution</th>
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<td>Bcc species</td>
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<td>ST number</td>
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<td>2003 (No of pts)</td>
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<td>2010 (No of pts)</td>
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Genetic fingerprinting of *Stenotrophomonas maltophilia* strains isolated from cystic fibrosis patients

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**Aim:** Rep-PCR-based DNA fingerprinting was used to compare isolates *Stenotrophomonas maltophilia* (Sm) of recovered from CF patients (pts).

**Materials and Methods:** In 2009, 48 Sm strains were isolated from respiratory samples of 33 CF pts. DNA fingerprints were obtained from the products of rep-PCR amplification and analyzed using dedicated software to determine strain genetic relatedness.

**Results:** The dendrogram showed a strain distribution as follows:

- 21 strains from 18 pts were considered unrelated to each other
- Cluster 1 included 3 different strains (3 pts), similar to each other (92%)
- Cluster 2 and 3 each consisting of 2 strains (2 pts in both) similar to each other (both 98%)
- Cluster 4 and 5 each consisting of 3 strains (2 pts in both) with a similarity of 93% and 95% respectively
- Cluster 6 composed by 5 strains (3 pts) with a similarity of 94% to each other. From 11 patients, colonized by Sm and followed in 2009, were isolated 26 strains (3 strains from 4 pts and 7 strains from 2 pts) showing a similarity range of 65−99%.

Furthermore 60% of these 11 pts, showed to have the same strain (similarity range 95−99%).

**Conclusion:** The use of rep-PCR has allowed us to define the correlation between the strains isolated from both the same and different pts. As for the identified clusters, we could only note that 48 strains showed no significant similarity, thus excluding a cross-infection among pts. Therefore the presence of these six clusters could be justified by the ubiquitous presence of Sm both in nature and in hospitals.

The high rate of colonization events suggested that a re-infection with the same strain or no eradication are frequent.

Diagnosis of nontuberculous mycobacteria infection in cystic fibrosis: how to decontaminate respiratory samples?

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**Objectives:** Nontuberculous mycobacteria (NTM) are potential respiratory pathogens in CF patients. In this setting, the most widely used decontamination method preceeding NTM culture, is the N-acetylcysteine-NaOH-oxalic acid (REF) method. However, some reports suggest that this method affects the viability of mycobacteria. Recently, a chlorohexidine (CHX) decontamination method showed to be superior. Our aim was to compare these 2 decontamination methods.

**Methods:** 795 respiratory samples collected at 4 different centers from 312 CF patients were divided equally into two aliquots. After REF or CHX decontamination, they were processed for staining and culture by inoculating 1 Löwenstein-Jensen and 1 Ogawa slant. Samples were scored as contaminated if both slants were overgrown.

**Results:** Overall, 3 smears were positive. Smears produced after CHX decontamination were difficult to interpret. 16 sputa cultures from 9 patients were found to be NTM positive. The recovered NTM species were *Mycobacterium acinum-intracellulare* (n=6), *M. abscessus* (n=6), *M. chelonae* (n=2), *M. gordonae* (n=1), and *M. lentiflavum* (n=1). Of the 16 positive sputa, 11 were positive with the CHX method alone, 1 with the REF method alone and 4 with both methods (P=0.043). 123 specimens were contaminated after CHX decontamination, whereas 179 were overgrown after REF treatment (P=0.001).

**Conclusion:** This work shows that CHX decontamination is more sensitive than the REF decontamination for the recovery of NTM from respiratory samples of CF patients. CHX decontamination yielded a lower contamination rate but smears produced after CHX decontamination were difficult to interpret.

Retrospective analysis of isolation of non-tuberculous mycobacteria from cystic fibrosis sputum samples

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**Objective:** To compare the relative capabilities of automated liquid culture and solid media for isolation of non-tuberculous mycobacteria (NTM) from CF sputum samples.

**Method:** A retrospective analysis of 2,962 CF sputum samples submitted for NTM culture between July 2004 and December 2009. All samples were cultured using an automated liquid culture device (MGIT 960) and on solid media (Lowenstein-Jensen slopes).

**Results:** NTM were isolated from 287 samples (9.8%). Of these, 282 (98.3%) were isolated in liquid culture alone, 168 (58.5%) were isolated from both media and only five (1.7%) were isolated from solid media alone. None of these five isolates resulted in a change to clinical management. The median time to positivity for liquid culture was 4 days (range 1–39 days) compared with 14 days (range 5–48 days) for solid media. The most common isolates were *Mycobacterium chelonae* (112; 39%), *M. abscessus* (86; 30%), *M. avium* (42; 22%) and *M. intracellulare* (21; 7%). The remaining six isolates could not be identified to species level by the reference laboratory and were classified as ‘AAFB’ (2%). There were no mixed infections identified during the study period.

**Conclusion:** Automated liquid culture was superior to solid media for isolation of NTM from CF sputum samples in terms of isolation rates and time to positivity. The inclusion of solid media in addition to automated liquid culture provided no extra value.