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 remains 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 1m from patients, working at a rate of 100L/min with a sampling time of 10min. 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 61CFU/m³ vs 0–3CFU/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.

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 (46.7%) 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 multiplex locus sequence typing (MLST). Of 265 PA positive patients 60% harbouring a strain found in at least 2 other patients. ST406 was found in 15% of the patients colonised with PA, mainly among patients 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 more than two patients were found in 50% of patients. ST406, the prevalent clone, was found in 14% of patients with a higher average age compared to 2007 (20–30 yrs). In >99% of the patients that were included in both studies (157) genotypes persisted. The combined data of two cross-sectional studies in 2007 and 2011 demonstrate that the population structure of PA is highly diverse with >90% persistence of strain in individual patients leading to airborne dissemination in a UK CF centre.

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 Centres. 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 Biomumetics 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 potential cross infection accuses. 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.