Evidence of Pseudomonas aeruginosa super-shedding from individual patients leading to airborne dissemination in a UK CF centre

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Objectives: The extent and mechanism of cross-infection with Pseudomonas aeruginosa (PA) in specialist cystic fibrosis (CF) units remain controversial. Prevention of droplet spread by segregation and use of single patient rooms is advised by most authorities. Despite these measures, many centres continue to report outbreaks of clonal “epidemic” strains. We conducted an aerobiological study to examine airborne dispersal of PA in a large CF centre in the UK.

Methods: Microbiological air sampling was conducted in outpatient and inpatient areas inhabited by patients known to harbour the Liverpool Epidemic Strain (LES) of PA. A volumetric air sampler was placed at least 1 m from patients, working at a rate of 100 L/min with a sampling time of 10 min. Any colonies growing on Pseudomonas selective agar were identified by phenotypic and molecular methods and the number of colony-forming units (CFUs) counted.

Conclusion: Out of 177 samples obtained from 8 separate patient environments, 33 (19%) grew PA. Contamination was greater in patient rooms than corridor areas; 23% (29/125) vs 10% (4/51) respectively. Rooms inhabited by 3 of 8 patients yielded positive growth. Corridor air was positive in the vicinity of 1 patient’s closed room. Samples from this patient’s room demonstrated much higher counts than those from other rooms (mean 61 CFU/m³ vs 0–3 CFU/m³). These data confirm that PA can contaminate air >1m from patients and suggest that certain patients may act as “super-shedders”. Ventilation strategies and infection control precautions in CF centres should take into account the possibility of true airborne transmission of PA.

An investigation into the clinical relevance and cross-infection risk of Pseudomonas aeruginosa cluster A in CF patients


Objectives: Pseudomonas aeruginosa cluster A (Variable Number Tandem Repeat profile 3, 4, 5, 2, 3, 2, x, where the repeat number at the last, most discriminatory locus is variable) or ST27 was first reported in UK CF patients by our group at the ECFS conference in 2011. Between June 2010 and June 2012 we received P. aeruginosa isolates from approximately 1204 CF patients and 1026 non-CF patients for molecular comparison. Within this time, cluster A was isolated from approximately 5% (n=61) of CF patients from 26 hospitals in the UK, as opposed to from 1% (n=10) non-CF patients, suggesting a propensity for the CF lung. We aimed to examine the clinical relevance of this strain in CF.

Methods: A simple questionnaire was submitted to clinicians requesting information regarding the affected patients’ general health (co-morbidities, numbers of exacerbations and co-infections), in addition to specific questions regarding this strain (estimated time of infection, whether the patient was considered to be chronically infected, and the possible source of infection). The information received back from hospitals was correlated with PCR assay results for the presence or absence of patient’s genes, permitting examination of isolates from patients attending the same hospital for any evidence of cross-infection.

Conclusion: In the majority of cases these combined data suggested this strain was being acquired independently by CF patients attending the same hospital, rather than through cross-infection. In addition, the evidence suggested that this strain is not thought to be especially pathogenic to CF patients.

Population structure of Pseudomonas aeruginosa and the prevalence of epidemic clones in patients with cystic fibrosis over four years

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In a cross-sectional study in 2007, we investigated the population structure of Pseudomonas aeruginosa (PA) in 596 (46%) cystic fibrosis (CF) patients in the Netherlands. PA carriage in the respiratory tract of all CF patients visiting two major CF centres was determined by standard microbiological techniques, and all obtained phenotypically different isolates in the first positive culture were typed with multi locus sequence typing (MLST). Of 265 PA positive patients 60% harboured a strain found in at least 2 other patients. ST406 was found in 15% of the patients colonised with PA, mainly among patients aged 15–25 yrs of age. ST406 is not genetically linked to other international epidemic clones.

In this follow-up 2011 study we investigated the effects of segregating CF patients (which started in 2006) on the population structure of PA in CF patients and persistence of sequence types (STs), using identical methodology as in the previous study.

PA was detected in 52% of the 621 cultured patients and from 280 patients with PA (86%), 414 isolates were genotyped. This yielded 157 STs. STs shared between the same CF center were identified by automated ribotyping and compared to databases of reference strains.

To confirm that this strain was not naturally occurring among patients, the combined data of two cross-sectional studies in 2007 and 2011 demonstrate that the three most frequent STs were shared among patients from different CF centers.

Cross infection of Pseudomonas aeruginosa (PA) among children under 24 months of age

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Objectives: Prevention of PA cross infection among patients is mandatory for CF Centers. In order to reduce this risk, in our Center patients are categorized into negative, intermittent, and chronic infection groups. During 2011 we noted the first isolation of PA in 5 children aged less than 24 mo. This study was carried out to clarify if a cross infection happened.

Methods: Ten PA strains were isolated and subtyped by automated ribotyping with DuPont Qualicon Riboprinter system using the enzyme EcoRI. In order to obtain dendrogram, generated results were analyzed by software BIOMERiC v.6.6 (Applied Maths).

Results: The majority of strains have no genetic homoLOGY, due to an environmental acquisition. On the contrary, PA strains identified in three patients (nr. 2, 4, 5) presented in cluster with their affinity over the cut off of 85%, thus showing a significant cross infection accuracy.

Retrospective analysis of their scheduled clinical visits showed that the three children were present at the same time in our outpatient clinic since PA in patient 4 was considered eradicated after therapy (repeated negative microbiological cultures).

Conclusion: Our study highlights the possibility of cross infection among not exacerbating children aged less than 24 months. Further studies are needed to clarify the risk of cross infection also in the first years of life. Our results also showed that much more attention needs to be paid to segregation measures for not colonized patients, in order to reduce the risk of cross-infection.